



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2024 – 01:30 PM JST

PDB ID : 8IRA
Title : XFEL structure of cyanobacterial photosystem II following one flash (1F) with a 200-microsecond delay
Authors : Li, H.; Suga, M.; Shen, J.R.
Deposited on : 2023-03-17
Resolution : 2.20 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

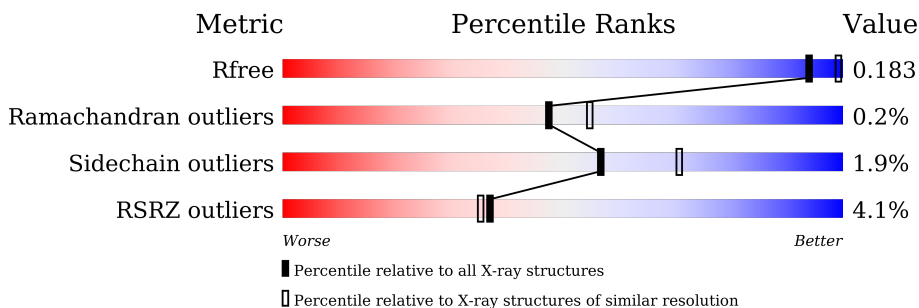
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

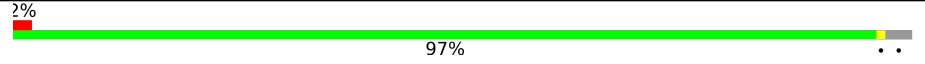
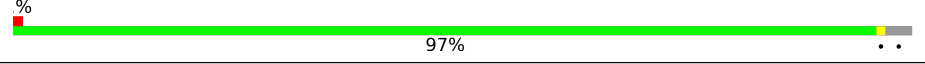
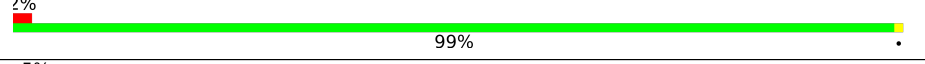
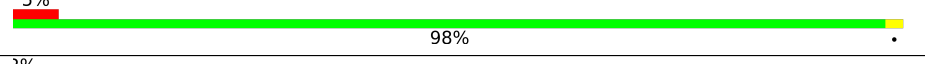
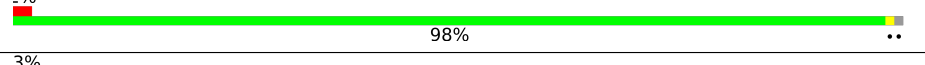
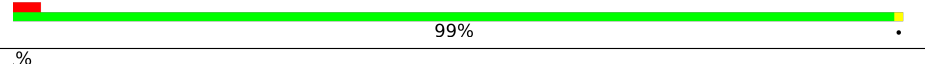
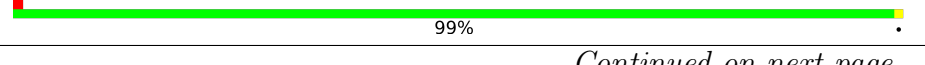
The reported resolution of this entry is 2.20 Å.

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}	130704	4898 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	 2% 97% ..
1	a	344	 2% 97% ..
2	B	505	 2% 99% .
2	b	505	 5% 98% .
3	C	455	 2% 98% ..
3	c	455	 3% 99% .
4	D	342	 2% 99% .

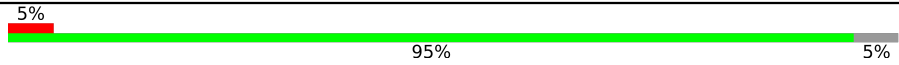
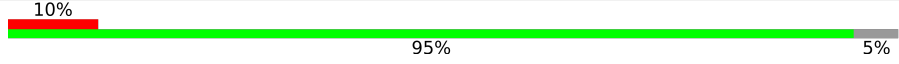
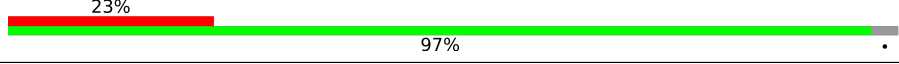
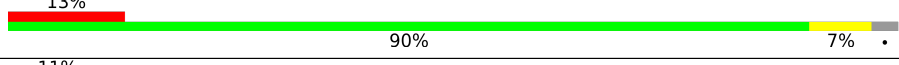
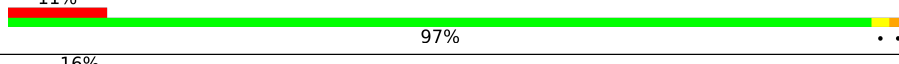
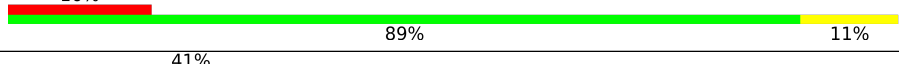
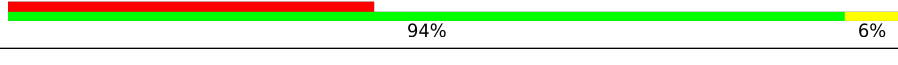
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Mol	Chain	Length	Quality of chain
4	d	342	99%
5	E	84	93%
5	e	84	90% 6%
6	F	44	77% 23%
6	f	44	70% 30%
7	H	65	94% 5%
7	h	65	95%
8	I	38	89% 11%
8	i	38	95% 5%
9	J	39	95%
9	j	39	97%
10	K	37	89% 11%
10	k	37	92% 8%
11	L	37	97%
11	l	37	97%
12	M	36	86% 6% 8%
12	m	36	89% 6% 6%
13	O	244	98%
13	o	244	98%
14	T	32	88% 6% 6%
14	t	32	91% 6%
15	U	104	90% 8%
15	u	104	92% 7%
16	V	137	99%
16	v	137	98%

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Mol	Chain	Length	Quality of chain
17	X	40	
17	x	40	
18	Y	30	
18	y	30	
19	Z	62	
19	z	62	
20	R	34	

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
23	CLA	A	404[A]	X	-	-	-
23	CLA	A	404[B]	X	-	-	-
23	CLA	A	405[B]	X	-	-	-
23	CLA	A	408	X	-	-	-
23	CLA	B	601	X	-	-	-
23	CLA	B	602	X	-	-	-
23	CLA	B	603	X	-	-	-
23	CLA	B	604	X	-	-	-
23	CLA	B	605	X	-	-	-
23	CLA	B	606	X	-	-	-
23	CLA	B	607	X	-	-	-
23	CLA	B	609	X	-	-	-
23	CLA	B	610	X	-	-	-
23	CLA	B	611	X	-	-	-
23	CLA	B	612	X	-	-	-
23	CLA	B	613	X	-	-	-
23	CLA	B	614	X	-	-	-
23	CLA	B	615	X	-	-	-
23	CLA	B	616	X	-	-	-
23	CLA	C	502	X	-	-	-
23	CLA	C	505	X	-	-	-
23	CLA	C	506	X	-	-	-
23	CLA	C	507	X	-	-	-
23	CLA	C	508	X	-	-	-
23	CLA	C	509	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	CLA	C	510	X	-	-	-
23	CLA	C	511	X	-	-	-
23	CLA	C	512	X	-	-	-
23	CLA	C	513	X	-	-	-
23	CLA	C	514	X	-	-	-
23	CLA	D	402[A]	X	-	-	-
23	CLA	D	402[B]	X	-	-	-
23	CLA	D	403	X	-	-	-
23	CLA	a	404[A]	X	-	-	-
23	CLA	a	404[B]	X	-	-	-
23	CLA	a	407	X	-	-	-
23	CLA	b	601	X	-	-	-
23	CLA	b	602	X	-	-	-
23	CLA	b	603	X	-	-	-
23	CLA	b	604	X	-	-	-
23	CLA	b	605	X	-	-	-
23	CLA	b	606	X	-	-	-
23	CLA	b	607	X	-	-	-
23	CLA	b	609	X	-	-	-
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23	CLA	b	612	X	-	-	-
23	CLA	b	613	X	-	-	-
23	CLA	b	614	X	-	-	-
23	CLA	b	615	X	-	-	-
23	CLA	b	616	X	-	-	-
23	CLA	c	501	X	-	-	-
23	CLA	c	502	X	-	-	-
23	CLA	c	503	X	-	-	-
23	CLA	c	504	X	-	-	-
23	CLA	c	505	X	-	-	-
23	CLA	c	506	X	-	-	-
23	CLA	c	507	X	-	-	-
23	CLA	c	508	X	-	-	-
23	CLA	c	509	X	-	-	-
23	CLA	c	510	X	-	-	-
23	CLA	c	511	X	-	-	-
23	CLA	c	512	X	-	-	-
23	CLA	c	513	X	-	-	-
23	CLA	d	402[A]	X	-	-	-
23	CLA	d	402[B]	X	-	-	-
23	CLA	d	403[A]	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	CLA	d	403[B]	X	-	-	-
23	CLA	d	404	X	-	-	-
27	GOL	D	412	-	X	-	-
27	GOL	a	417	-	-	-	X
27	GOL	l	801[A]	-	-	-	X
27	GOL	l	801[B]	-	-	-	X
31	LMT	F	101	-	-	-	X
31	LMT	e	101	-	-	-	X
34	HTG	b	623	-	-	-	X

2 Entry composition [i](#)

There are 41 unique types of molecules in this entry. The entry contains 62674 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
			Total	C	N	O	S			
1	A	334	4338	2836	717	760	25	0	222	0
1	a	334	4318	2821	715	757	25	0	220	0

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
			Total	C	N	O	S			
2	B	504	4166	2735	694	724	13	0	22	0
2	b	504	4134	2718	687	716	13	0	19	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	451	4272	2796	715	743	18	0	99	0
3	c	455	4316	2827	720	751	18	0	101	0

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	115	0
			3625	2390	597	623	15			
4	d	341	Total	C	N	O	S	0	119	0
			3658	2412	605	626	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
			Total	C	N	O	S			
12	m	34	286	190	43	52	1	0	2	0

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
			Total	C	N	O	S			
13	O	243	1958	1221	335	398	4	0	10	0
13	o	243	1933	1207	330	392	4	0	8	0

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
15	U	96	800	508	133	159	0	4	0
15	u	97	815	519	135	161	0	5	0

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

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

- 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 FE (II) ION (three-letter code: FE2) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
21	A	1	Total	Fe	0	1
			2	2		
21	a	1	Total	Fe	0	1
			2	2		

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

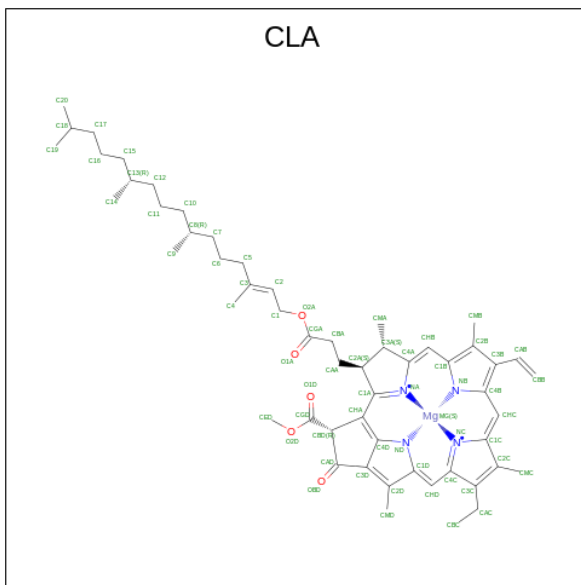
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	2	Total	Cl	0	2
			4	4		

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

- Molecule 23 is CHLOROPHYLL A (three-letter code: CLA) (formula: $C_{55}H_{72}MgN_4O_5$) (labeled as "Ligand of Interest" by depositor).



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

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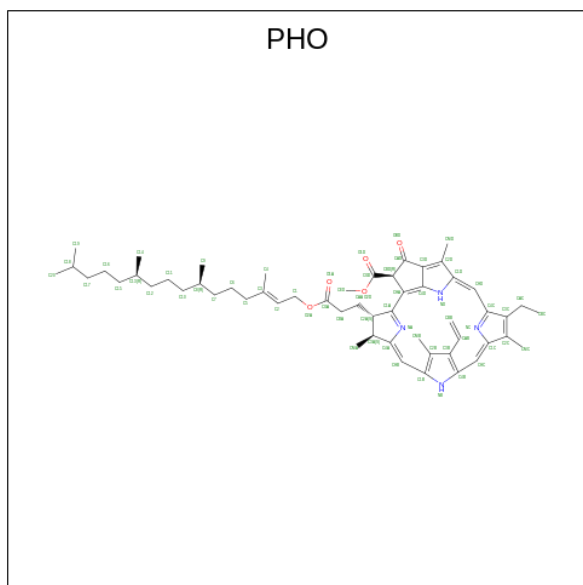
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
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		

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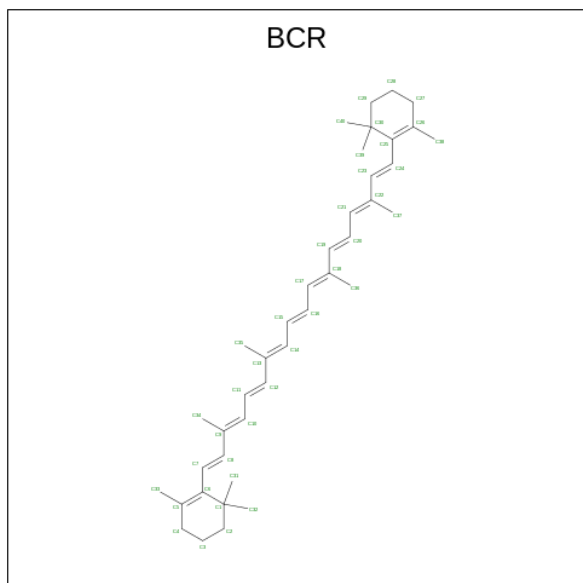
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
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	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 (three-letter code: PHO) (formula: C₅₅H₇₄N₄O₅).



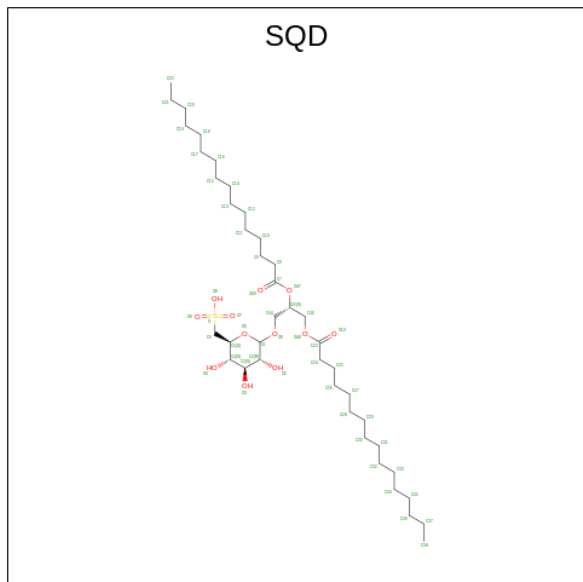
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
24	A	1	Total	C	N	O	0	1
			128	110	8	10		
24	A	1	Total	C	N	O	0	1
			128	110	8	10		
24	a	1	Total	C	N	O	0	1
			128	110	8	10		
24	a	1	Total	C	N	O	0	1
			128	110	8	10		

- Molecule 25 is BETA-CAROTENE (three-letter code: BCR) (formula: $C_{40}H_{56}$).



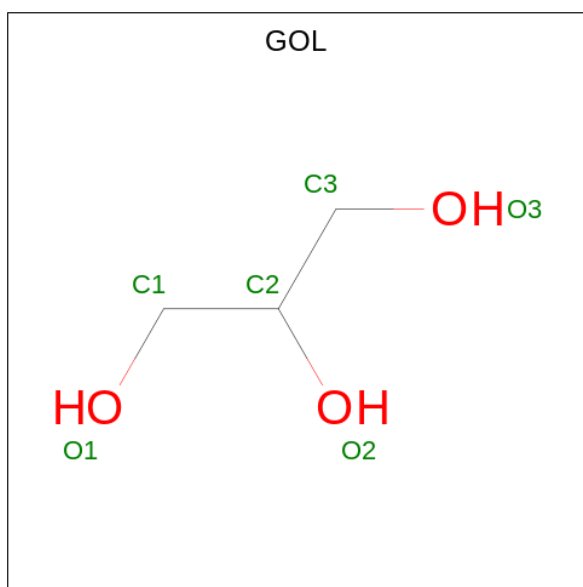
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
25	A	1	Total C 40 40	0	0
25	B	1	Total C 40 40	0	0
25	B	1	Total C 40 40	0	0
25	B	1	Total C 40 40	0	0
25	C	1	Total C 40 40	0	0
25	C	1	Total C 40 40	0	0
25	D	1	Total C 40 40	0	0
25	H	1	Total C 40 40	0	0
25	K	1	Total C 40 40	0	0
25	T	1	Total C 40 40	0	0
25	Y	1	Total 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 (three-letter code: SQD) (formula: $C_{41}H_{78}O_{12}S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
26	A	1	Total 108	C 82	O 24	S 2	0	1
26	A	1	Total 54	C 41	O 12	S 1	0	0
26	B	1	Total 54	C 41	O 12	S 1	0	0
26	F	1	Total 43	C 30	O 12	S 1	0	0
26	a	1	Total 108	C 82	O 24	S 2	0	1
26	a	1	Total 54	C 41	O 12	S 1	0	0
26	b	1	Total 54	C 41	O 12	S 1	0	0
26	f	1	Total 43	C 30	O 12	S 1	0	0

- Molecule 27 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



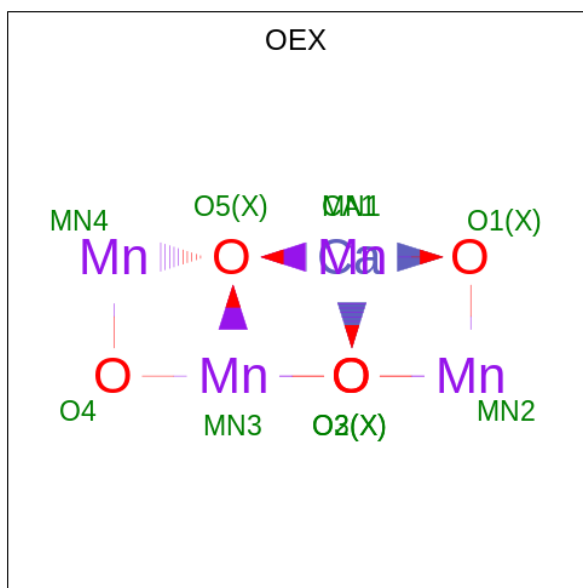
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
27	A	1	Total C O 6 3 3	0	0
27	A	1	Total C O 6 3 3	0	0
27	B	1	Total C O 6 3 3	0	0
27	B	1	Total C O 6 3 3	0	0
27	B	1	Total C O 6 3 3	0	0
27	C	1	Total C O 12 6 6	0	1
27	D	1	Total C O 6 3 3	0	0
27	O	1	Total C O 6 3 3	0	0
27	O	1	Total C O 6 3 3	0	0
27	V	1	Total C O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

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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		

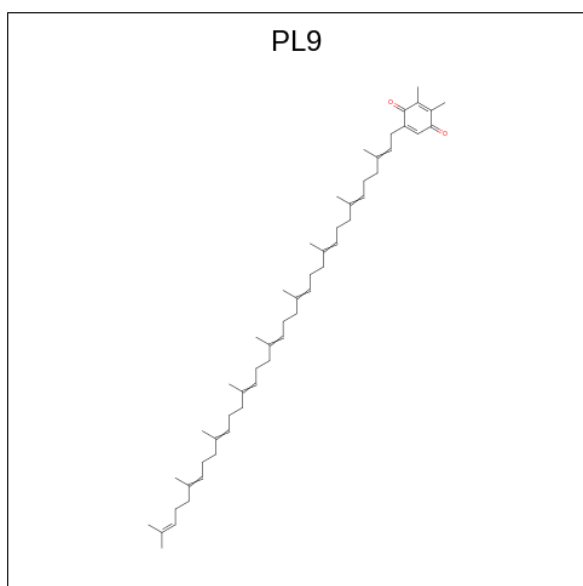
- Molecule 28 is CA-MN4-O5 CLUSTER (three-letter code: OEX) (formula: CaMn_4O_5) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
28	A	1	Total	Ca	Mn	O	0	1
			20	2	8	10		
28	a	1	Total	Ca	Mn	O	0	1
			20	2	8	10		

- 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 (three-letter code: PL9) (formula:

C₅₃H₈₀O₂) (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 (three-letter code: UNL) (formula:).

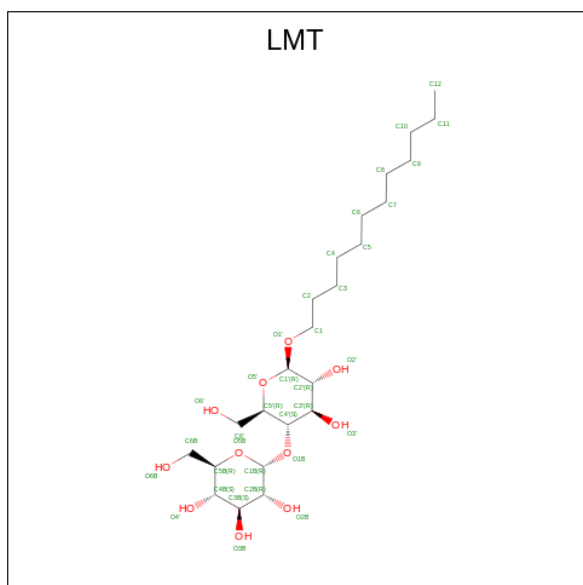
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
30	A	1	Total	C	O	0	0
			28	23	5		
30	B	1	Total	C	O	0	0
			33	28	5		
30	D	2	Total	C	O	0	0
			57	51	6		
30	I	1	Total	C	O	0	0
			40	35	5		
30	J	1	Total	C		0	0
			10	10			
30	K	1	Total	C	O	0	1
			68	58	10		
30	M	1	Total	C		0	0
			10	10			

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
30	X	1	Total	C	O	0	0
			18	16	2		
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	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 (three-letter code: LMT) (formula: $C_{24}H_{46}O_{11}$).



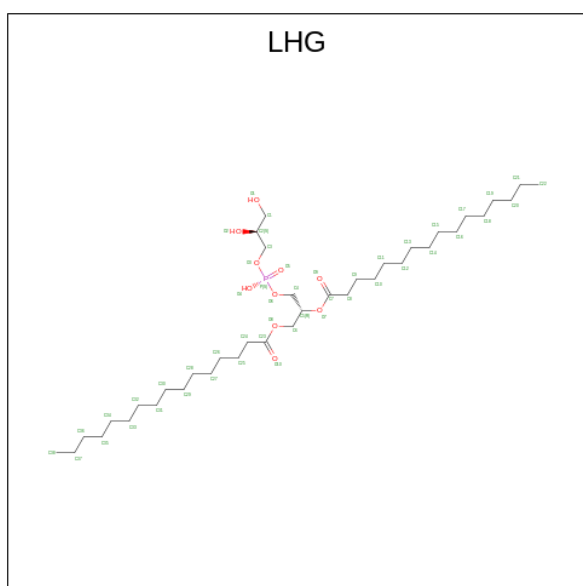
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
31	A	1	Total	C	O	0	0
			35	24	11		
31	A	1	Total	C	O	0	0
			35	24	11		

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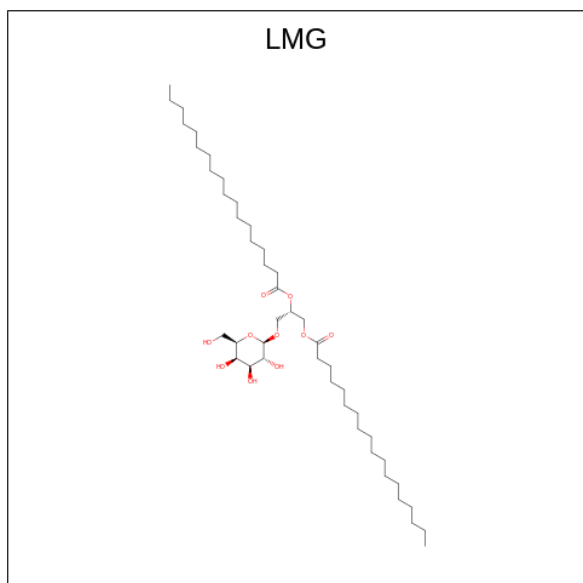
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
31	B	1	Total	C	O	0	0
			35	24	11		
31	B	1	Total	C	O	0	0
			35	24	11		
31	B	1	Total	C	O	0	0
			25	19	6		
31	F	1	Total	C	O	0	0
			35	24	11		
31	M	1	Total	C	O	0	0
			35	24	11		
31	T	1	Total	C	O	0	0
			35	24	11		
31	a	1	Total	C	O	0	0
			35	24	11		
31	b	1	Total	C	O	0	0
			25	19	6		
31	b	1	Total	C	O	0	0
			25	19	6		
31	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 (three-letter code: 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 (three-letter code: LMG) (formula: C₄₅H₈₆O₁₀).



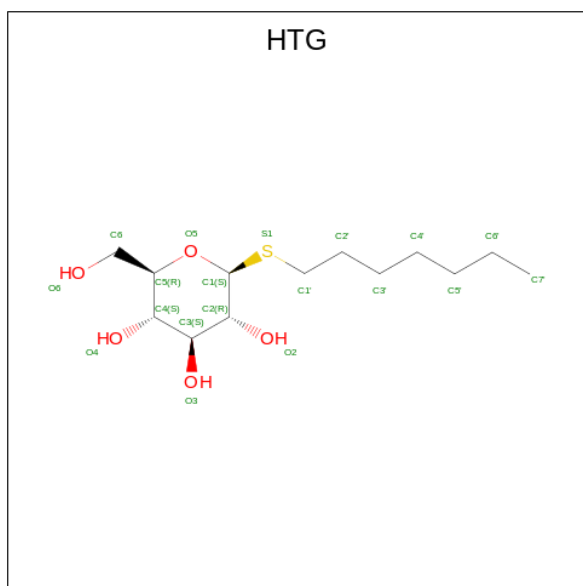
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
33	B	1	Total	C	O	0	0
			51	41	10		

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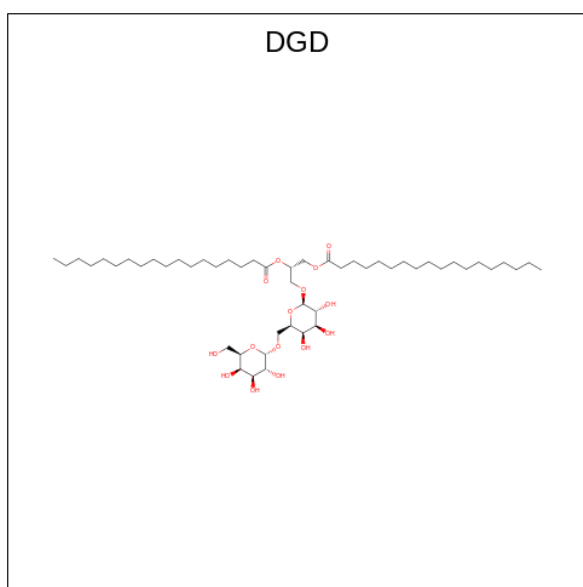
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
33	C	1	Total	C	O	0	0
			51	41	10		
33	C	1	Total	C	O	0	0
			51	41	10		
33	C	1	Total	C	O	0	0
			51	41	10		
33	D	1	Total	C	O	0	0
			51	41	10		
33	a	1	Total	C	O	0	0
			51	41	10		
33	c	1	Total	C	O	0	0
			51	41	10		
33	c	1	Total	C	O	0	0
			51	41	10		
33	d	1	Total	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 (three-letter code: HTG) (formula: $C_{13}H_{26}O_5S$).



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) (three-letter code: DGD) (formula: $C_{51}H_{96}O_{15}$).

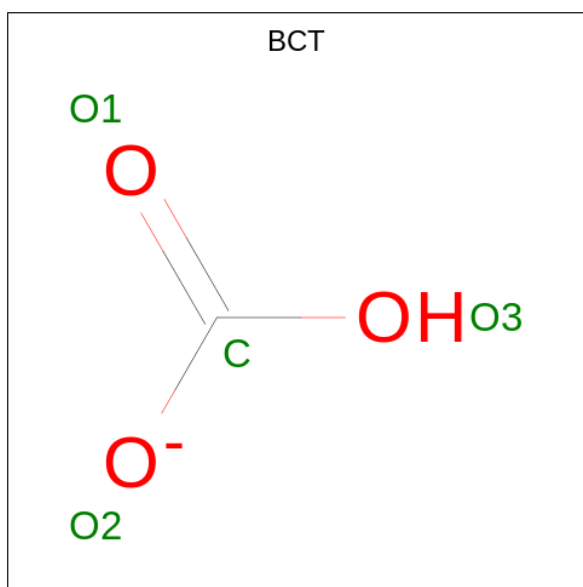


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
35	C	1	Total	C	O	0	1
			124	94	30		
35	C	1	Total	C	O	0	1
			124	94	30		
35	C	1	Total	C	O	0	0
			62	47	15		
35	H	1	Total	C	O	0	0
			62	47	15		
35	c	1	Total	C	O	0	1
			124	94	30		
35	c	1	Total	C	O	0	1
			124	94	30		
35	c	1	Total	C	O	0	0
			62	47	15		
35	h	1	Total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

- Molecule 36 is CALCIUM ION (three-letter code: CA) (formula: Ca).

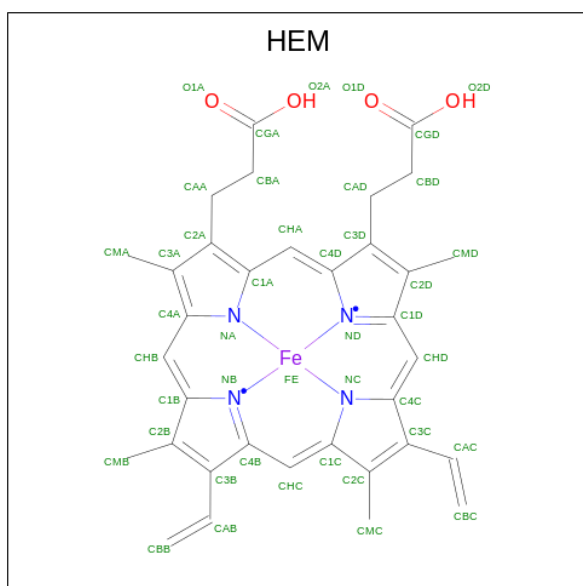
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	C	1	Total	Ca	0	0
			1	1		
36	F	1	Total	Ca	0	0
			1	1		
36	O	1	Total	Ca	0	0
			1	1		
36	c	2	Total	Ca	0	0
			2	2		
36	f	1	Total	Ca	0	0
			1	1		
36	o	1	Total	Ca	0	0
			1	1		

- Molecule 37 is BICARBONATE ION (three-letter code: BCT) (formula: CHO₃) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 38 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

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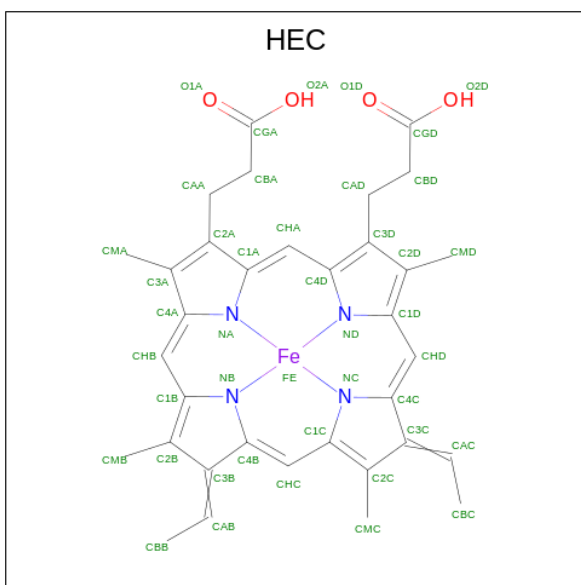
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
38	f	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 39 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 40 is HEME C (three-letter code: HEC) (formula: C₃₄H₃₄FeN₄O₄).



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

- Molecule 41 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
41	A	142	Total	O	0	86
			227	227		
41	B	187	Total	O	0	2
			189	189		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
41	C	169	Total O 206 206	0	38
41	D	120	Total O 155 155	0	35
41	E	17	Total O 17 17	0	0
41	F	4	Total O 4 4	0	0
41	H	22	Total O 22 22	0	0
41	I	4	Total O 4 4	0	0
41	J	6	Total O 6 6	0	0
41	K	5	Total O 5 5	0	0
41	L	9	Total O 10 10	0	1
41	M	6	Total O 6 6	0	0
41	O	104	Total O 108 108	0	4
41	T	11	Total O 14 14	0	3
41	U	47	Total O 49 49	0	2
41	V	79	Total O 80 80	0	1
41	X	7	Total O 7 7	0	0
41	a	131	Total O 211 211	0	81
41	b	201	Total O 204 204	0	3
41	c	160	Total O 193 193	0	34
41	d	117	Total O 149 149	0	32
41	e	8	Total O 8 8	0	0
41	f	3	Total O 3 3	0	0

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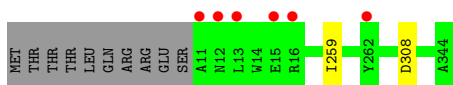
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
41	h	17	Total O 17 17	0	0
41	i	2	Total O 2 2	0	0
41	j	1	Total O 1 1	0	0
41	k	3	Total O 3 3	0	0
41	l	8	Total O 10 10	0	2
41	m	13	Total O 13 13	0	0
41	o	99	Total O 103 103	0	4
41	t	8	Total O 11 11	0	3
41	u	51	Total O 52 52	0	1
41	v	56	Total O 58 58	0	2
41	x	6	Total O 6 6	0	0
41	y	2	Total O 2 2	0	0

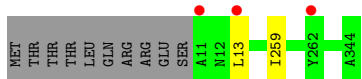
3 Residue-property plots [i](#)

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



- Molecule 1: Photosystem II protein D1



- Molecule 2: Photosystem II CP47 reaction center protein



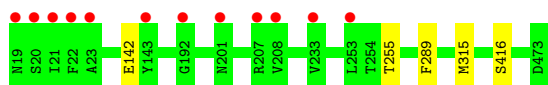
- Molecule 2: Photosystem II CP47 reaction center protein



- Molecule 3: Photosystem II CP43 reaction center protein



- Molecule 3: Photosystem II CP43 reaction center protein



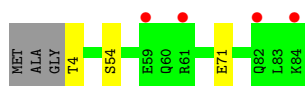
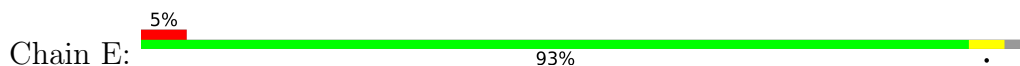
• Molecule 4: Photosystem II D2 protein



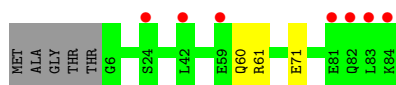
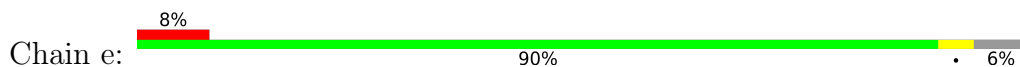
• Molecule 4: Photosystem II D2 protein



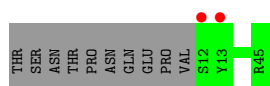
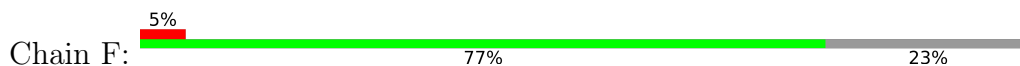
• Molecule 5: Cytochrome b559 subunit alpha



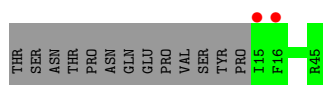
• Molecule 5: Cytochrome b559 subunit alpha



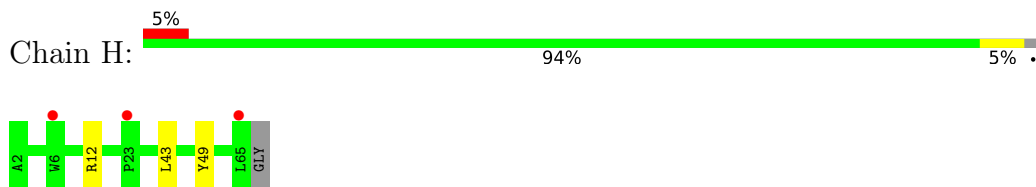
• Molecule 6: Cytochrome b559 subunit beta



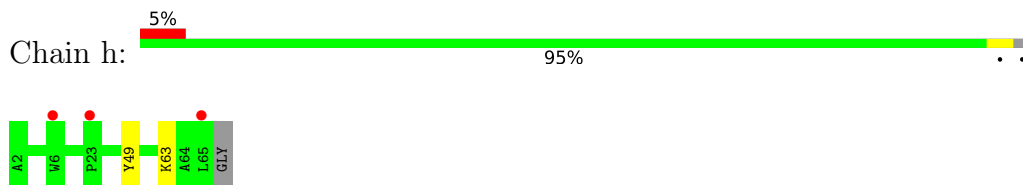
• Molecule 6: Cytochrome b559 subunit beta



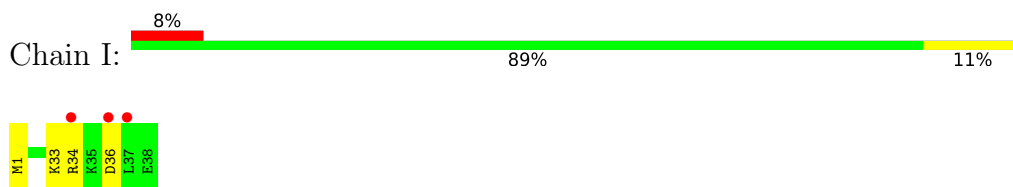
- Molecule 7: Photosystem II reaction center protein H



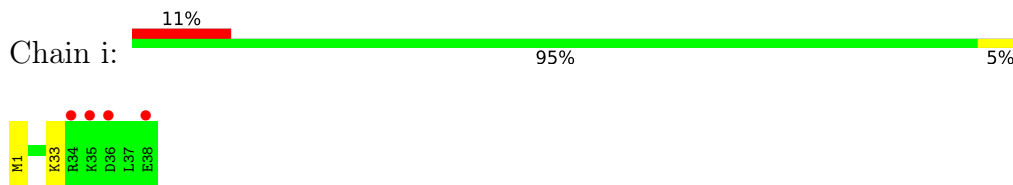
- Molecule 7: Photosystem II reaction center protein H



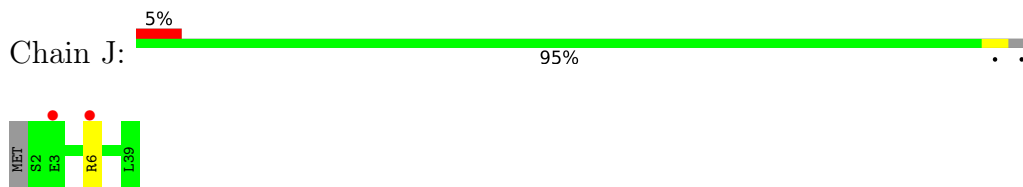
- Molecule 8: Photosystem II reaction center protein I



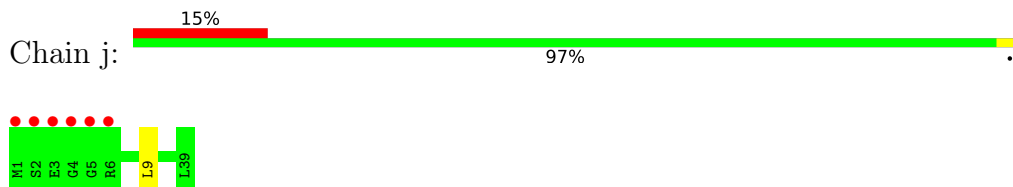
- Molecule 8: Photosystem II reaction center protein I



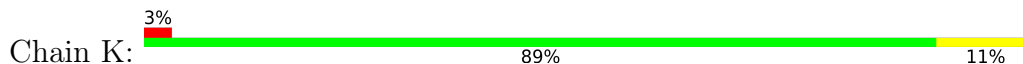
- Molecule 9: Photosystem II reaction center protein J



- Molecule 9: Photosystem II reaction center protein J



- Molecule 10: Photosystem II reaction center protein K

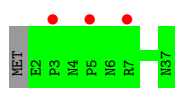




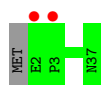
- Molecule 10: Photosystem II reaction center protein K



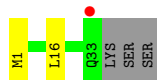
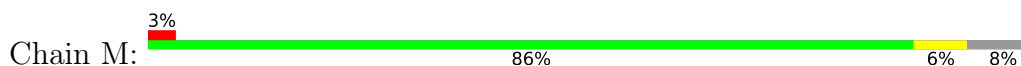
- Molecule 11: Photosystem II reaction center protein L



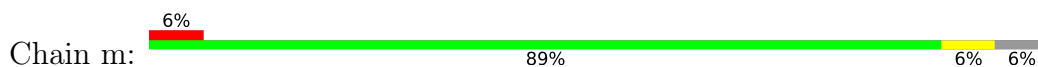
- Molecule 11: Photosystem II reaction center protein L



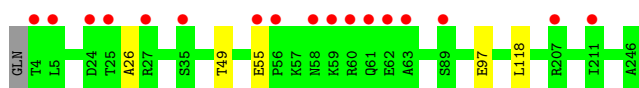
- Molecule 12: Photosystem II reaction center protein M



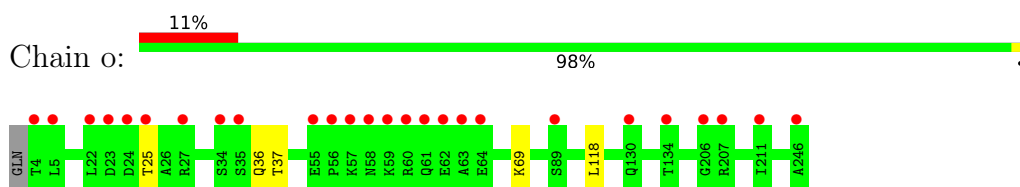
- Molecule 12: Photosystem II reaction center protein M



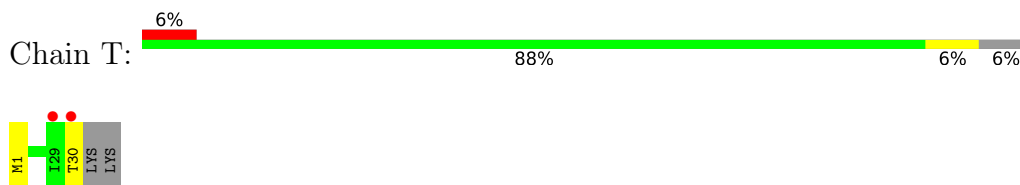
- Molecule 13: Photosystem II manganese-stabilizing polypeptide



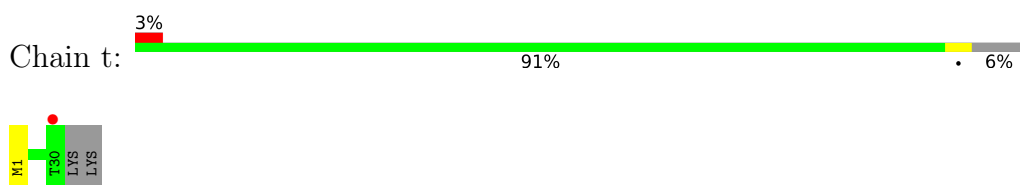
- Molecule 13: Photosystem II manganese-stabilizing polypeptide



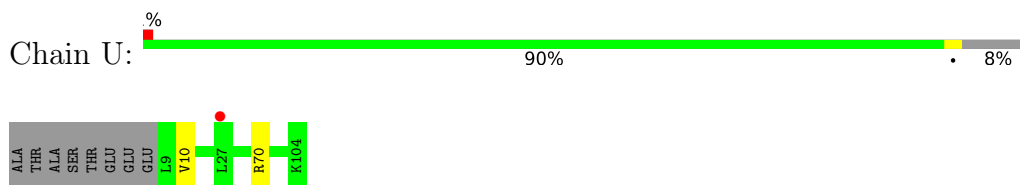
- Molecule 14: Photosystem II reaction center protein T



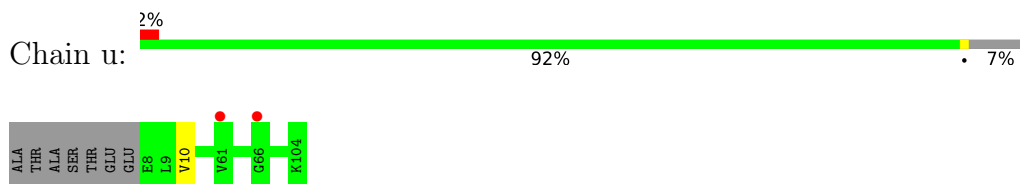
- Molecule 14: Photosystem II reaction center protein T



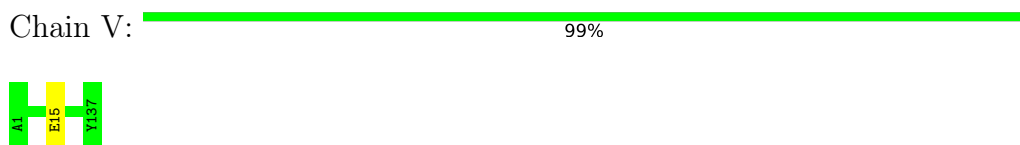
- Molecule 15: Photosystem II 12 kDa extrinsic protein



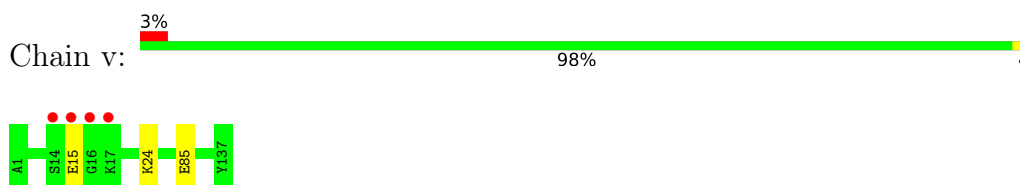
- Molecule 15: Photosystem II 12 kDa extrinsic protein



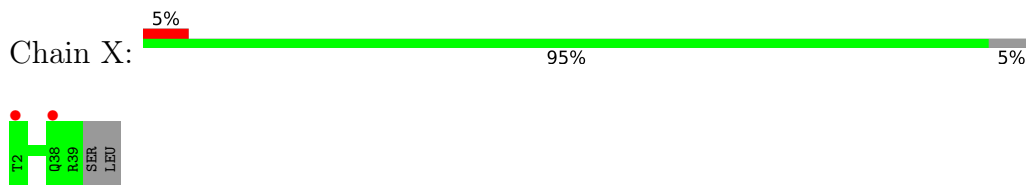
- Molecule 16: Cytochrome c-550



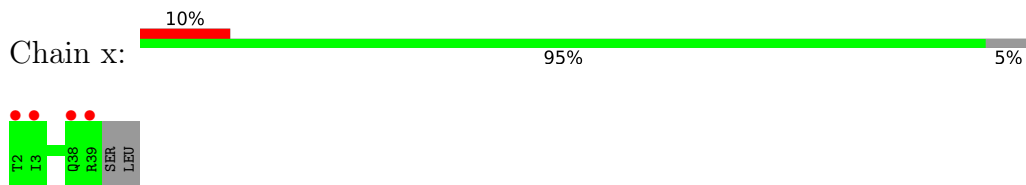
- Molecule 16: Cytochrome c-550



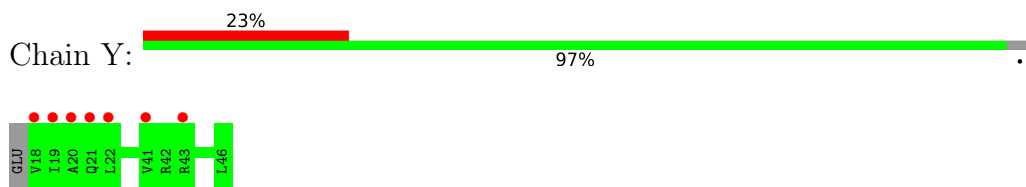
- Molecule 17: Photosystem II reaction center protein X



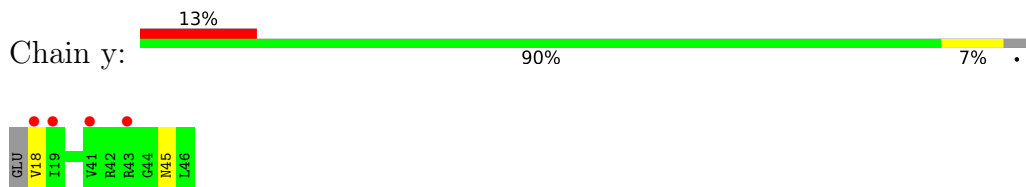
- Molecule 17: Photosystem II reaction center protein X



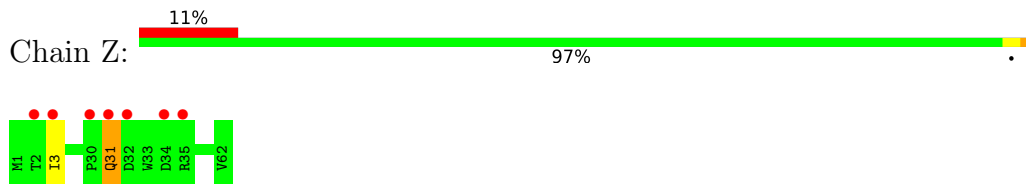
- Molecule 18: Photosystem II reaction center protein Ycf12



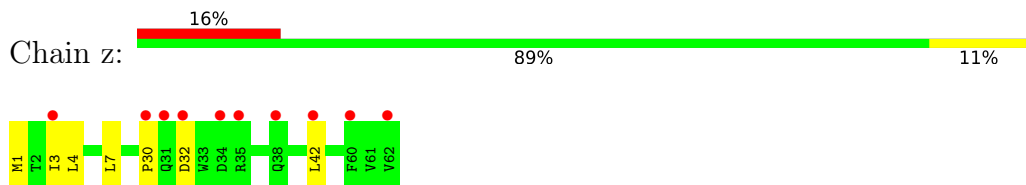
- Molecule 18: Photosystem II reaction center protein Ycf12



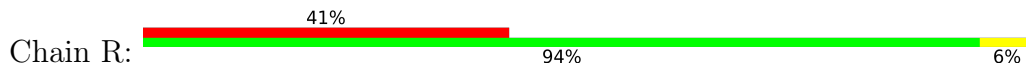
- Molecule 19: Photosystem II reaction center protein Z

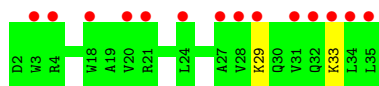


- Molecule 19: Photosystem II reaction center protein Z



- 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	125.75Å 231.60Å 288.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.98 – 2.20 19.98 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.98-2.20) 99.9 (19.98-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.19Å)	Xtrriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.142 , 0.178 0.153 , 0.183	Depositor DCC
R_{free} test set	21144 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	50.0	Xtrriage
Anisotropy	0.485	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 81.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	62674	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.73% 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 [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.43	0/4478	0.58	1/6098 (0.0%)
1	a	0.42	0/4457	0.57	0/6069
2	B	0.43	0/4314	0.58	0/5879
2	b	0.41	0/4285	0.57	0/5841
3	C	0.40	0/4416	0.55	0/6013
3	c	0.41	0/4467	0.54	0/6082
4	D	0.46	0/3746	0.60	0/5102
4	d	0.44	0/3780	0.58	0/5147
5	E	0.40	0/681	0.57	0/928
5	e	0.38	0/690	0.54	0/939
6	F	0.40	0/284	0.54	0/387
6	f	0.36	0/269	0.50	0/365
7	H	0.39	0/519	0.58	0/708
7	h	0.36	0/530	0.58	0/722
8	I	0.38	0/311	0.51	0/419
8	i	0.39	0/311	0.56	0/419
9	J	0.38	0/278	0.52	0/376
9	j	0.36	0/283	0.54	0/383
10	K	0.37	0/303	0.51	0/416
10	k	0.38	0/303	0.51	0/416
11	L	0.42	0/318	0.56	0/433
11	l	0.44	0/318	0.54	0/433
12	M	0.45	0/261	0.53	0/357
12	m	0.40	0/279	0.52	0/380
13	O	0.41	0/1991	0.64	0/2698
13	o	0.40	0/1966	0.63	0/2665
14	T	0.46	0/310	0.60	0/419
14	t	0.48	0/301	0.58	0/406
15	U	0.44	0/811	0.62	0/1095
15	u	0.44	0/826	0.61	0/1116
16	V	0.40	0/1142	0.57	0/1545

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	v	0.37	0/1139	0.54	0/1542
17	X	0.32	0/292	0.50	0/395
17	x	0.34	0/284	0.49	0/384
18	Y	0.32	0/216	0.54	0/289
18	y	0.30	0/216	0.49	0/289
19	Z	0.32	0/490	0.45	0/669
19	z	0.32	0/490	0.42	0/669
20	R	0.32	0/279	0.52	0/383
All	All	0.41	0/50634	0.57	1/68876 (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	308	ASP	CB-CG-OD1	5.49	123.24	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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%)	34	37
1	a	551/344 (160%)	540 (98%)	9 (2%)	2 (0%)	34	37
2	B	524/505 (104%)	517 (99%)	7 (1%)	0	100	100
2	b	521/505 (103%)	507 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	548/455 (120%)	540 (98%)	7 (1%)	1 (0%)	47	55
3	c	554/455 (122%)	545 (98%)	8 (1%)	1 (0%)	47	55
4	D	454/342 (133%)	439 (97%)	15 (3%)	0	100	100
4	d	457/342 (134%)	446 (98%)	11 (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%)	62 (100%)	0	0	100	100
7	h	63/65 (97%)	60 (95%)	2 (3%)	1 (2%)	9	7
8	I	36/38 (95%)	33 (92%)	2 (6%)	1 (3%)	5	2
8	i	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
9	J	36/39 (92%)	35 (97%)	1 (3%)	0	100	100
9	j	37/39 (95%)	37 (100%)	0	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%)	33 (97%)	1 (3%)	0	100	100
13	O	251/244 (103%)	242 (96%)	8 (3%)	1 (0%)	34	37
13	o	249/244 (102%)	244 (98%)	5 (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	99/104 (95%)	94 (95%)	5 (5%)	0	100	100
16	V	140/137 (102%)	136 (97%)	4 (3%)	0	100	100
16	v	140/137 (102%)	135 (96%)	5 (4%)	0	100	100
17	X	37/40 (92%)	36 (97%)	1 (3%)	0	100	100
17	x	36/40 (90%)	36 (100%)	0	0	100	100
18	Y	27/30 (90%)	24 (89%)	3 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	y	27/30 (90%)	27 (100%)	0	0	100	100
19	Z	60/62 (97%)	58 (97%)	1 (2%)	1 (2%)	9	6
19	z	60/62 (97%)	59 (98%)	0	1 (2%)	9	6
20	R	32/34 (94%)	31 (97%)	1 (3%)	0	100	100
All	All	6180/5384 (115%)	6042 (98%)	127 (2%)	11 (0%)	47	55

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	I	36	ASP
3	C	416	SER
13	O	26	ALA
3	c	416	SER
19	Z	31	GLN

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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%)	444 (100%)	0	100	100
1	a	442/279 (158%)	441 (100%)	1 (0%)	93	97
2	B	423/403 (105%)	418 (99%)	5 (1%)	71	83
2	b	420/403 (104%)	410 (98%)	10 (2%)	49	62
3	C	431/356 (121%)	426 (99%)	5 (1%)	71	83
3	c	437/356 (123%)	432 (99%)	5 (1%)	73	85
4	D	368/277 (133%)	366 (100%)	2 (0%)	88	94
4	d	372/277 (134%)	368 (99%)	4 (1%)	73	85
5	E	72/73 (99%)	69 (96%)	3 (4%)	30	38
5	e	72/73 (99%)	69 (96%)	3 (4%)	30	38
6	F	28/38 (74%)	28 (100%)	0	100	100
6	f	26/38 (68%)	26 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	H	54/54 (100%)	51 (94%)	3 (6%)	21	25
7	h	55/54 (102%)	54 (98%)	1 (2%)	59	72
8	I	34/34 (100%)	32 (94%)	2 (6%)	19	23
8	i	34/34 (100%)	33 (97%)	1 (3%)	42	54
9	J	26/27 (96%)	25 (96%)	1 (4%)	33	42
9	j	26/27 (96%)	25 (96%)	1 (4%)	33	42
10	K	30/30 (100%)	26 (87%)	4 (13%)	4	3
10	k	30/30 (100%)	27 (90%)	3 (10%)	7	7
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%)	16	18
12	m	32/32 (100%)	30 (94%)	2 (6%)	18	20
13	O	216/207 (104%)	212 (98%)	4 (2%)	57	71
13	o	213/207 (103%)	208 (98%)	5 (2%)	50	63
14	T	32/28 (114%)	30 (94%)	2 (6%)	18	20
14	t	31/28 (111%)	31 (100%)	0	100	100
15	U	86/89 (97%)	84 (98%)	2 (2%)	50	63
15	u	88/89 (99%)	86 (98%)	2 (2%)	50	63
16	V	123/117 (105%)	122 (99%)	1 (1%)	81	90
16	v	123/117 (105%)	120 (98%)	3 (2%)	49	62
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%)	20 (91%)	2 (9%)	9	9
19	Z	52/52 (100%)	50 (96%)	2 (4%)	33	42
19	z	52/52 (100%)	46 (88%)	6 (12%)	5	5
20	R	29/29 (100%)	27 (93%)	2 (7%)	15	16
All	All	5110/4403 (116%)	5021 (98%)	89 (2%)	57	74

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	e	61	ARG

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Mol	Chain	Res	Type
13	o	118	LEU
7	h	49	TYR
12	m	16[A]	LEU
16	v	24	LYS

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

Mol	Chain	Res	Type
5	E	60	GLN
13	o	58	ASN
16	v	86	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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	$\# Z > 2$
8	FME	i	1	8	8,9,10	0.66	0	7,9,11	1.16	1 (14%)
14	FME	T	1	14	8,9,10	0.63	0	7,9,11	1.31	1 (14%)
12	FME	m	1	12	8,9,10	0.58	0	7,9,11	1.51	2 (28%)
8	FME	I	1	8	8,9,10	0.58	0	7,9,11	1.16	1 (14%)
12	FME	M	1	12	8,9,10	0.64	0	7,9,11	1.18	1 (14%)
14	FME	t	1	14	8,9,10	0.71	0	7,9,11	1.53	2 (28%)

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

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	m	1	FME	O1-CN-N	-2.55	118.54	125.27
14	t	1	FME	O-C-CA	-2.40	118.48	124.78
14	T	1	FME	CG-CB-CA	2.39	119.60	112.95
12	m	1	FME	CA-N-CN	-2.26	119.34	122.82
14	t	1	FME	CA-N-CN	-2.22	119.40	122.82

There are no chirality outliers.

All (5) torsion outliers are listed below:

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

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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$
25	BCR	d	405	-	41,41,41	1.13	2 (4%)	56,56,56	1.98	15 (26%)
23	CLA	C	505	41	65,73,73	2.01	17 (26%)	76,113,113	2.76	26 (34%)
32	LHG	D	406[A]	-	48,48,48	0.86	2 (4%)	51,54,54	0.99	3 (5%)
27	GOL	c	525[B]	-	5,5,5	1.04	0	5,5,5	0.87	0
31	LMT	b	621	-	25,25,36	0.98	1 (4%)	30,30,47	1.20	2 (6%)
25	BCR	A	409	-	41,41,41	1.01	1 (2%)	56,56,56	1.43	8 (14%)
23	CLA	B	606	-	65,73,73	1.96	16 (24%)	76,113,113	2.97	28 (36%)
23	CLA	B	616	-	65,73,73	2.02	16 (24%)	76,113,113	2.88	27 (35%)
29	PL9	d	406[B]	-	55,55,55	0.68	1 (1%)	68,69,69	1.62	17 (25%)
27	GOL	l	801[B]	-	5,5,5	0.88	0	5,5,5	0.97	0
33	LMG	Z	101	-	37,37,55	1.01	2 (5%)	45,45,63	1.44	6 (13%)
34	HTG	d	411	-	16,16,19	0.96	1 (6%)	20,21,24	1.55	1 (5%)
23	CLA	B	603	-	65,73,73	2.03	17 (26%)	76,113,113	2.92	29 (38%)
27	GOL	d	413	-	5,5,5	1.07	0	5,5,5	0.97	0
32	LHG	A	419[A]	-	48,48,48	0.84	2 (4%)	51,54,54	1.31	6 (11%)
26	SQD	a	410	-	53,54,54	1.05	4 (7%)	62,65,65	1.21	8 (12%)
35	DGD	C	518[B]	-	63,63,67	0.87	2 (3%)	77,77,81	1.07	5 (6%)
23	CLA	a	404[A]	-	65,73,73	1.99	15 (23%)	76,113,113	2.87	32 (42%)
34	HTG	c	521	-	19,19,19	0.93	1 (5%)	23,24,24	1.51	1 (4%)
32	LHG	d	407[A]	-	48,48,48	0.86	2 (4%)	51,54,54	1.08	4 (7%)
27	GOL	a	417	-	5,5,5	0.99	0	5,5,5	1.03	0
32	LHG	D	406[B]	-	48,48,48	0.87	2 (4%)	51,54,54	0.93	3 (5%)
33	LMG	c	520	-	51,51,55	1.00	2 (3%)	59,59,63	1.36	6 (10%)
23	CLA	b	611	-	65,73,73	1.99	16 (24%)	76,113,113	2.87	29 (38%)
33	LMG	B	621	-	51,51,55	0.91	2 (3%)	59,59,63	1.32	5 (8%)
23	CLA	B	615	-	65,73,73	2.06	16 (24%)	76,113,113	2.79	28 (36%)
23	CLA	d	402[A]	41	65,73,73	2.00	14 (21%)	76,113,113	2.75	26 (34%)
31	LMT	B	630	-	36,36,36	1.02	3 (8%)	47,47,47	1.15	5 (10%)
23	CLA	A	404[B]	-	65,73,73	2.05	16 (24%)	76,113,113	2.81	31 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	CLA	A	408	-	65,73,73	2.04	16 (24%)	76,113,113	2.86	32 (42%)
33	LMG	z	101	-	39,39,55	1.09	2 (5%)	47,47,63	1.08	3 (6%)
33	LMG	a	415	-	51,51,55	0.92	2 (3%)	59,59,63	1.22	5 (8%)
23	CLA	b	610	41	65,73,73	2.04	16 (24%)	76,113,113	2.81	31 (40%)
23	CLA	a	404[B]	-	65,73,73	2.02	16 (24%)	76,113,113	2.82	33 (43%)
23	CLA	c	501	-	65,73,73	2.00	17 (26%)	76,113,113	2.87	26 (34%)
38	HEM	E	102	5,6	41,50,50	1.29	4 (9%)	45,82,82	2.09	14 (31%)
37	BCT	d	401[A]	21	2,3,3	0.57	0	2,3,3	1.58	1 (50%)
23	CLA	C	507	-	65,73,73	2.05	17 (26%)	76,113,113	2.75	30 (39%)
35	DGD	c	517[A]	-	63,63,67	0.84	2 (3%)	77,77,81	0.97	5 (6%)
31	LMT	m	103	-	36,36,36	1.10	3 (8%)	47,47,47	1.12	3 (6%)
23	CLA	C	508	41	65,73,73	2.01	16 (24%)	76,113,113	2.77	27 (35%)
40	HEC	v	201	16	32,50,50	2.05	3 (9%)	24,82,82	1.99	6 (25%)
31	LMT	t	101	-	26,26,36	0.93	2 (7%)	31,31,47	1.35	2 (6%)
23	CLA	B	609	-	65,73,73	2.02	16 (24%)	76,113,113	2.81	25 (32%)
23	CLA	d	402[B]	41	65,73,73	2.07	16 (24%)	76,113,113	2.76	30 (39%)
26	SQD	a	409[A]	-	53,54,54	0.95	3 (5%)	62,65,65	1.77	13 (20%)
34	HTG	b	625	-	19,19,19	1.03	2 (10%)	23,24,24	1.58	3 (13%)
23	CLA	C	503	-	65,73,73	2.04	16 (24%)	76,113,113	2.71	26 (34%)
25	BCR	C	516	-	41,41,41	1.03	1 (2%)	56,56,56	1.46	8 (14%)
33	LMG	C	520	-	51,51,55	0.93	2 (3%)	59,59,63	1.18	6 (10%)
32	LHG	d	408[B]	-	48,48,48	0.93	2 (4%)	51,54,54	1.01	3 (5%)
25	BCR	c	514	-	41,41,41	1.00	1 (2%)	56,56,56	1.68	13 (23%)
23	CLA	D	402[A]	-	65,73,73	1.99	16 (24%)	76,113,113	2.87	29 (38%)
23	CLA	C	513	-	65,73,73	2.03	15 (23%)	76,113,113	2.79	30 (39%)
32	LHG	a	419[A]	-	41,41,48	1.04	2 (4%)	44,47,54	0.92	2 (4%)
23	CLA	b	616	-	65,73,73	2.01	16 (24%)	76,113,113	2.89	28 (36%)
27	GOL	V	203[A]	-	5,5,5	1.22	0	5,5,5	0.91	0
23	CLA	D	403	-	65,73,73	2.07	15 (23%)	76,113,113	2.72	29 (38%)
25	BCR	Y	101	-	41,41,41	0.99	1 (2%)	56,56,56	1.78	13 (23%)
23	CLA	c	507	41	65,73,73	2.02	15 (23%)	76,113,113	2.87	28 (36%)
26	SQD	A	410[A]	-	53,54,54	0.93	3 (5%)	62,65,65	1.81	10 (16%)
23	CLA	c	509	-	65,73,73	2.02	15 (23%)	76,113,113	2.81	29 (38%)
37	BCT	d	401[B]	21	2,3,3	0.61	0	2,3,3	1.23	0
23	CLA	c	508	-	65,73,73	2.14	16 (24%)	76,113,113	2.71	26 (34%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	GOL	c	526	-	5,5,5	1.01	0	5,5,5	0.99	0
35	DGD	c	517[B]	-	63,63,67	0.86	2 (3%)	77,77,81	0.97	5 (6%)
25	BCR	C	515	-	41,41,41	1.05	1 (2%)	56,56,56	1.36	6 (10%)
26	SQD	A	412	-	53,54,54	1.03	3 (5%)	62,65,65	1.22	7 (11%)
26	SQD	a	409[B]	-	53,54,54	0.97	3 (5%)	62,65,65	1.64	12 (19%)
27	GOL	b	624	-	5,5,5	1.22	1 (20%)	5,5,5	0.81	0
25	BCR	a	408	-	41,41,41	1.04	1 (2%)	56,56,56	1.29	7 (12%)
31	LMT	B	628	-	36,36,36	1.19	4 (11%)	47,47,47	1.37	6 (12%)
23	CLA	C	510	-	65,73,73	2.08	16 (24%)	76,113,113	2.78	28 (36%)
23	CLA	c	505	-	65,73,73	2.01	16 (24%)	76,113,113	2.72	25 (32%)
26	SQD	B	620	-	53,54,54	1.07	4 (7%)	62,65,65	1.76	11 (17%)
33	LMG	D	411	39	51,51,55	0.84	2 (3%)	59,59,63	0.99	4 (6%)
37	BCT	D	401[A]	21	2,3,3	0.54	0	2,3,3	1.81	1 (50%)
23	CLA	c	506	-	65,73,73	2.05	16 (24%)	76,113,113	2.75	28 (36%)
32	LHG	a	419[B]	-	41,41,48	1.03	2 (4%)	44,47,54	0.92	2 (4%)
25	BCR	B	618	-	41,41,41	1.00	1 (2%)	56,56,56	1.31	7 (12%)
25	BCR	b	619	-	41,41,41	1.07	1 (2%)	56,56,56	1.36	6 (10%)
23	CLA	c	512	-	65,73,73	2.08	16 (24%)	76,113,113	2.74	29 (38%)
27	GOL	V	203[B]	-	5,5,5	1.10	0	5,5,5	0.89	0
35	DGD	c	516[A]	-	63,63,67	0.85	2 (3%)	77,77,81	1.12	6 (7%)
23	CLA	B	605	-	65,73,73	1.96	16 (24%)	76,113,113	2.89	26 (34%)
25	BCR	K	102	-	41,41,41	1.02	1 (2%)	56,56,56	1.41	10 (17%)
23	CLA	b	615	-	65,73,73	2.00	16 (24%)	76,113,113	2.76	27 (35%)
34	HTG	B	625	-	19,19,19	0.97	2 (10%)	23,24,24	1.12	2 (8%)
25	BCR	c	515	-	41,41,41	1.04	1 (2%)	56,56,56	1.45	13 (23%)
23	CLA	B	602	-	65,73,73	2.10	17 (26%)	76,113,113	2.81	31 (40%)
24	PHO	a	406[A]	-	51,69,69	1.83	8 (15%)	47,99,99	1.71	10 (21%)
31	LMT	T	101	-	36,36,36	1.05	3 (8%)	47,47,47	1.04	2 (4%)
29	PL9	A	414[A]	-	55,55,55	0.68	2 (3%)	68,69,69	2.08	25 (36%)
35	DGD	h	102	-	63,63,67	0.87	3 (4%)	77,77,81	1.07	6 (7%)
23	CLA	b	601	41	65,73,73	2.13	16 (24%)	76,113,113	2.73	27 (35%)
23	CLA	b	609	-	65,73,73	2.04	16 (24%)	76,113,113	2.80	30 (39%)
23	CLA	d	404	-	65,73,73	2.04	15 (23%)	76,113,113	2.84	27 (35%)
23	CLA	B	601	41	65,73,73	2.09	16 (24%)	76,113,113	2.78	26 (34%)
37	BCT	D	401[B]	21	2,3,3	0.63	0	2,3,3	1.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
29	PL9	a	412[A]	-	55,55,55	0.65	2 (3%)	68,69,69	2.00	22 (32%)
31	LMT	A	417	-	36,36,36	0.96	3 (8%)	47,47,47	0.99	1 (2%)
31	LMT	b	627	-	25,25,36	0.89	1 (4%)	30,30,47	1.09	2 (6%)
32	LHG	A	419[B]	-	48,48,48	0.87	2 (4%)	51,54,54	1.17	5 (9%)
23	CLA	b	613	-	65,73,73	1.98	16 (24%)	76,113,113	2.76	29 (38%)
23	CLA	C	506	-	65,73,73	1.99	16 (24%)	76,113,113	2.72	29 (38%)
24	PHO	A	416[A]	-	51,69,69	1.87	8 (15%)	47,99,99	1.93	12 (25%)
25	BCR	k	101	-	41,41,41	1.06	1 (2%)	56,56,56	1.51	13 (23%)
27	GOL	o	302	-	5,5,5	1.00	0	5,5,5	1.00	0
24	PHO	A	407[A]	-	51,69,69	1.78	8 (15%)	47,99,99	1.77	11 (23%)
32	LHG	d	407[B]	-	48,48,48	0.88	2 (4%)	51,54,54	0.99	3 (5%)
25	BCR	B	617	-	41,41,41	1.05	1 (2%)	56,56,56	1.32	6 (10%)
25	BCR	D	404	-	41,41,41	1.11	1 (2%)	56,56,56	1.80	17 (30%)
34	HTG	C	522	-	19,19,19	0.86	1 (5%)	23,24,24	1.36	2 (8%)
23	CLA	b	604	-	65,73,73	2.02	15 (23%)	76,113,113	2.75	25 (32%)
23	CLA	B	608	-	65,73,73	1.97	16 (24%)	76,113,113	2.77	32 (42%)
26	SQD	b	620	-	53,54,54	1.04	3 (5%)	62,65,65	1.68	11 (17%)
29	PL9	A	414[B]	-	55,55,55	0.65	2 (3%)	68,69,69	1.98	25 (36%)
27	GOL	o	303	-	5,5,5	1.07	1 (20%)	5,5,5	1.08	0
27	GOL	O	302	-	5,5,5	0.91	0	5,5,5	0.87	0
23	CLA	d	403[A]	-	65,73,73	1.94	17 (26%)	76,113,113	2.79	29 (38%)
27	GOL	v	202[A]	-	5,5,5	1.27	0	5,5,5	0.72	0
29	PL9	a	412[B]	-	55,55,55	0.64	2 (3%)	68,69,69	1.96	22 (32%)
24	PHO	A	416[B]	-	51,69,69	1.90	7 (13%)	47,99,99	1.84	10 (21%)
25	BCR	y	101	-	41,41,41	1.09	1 (2%)	56,56,56	1.63	12 (21%)
23	CLA	b	602	-	65,73,73	2.07	16 (24%)	76,113,113	2.84	33 (43%)
24	PHO	A	407[B]	-	51,69,69	1.80	8 (15%)	47,99,99	1.80	10 (21%)
34	HTG	b	623	-	19,19,19	1.01	1 (5%)	23,24,24	1.78	2 (8%)
23	CLA	C	502	-	65,73,73	1.99	16 (24%)	76,113,113	2.76	28 (36%)
23	CLA	C	514	-	65,73,73	2.06	16 (24%)	76,113,113	2.79	28 (36%)
35	DGD	C	517[A]	-	63,63,67	0.81	2 (3%)	77,77,81	1.21	8 (10%)
23	CLA	b	608	-	65,73,73	2.02	15 (23%)	76,113,113	2.78	32 (42%)
40	HEC	V	201	16	32,50,50	1.97	4 (12%)	24,82,82	2.18	7 (29%)
28	OEX	a	411[A]	3,41,1	0,15,15	-	-	-	-	-
29	PL9	D	405[A]	-	55,55,55	0.62	2 (3%)	68,69,69	1.64	18 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
31	LMT	F	101	-	36,36,36	1.07	1 (2%)	47,47,47	1.06	2 (4%)
23	CLA	d	403[B]	-	65,73,73	1.96	17 (26%)	76,113,113	2.83	25 (32%)
27	GOL	v	202[B]	-	5,5,5	1.13	0	5,5,5	0.87	0
23	CLA	B	611	-	65,73,73	2.68	18 (27%)	76,113,113	3.09	28 (36%)
25	BCR	t	102	-	41,41,41	1.00	1 (2%)	56,56,56	1.55	11 (19%)
27	GOL	C	523[A]	-	5,5,5	1.18	0	5,5,5	0.83	0
23	CLA	D	402[B]	-	65,73,73	2.02	16 (24%)	76,113,113	2.84	30 (39%)
31	LMT	e	101	-	36,36,36	1.03	4 (11%)	47,47,47	0.98	1 (2%)
34	HTG	B	622	-	19,19,19	1.07	2 (10%)	23,24,24	1.59	5 (21%)
23	CLA	A	405[A]	41	65,73,73	1.90	16 (24%)	76,113,113	2.85	30 (39%)
32	LHG	D	407[A]	-	48,48,48	0.92	2 (4%)	51,54,54	0.99	4 (7%)
26	SQD	F	102	-	42,43,54	1.19	4 (9%)	51,54,65	2.18	14 (27%)
26	SQD	A	410[B]	-	53,54,54	0.93	3 (5%)	62,65,65	1.79	11 (17%)
25	BCR	T	102	-	41,41,41	1.04	1 (2%)	56,56,56	1.68	15 (26%)
35	DGD	C	517[B]	-	63,63,67	0.84	2 (3%)	77,77,81	1.11	7 (9%)
28	OEX	a	411[B]	3,41,1	0,15,15	-	-	-	-	-
24	PHO	a	414[A]	-	51,69,69	1.86	9 (17%)	47,99,99	1.99	13 (27%)
29	PL9	D	405[B]	-	55,55,55	0.63	2 (3%)	68,69,69	1.68	17 (25%)
23	CLA	c	513	-	65,73,73	2.10	16 (24%)	76,113,113	2.78	26 (34%)
27	GOL	A	411	-	5,5,5	1.13	0	5,5,5	0.74	0
31	LMT	a	416	-	36,36,36	1.01	1 (2%)	47,47,47	1.03	1 (2%)
32	LHG	L	101[A]	-	48,48,48	0.89	2 (4%)	51,54,54	1.15	3 (5%)
34	HTG	D	410	-	16,16,19	1.04	1 (6%)	20,21,24	1.46	1 (5%)
23	CLA	C	509	-	65,73,73	2.11	16 (24%)	76,113,113	2.78	27 (35%)
38	HEM	f	101	5,6	41,50,50	1.29	5 (12%)	45,82,82	1.81	10 (22%)
27	GOL	C	523[B]	-	5,5,5	1.07	0	5,5,5	0.91	0
35	DGD	c	516[B]	-	63,63,67	0.86	2 (3%)	77,77,81	1.01	3 (3%)
23	CLA	a	405[A]	41	65,73,73	1.94	16 (24%)	76,113,113	2.81	27 (35%)
23	CLA	A	405[B]	41	65,73,73	2.04	16 (24%)	76,113,113	2.78	29 (38%)
32	LHG	D	407[B]	-	48,48,48	0.92	2 (4%)	51,54,54	0.97	3 (5%)
33	LMG	m	101	-	51,51,55	0.87	2 (3%)	59,59,63	1.24	6 (10%)
27	GOL	A	418	-	5,5,5	1.62	2 (40%)	5,5,5	0.97	1 (20%)
35	DGD	C	519	-	63,63,67	0.86	3 (4%)	77,77,81	0.98	3 (3%)
23	CLA	B	607	41	65,73,73	1.98	17 (26%)	76,113,113	2.93	31 (40%)
23	CLA	B	610	41	65,73,73	2.05	17 (26%)	76,113,113	2.87	27 (35%)
23	CLA	a	407	-	65,73,73	1.97	15 (23%)	76,113,113	3.01	30 (39%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	CLA	b	605	-	65,73,73	1.93	15 (23%)	76,113,113	2.94	27 (35%)
24	PHO	a	414[B]	-	51,69,69	1.88	8 (15%)	47,99,99	1.90	12 (25%)
24	PHO	a	406[B]	-	51,69,69	1.84	8 (15%)	47,99,99	1.77	9 (19%)
23	CLA	b	614	-	65,73,73	2.00	16 (24%)	76,113,113	2.85	30 (39%)
32	LHG	L	101[B]	-	48,48,48	0.92	2 (4%)	51,54,54	1.09	4 (7%)
25	BCR	h	101	-	41,41,41	1.03	1 (2%)	56,56,56	1.44	11 (19%)
32	LHG	E	101[A]	-	41,41,48	1.06	2 (4%)	44,47,54	1.11	3 (6%)
34	HTG	B	623	-	19,19,19	0.81	1 (5%)	23,24,24	1.46	3 (13%)
33	LMG	C	501	-	51,51,55	0.92	2 (3%)	59,59,63	1.53	7 (11%)
23	CLA	B	614	-	65,73,73	2.03	18 (27%)	76,113,113	2.89	30 (39%)
23	CLA	a	405[B]	41	65,73,73	2.00	16 (24%)	76,113,113	2.79	28 (36%)
23	CLA	b	606	-	65,73,73	1.98	15 (23%)	76,113,113	2.85	29 (38%)
27	GOL	B	624	-	5,5,5	0.75	0	5,5,5	1.10	1 (20%)
33	LMG	C	521	-	51,51,55	1.07	3 (5%)	59,59,63	1.33	6 (10%)
23	CLA	A	404[A]	-	65,73,73	2.02	16 (24%)	76,113,113	2.77	32 (42%)
23	CLA	b	612	-	65,73,73	2.01	16 (24%)	76,113,113	2.80	29 (38%)
27	GOL	a	418	-	5,5,5	1.23	1 (20%)	5,5,5	1.03	0
23	CLA	B	604	-	65,73,73	1.99	18 (27%)	76,113,113	2.63	27 (35%)
23	CLA	B	613	-	65,73,73	2.04	16 (24%)	76,113,113	2.74	29 (38%)
32	LHG	d	414[A]	-	48,48,48	0.89	2 (4%)	51,54,54	1.12	4 (7%)
23	CLA	A	406[A]	41	65,73,73	1.96	16 (24%)	76,113,113	2.81	29 (38%)
33	LMG	d	412	39	51,51,55	0.88	2 (3%)	59,59,63	1.13	5 (8%)
23	CLA	c	502	-	65,73,73	2.02	13 (20%)	76,113,113	2.70	25 (32%)
32	LHG	E	101[B]	-	41,41,48	1.06	2 (4%)	44,47,54	1.09	3 (6%)
27	GOL	B	627	-	5,5,5	1.00	0	5,5,5	1.06	1 (20%)
23	CLA	b	603	-	65,73,73	2.04	14 (21%)	76,113,113	2.92	29 (38%)
23	CLA	b	607	41	65,73,73	1.97	17 (26%)	76,113,113	2.75	27 (35%)
23	CLA	c	504	41	65,73,73	2.09	17 (26%)	76,113,113	2.79	29 (38%)
23	CLA	C	504	-	65,73,73	1.94	16 (24%)	76,113,113	2.89	26 (34%)
34	HTG	b	622	-	19,19,19	1.16	2 (10%)	23,24,24	1.96	7 (30%)
28	OEX	A	413[A]	3,41,1	0,15,15	-	-	-	-	-
32	LHG	b	629[A]	-	48,48,48	0.85	3 (6%)	51,54,54	1.03	4 (7%)
31	LMT	B	631	-	25,25,36	0.88	2 (8%)	30,30,47	1.15	3 (10%)
32	LHG	d	408[A]	-	48,48,48	0.92	2 (4%)	51,54,54	0.99	3 (5%)
32	LHG	d	414[B]	-	48,48,48	0.91	2 (4%)	51,54,54	1.07	5 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	CLA	A	406[B]	41	65,73,73	2.02	16 (24%)	76,113,113	2.79	28 (36%)
35	DGD	H	102	-	63,63,67	0.85	3 (4%)	77,77,81	1.04	6 (7%)
27	GOL	O	303	-	5,5,5	0.98	0	5,5,5	1.11	1 (20%)
35	DGD	c	518	-	63,63,67	0.86	3 (4%)	77,77,81	1.04	4 (5%)
27	GOL	D	412	-	5,5,5	1.42	2 (40%)	5,5,5	0.81	0
23	CLA	B	612	-	65,73,73	2.07	19 (29%)	76,113,113	2.84	29 (38%)
25	BCR	H	101	-	41,41,41	1.05	1 (2%)	56,56,56	1.48	9 (16%)
27	GOL	B	629	-	5,5,5	0.99	0	5,5,5	1.00	0
27	GOL	c	525[A]	-	5,5,5	0.94	0	5,5,5	0.95	0
33	LMG	c	519	-	51,51,55	0.93	2 (3%)	59,59,63	1.10	4 (6%)
28	OEX	A	413[B]	3,41,1	0,15,15	-	-	-	-	-
23	CLA	c	503	-	65,73,73	1.99	16 (24%)	76,113,113	2.81	26 (34%)
26	SQD	f	102	-	42,43,54	1.18	3 (7%)	51,54,65	1.55	11 (21%)
27	GOL	b	628	-	5,5,5	0.54	0	5,5,5	1.35	1 (20%)
32	LHG	b	629[B]	-	48,48,48	0.88	2 (4%)	51,54,54	1.02	3 (5%)
31	LMT	A	420	-	36,36,36	1.04	2 (5%)	47,47,47	1.15	4 (8%)
23	CLA	C	511	-	65,73,73	2.05	16 (24%)	76,113,113	2.88	30 (39%)
29	PL9	d	406[A]	-	55,55,55	0.65	1 (1%)	68,69,69	1.63	17 (25%)
27	GOL	l	801[A]	-	5,5,5	0.96	0	5,5,5	0.97	0
25	BCR	B	619	-	41,41,41	1.11	2 (4%)	56,56,56	1.31	8 (14%)
23	CLA	C	512	3	65,73,73	2.06	16 (24%)	76,113,113	2.68	25 (32%)
25	BCR	b	618	-	41,41,41	1.01	1 (2%)	56,56,56	1.16	6 (10%)
25	BCR	b	617	-	41,41,41	1.04	1 (2%)	56,56,56	1.37	6 (10%)
23	CLA	c	510	-	65,73,73	2.05	16 (24%)	76,113,113	2.78	30 (39%)
34	HTG	V	202	-	11,11,19	0.29	0	15,15,24	1.17	1 (6%)
31	LMT	M	101	-	36,36,36	1.12	3 (8%)	47,47,47	1.17	4 (8%)
35	DGD	C	518[A]	-	63,63,67	0.89	3 (4%)	77,77,81	1.02	5 (6%)
23	CLA	c	511	3	65,73,73	2.10	16 (24%)	76,113,113	2.77	30 (39%)

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
25	BCR	d	405	-	-	5/29/63/63	0/2/2/2
23	CLA	C	505	41	1/1/15/20	6/37/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	LHG	D	406[A]	-	-	16/53/53/53	-
27	GOL	c	525[B]	-	-	0/4/4/4	-
31	LMT	b	621	-	-	8/17/37/61	0/1/1/2
25	BCR	A	409	-	-	0/29/63/63	0/2/2/2
23	CLA	B	606	-	1/1/15/20	9/37/115/115	-
23	CLA	B	616	-	1/1/15/20	8/37/115/115	-
29	PL9	d	406[B]	-	-	6/53/73/73	0/1/1/1
27	GOL	l	801[B]	-	-	3/4/4/4	-
33	LMG	Z	101	-	-	10/31/51/70	0/1/1/1
34	HTG	d	411	-	-	1/7/27/30	0/1/1/1
23	CLA	B	603	-	1/1/15/20	8/37/115/115	-
27	GOL	d	413	-	-	3/4/4/4	-
32	LHG	A	419[A]	-	-	10/53/53/53	-
26	SQD	a	410	-	-	14/49/69/69	0/1/1/1
35	DGD	C	518[B]	-	-	13/51/91/95	0/2/2/2
23	CLA	a	404[A]	-	1/1/15/20	3/37/115/115	-
34	HTG	c	521	-	-	2/10/30/30	0/1/1/1
32	LHG	d	407[A]	-	-	13/53/53/53	-
27	GOL	a	417	-	-	2/4/4/4	-
32	LHG	D	406[B]	-	-	16/53/53/53	-
33	LMG	c	520	-	-	10/46/66/70	0/1/1/1
23	CLA	b	611	-	1/1/15/20	2/37/115/115	-
33	LMG	B	621	-	-	19/46/66/70	0/1/1/1
23	CLA	B	615	-	1/1/15/20	8/37/115/115	-
23	CLA	d	402[A]	41	1/1/15/20	8/37/115/115	-
31	LMT	B	630	-	-	12/21/61/61	0/2/2/2
23	CLA	A	404[B]	-	1/1/15/20	4/37/115/115	-
23	CLA	A	408	-	1/1/15/20	9/37/115/115	-
33	LMG	z	101	-	-	9/34/54/70	0/1/1/1
33	LMG	a	415	-	-	12/46/66/70	0/1/1/1
23	CLA	b	610	41	1/1/15/20	5/37/115/115	-
23	CLA	a	404[B]	-	1/1/15/20	2/37/115/115	-
23	CLA	c	501	-	1/1/15/20	4/37/115/115	-
38	HEM	E	102	5,6	-	2/12/54/54	-
23	CLA	C	507	-	1/1/15/20	12/37/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	DGD	c	517[A]	-	-	17/51/91/95	0/2/2/2
31	LMT	m	103	-	-	4/21/61/61	0/2/2/2
23	CLA	C	508	41	1/1/15/20	4/37/115/115	-
40	HEC	v	201	16	-	2/10/54/54	-
31	LMT	t	101	-	-	8/17/38/61	0/1/1/2
23	CLA	B	609	-	1/1/15/20	2/37/115/115	-
23	CLA	d	402[B]	41	1/1/15/20	6/37/115/115	-
26	SQD	a	409[A]	-	-	10/49/69/69	0/1/1/1
34	HTG	b	625	-	-	3/10/30/30	0/1/1/1
23	CLA	C	503	-	-	10/37/115/115	-
25	BCR	C	516	-	-	2/29/63/63	0/2/2/2
33	LMG	C	520	-	-	9/46/66/70	0/1/1/1
32	LHG	d	408[B]	-	-	13/53/53/53	-
25	BCR	c	514	-	-	2/29/63/63	0/2/2/2
23	CLA	D	402[A]	-	1/1/15/20	0/37/115/115	-
23	CLA	C	513	-	1/1/15/20	9/37/115/115	-
32	LHG	a	419[A]	-	-	16/46/46/53	-
23	CLA	b	616	-	1/1/15/20	9/37/115/115	-
27	GOL	V	203[A]	-	-	2/4/4/4	-
23	CLA	D	403	-	1/1/15/20	14/37/115/115	-
25	BCR	Y	101	-	-	6/29/63/63	0/2/2/2
23	CLA	c	507	41	1/1/15/20	7/37/115/115	-
26	SQD	A	410[A]	-	-	12/49/69/69	0/1/1/1
23	CLA	c	509	-	1/1/15/20	14/37/115/115	-
23	CLA	c	508	-	1/1/15/20	5/37/115/115	-
27	GOL	c	526	-	-	4/4/4/4	-
35	DGD	c	517[B]	-	-	17/51/91/95	0/2/2/2
25	BCR	C	515	-	-	2/29/63/63	0/2/2/2
26	SQD	A	412	-	-	14/49/69/69	0/1/1/1
26	SQD	a	409[B]	-	-	9/49/69/69	0/1/1/1
27	GOL	b	624	-	-	2/4/4/4	-
25	BCR	a	408	-	-	1/29/63/63	0/2/2/2
31	LMT	B	628	-	-	12/21/61/61	0/2/2/2
23	CLA	C	510	-	1/1/15/20	4/37/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	CLA	c	505	-	1/1/15/20	7/37/115/115	-
26	SQD	B	620	-	-	13/49/69/69	0/1/1/1
33	LMG	D	411	39	-	9/46/66/70	0/1/1/1
23	CLA	c	506	-	1/1/15/20	8/37/115/115	-
32	LHG	a	419[B]	-	-	16/46/46/53	-
25	BCR	B	618	-	-	0/29/63/63	0/2/2/2
25	BCR	b	619	-	-	3/29/63/63	0/2/2/2
23	CLA	c	512	-	1/1/15/20	13/37/115/115	-
27	GOL	V	203[B]	-	-	2/4/4/4	-
35	DGD	c	516[A]	-	-	20/51/91/95	0/2/2/2
23	CLA	B	605	-	1/1/15/20	6/37/115/115	-
25	BCR	K	102	-	-	1/29/63/63	0/2/2/2
23	CLA	b	615	-	1/1/15/20	7/37/115/115	-
34	HTG	B	625	-	-	3/10/30/30	0/1/1/1
25	BCR	c	515	-	-	0/29/63/63	0/2/2/2
23	CLA	B	602	-	1/1/15/20	7/37/115/115	-
24	PHO	a	406[A]	-	-	6/37/103/103	0/5/6/6
31	LMT	T	101	-	-	10/21/61/61	0/2/2/2
29	PL9	A	414[A]	-	-	15/53/73/73	0/1/1/1
35	DGD	h	102	-	-	16/51/91/95	0/2/2/2
23	CLA	b	601	41	1/1/15/20	19/37/115/115	-
23	CLA	b	609	-	1/1/15/20	3/37/115/115	-
23	CLA	d	404	-	1/1/15/20	8/37/115/115	-
23	CLA	B	601	41	1/1/15/20	13/37/115/115	-
29	PL9	a	412[A]	-	-	14/53/73/73	0/1/1/1
31	LMT	A	417	-	-	7/21/61/61	0/2/2/2
31	LMT	b	627	-	-	11/17/37/61	0/1/1/2
32	LHG	A	419[B]	-	-	13/53/53/53	-
23	CLA	b	613	-	1/1/15/20	4/37/115/115	-
23	CLA	C	506	-	1/1/15/20	7/37/115/115	-
24	PHO	A	416[A]	-	-	1/37/103/103	0/5/6/6
25	BCR	k	101	-	-	0/29/63/63	0/2/2/2
27	GOL	o	302	-	-	2/4/4/4	-
24	PHO	A	407[A]	-	-	4/37/103/103	0/5/6/6
32	LHG	d	407[B]	-	-	11/53/53/53	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	BCR	B	617	-	-	2/29/63/63	0/2/2/2
25	BCR	D	404	-	-	4/29/63/63	0/2/2/2
34	HTG	C	522	-	-	0/10/30/30	0/1/1/1
23	CLA	b	604	-	1/1/15/20	10/37/115/115	-
23	CLA	B	608	-	-	4/37/115/115	-
26	SQD	b	620	-	-	19/49/69/69	0/1/1/1
29	PL9	A	414[B]	-	-	18/53/73/73	0/1/1/1
27	GOL	o	303	-	-	3/4/4/4	-
27	GOL	O	302	-	-	2/4/4/4	-
23	CLA	d	403[A]	-	1/1/15/20	2/37/115/115	-
27	GOL	v	202[A]	-	-	1/4/4/4	-
29	PL9	a	412[B]	-	-	15/53/73/73	0/1/1/1
24	PHO	A	416[B]	-	-	3/37/103/103	0/5/6/6
25	BCR	y	101	-	-	6/29/63/63	0/2/2/2
23	CLA	b	602	-	1/1/15/20	4/37/115/115	-
24	PHO	A	407[B]	-	-	2/37/103/103	0/5/6/6
34	HTG	b	623	-	-	5/10/30/30	0/1/1/1
23	CLA	C	502	-	1/1/15/20	5/37/115/115	-
23	CLA	C	514	-	1/1/15/20	7/37/115/115	-
35	DGD	C	517[A]	-	-	11/51/91/95	0/2/2/2
23	CLA	b	608	-	-	5/37/115/115	-
40	HEC	V	201	16	-	2/10/54/54	-
29	PL9	D	405[A]	-	-	8/53/73/73	0/1/1/1
31	LMT	F	101	-	-	8/21/61/61	0/2/2/2
23	CLA	d	403[B]	-	1/1/15/20	4/37/115/115	-
27	GOL	v	202[B]	-	-	2/4/4/4	-
23	CLA	B	611	-	1/1/15/20	2/37/115/115	-
25	BCR	t	102	-	-	1/29/63/63	0/2/2/2
27	GOL	C	523[A]	-	-	0/4/4/4	-
23	CLA	D	402[B]	-	1/1/15/20	0/37/115/115	-
31	LMT	e	101	-	-	15/21/61/61	0/2/2/2
34	HTG	B	622	-	-	4/10/30/30	0/1/1/1
23	CLA	A	405[A]	41	-	4/37/115/115	-
32	LHG	D	407[A]	-	-	14/53/53/53	-
26	SQD	F	102	-	-	14/38/58/69	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	SQD	A	410[B]	-	-	10/49/69/69	0/1/1/1
25	BCR	T	102	-	-	1/29/63/63	0/2/2/2
35	DGD	C	517[B]	-	-	14/51/91/95	0/2/2/2
24	PHO	a	414[A]	-	-	2/37/103/103	0/5/6/6
29	PL9	D	405[B]	-	-	8/53/73/73	0/1/1/1
23	CLA	c	513	-	1/1/15/20	10/37/115/115	-
27	GOL	A	411	-	-	2/4/4/4	-
31	LMT	a	416	-	-	10/21/61/61	0/2/2/2
32	LHG	L	101[A]	-	-	19/53/53/53	-
34	HTG	D	410	-	-	3/7/27/30	0/1/1/1
23	CLA	C	509	-	1/1/15/20	3/37/115/115	-
38	HEM	f	101	5,6	-	6/12/54/54	-
27	GOL	C	523[B]	-	-	0/4/4/4	-
35	DGD	c	516[B]	-	-	21/51/91/95	0/2/2/2
23	CLA	a	405[A]	41	-	5/37/115/115	-
23	CLA	A	405[B]	41	1/1/15/20	5/37/115/115	-
32	LHG	D	407[B]	-	-	13/53/53/53	-
33	LMG	m	101	-	-	10/46/66/70	0/1/1/1
27	GOL	A	418	-	-	1/4/4/4	-
35	DGD	C	519	-	-	16/51/91/95	0/2/2/2
23	CLA	B	607	41	1/1/15/20	3/37/115/115	-
23	CLA	B	610	41	1/1/15/20	7/37/115/115	-
23	CLA	a	407	-	1/1/15/20	10/37/115/115	-
23	CLA	b	605	-	1/1/15/20	5/37/115/115	-
24	PHO	a	414[B]	-	-	1/37/103/103	0/5/6/6
24	PHO	a	406[B]	-	-	6/37/103/103	0/5/6/6
23	CLA	b	614	-	1/1/15/20	15/37/115/115	-
32	LHG	L	101[B]	-	-	18/53/53/53	-
25	BCR	h	101	-	-	1/29/63/63	0/2/2/2
32	LHG	E	101[A]	-	-	22/46/46/53	-
34	HTG	B	623	-	-	4/10/30/30	0/1/1/1
33	LMG	C	501	-	-	13/46/66/70	0/1/1/1
23	CLA	B	614	-	1/1/15/20	14/37/115/115	-
23	CLA	a	405[B]	41	-	6/37/115/115	-
23	CLA	b	606	-	1/1/15/20	11/37/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	GOL	B	624	-	-	2/4/4/4	-
33	LMG	C	521	-	-	13/46/66/70	0/1/1/1
23	CLA	A	404[A]	-	1/1/15/20	5/37/115/115	-
23	CLA	b	612	-	1/1/15/20	3/37/115/115	-
27	GOL	a	418	-	-	0/4/4/4	-
23	CLA	B	604	-	1/1/15/20	4/37/115/115	-
23	CLA	B	613	-	1/1/15/20	8/37/115/115	-
32	LHG	d	414[A]	-	-	13/53/53/53	-
23	CLA	A	406[A]	41	-	5/37/115/115	-
33	LMG	d	412	39	-	11/46/66/70	0/1/1/1
23	CLA	c	502	-	1/1/15/20	6/37/115/115	-
32	LHG	E	101[B]	-	-	23/46/46/53	-
27	GOL	B	627	-	-	1/4/4/4	-
23	CLA	b	603	-	1/1/15/20	4/37/115/115	-
23	CLA	b	607	41	1/1/15/20	3/37/115/115	-
23	CLA	c	504	41	1/1/15/20	6/37/115/115	-
23	CLA	C	504	-	-	2/37/115/115	-
34	HTG	b	622	-	-	5/10/30/30	0/1/1/1
32	LHG	b	629[A]	-	-	20/53/53/53	-
31	LMT	B	631	-	-	11/17/37/61	0/1/1/2
32	LHG	d	408[A]	-	-	11/53/53/53	-
32	LHG	d	414[B]	-	-	12/53/53/53	-
23	CLA	A	406[B]	41	-	6/37/115/115	-
35	DGD	H	102	-	-	9/51/91/95	0/2/2/2
27	GOL	O	303	-	-	2/4/4/4	-
35	DGD	c	518	-	-	10/51/91/95	0/2/2/2
27	GOL	D	412	-	-	4/4/4/4	-
23	CLA	B	612	-	1/1/15/20	6/37/115/115	-
25	BCR	H	101	-	-	2/29/63/63	0/2/2/2
27	GOL	B	629	-	-	4/4/4/4	-
27	GOL	c	525[A]	-	-	0/4/4/4	-
33	LMG	c	519	-	-	12/46/66/70	0/1/1/1
23	CLA	c	503	-	1/1/15/20	2/37/115/115	-
26	SQD	f	102	-	-	10/38/58/69	0/1/1/1
27	GOL	b	628	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	LHG	b	629[B]	-	-	18/53/53/53	-
31	LMT	A	420	-	-	15/21/61/61	0/2/2/2
23	CLA	C	511	-	1/1/15/20	12/37/115/115	-
29	PL9	d	406[A]	-	-	6/53/73/73	0/1/1/1
27	GOL	l	801[A]	-	-	2/4/4/4	-
25	BCR	B	619	-	-	0/29/63/63	0/2/2/2
23	CLA	C	512	3	1/1/15/20	3/37/115/115	-
25	BCR	b	618	-	-	0/29/63/63	0/2/2/2
25	BCR	b	617	-	-	2/29/63/63	0/2/2/2
23	CLA	c	510	-	1/1/15/20	12/37/115/115	-
34	HTG	V	202	-	-	0/2/19/30	0/1/1/1
31	LMT	M	101	-	-	4/21/61/61	0/2/2/2
35	DGD	C	518[A]	-	-	15/51/91/95	0/2/2/2
23	CLA	c	511	3	1/1/15/20	3/37/115/115	-

The worst 5 of 1550 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	B	611	CLA	C3B-C2B	10.57	1.55	1.40
23	B	611	CLA	CMB-C2B	7.01	1.66	1.51
23	B	612	CLA	C3B-C2B	6.95	1.50	1.40
23	C	509	CLA	C3B-C2B	6.92	1.50	1.40
23	C	512	CLA	C3B-C2B	6.86	1.49	1.40

The worst 5 of 3102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	a	407	CLA	C1D-ND-C4D	-11.35	98.27	106.33
23	B	611	CLA	C1D-ND-C4D	-11.17	98.40	106.33
23	a	407	CLA	C2D-C1D-ND	10.70	117.99	110.10
23	B	612	CLA	C1D-ND-C4D	-10.60	98.81	106.33
23	C	504	CLA	C1D-ND-C4D	-10.32	99.00	106.33

5 of 69 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	A	404[A]	CLA	ND
23	A	404[B]	CLA	ND
23	A	405[B]	CLA	ND

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Mol	Chain	Res	Type	Atom
23	A	408	CLA	ND
23	B	601	CLA	ND

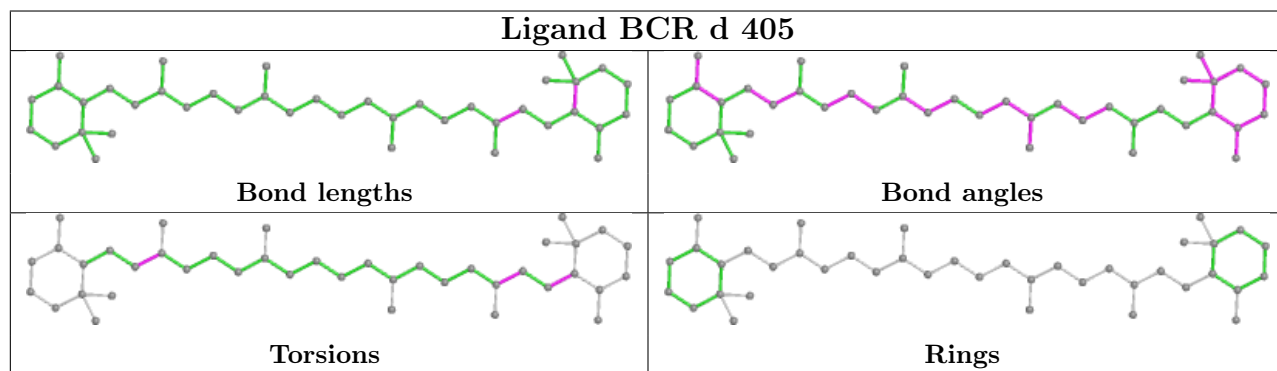
5 of 1632 torsion outliers are listed below:

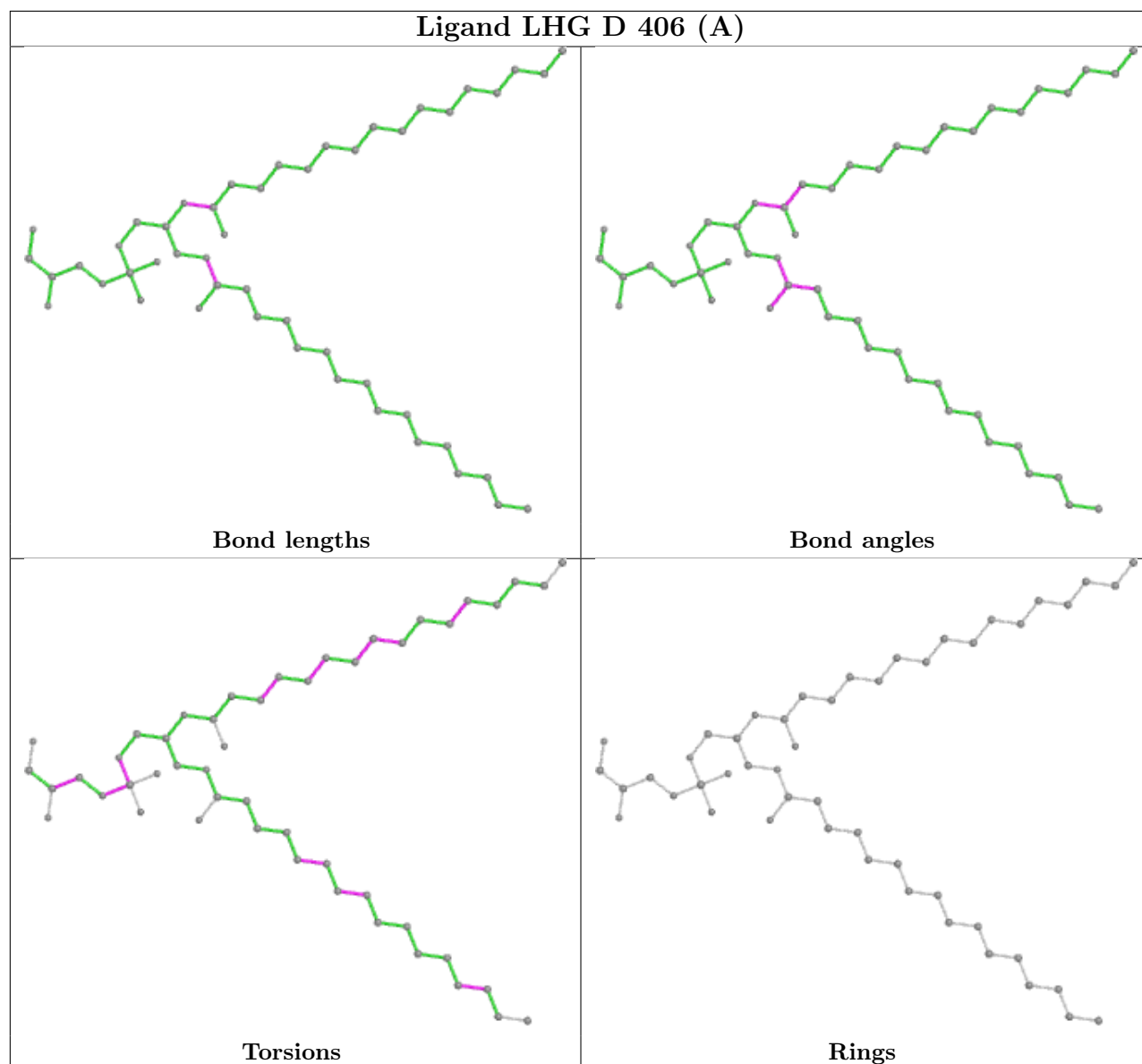
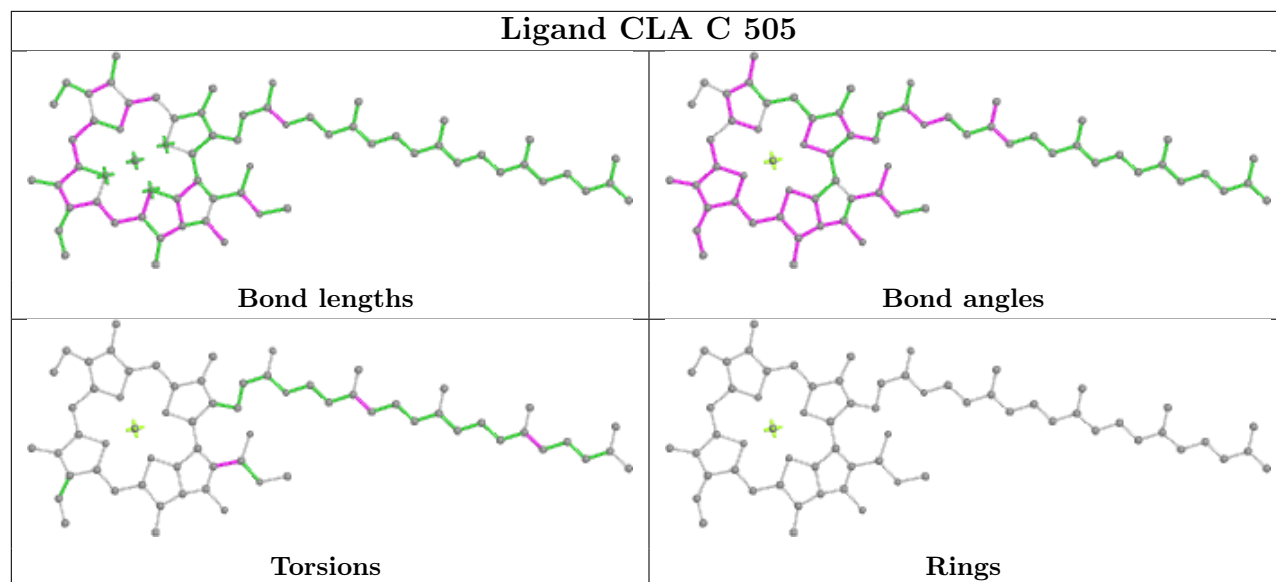
Mol	Chain	Res	Type	Atoms
23	A	408	CLA	C4-C3-C5-C6
23	B	614	CLA	CHA-CBD-CGD-O1D
23	B	614	CLA	CAD-CBD-CGD-O1D
23	B	614	CLA	CAD-CBD-CGD-O2D
23	C	507	CLA	C14-C13-C15-C16

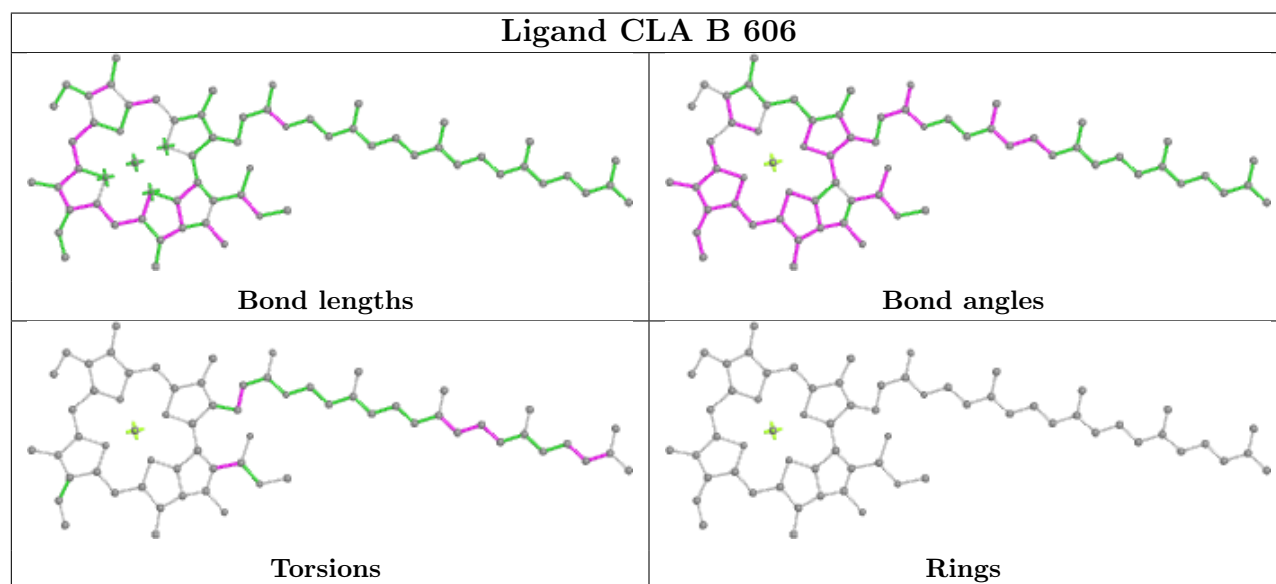
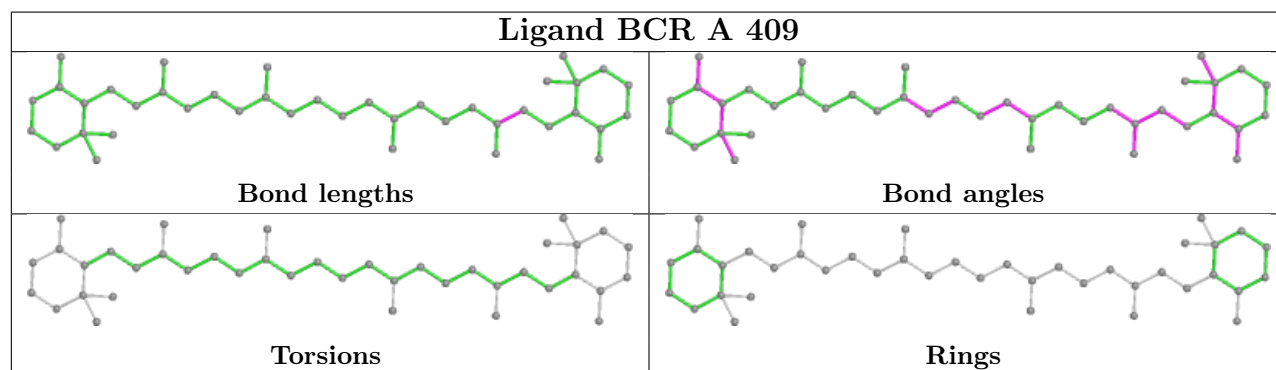
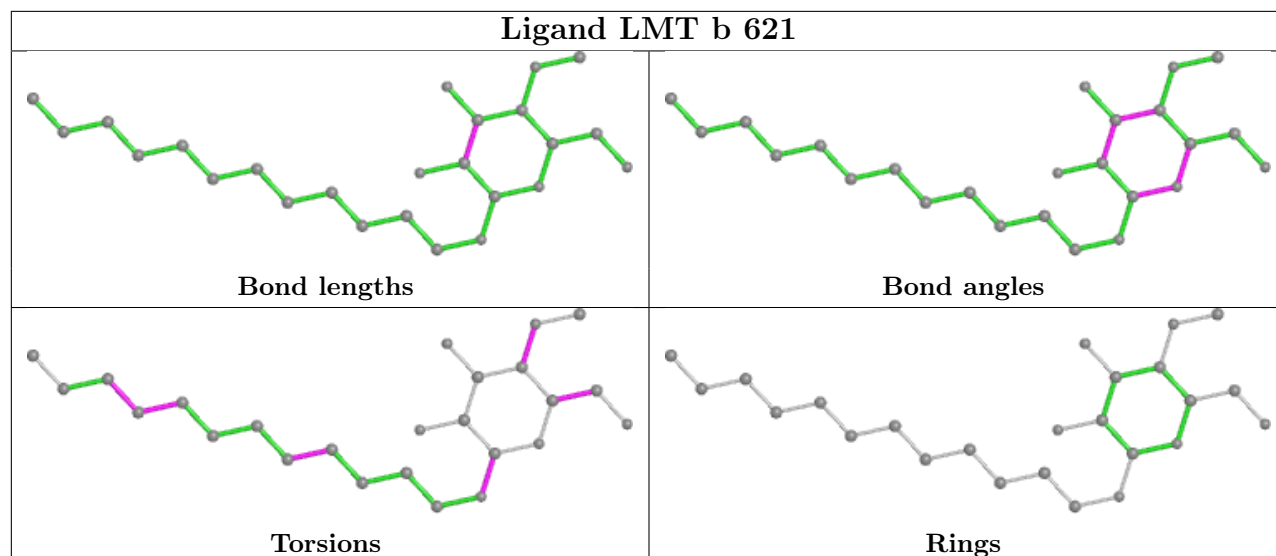
There are no ring outliers.

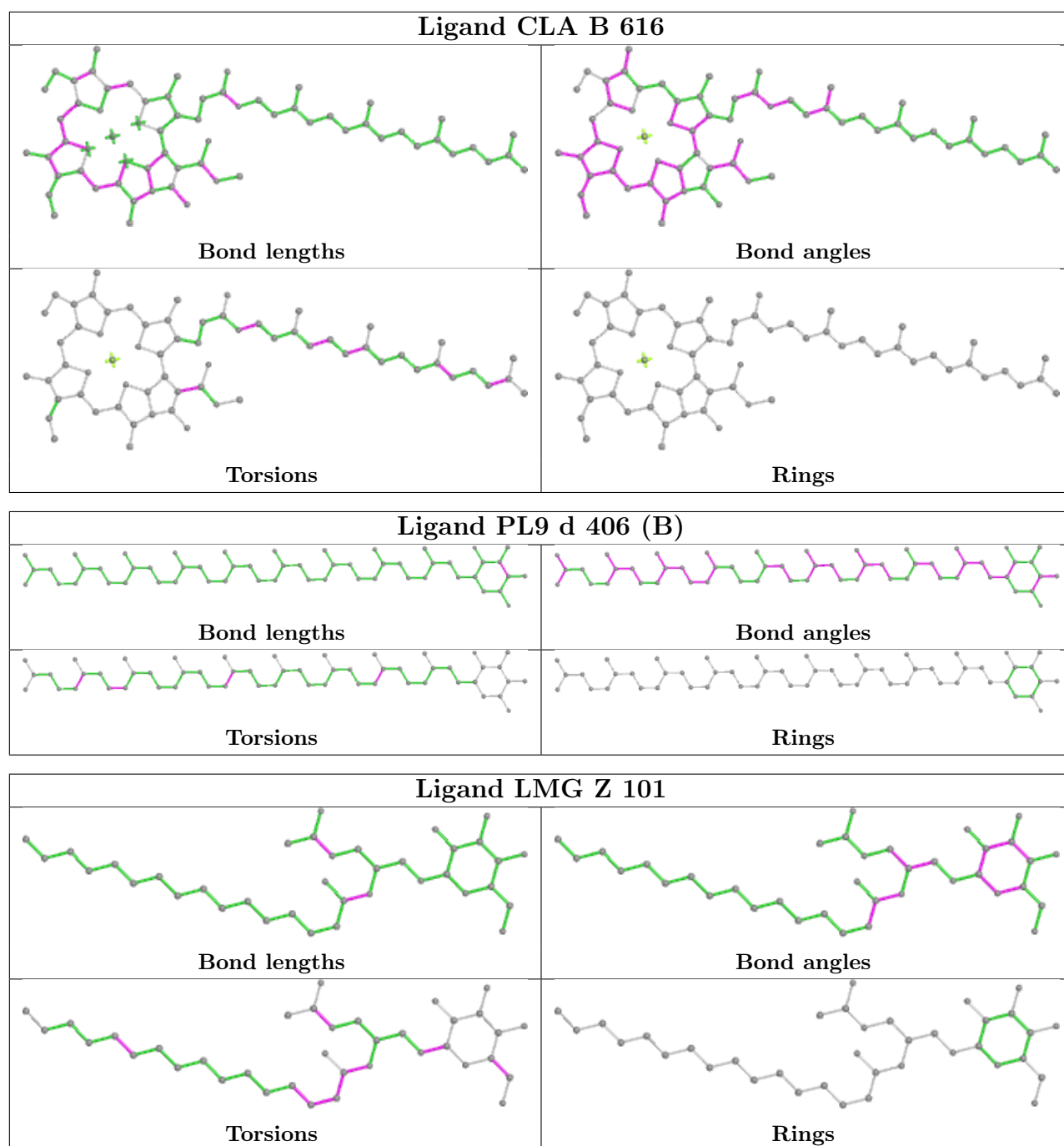
No monomer is involved in short contacts.

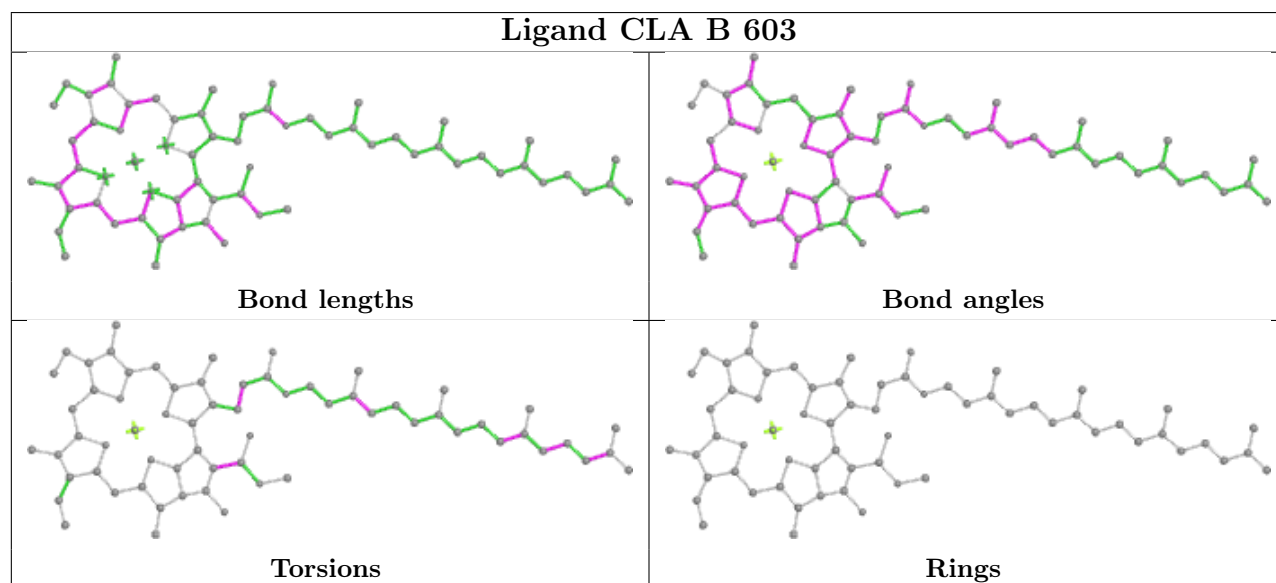
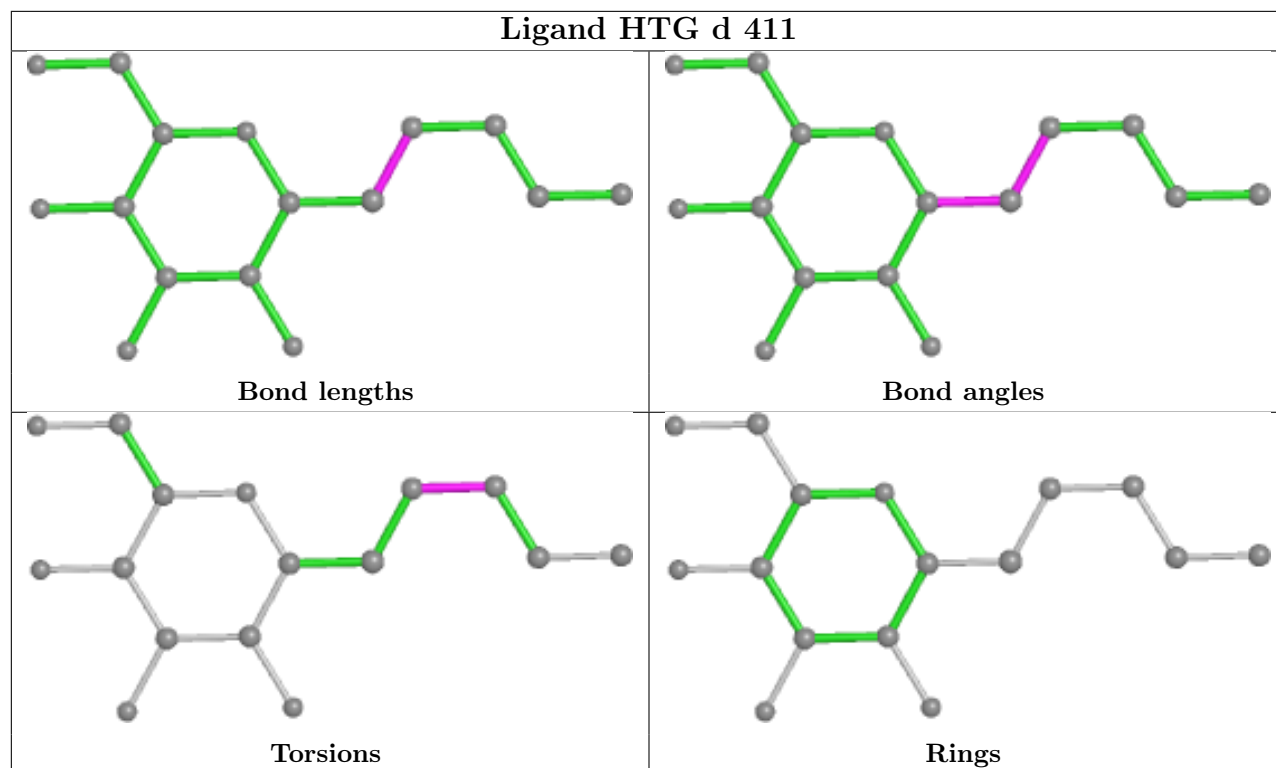
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

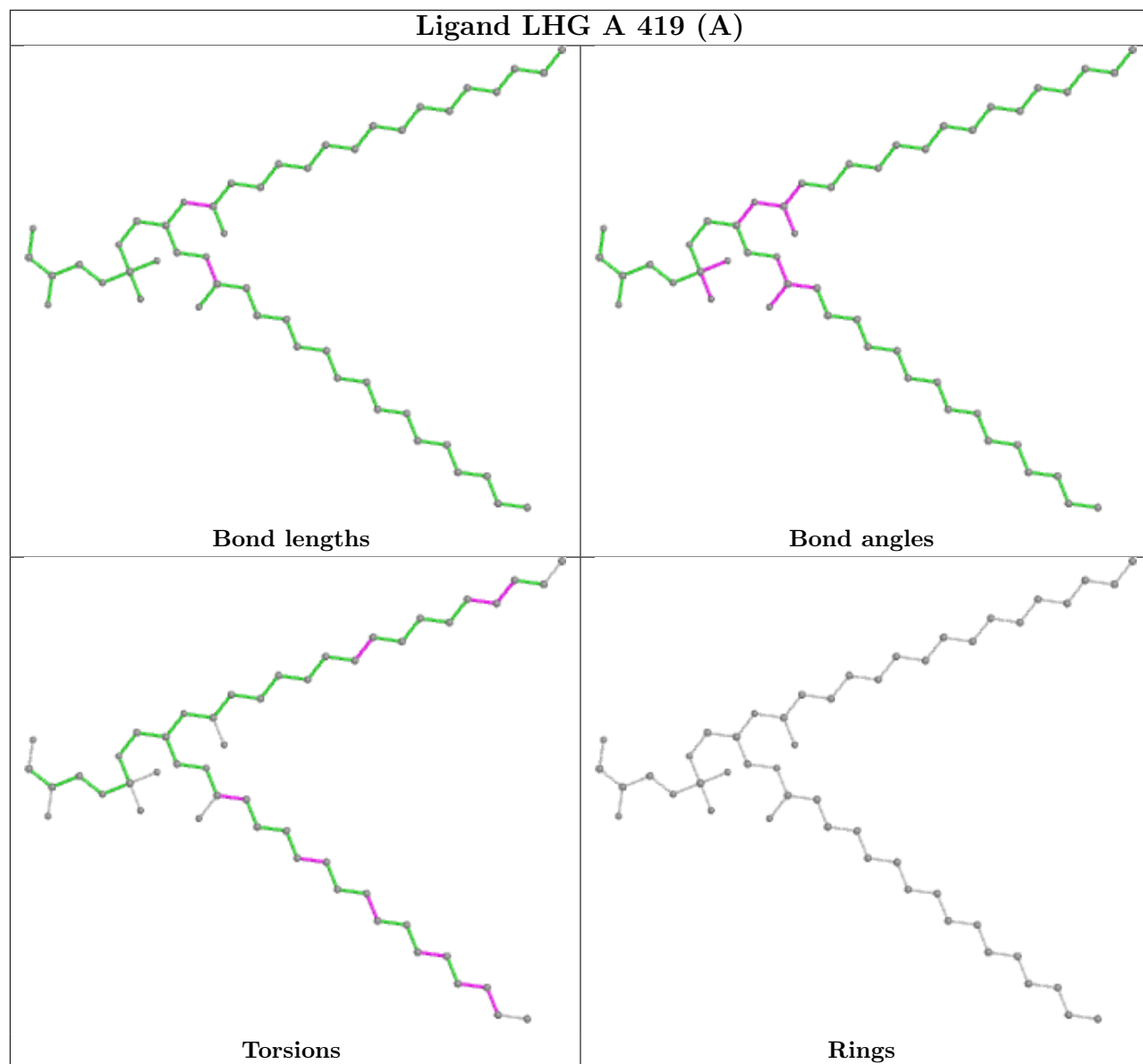


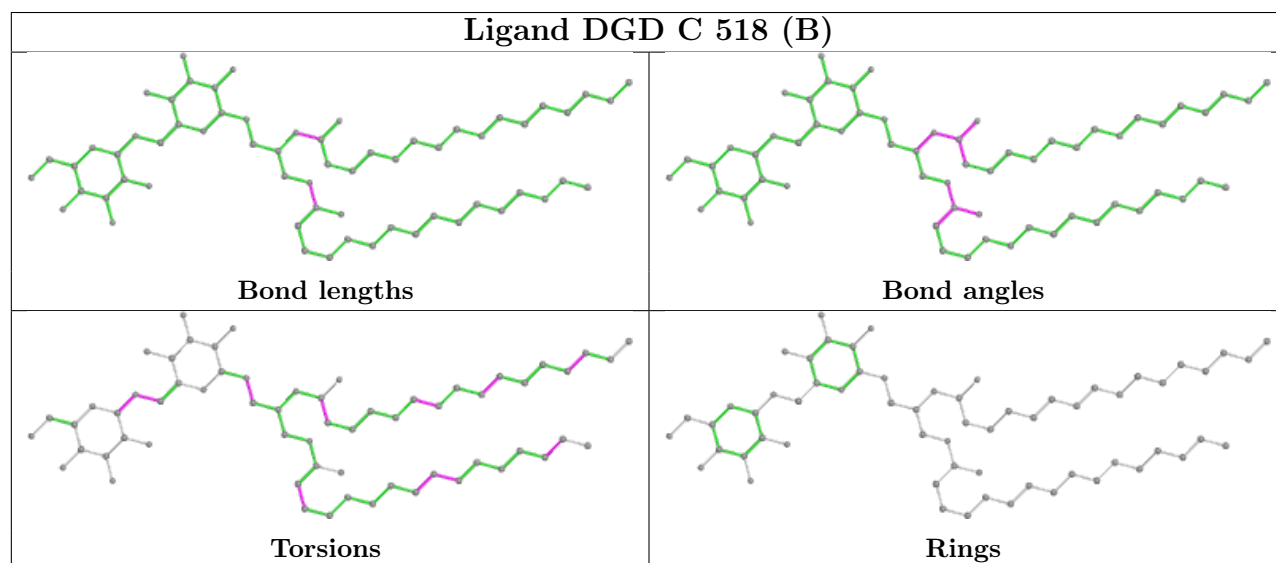
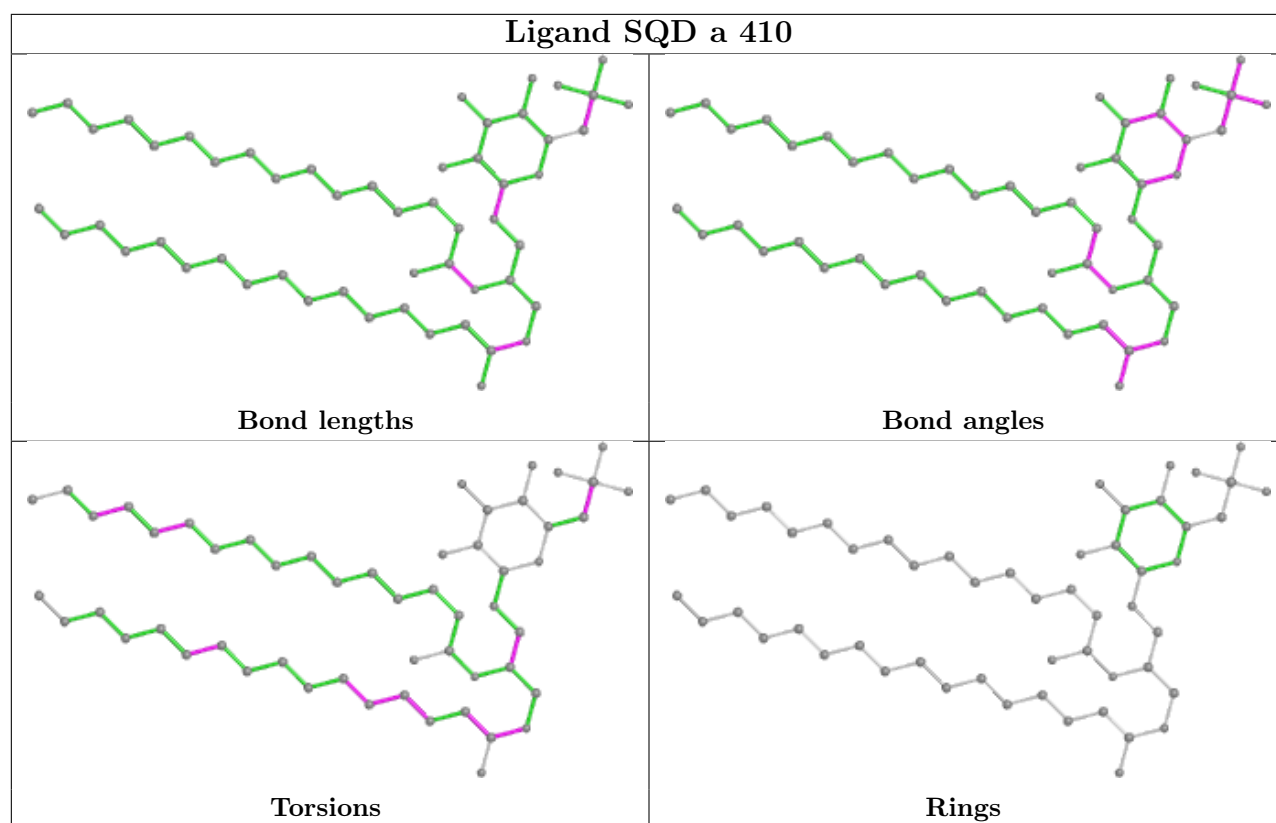


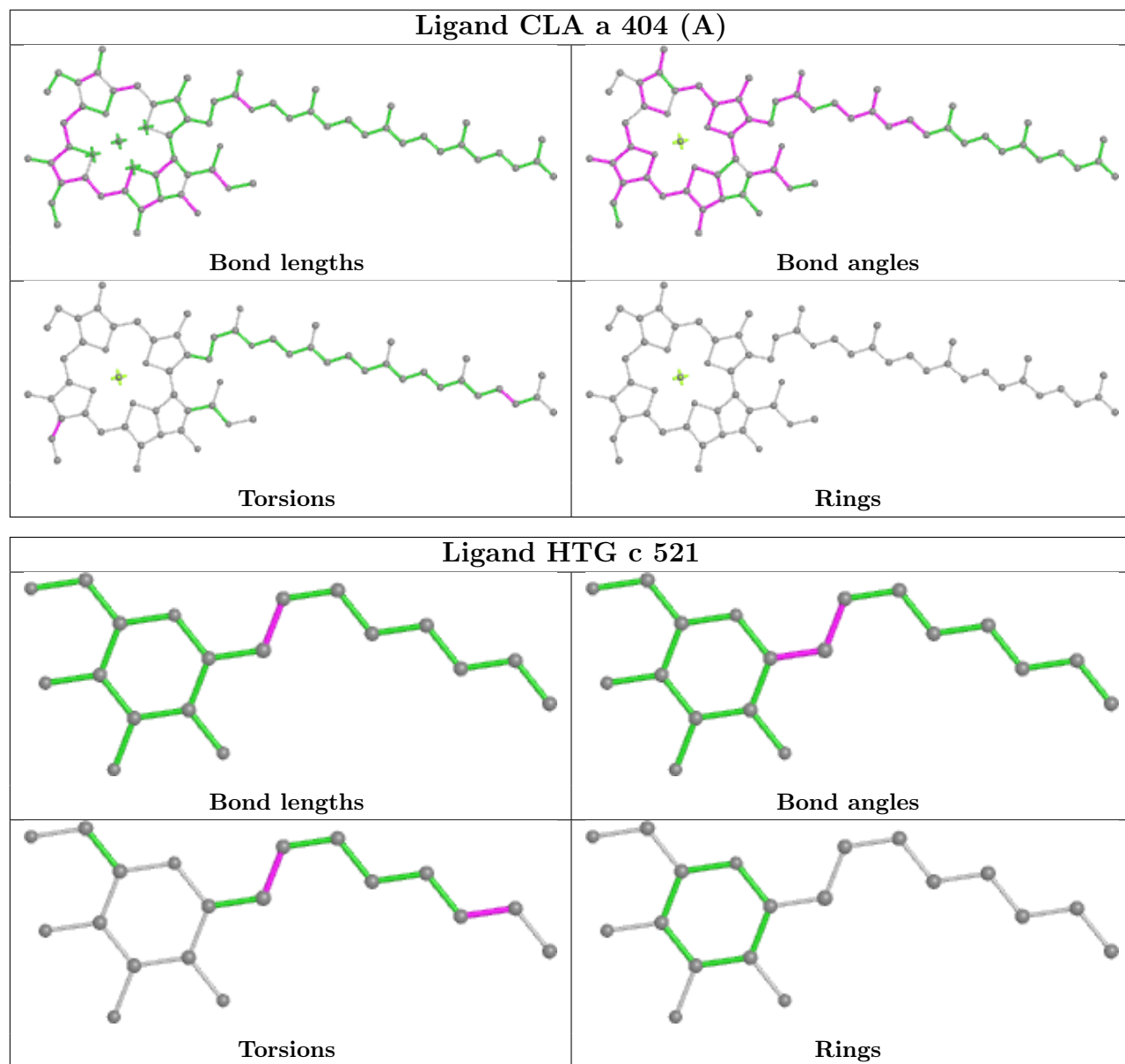


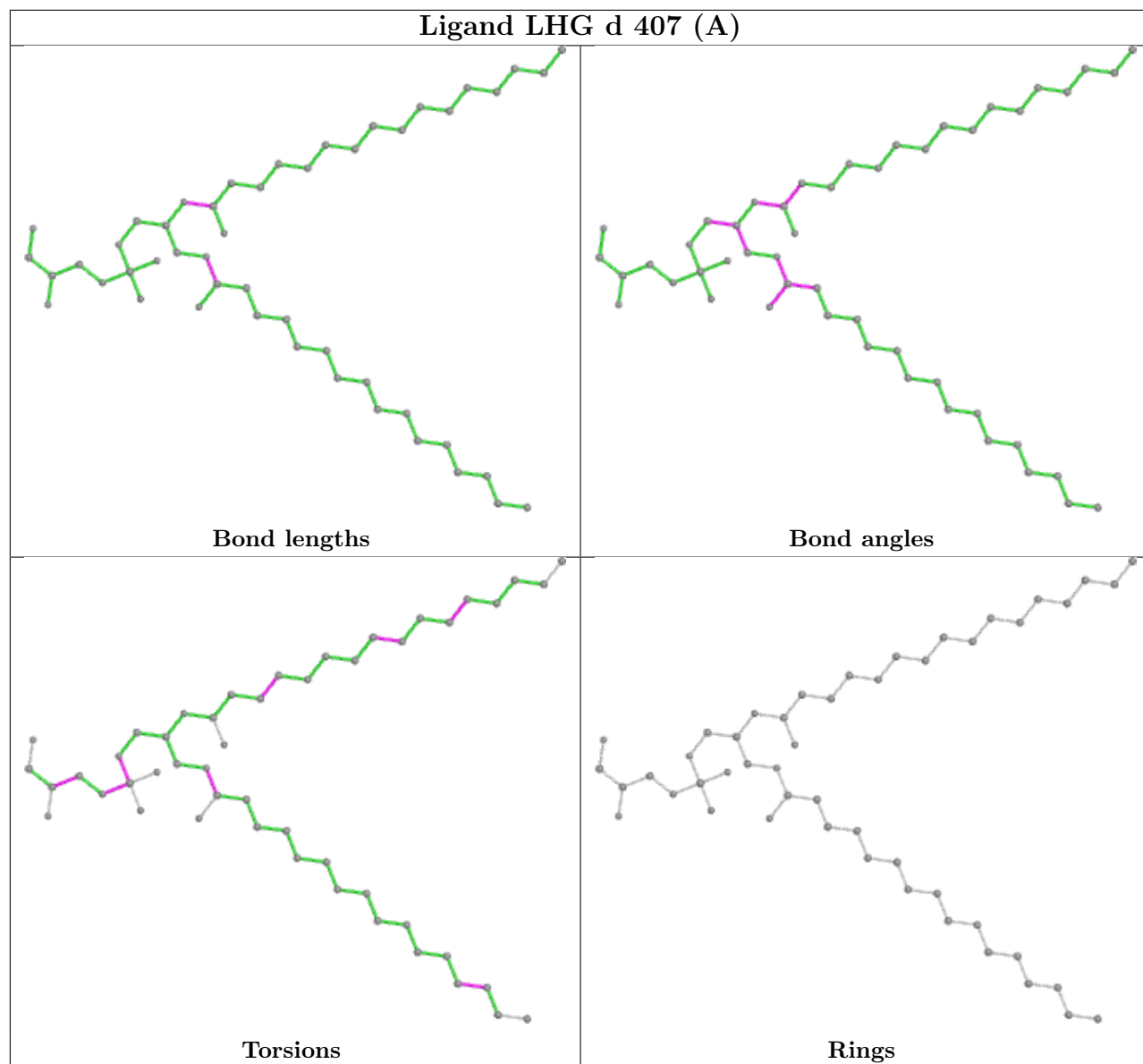


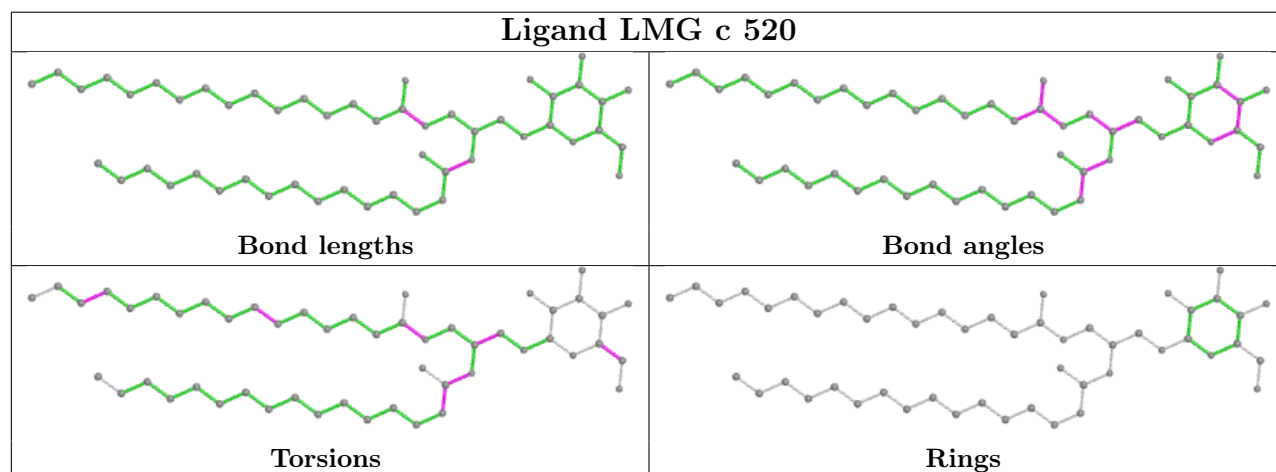
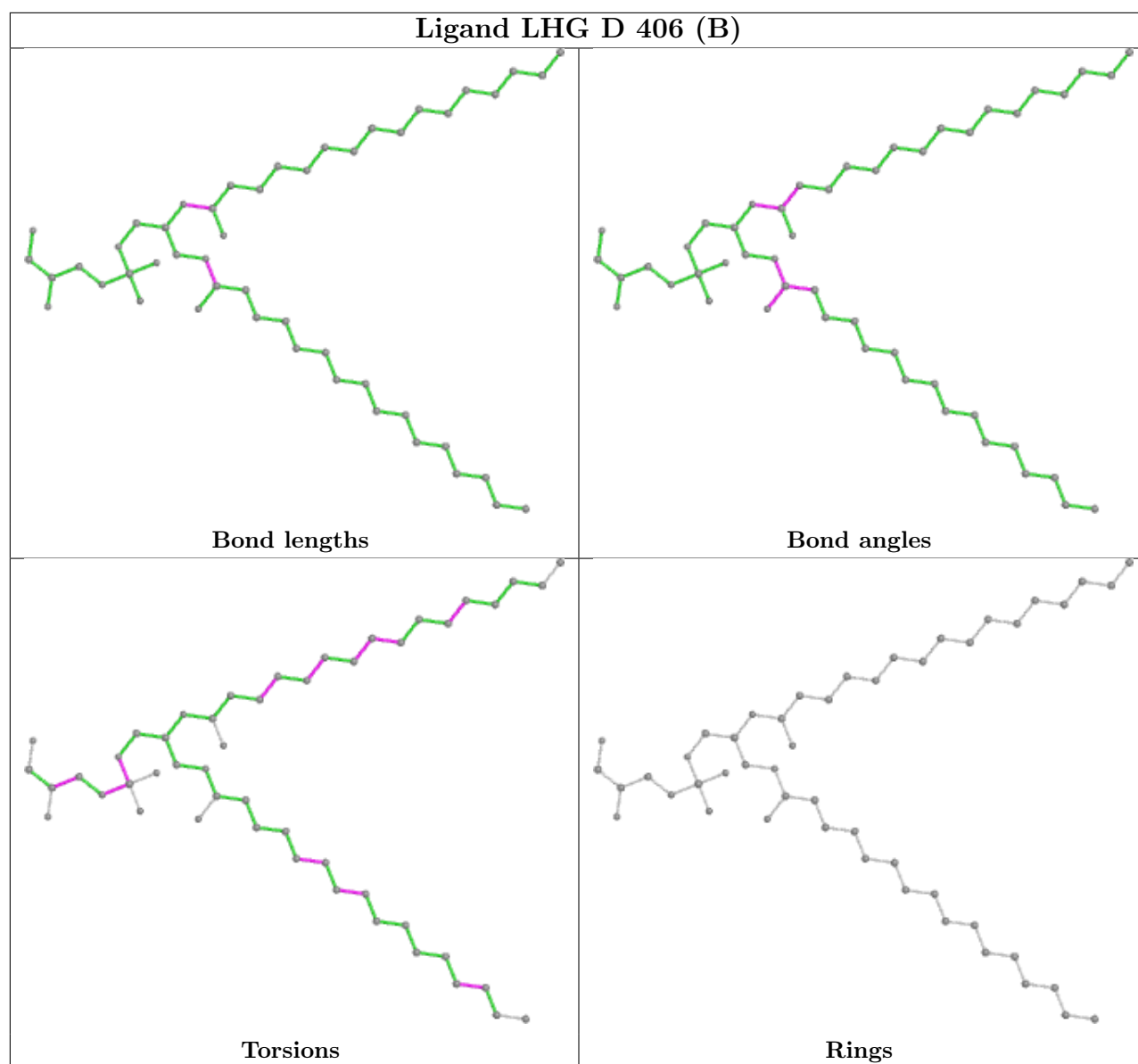


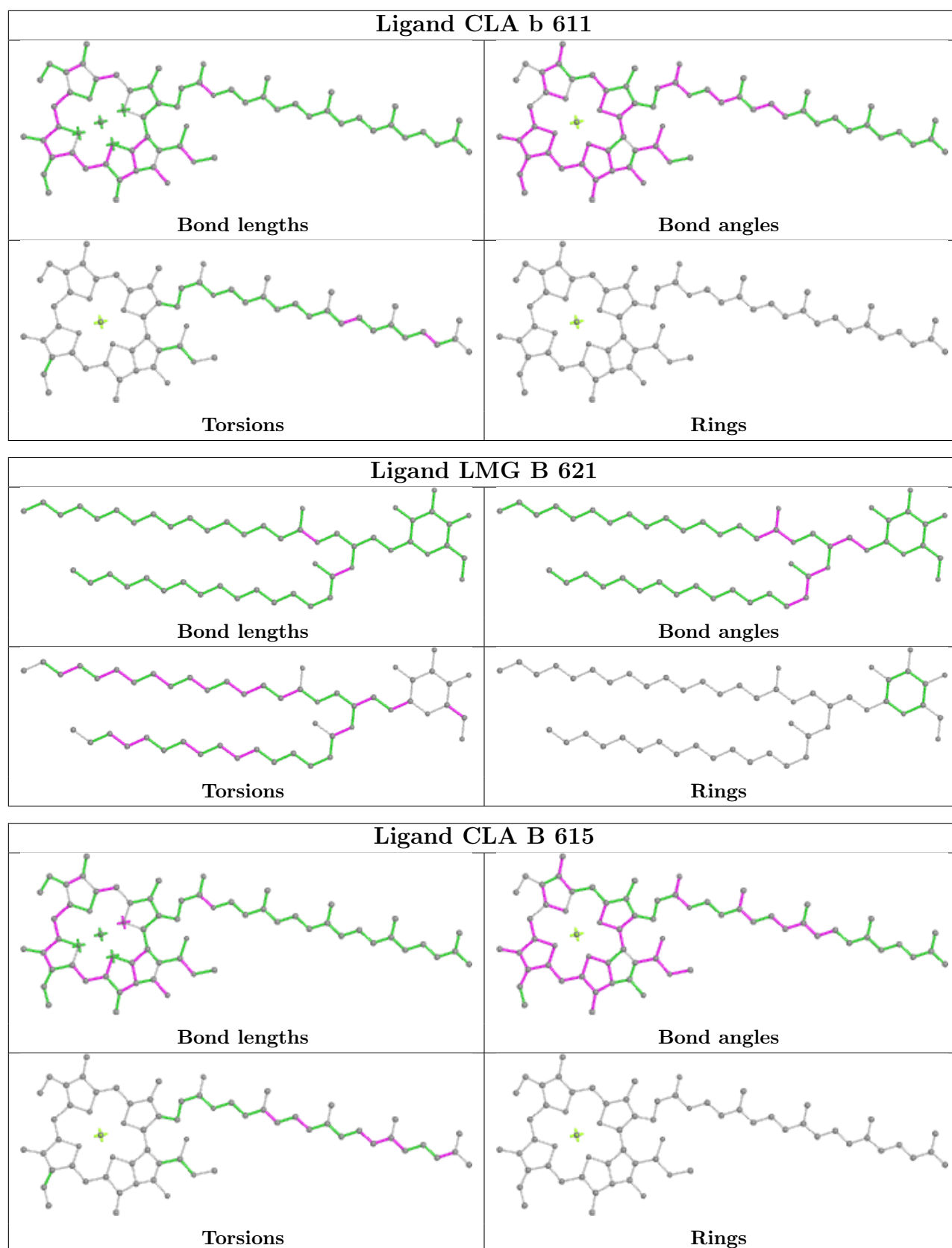


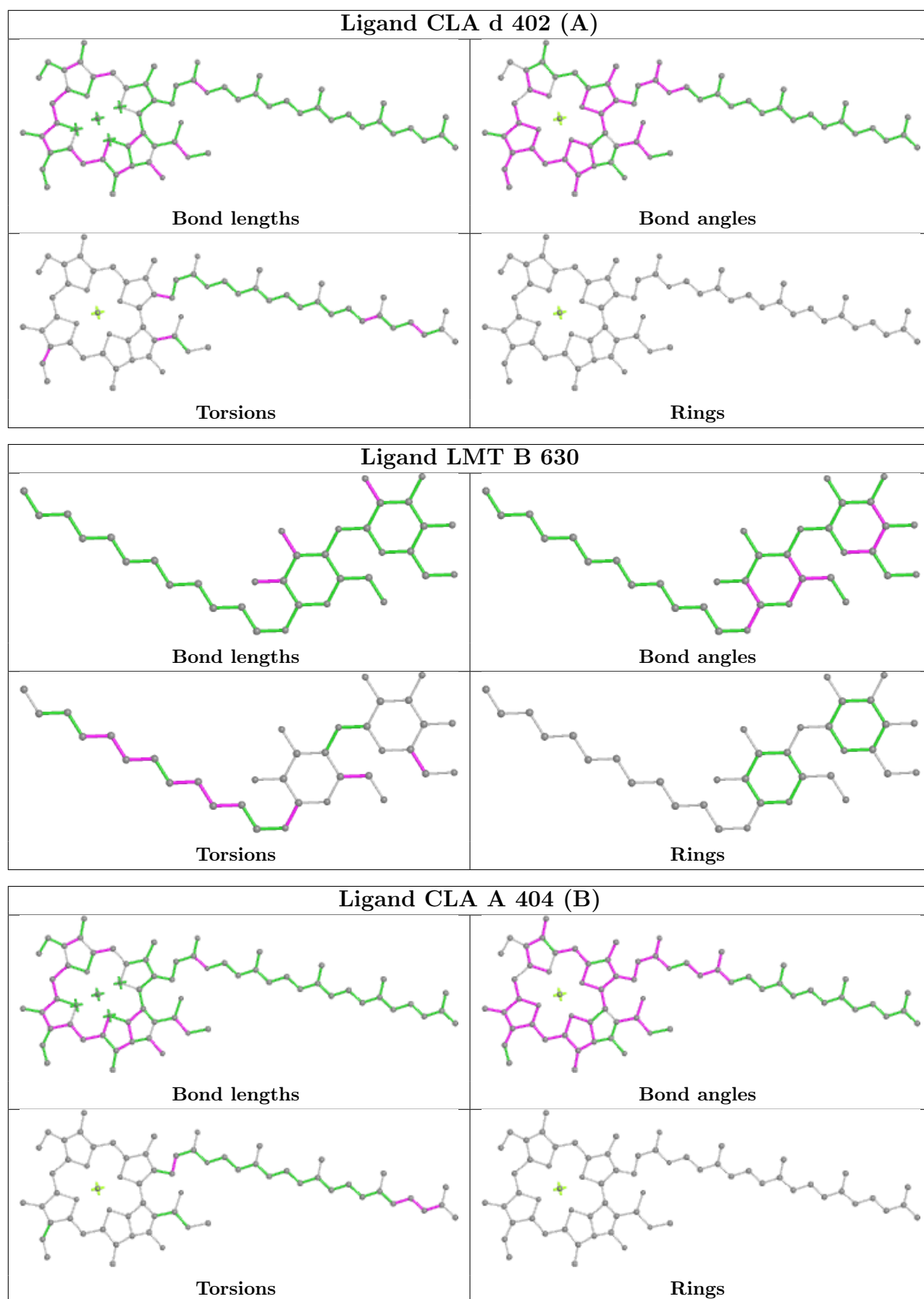


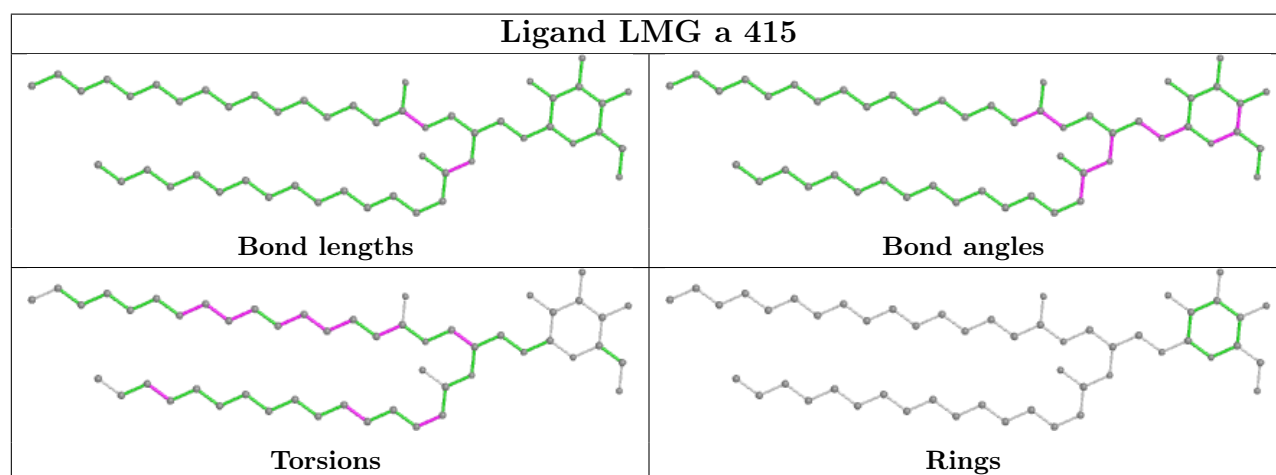
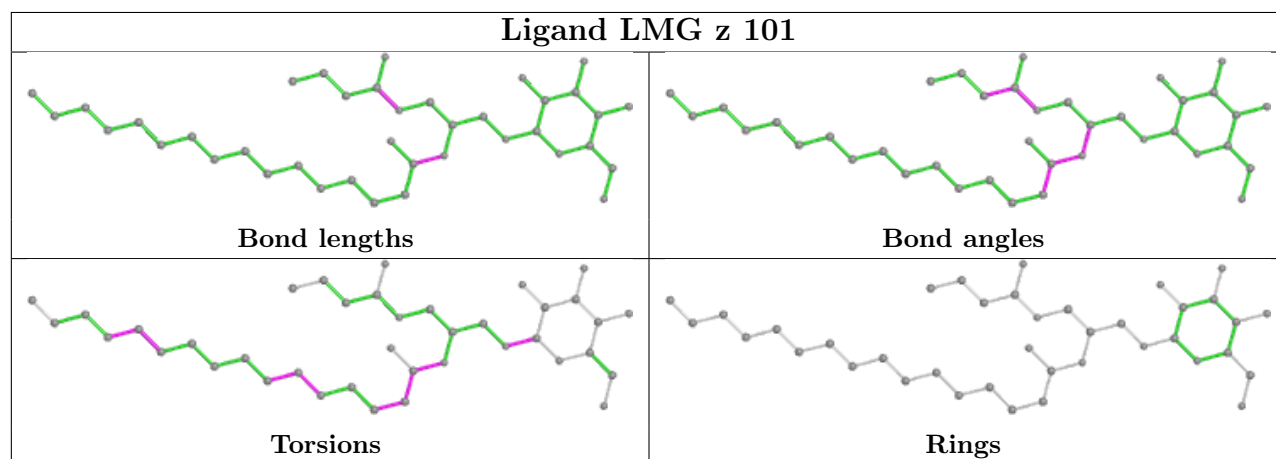
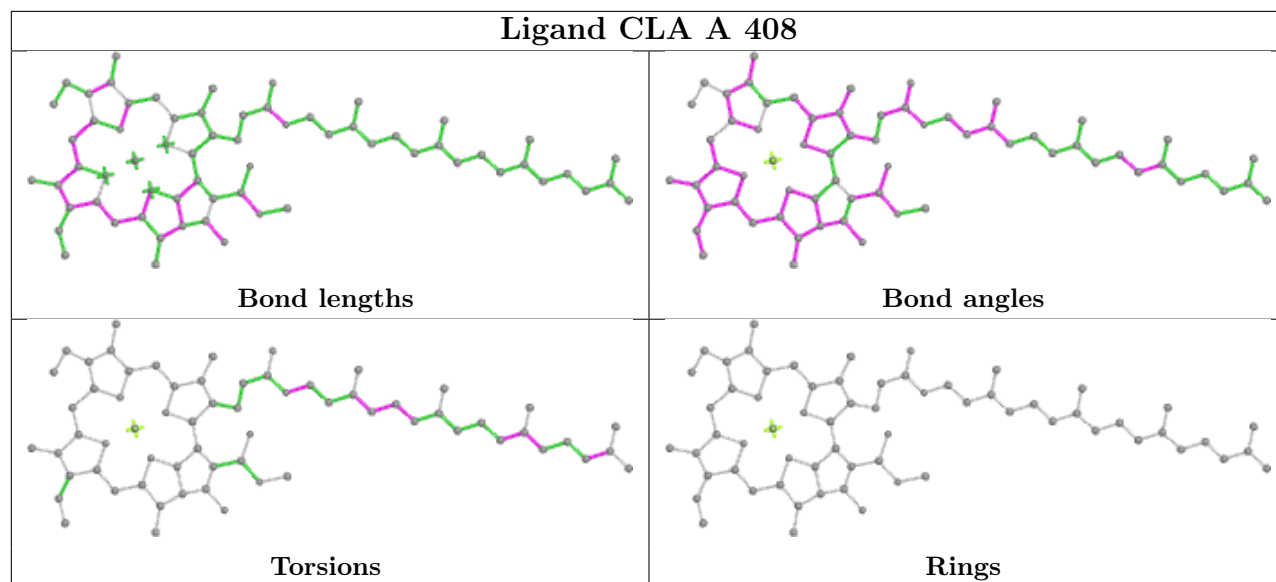


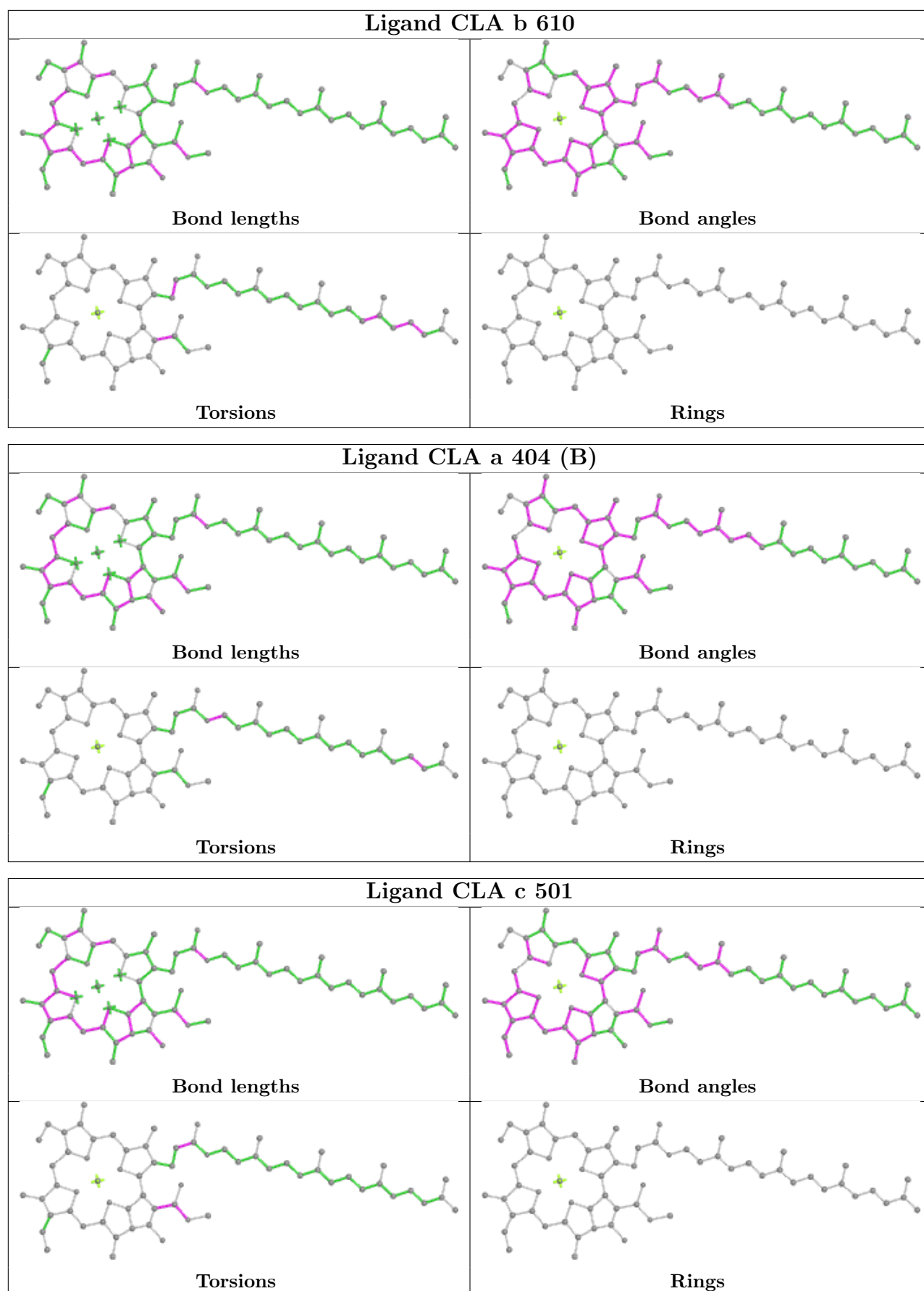


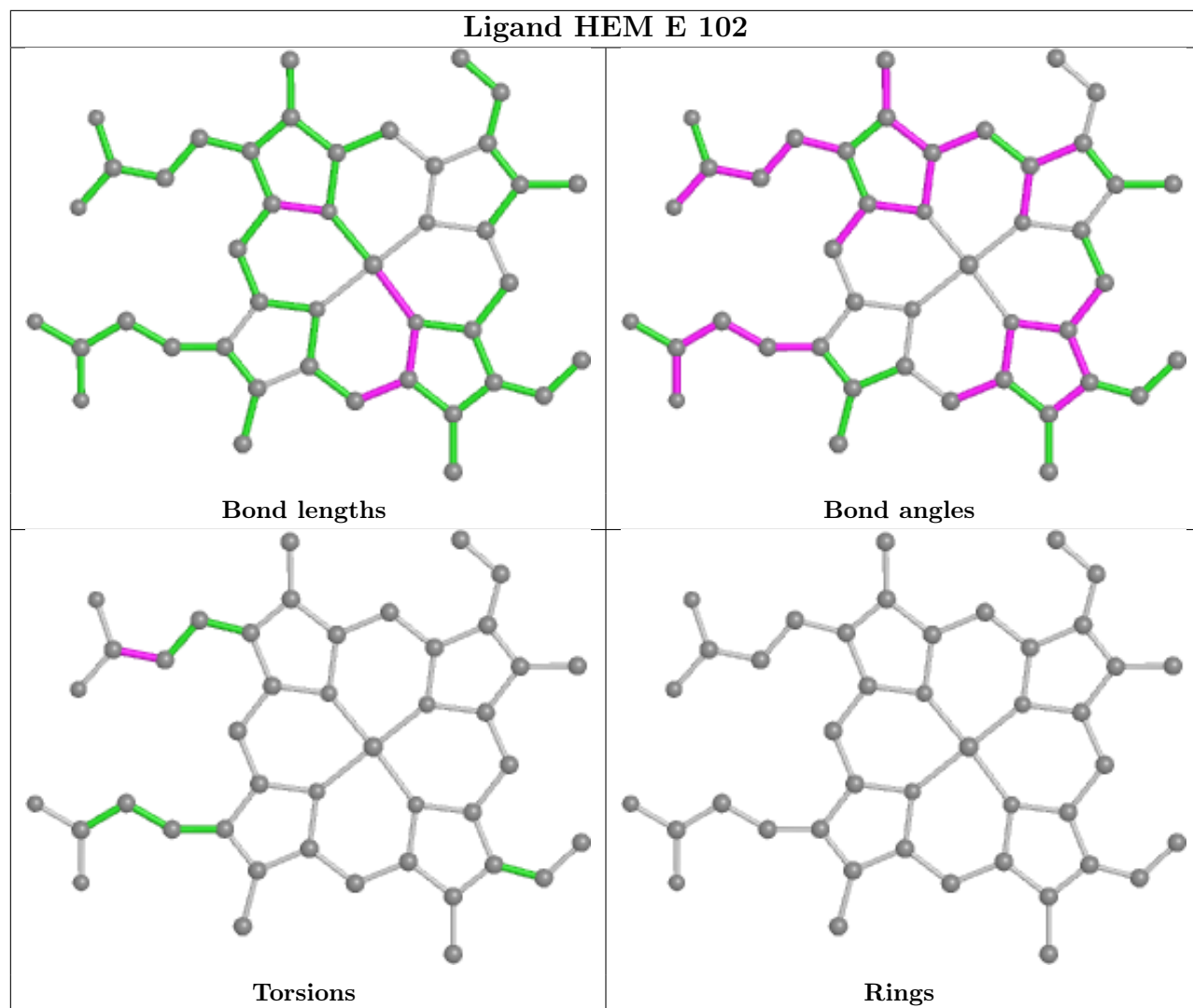


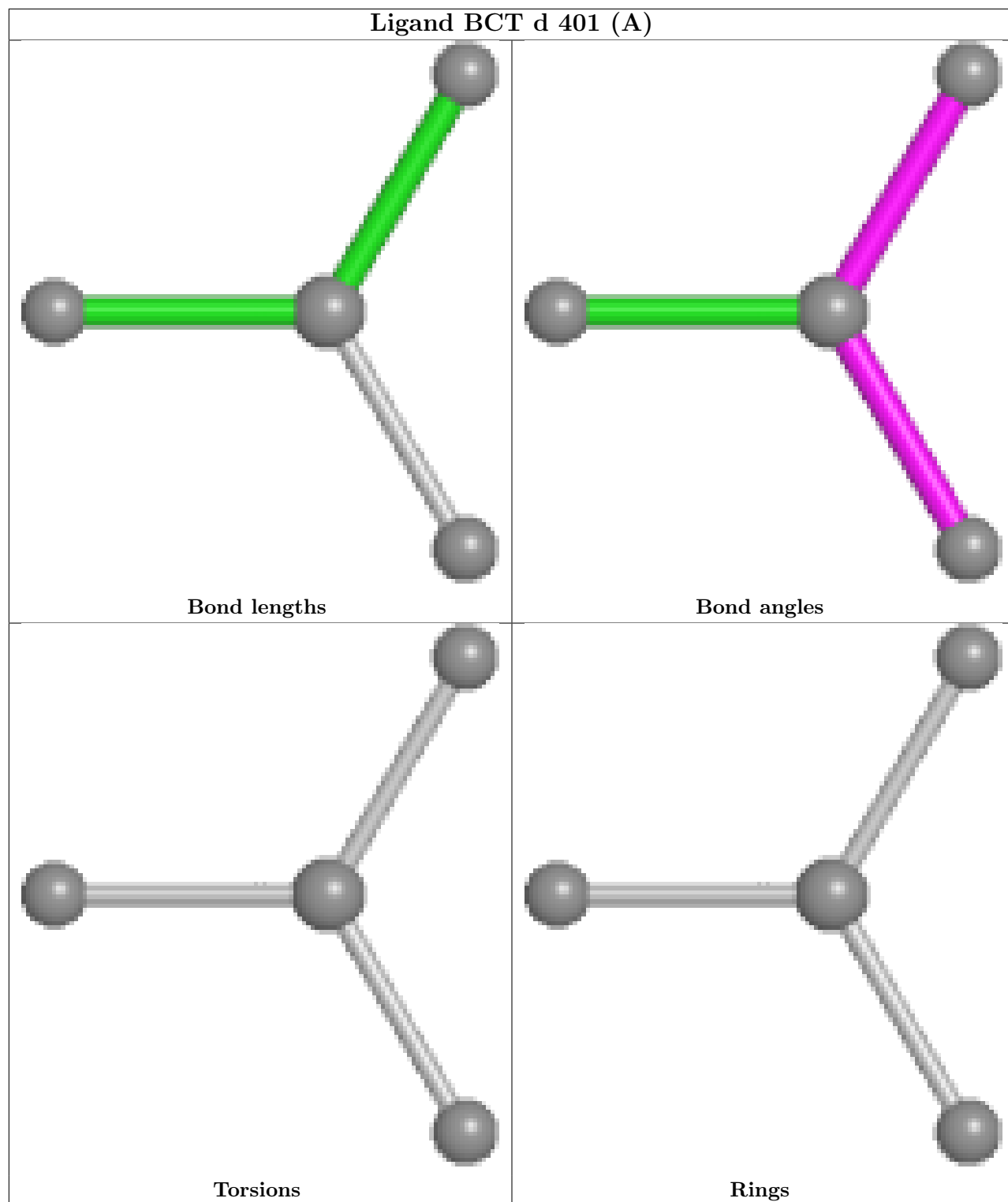


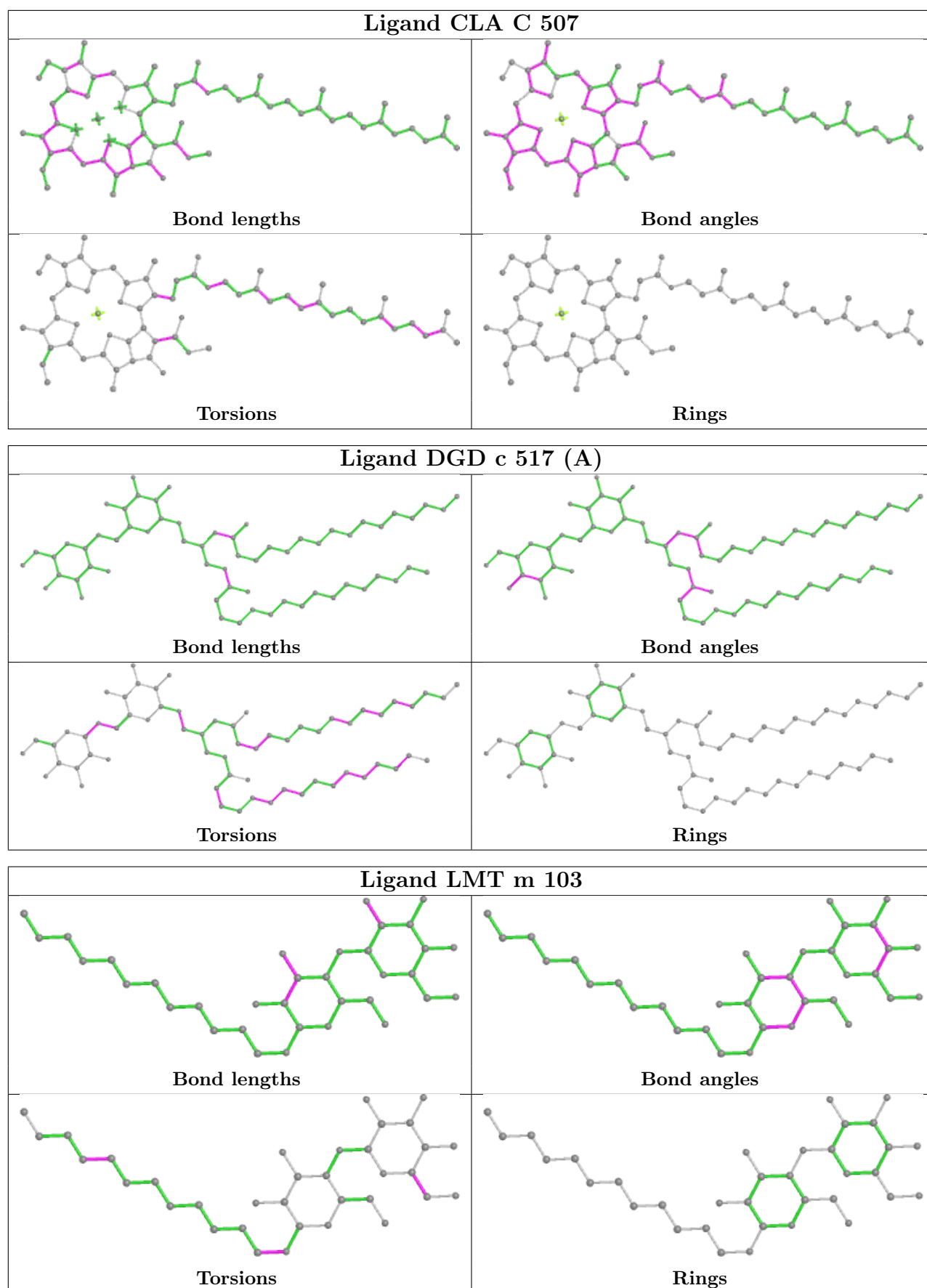


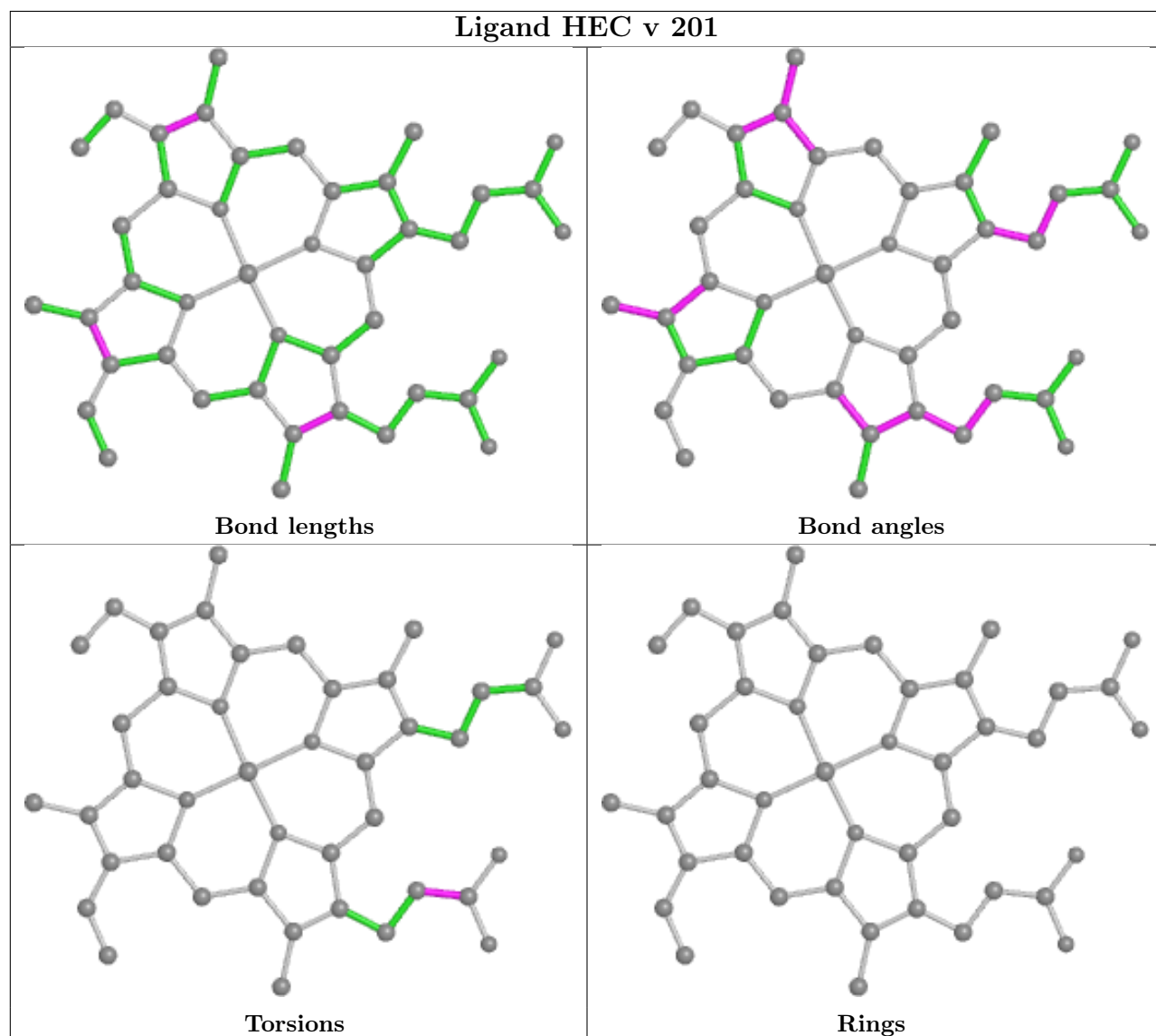
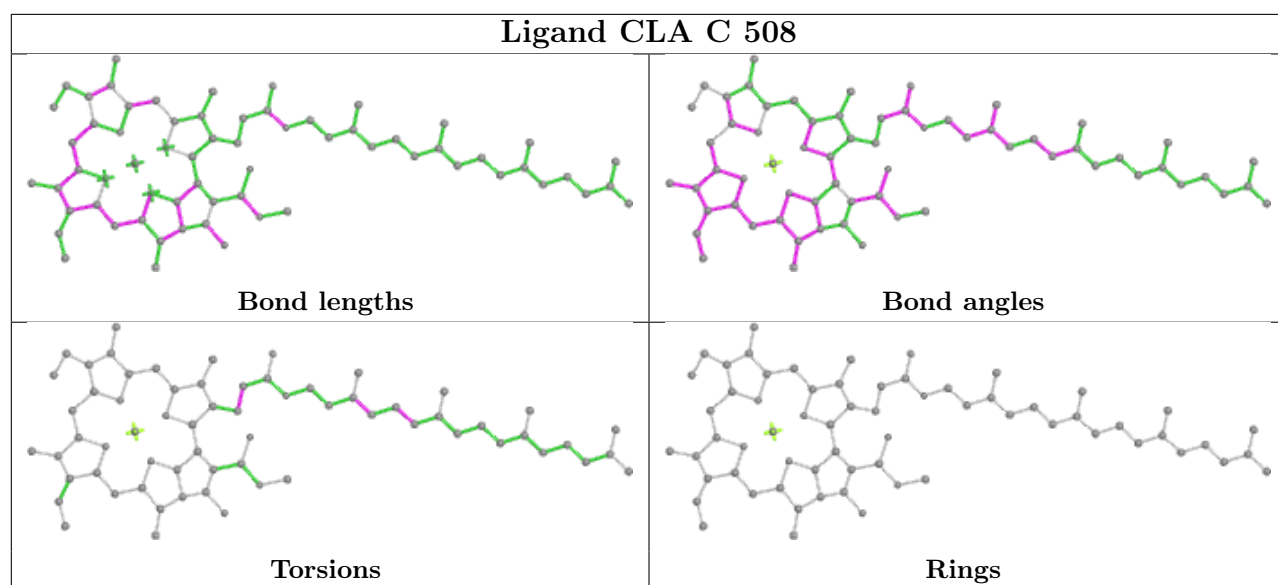


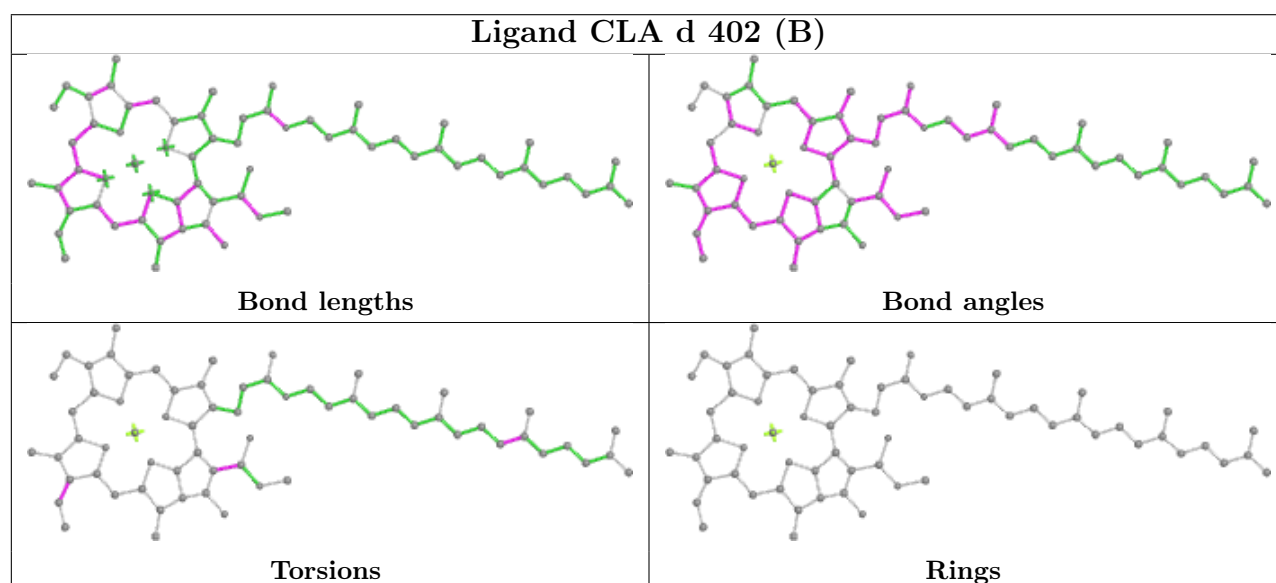
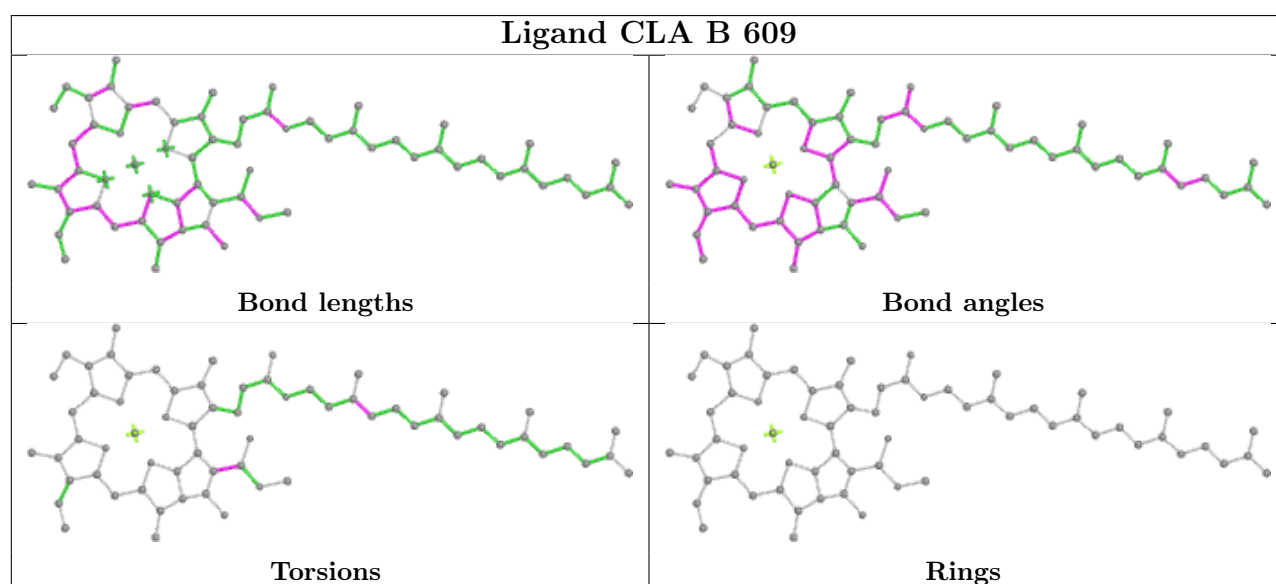
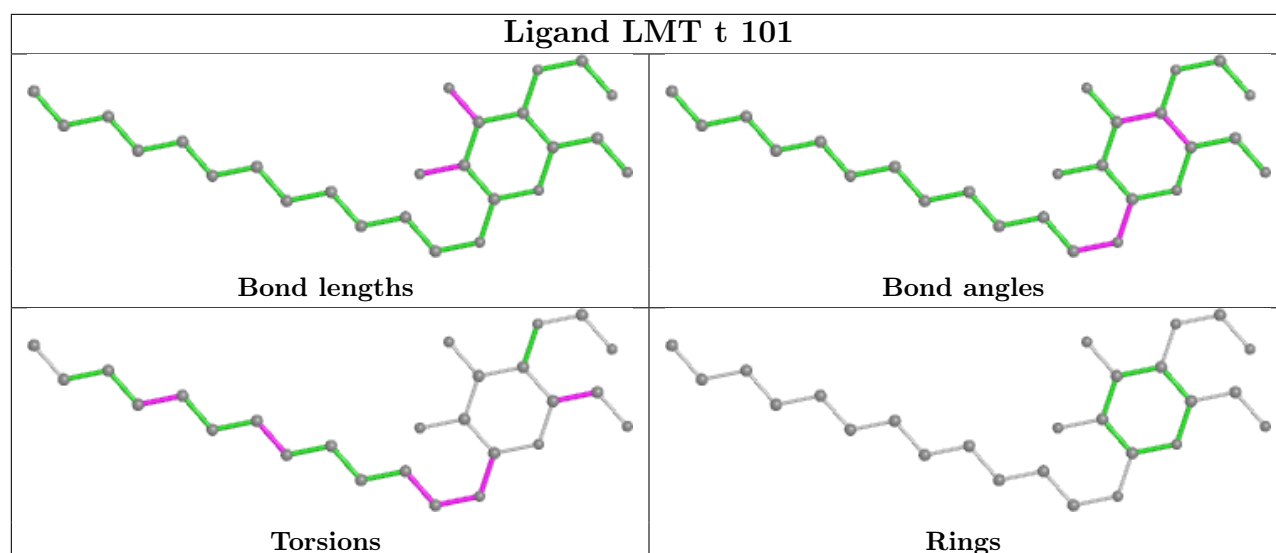


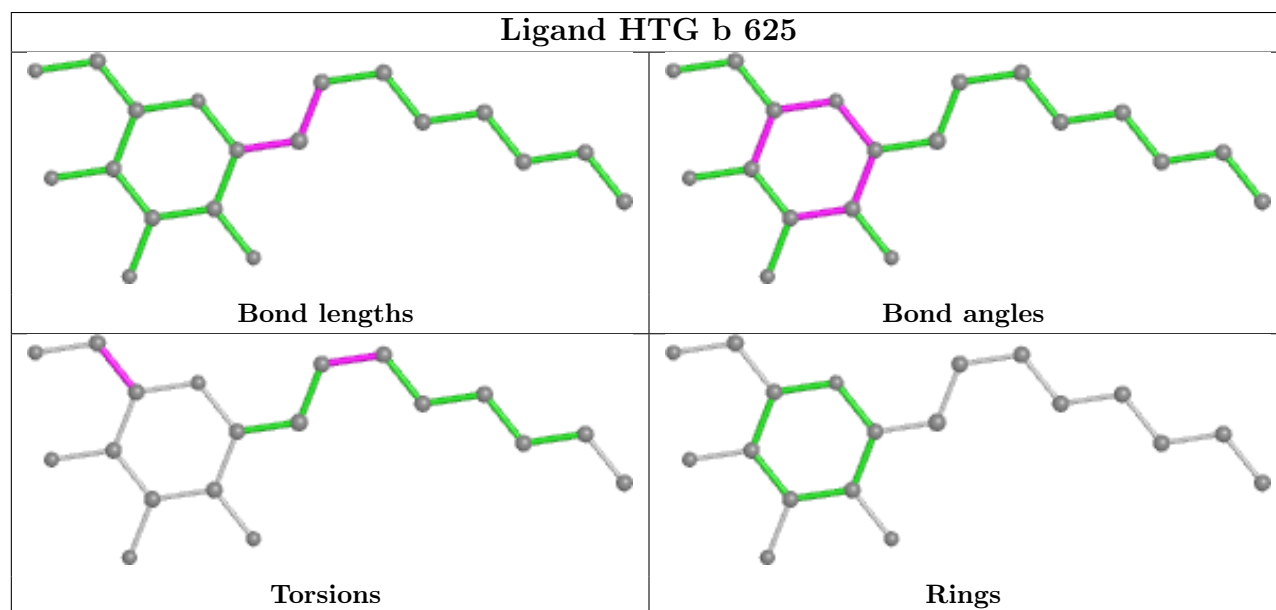
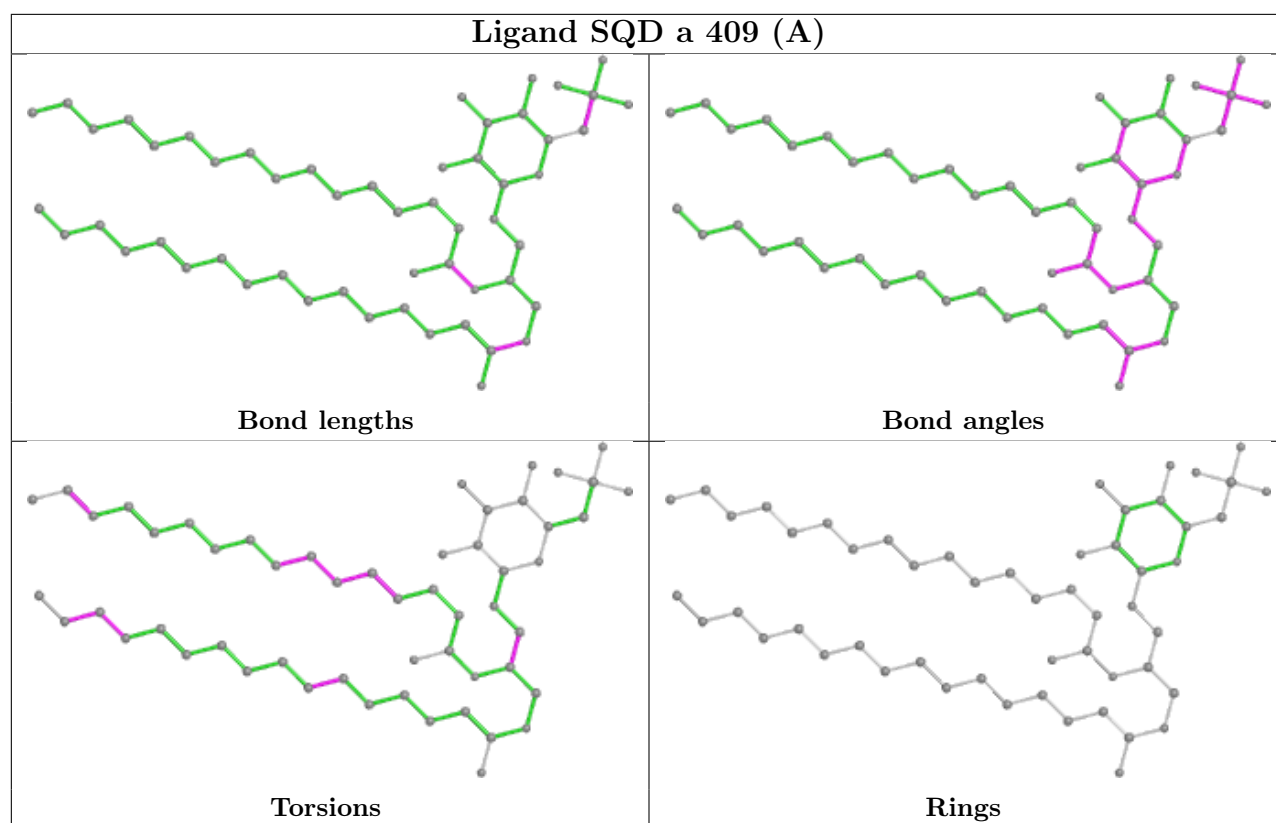


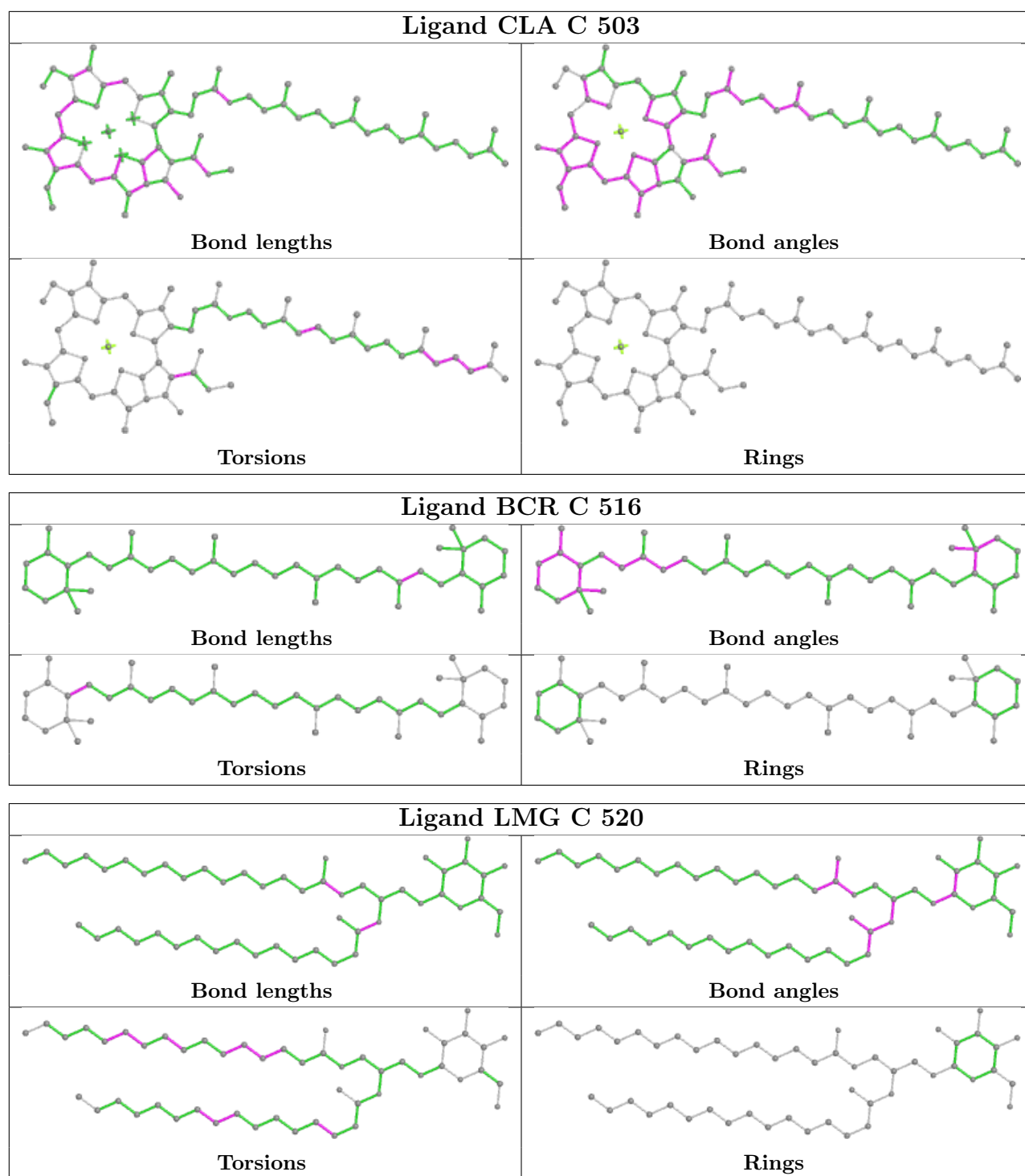


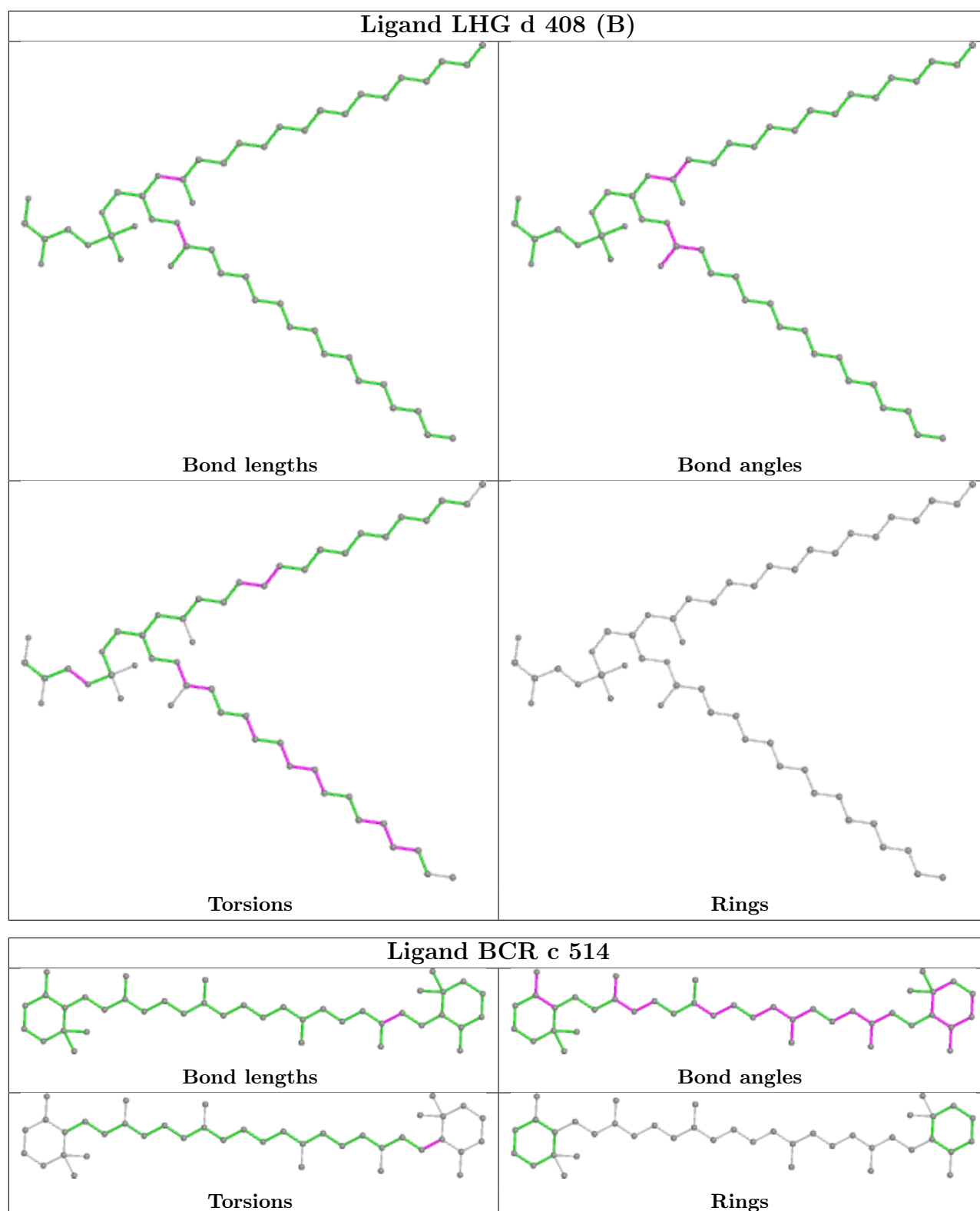


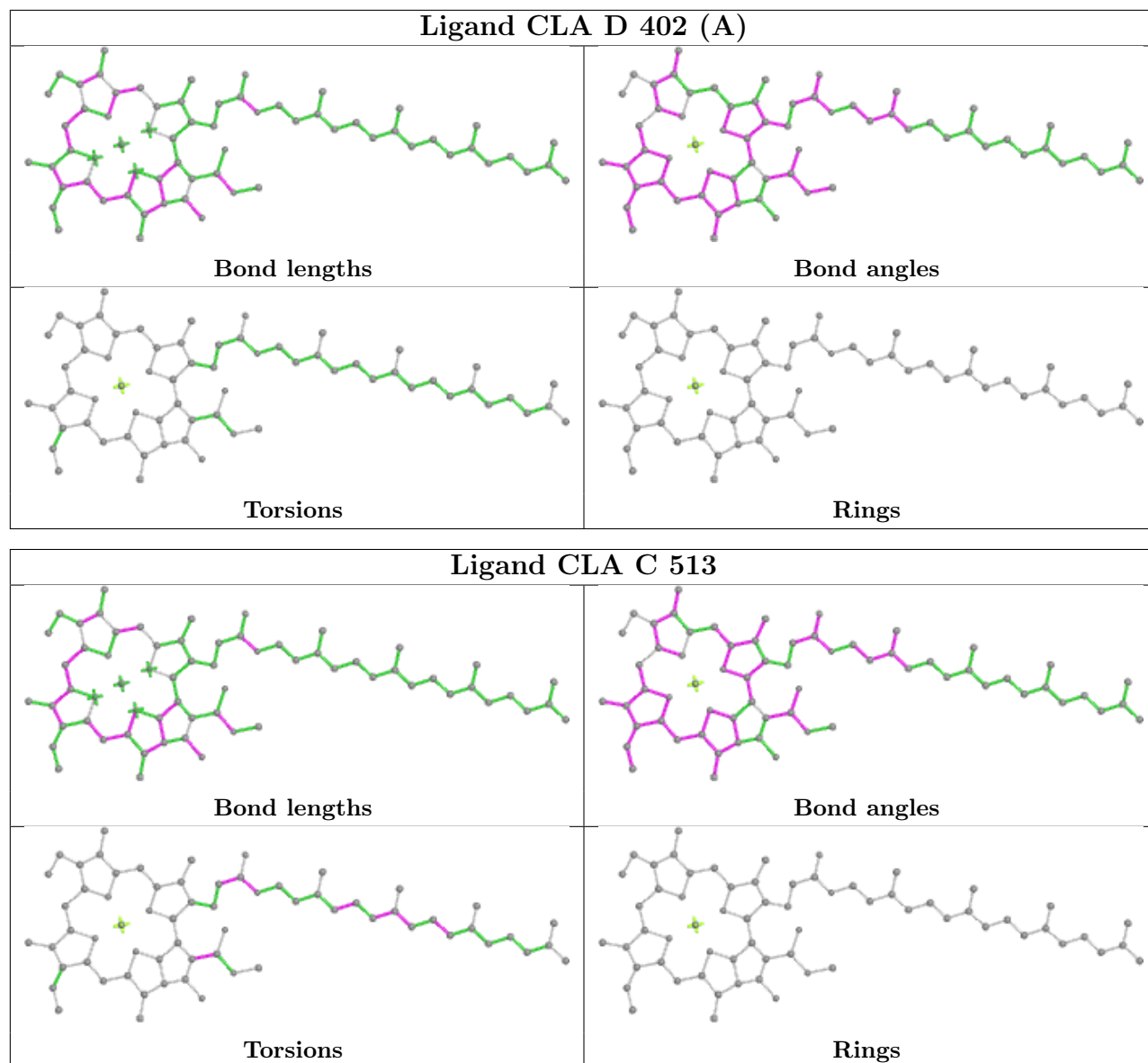


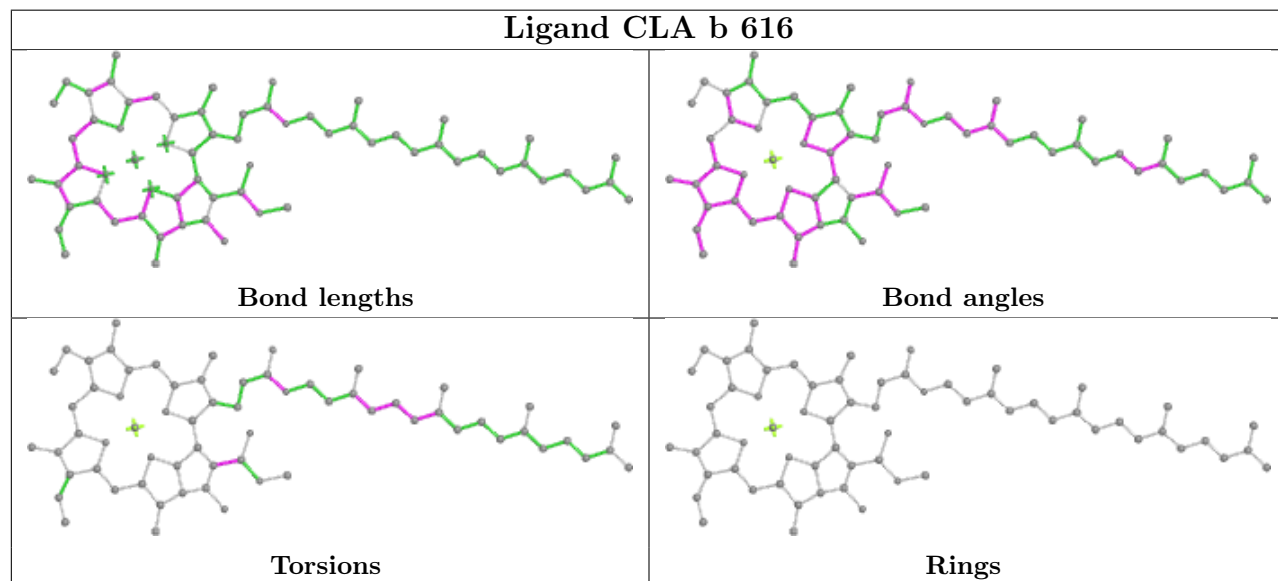
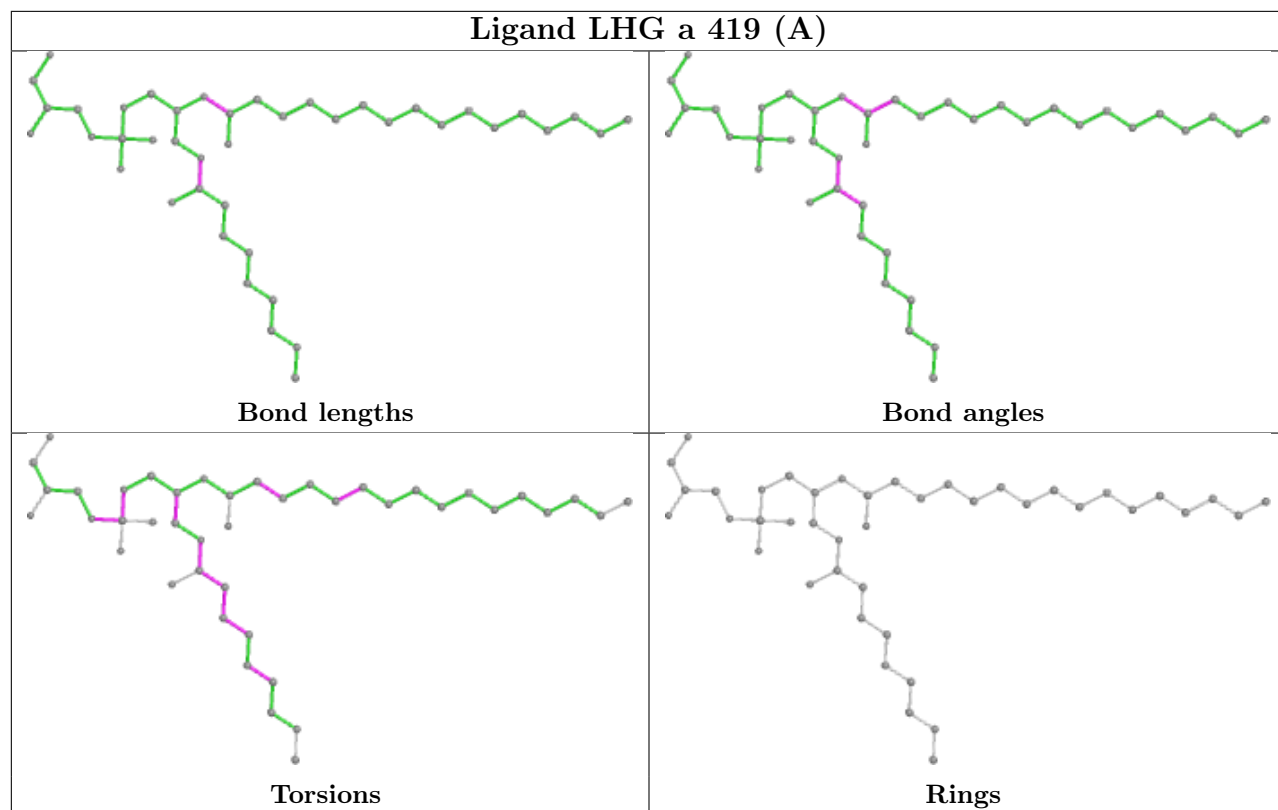


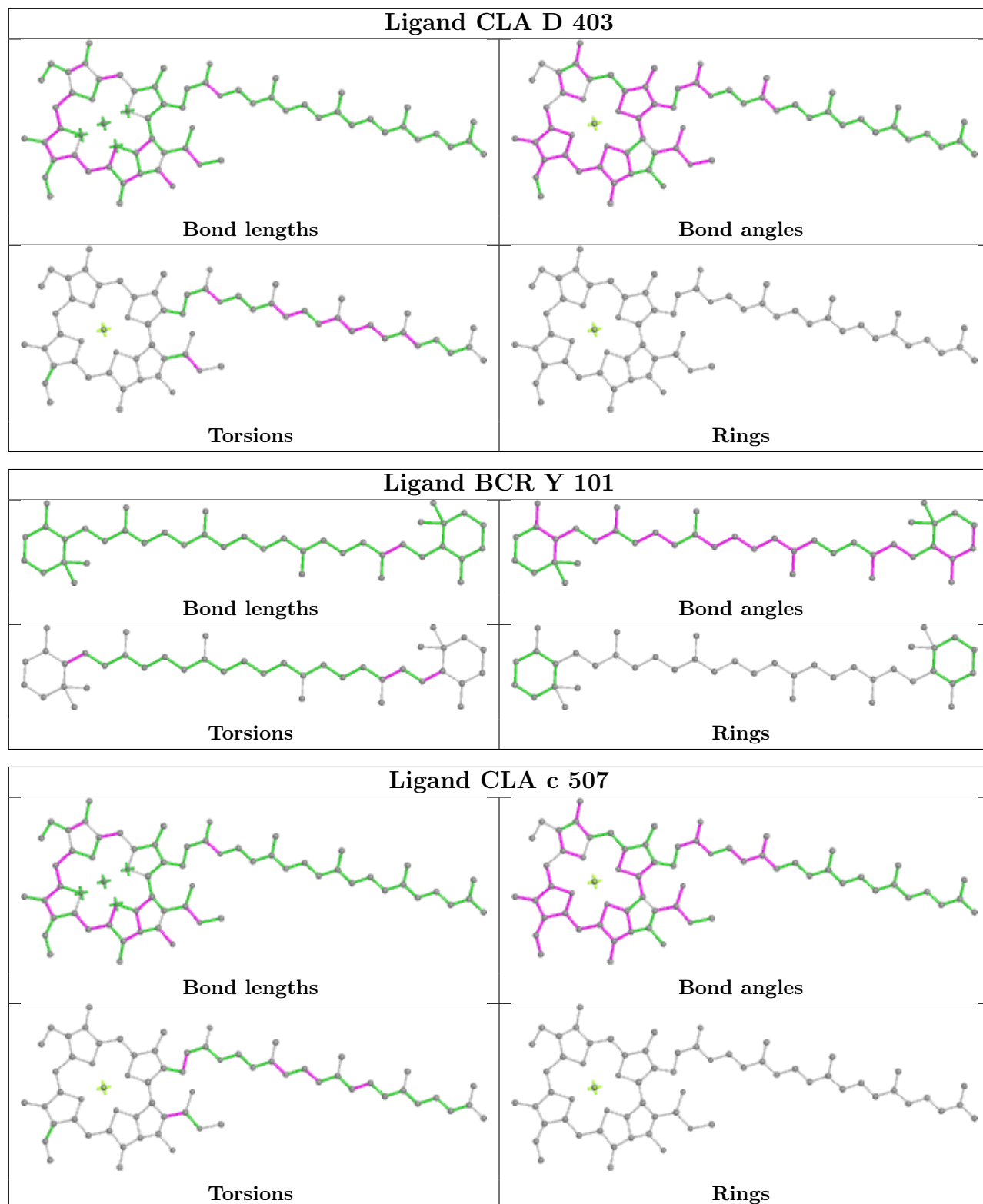


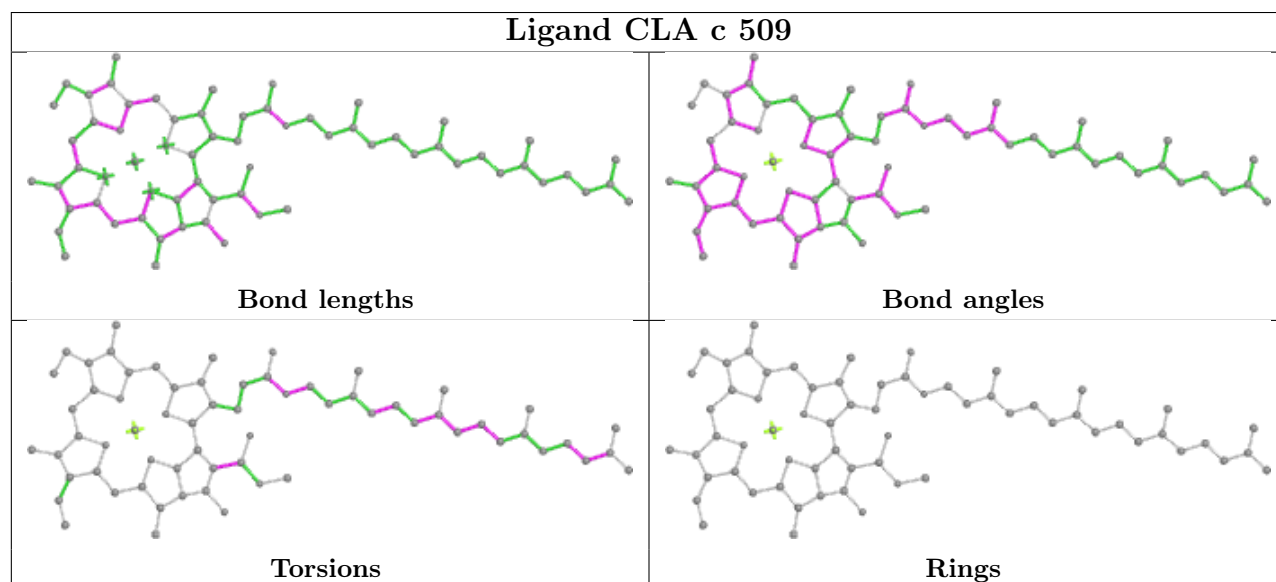
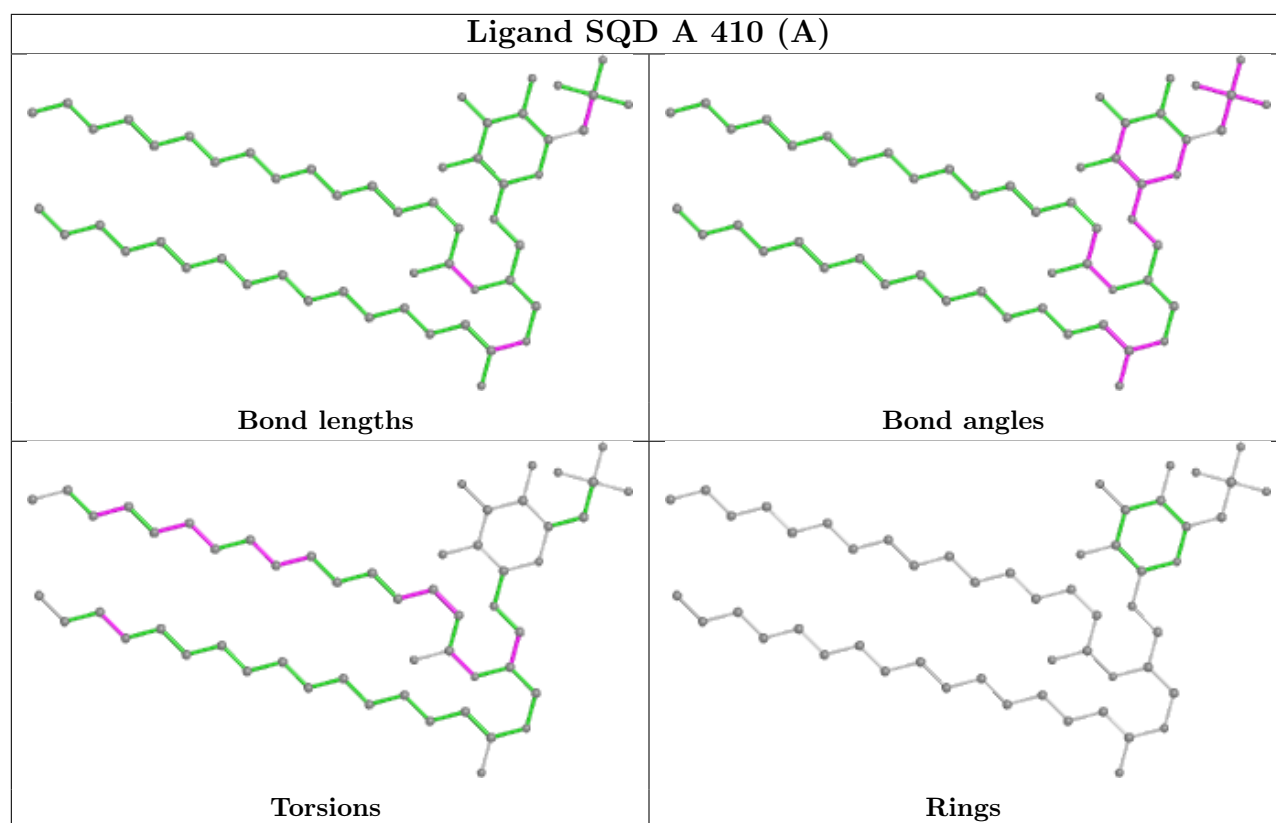


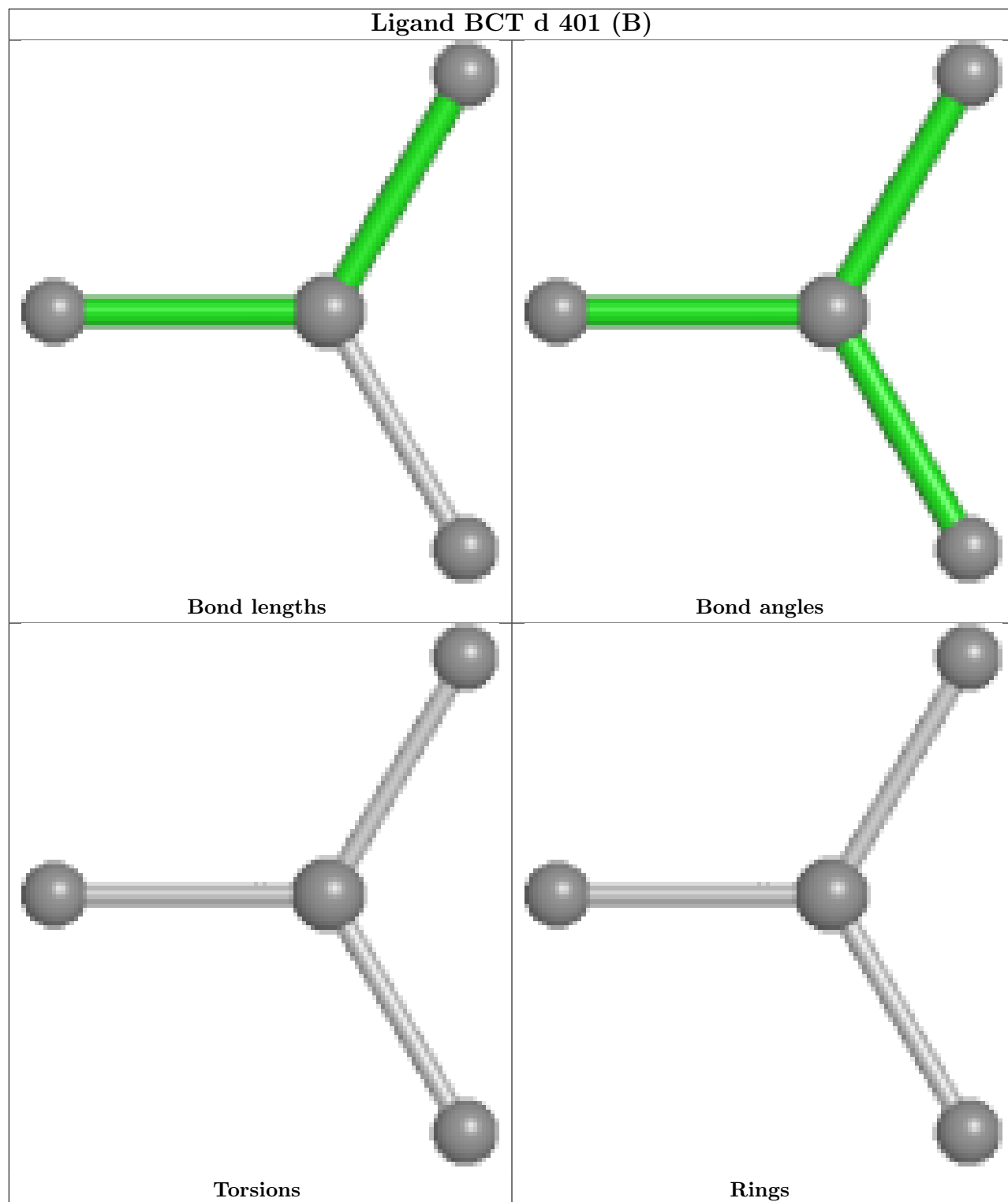


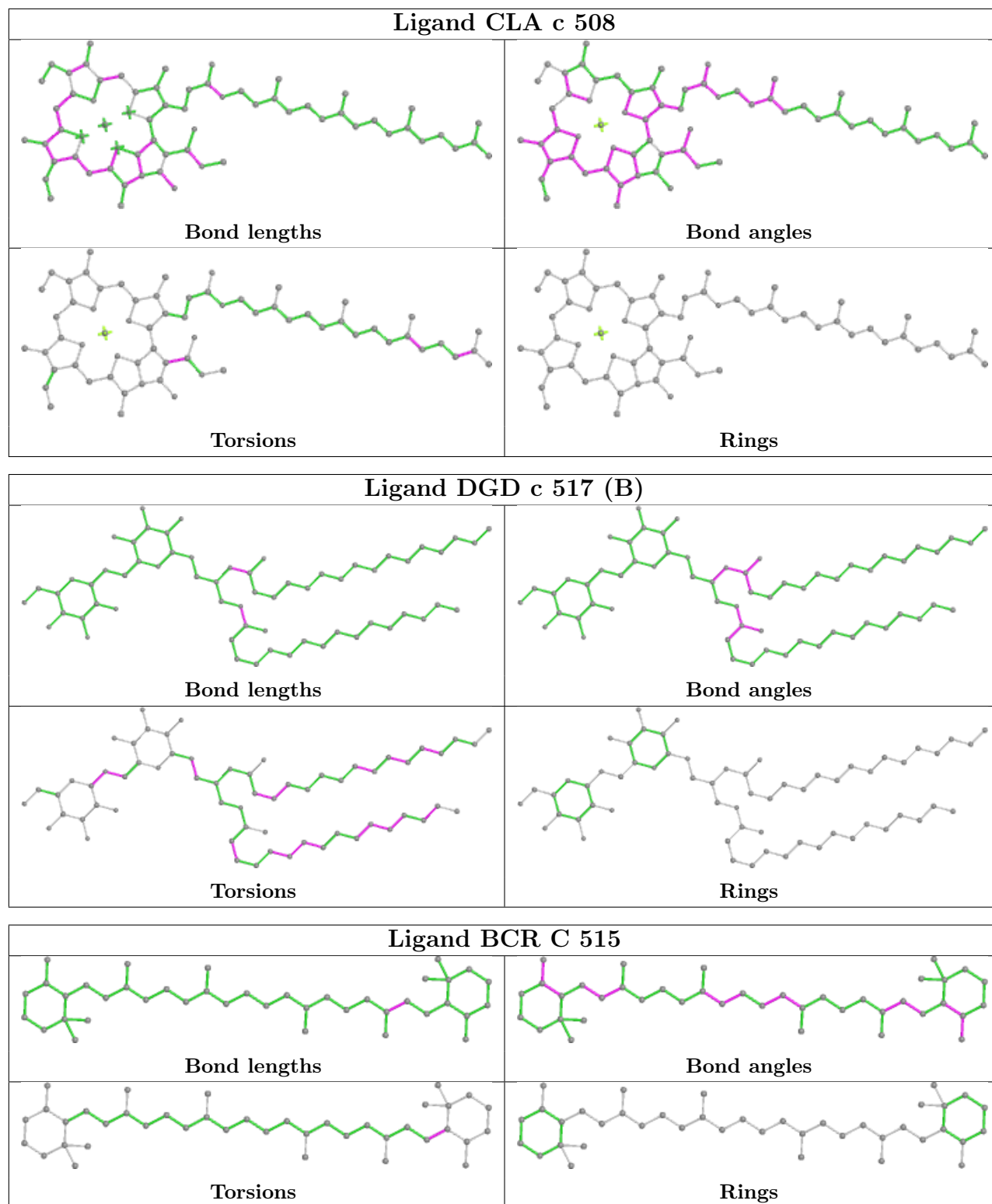


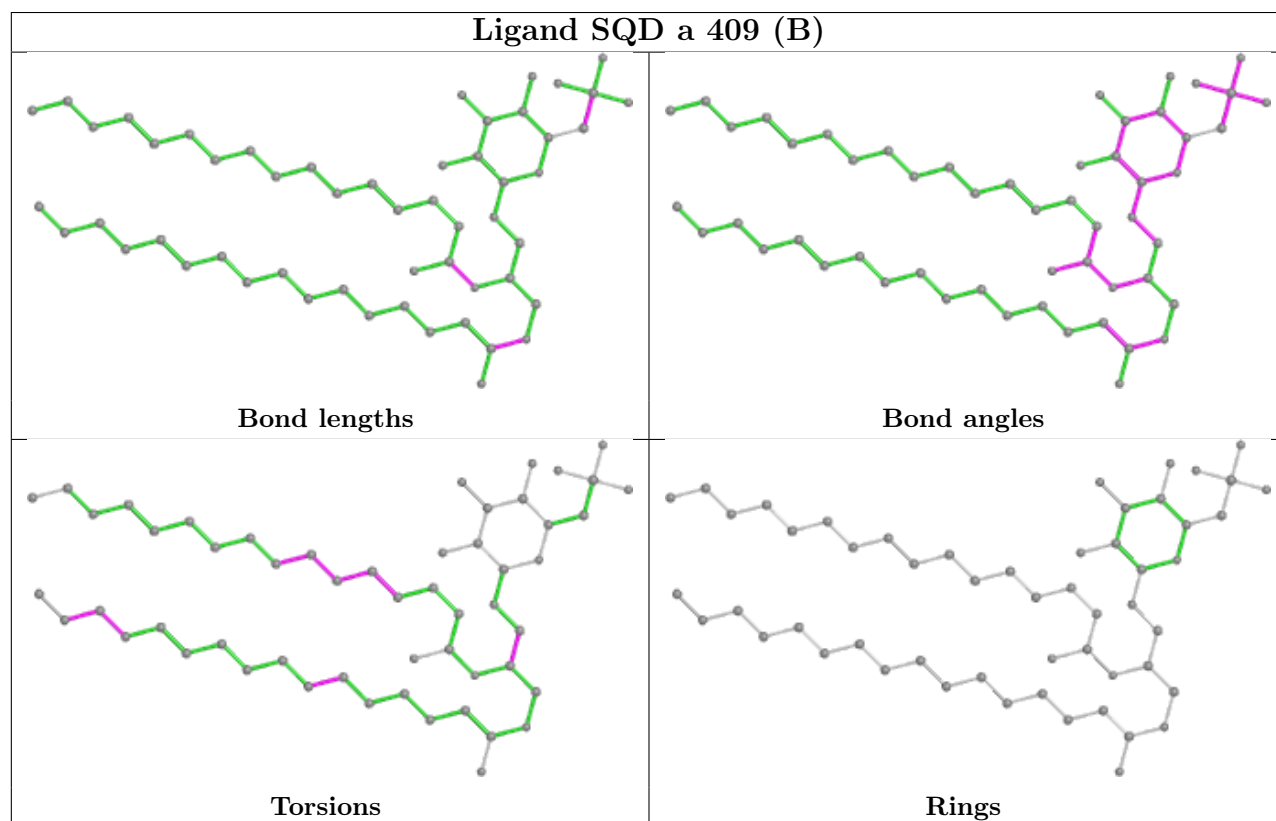
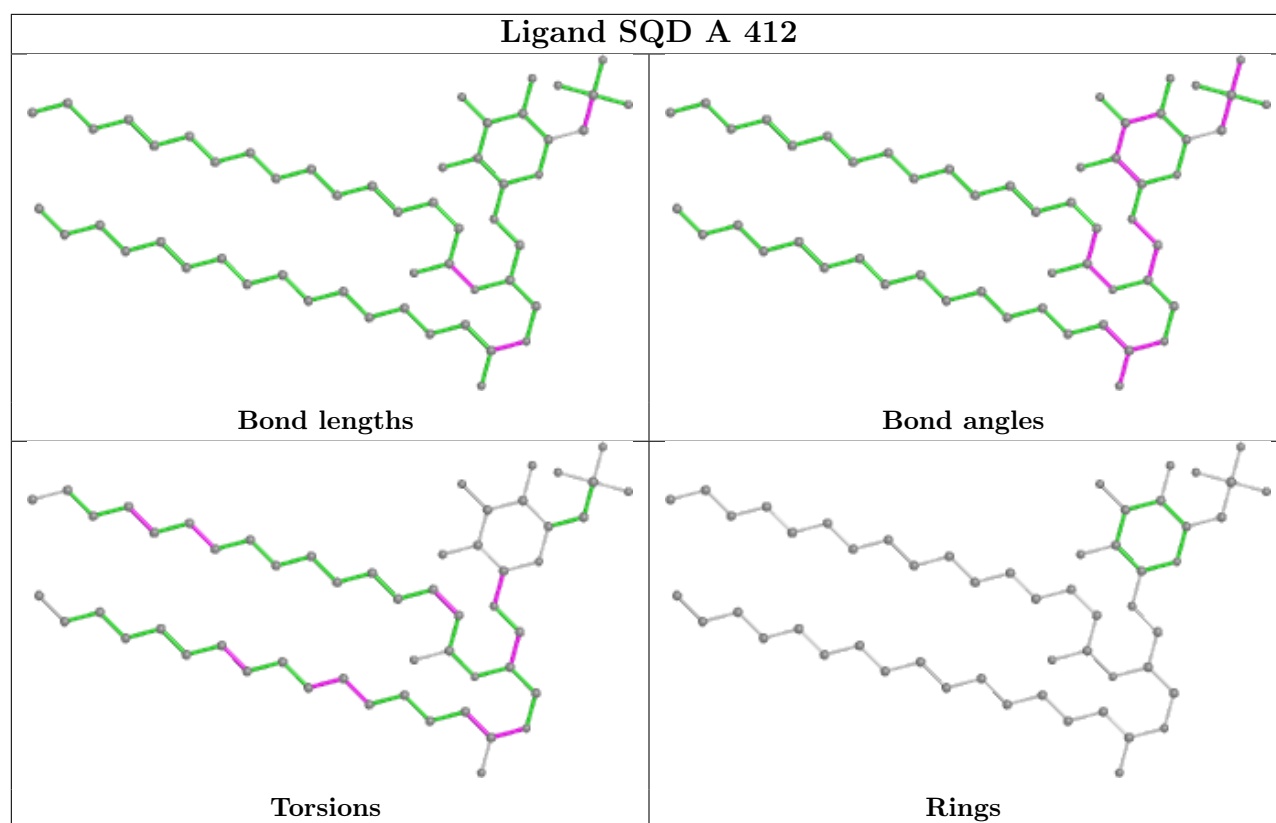


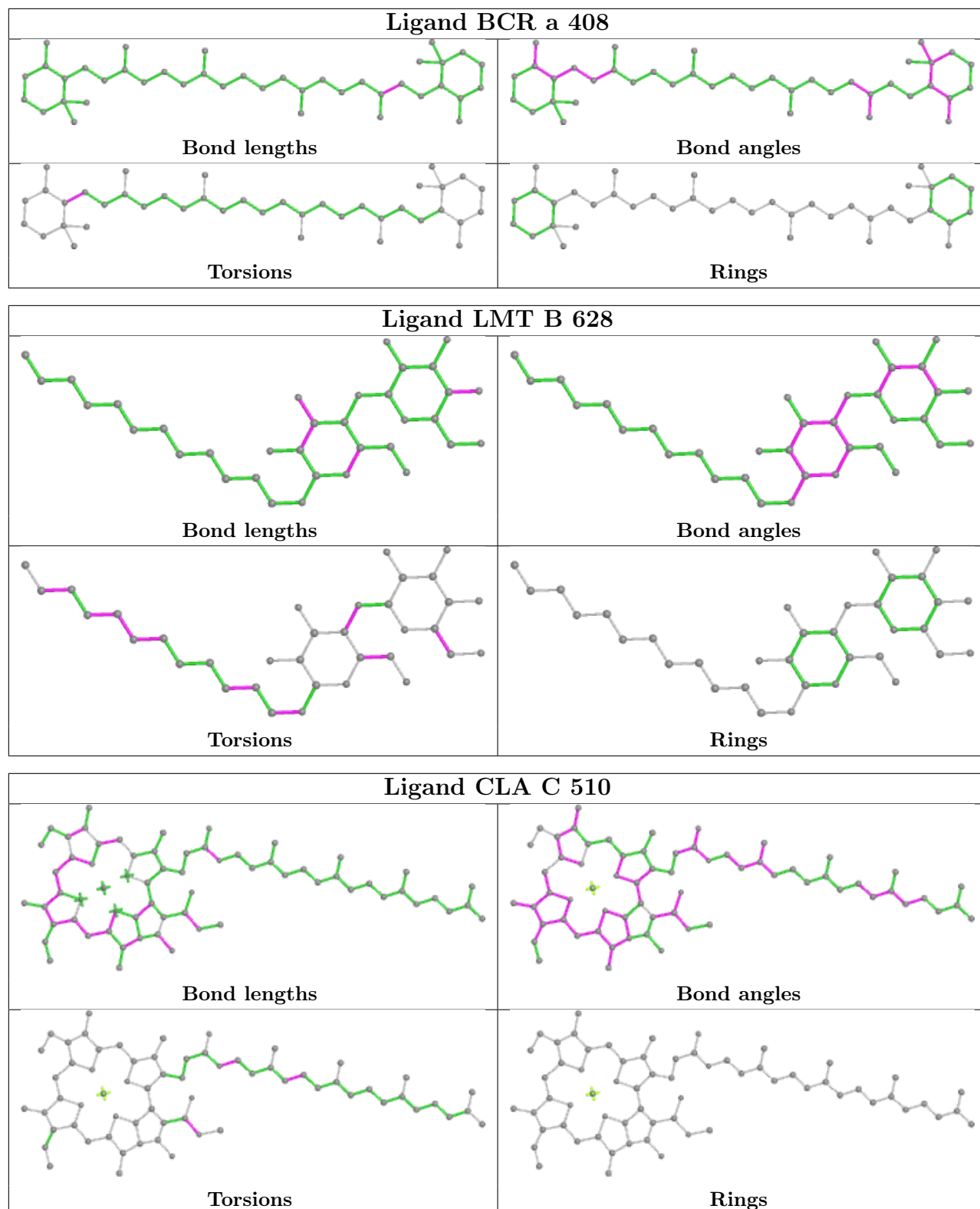


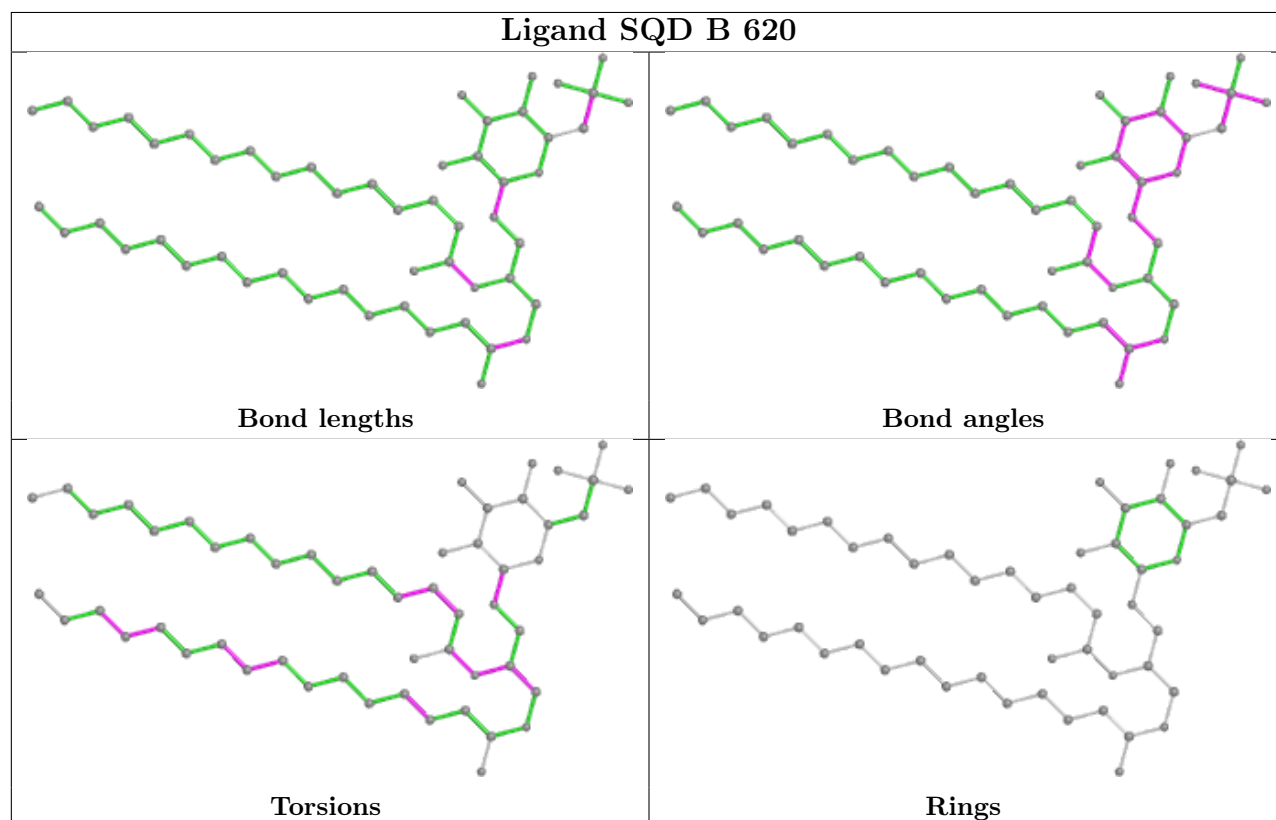
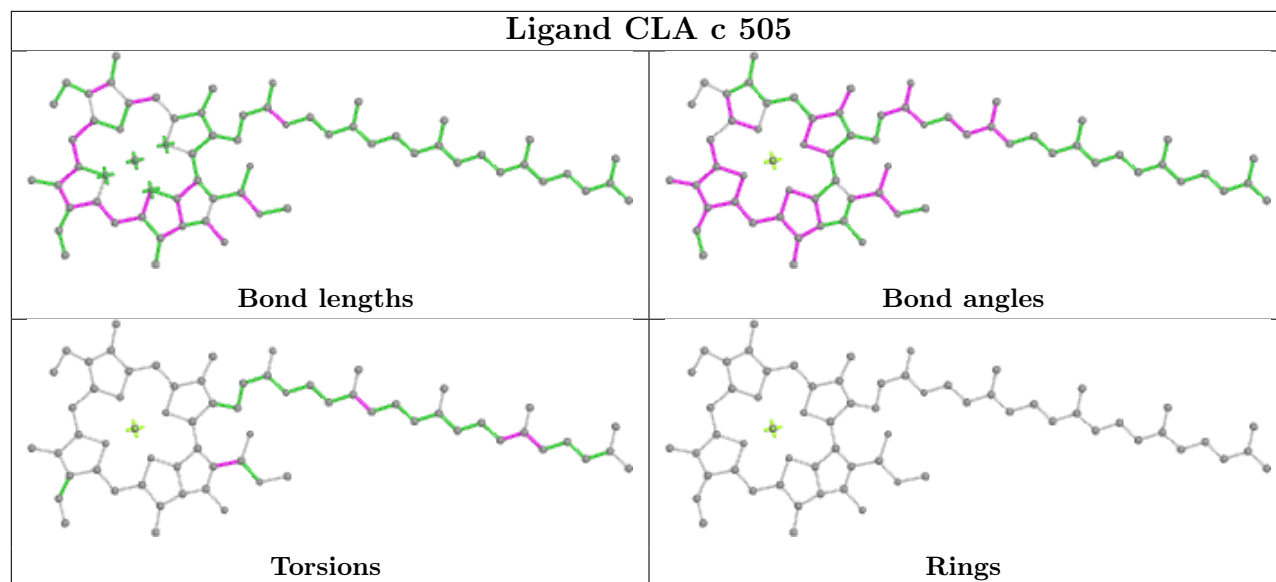


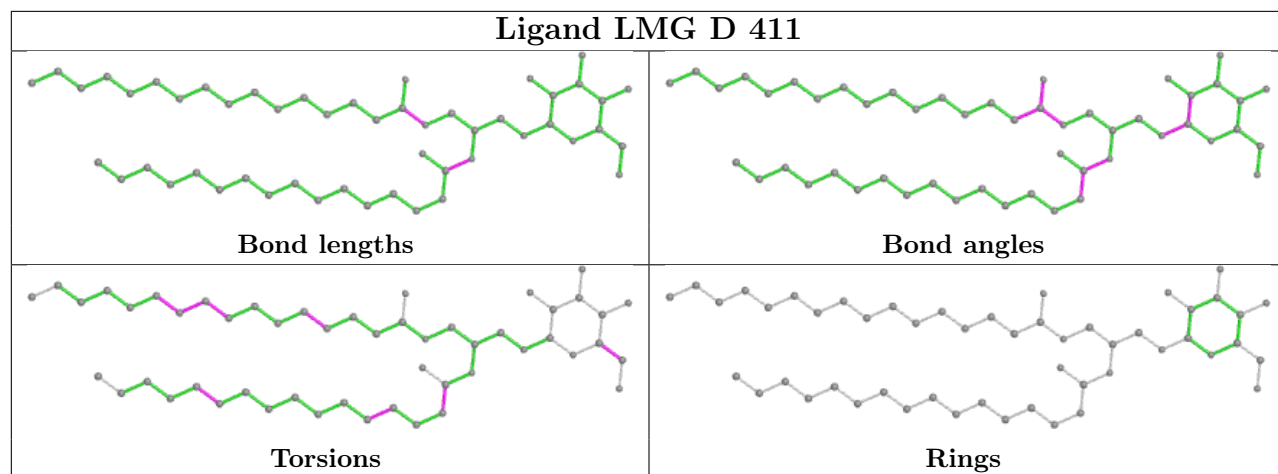


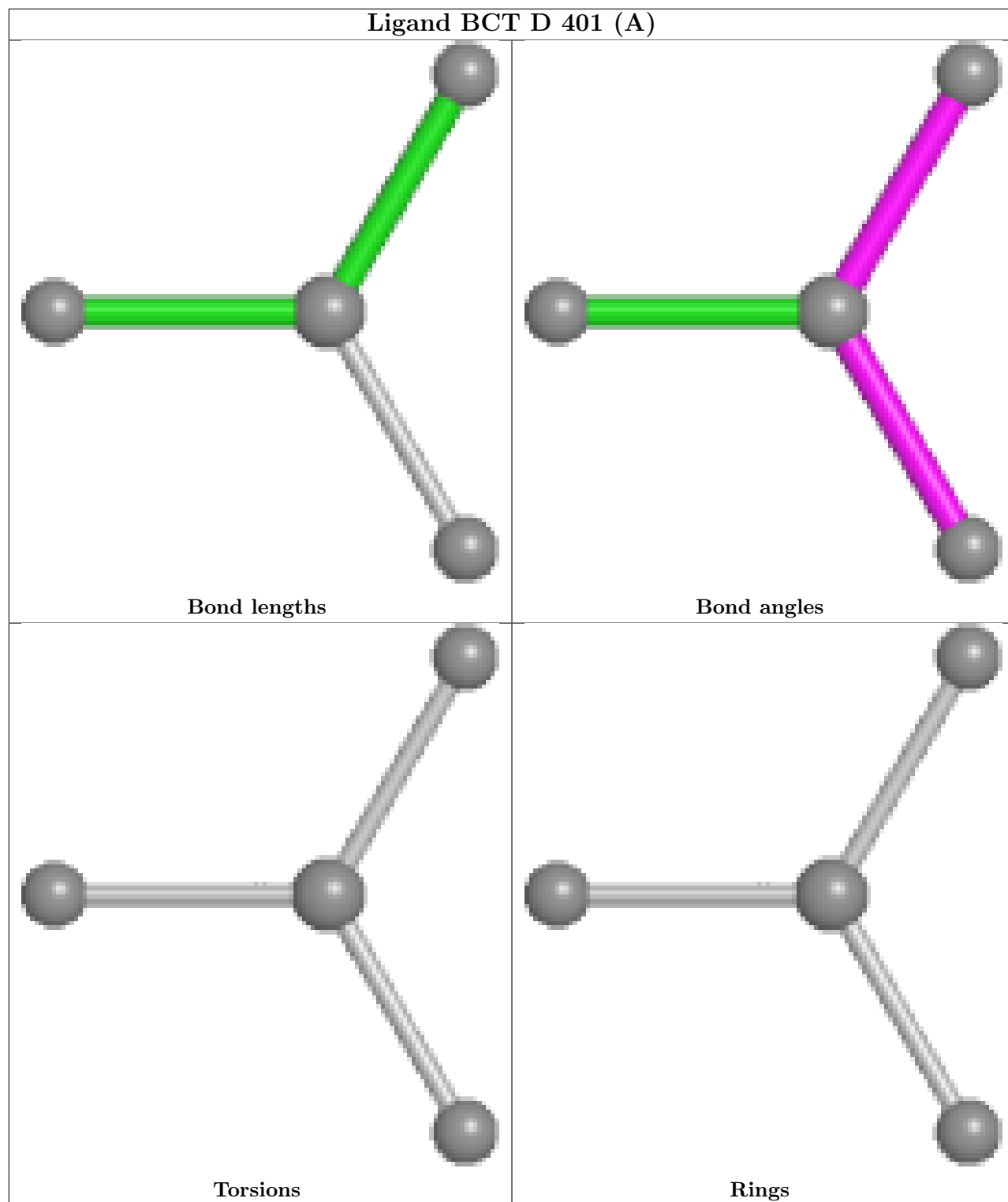


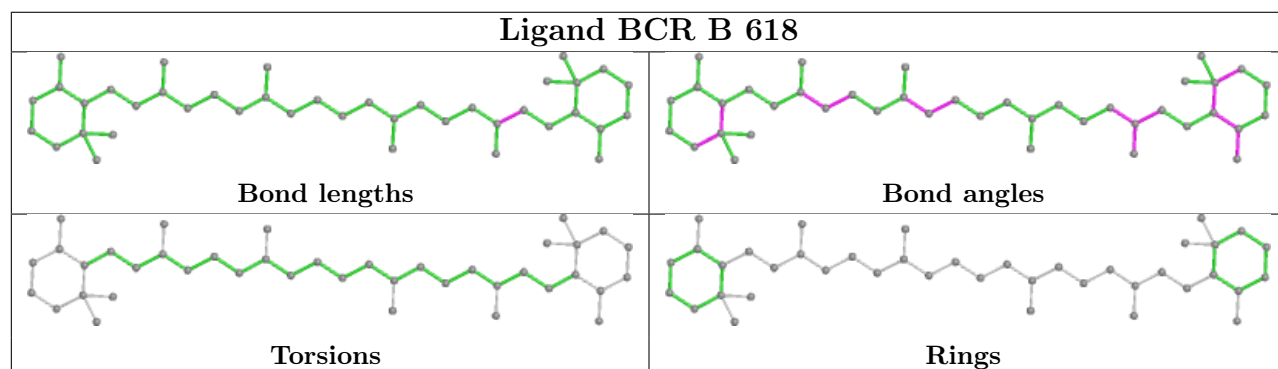
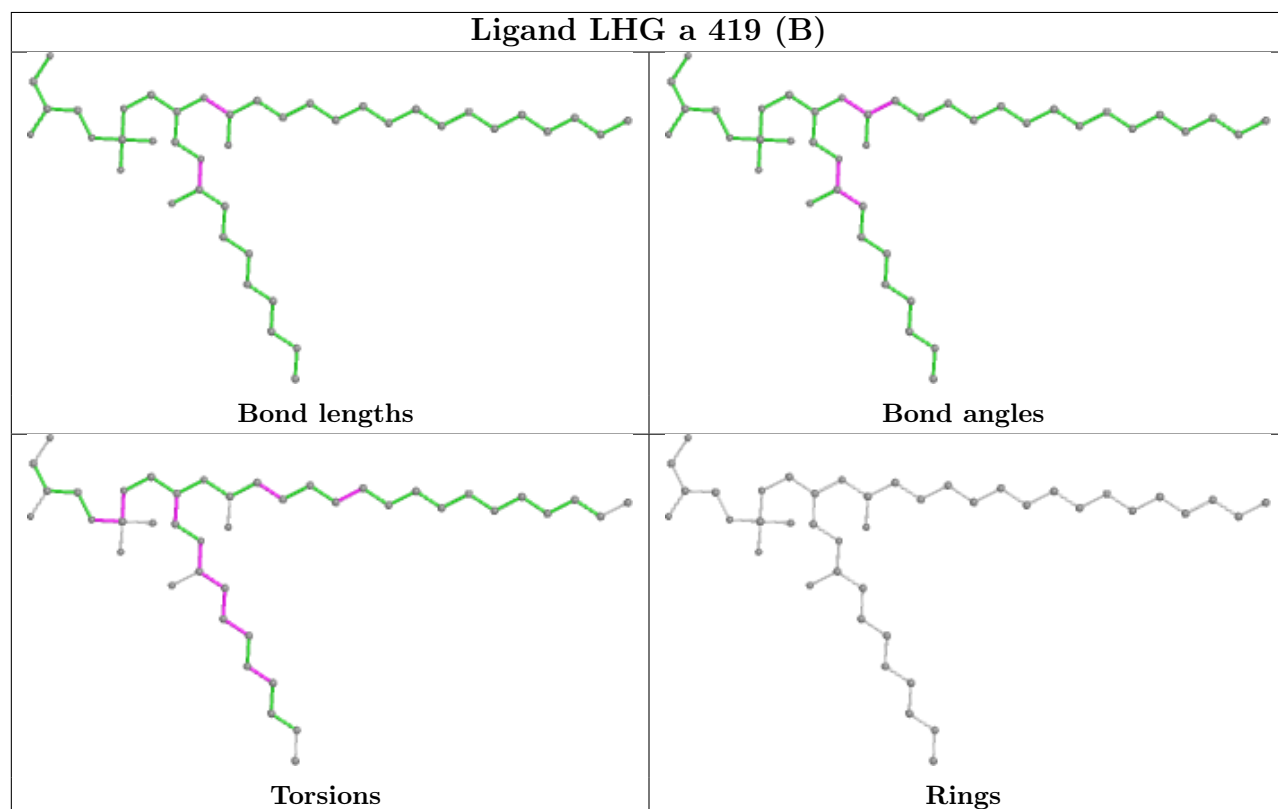
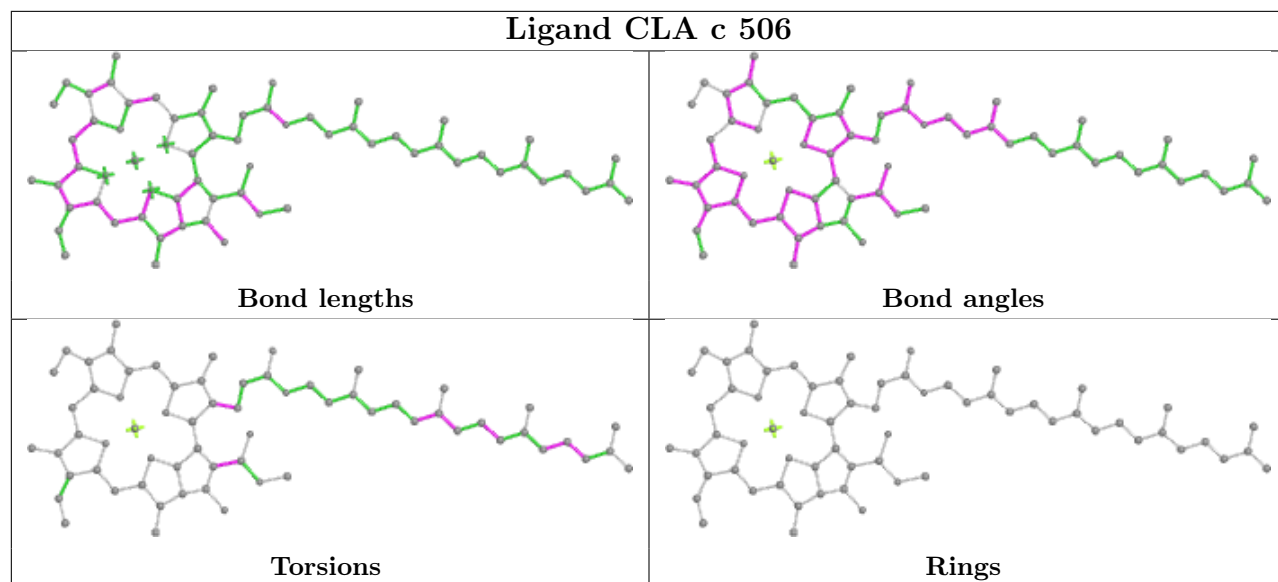


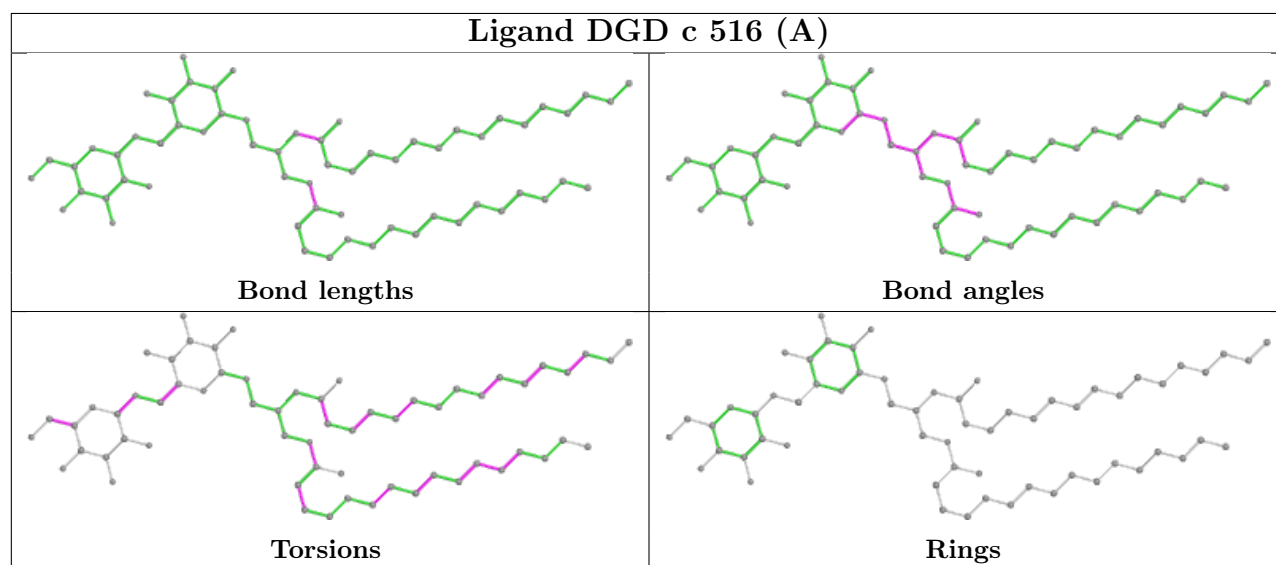
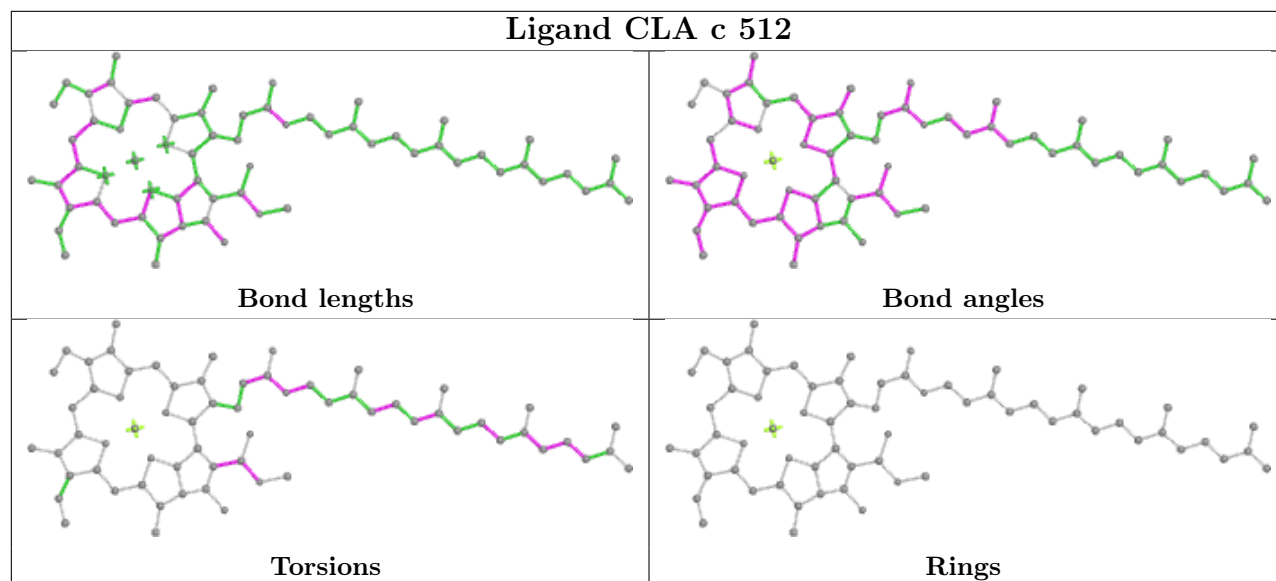
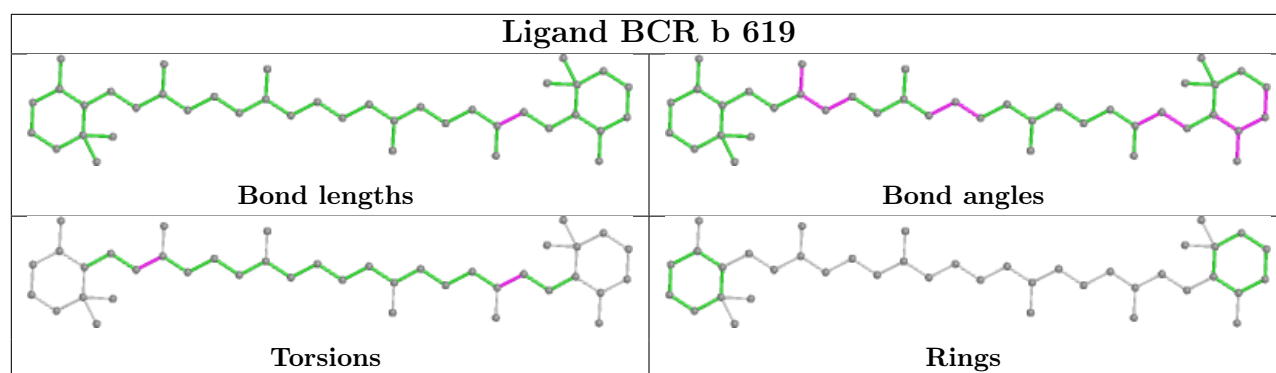


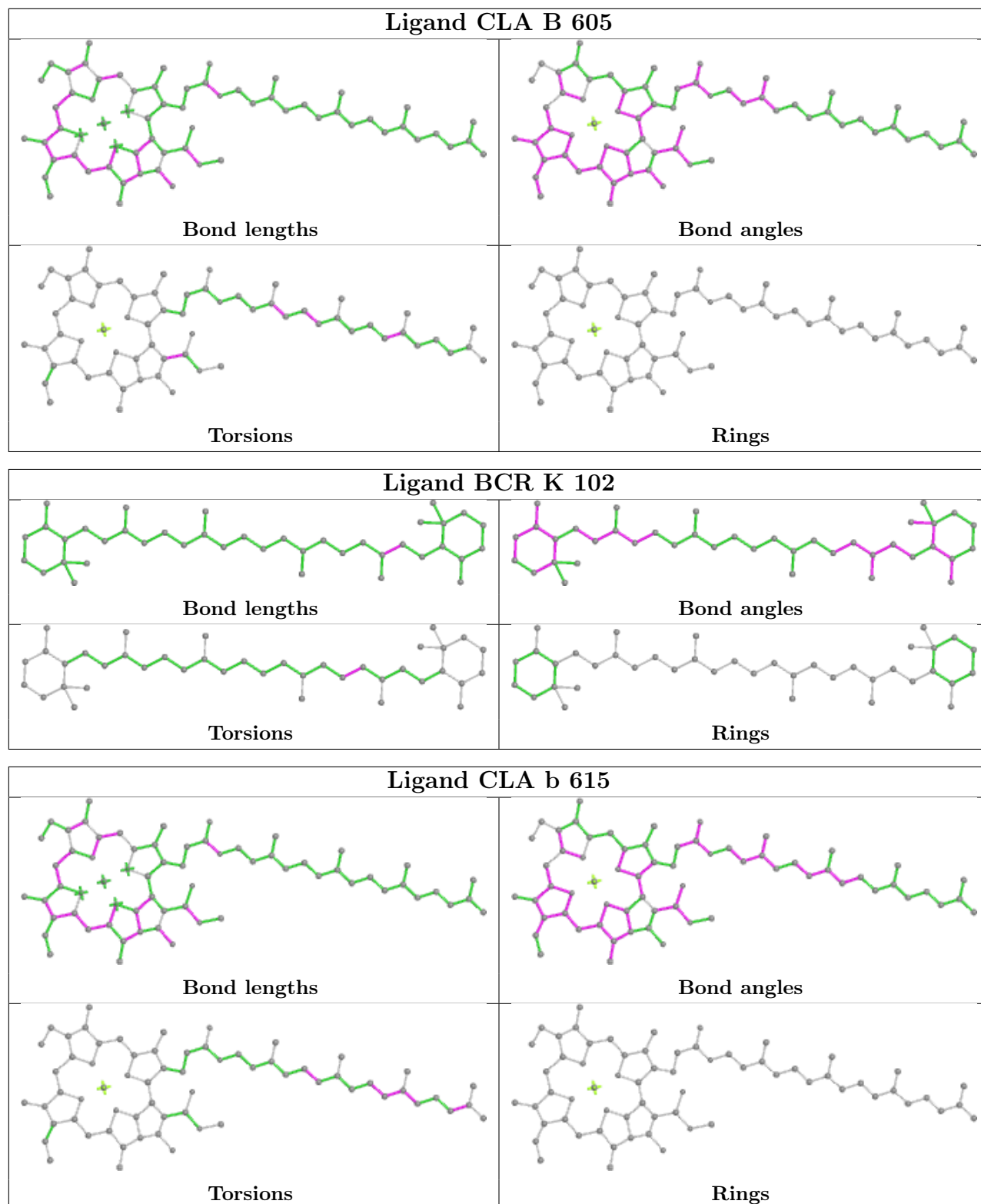


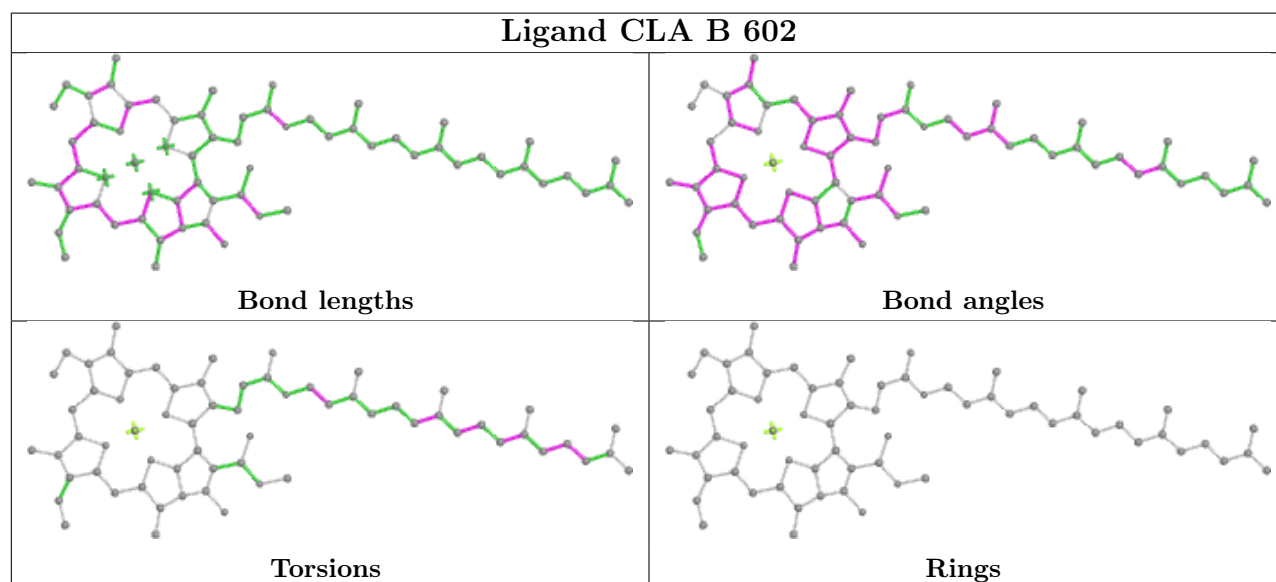
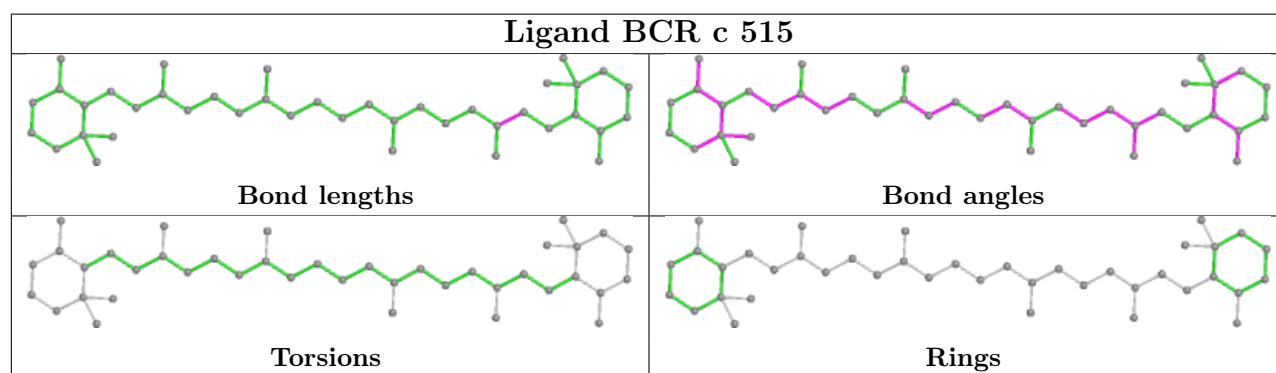
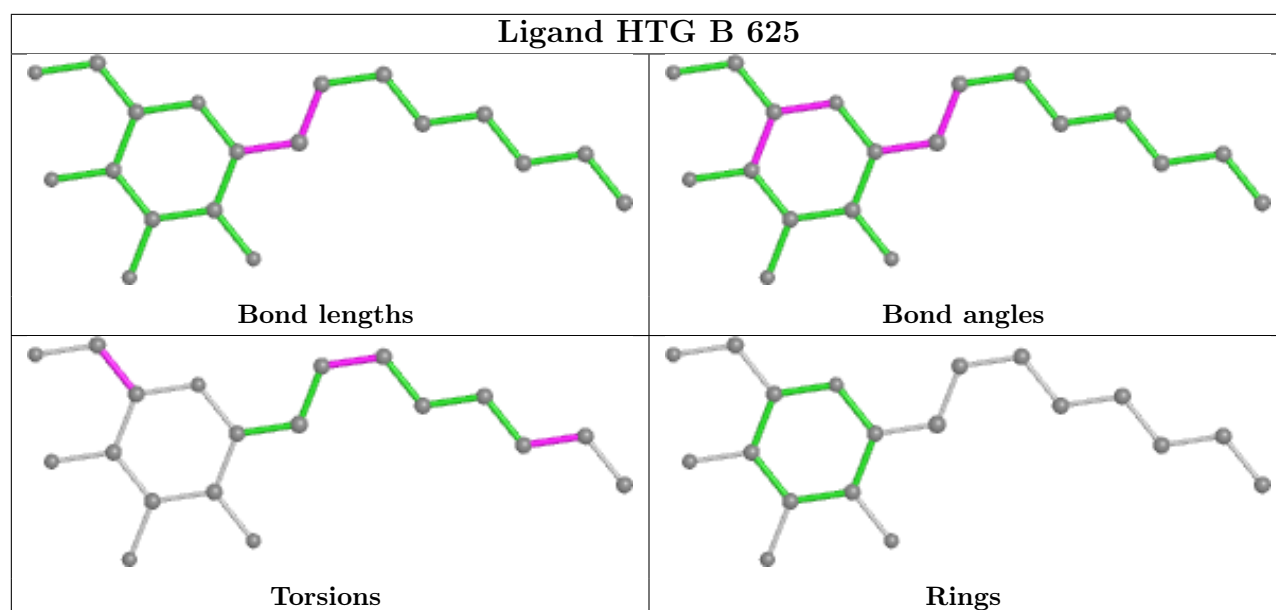


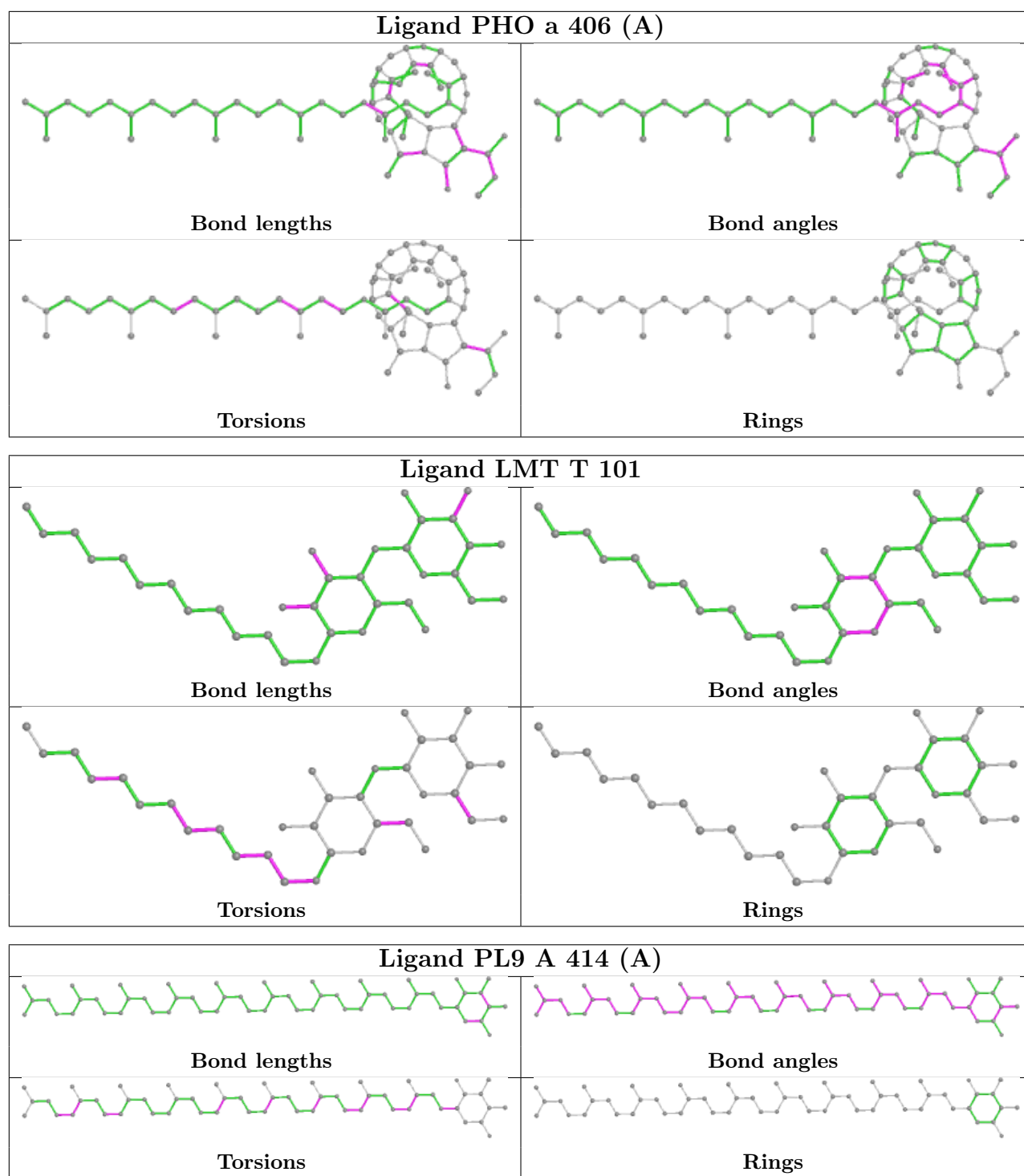


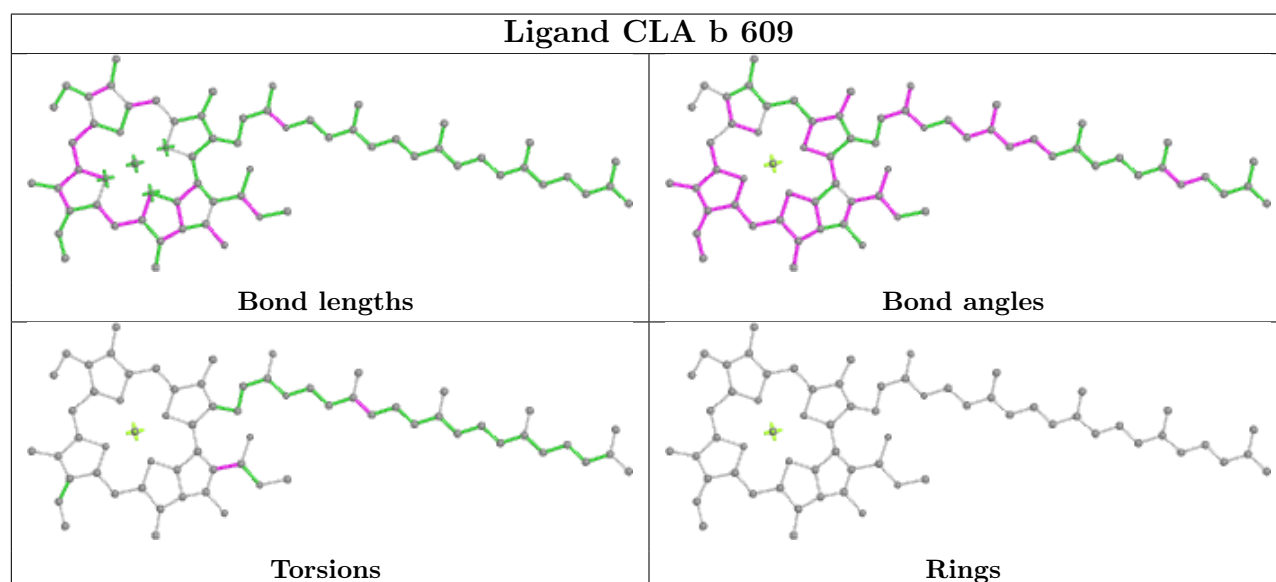
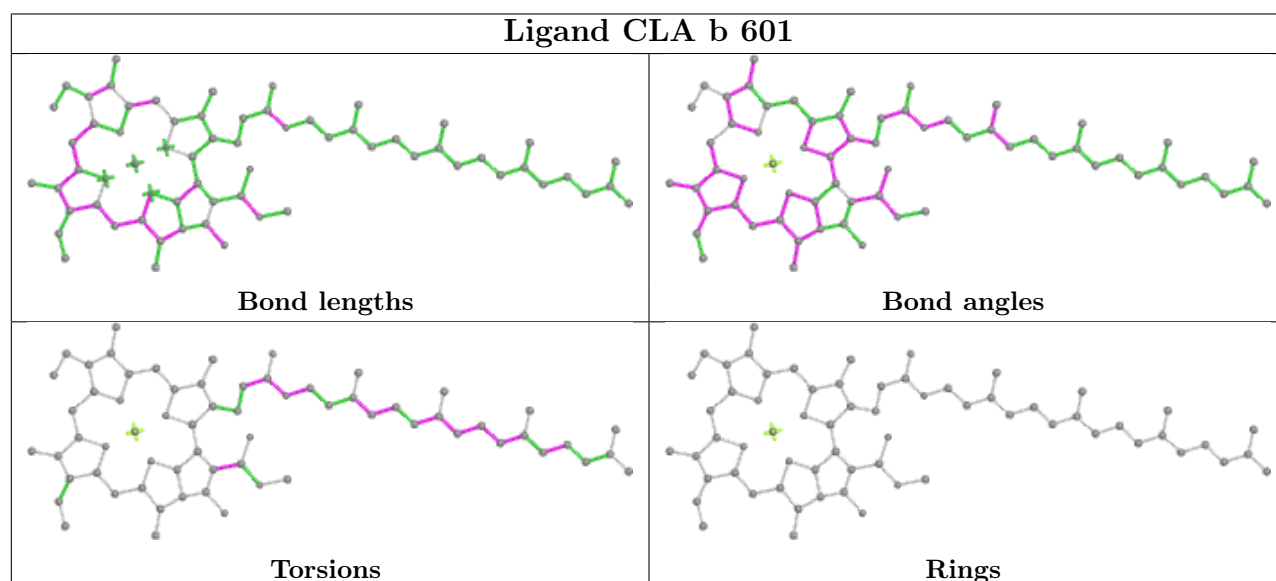
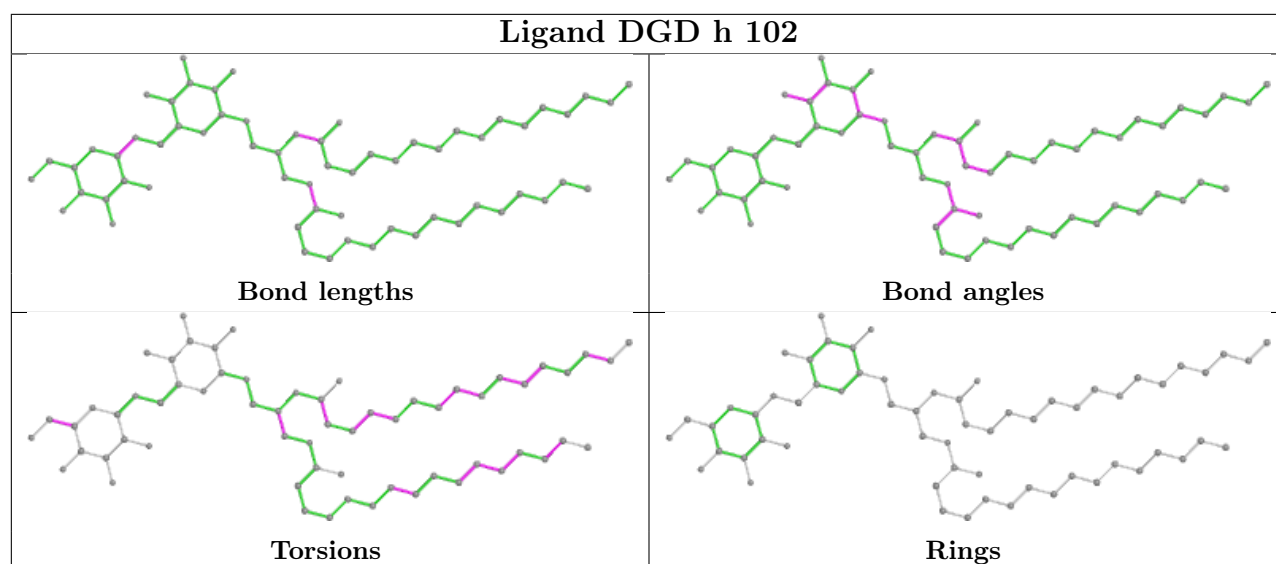


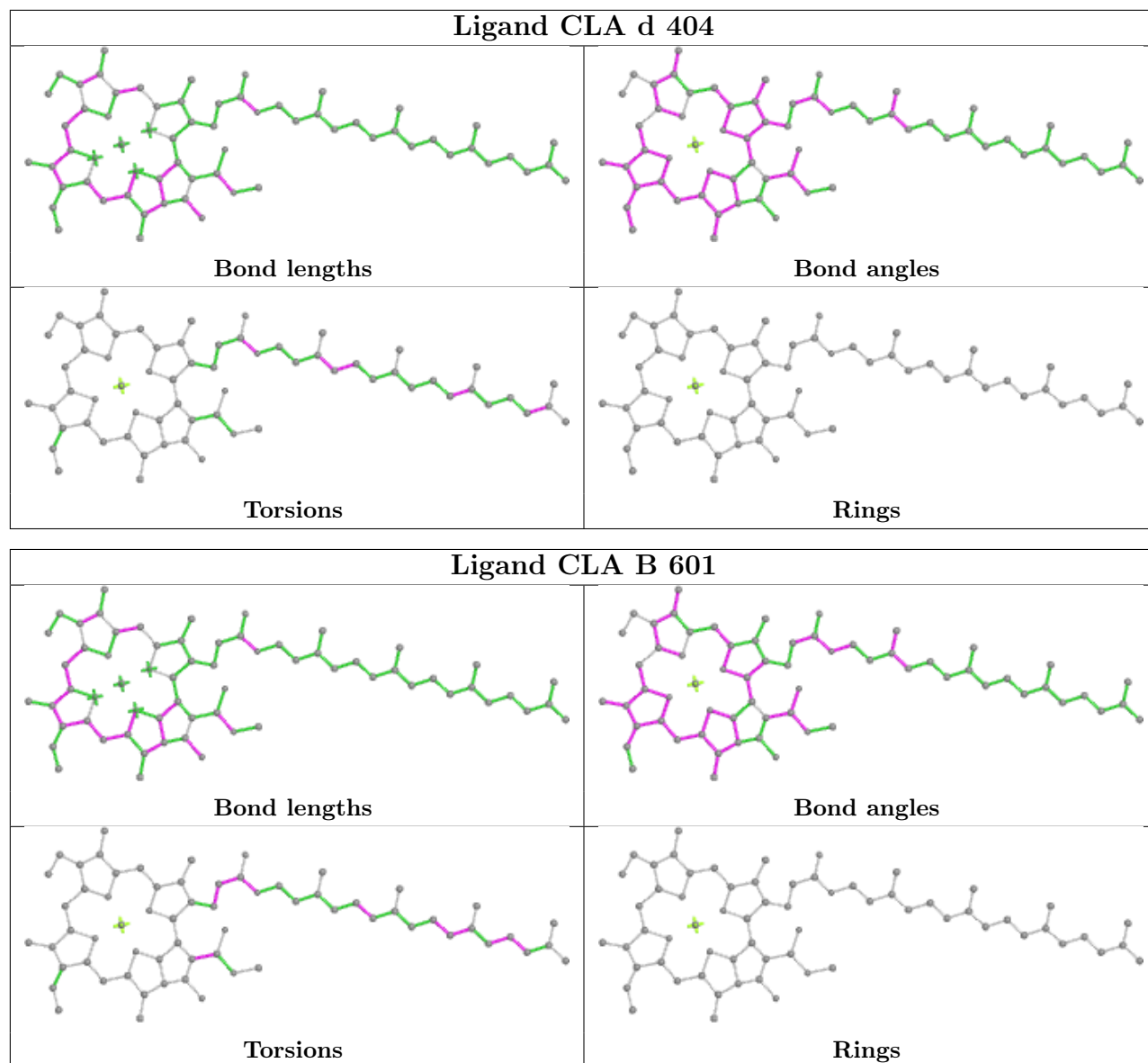


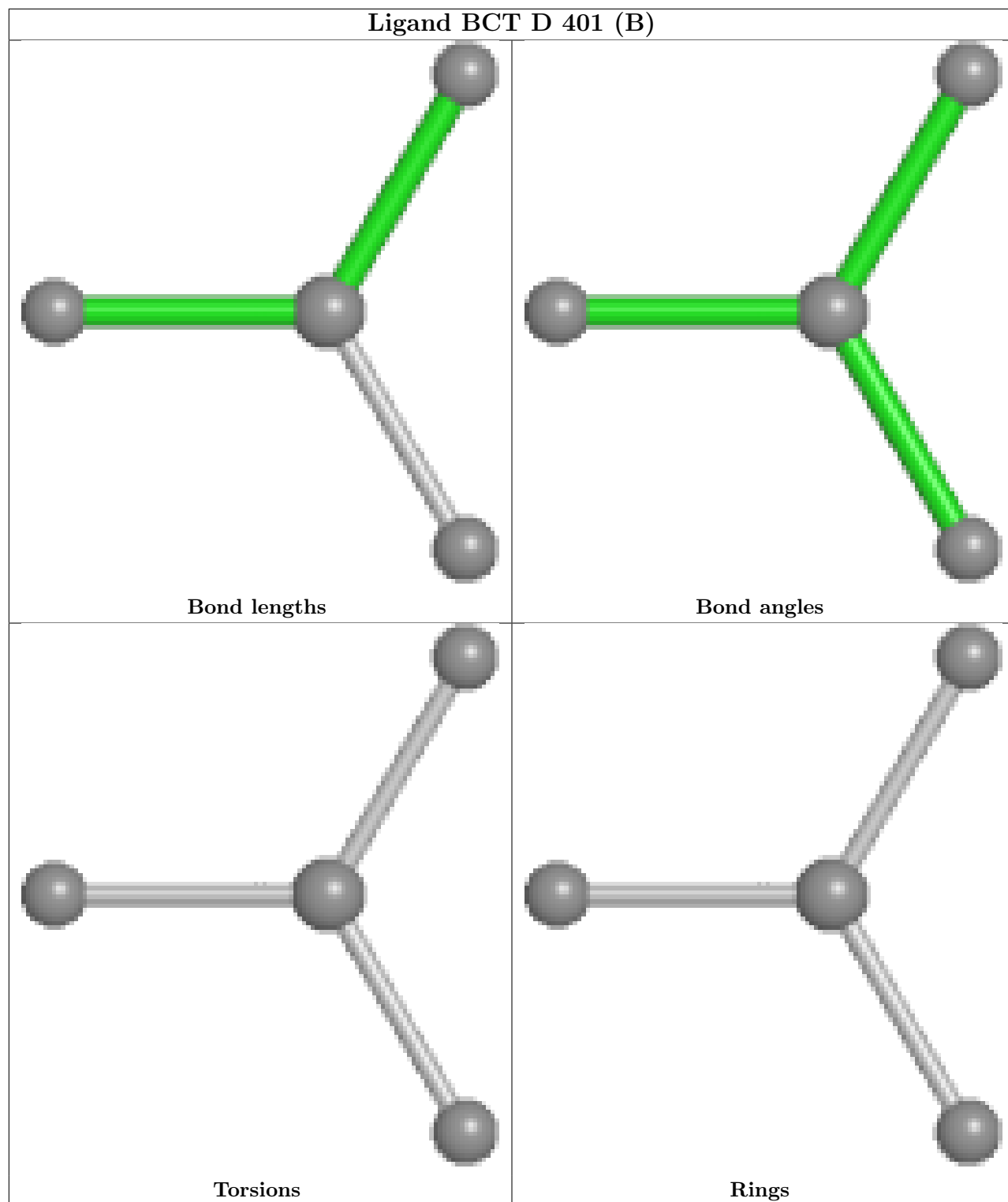


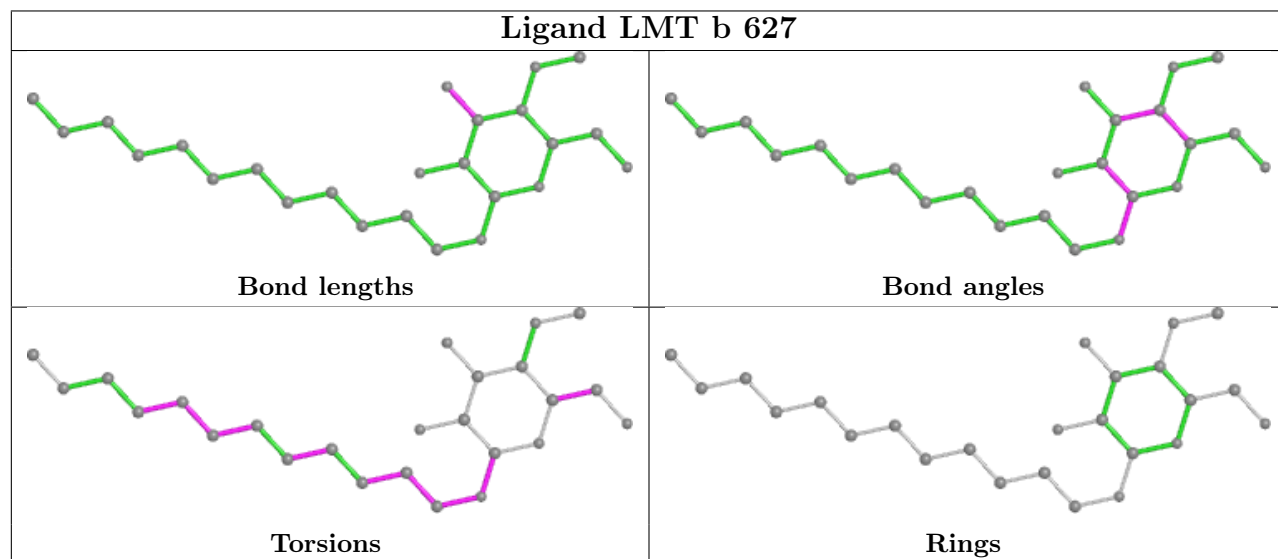
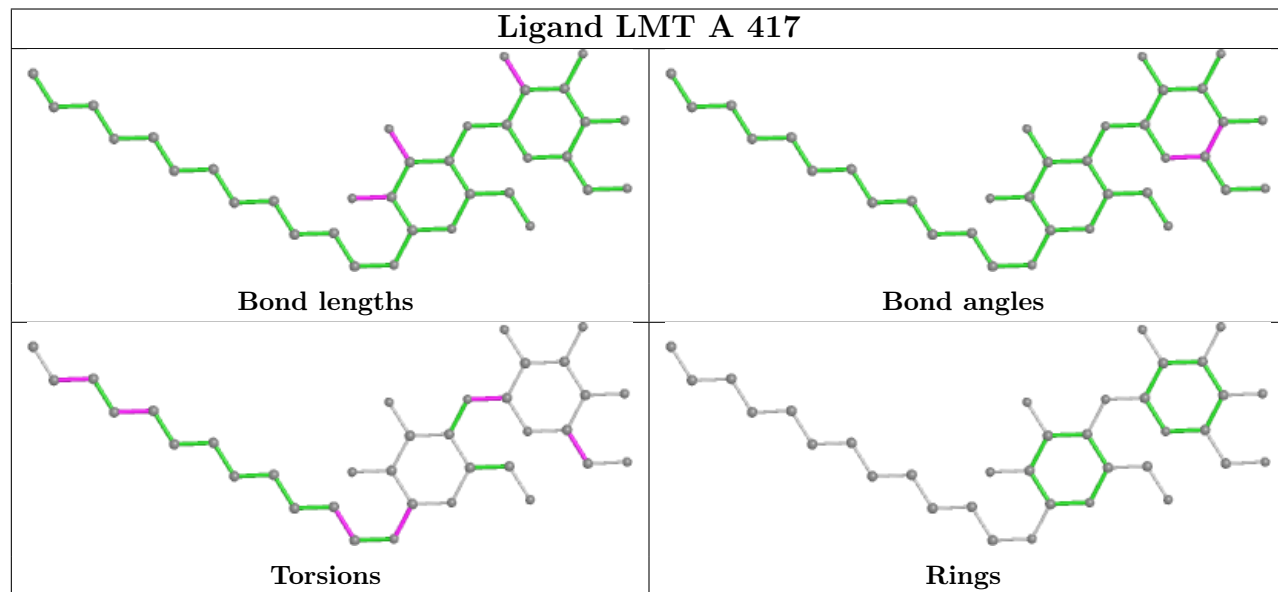
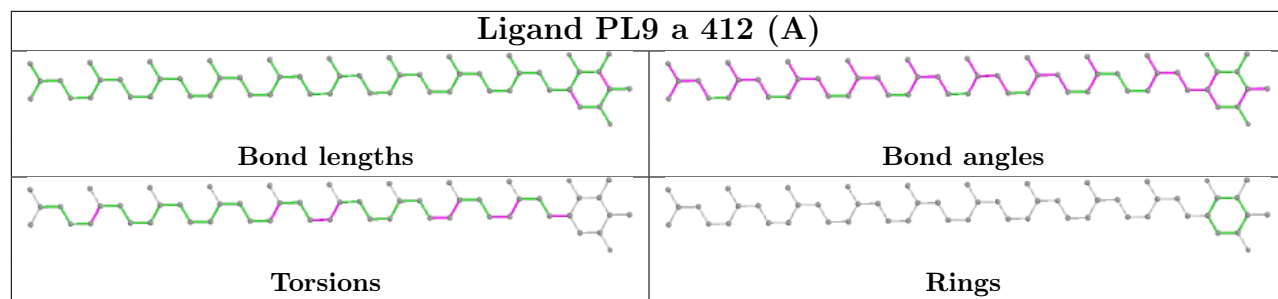


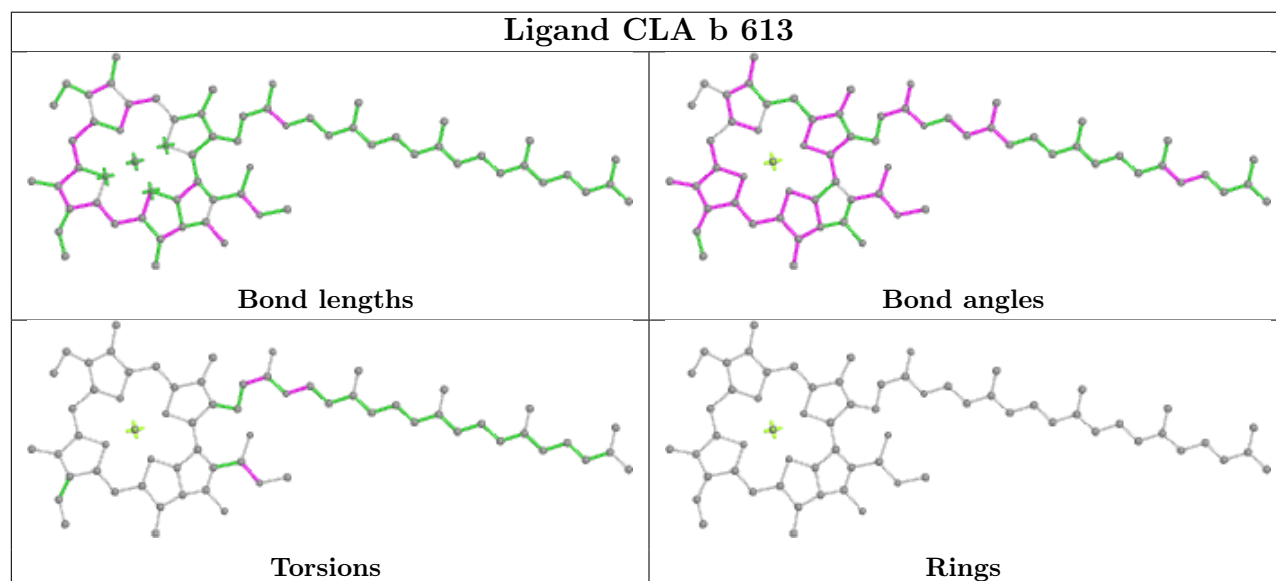
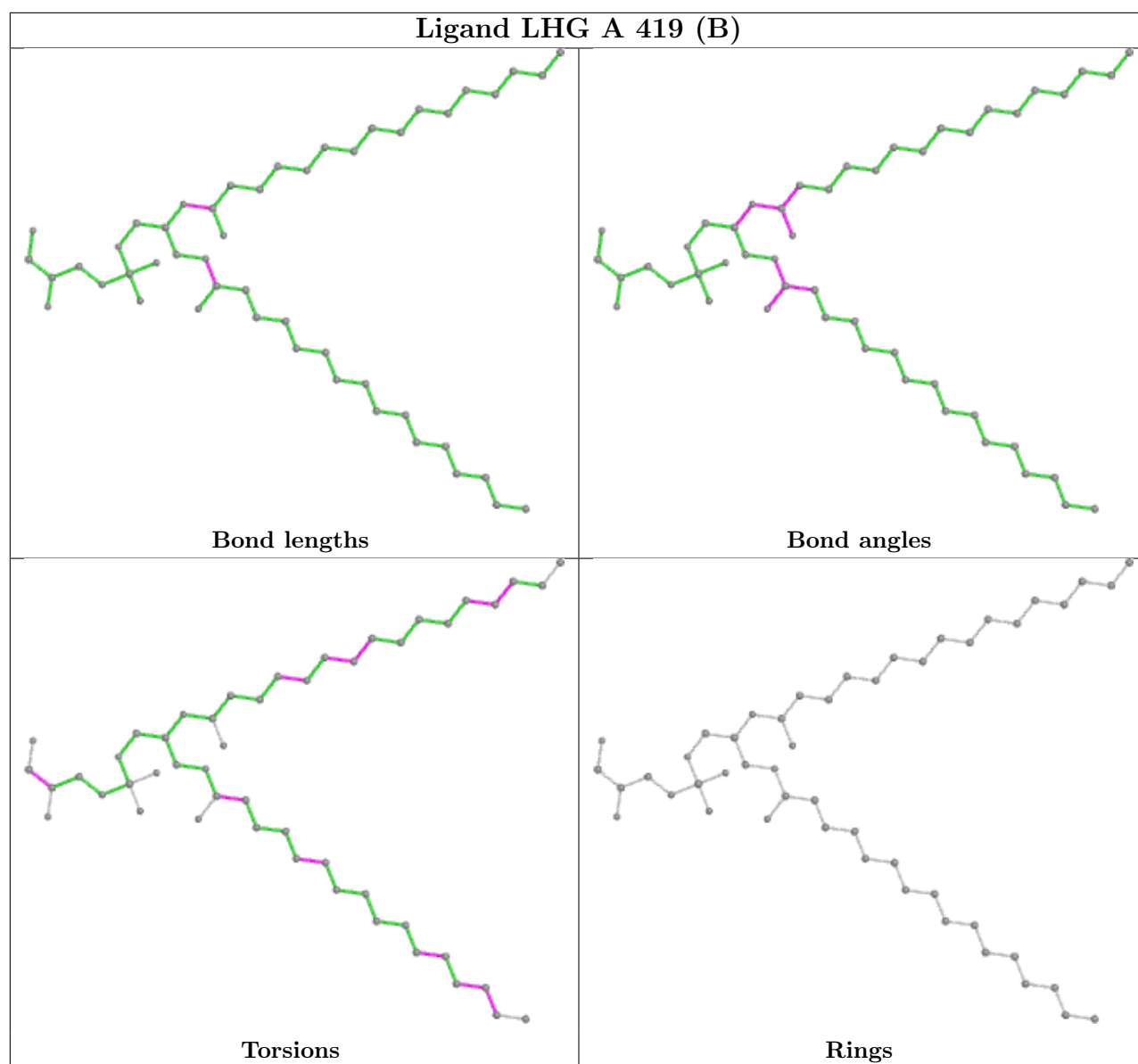


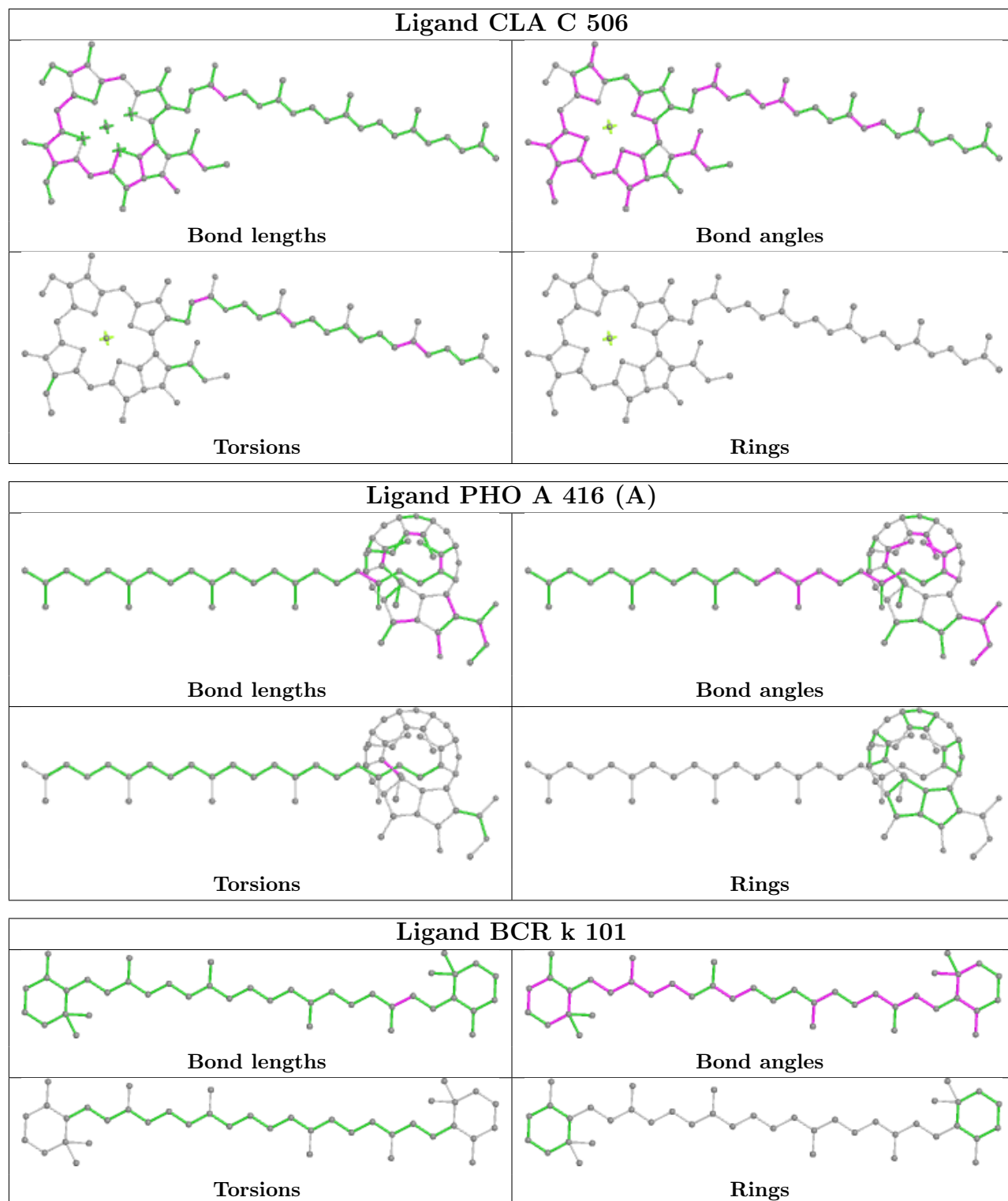


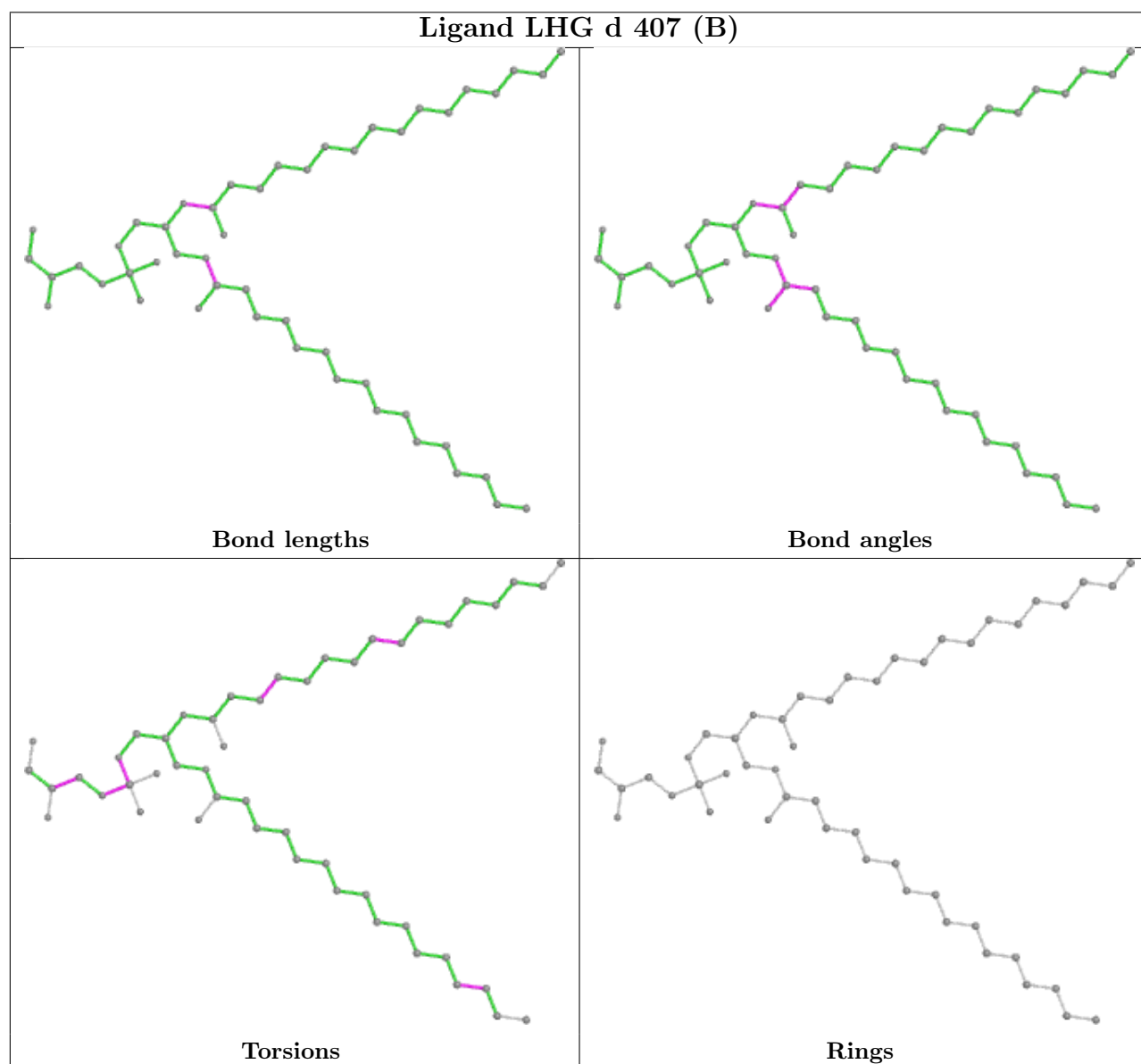
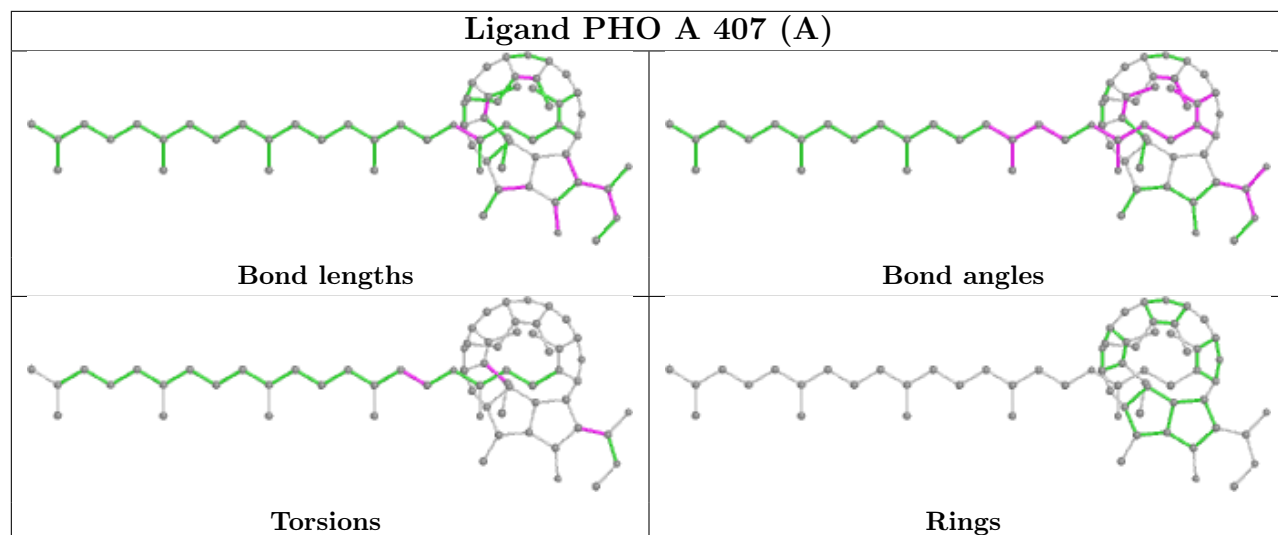


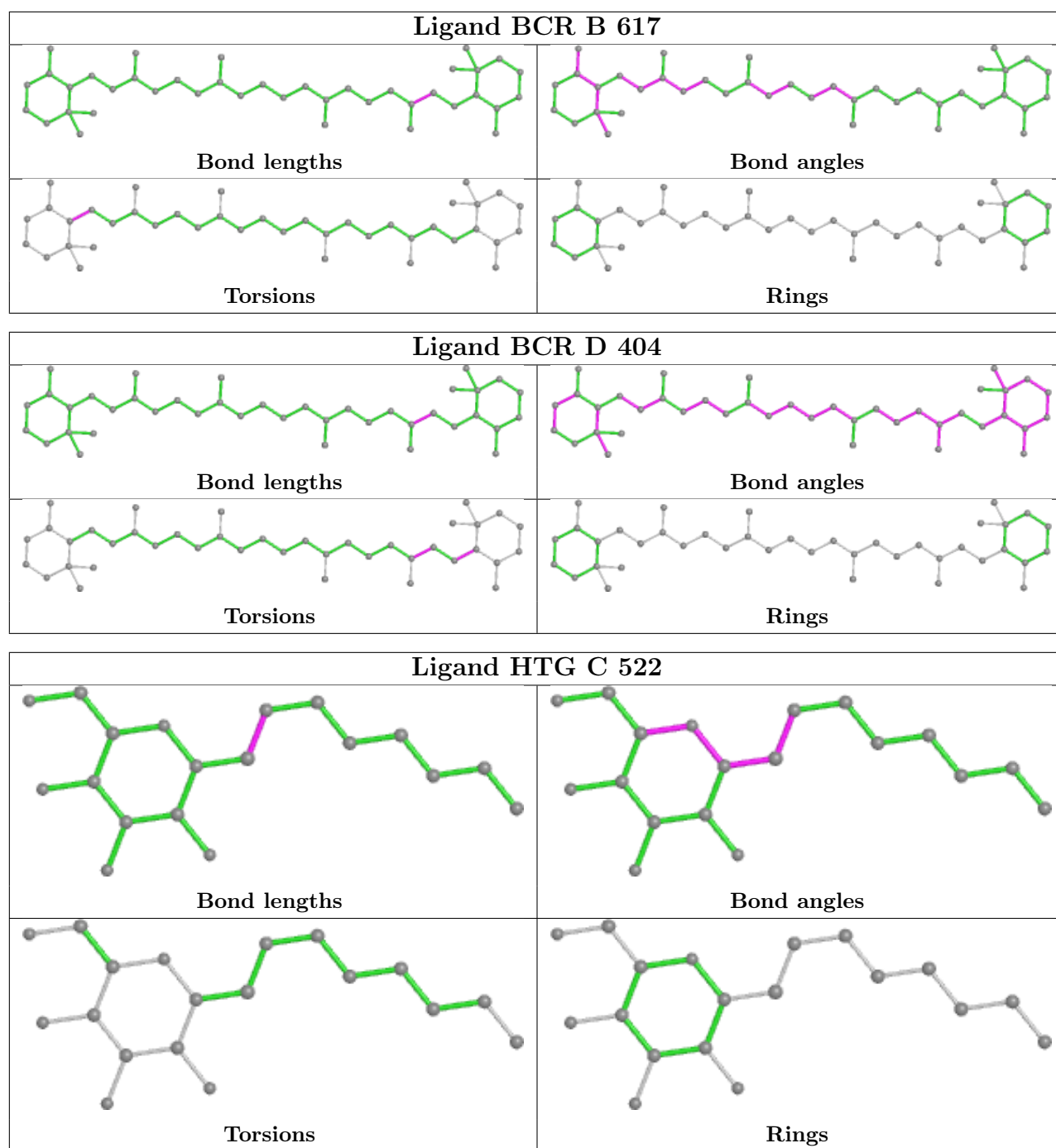


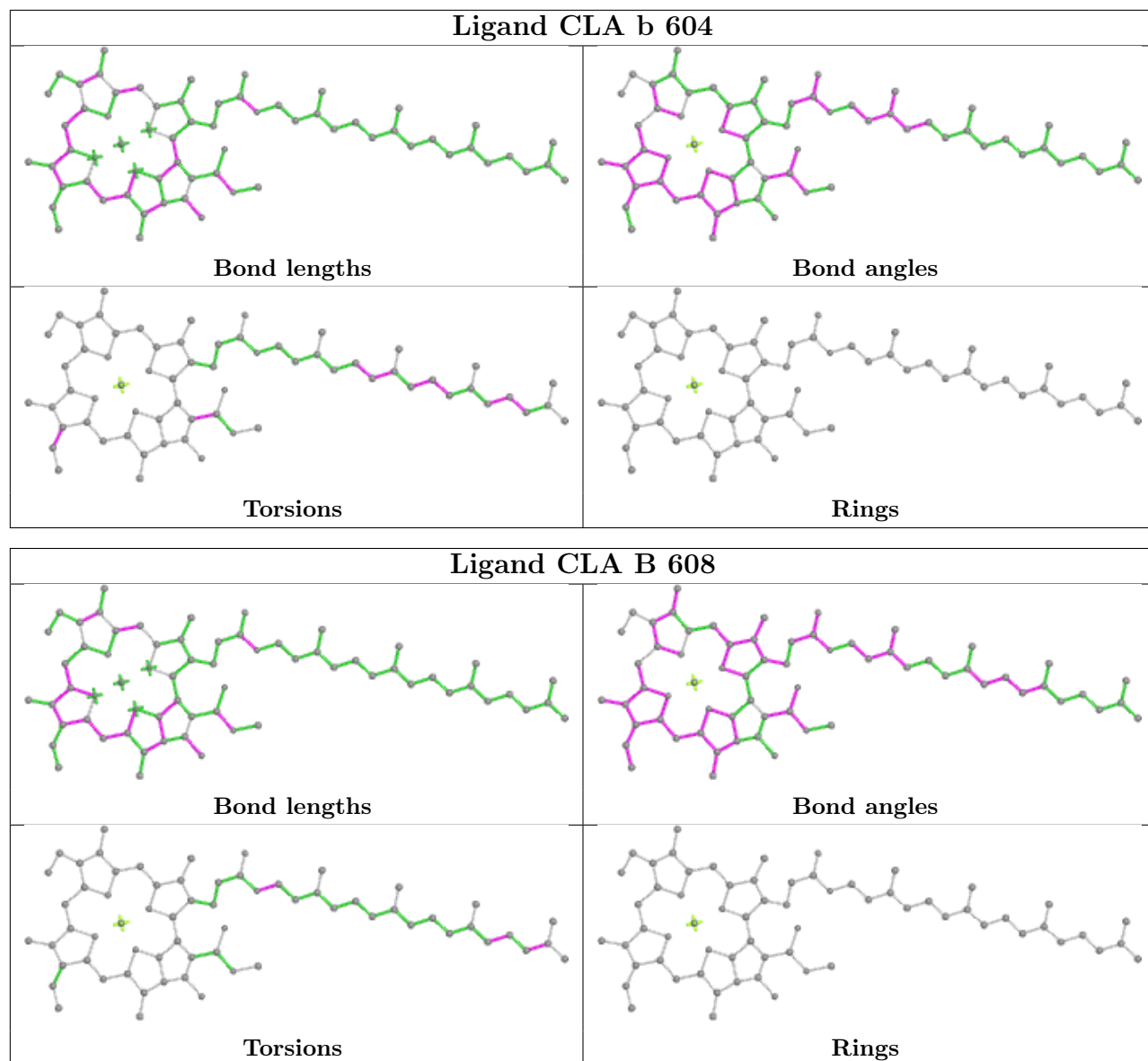


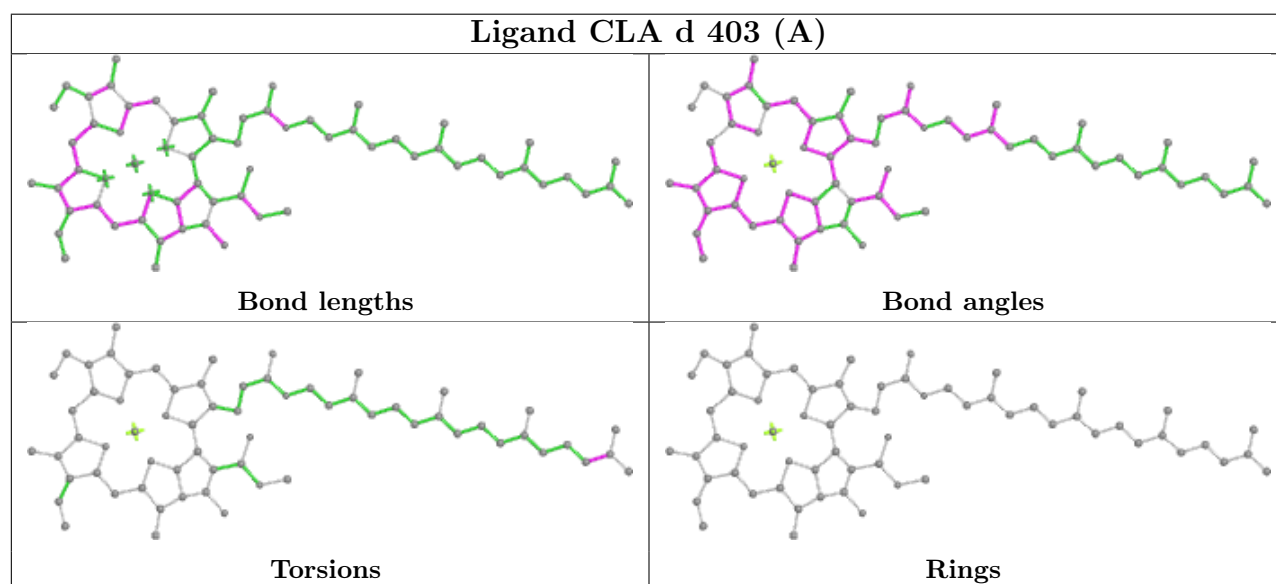
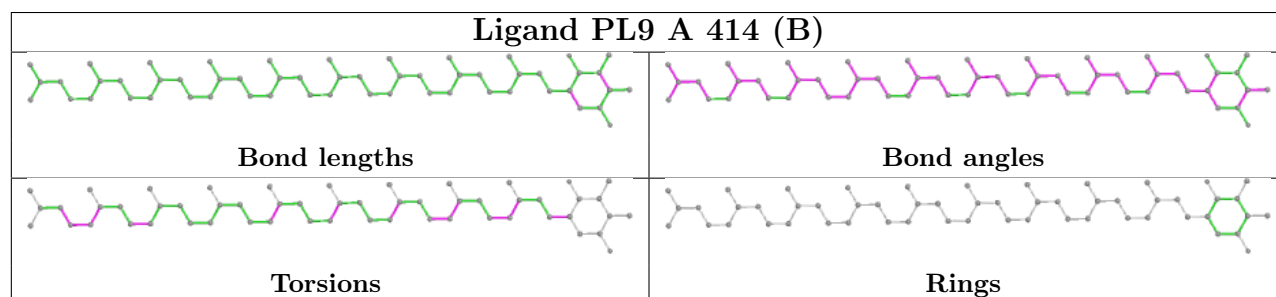
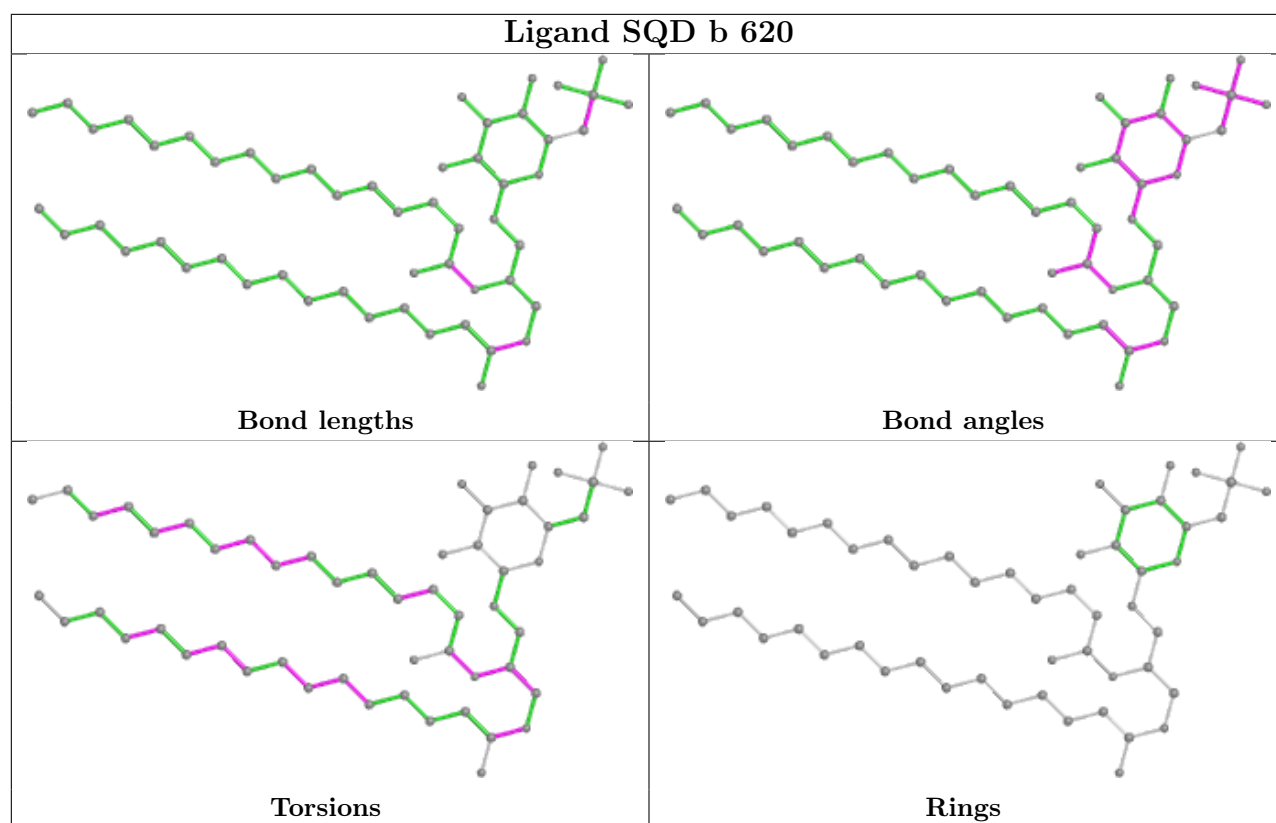


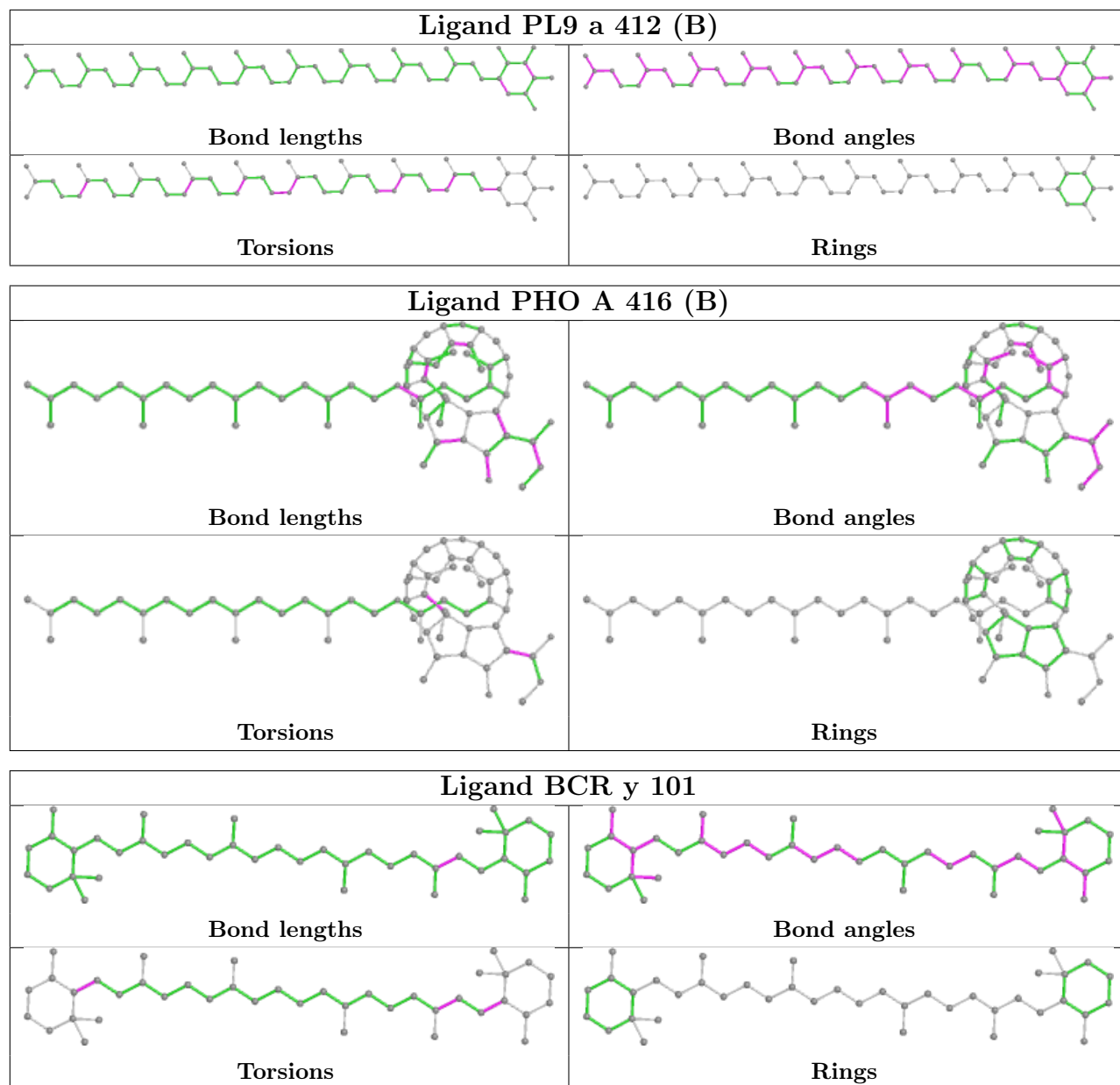


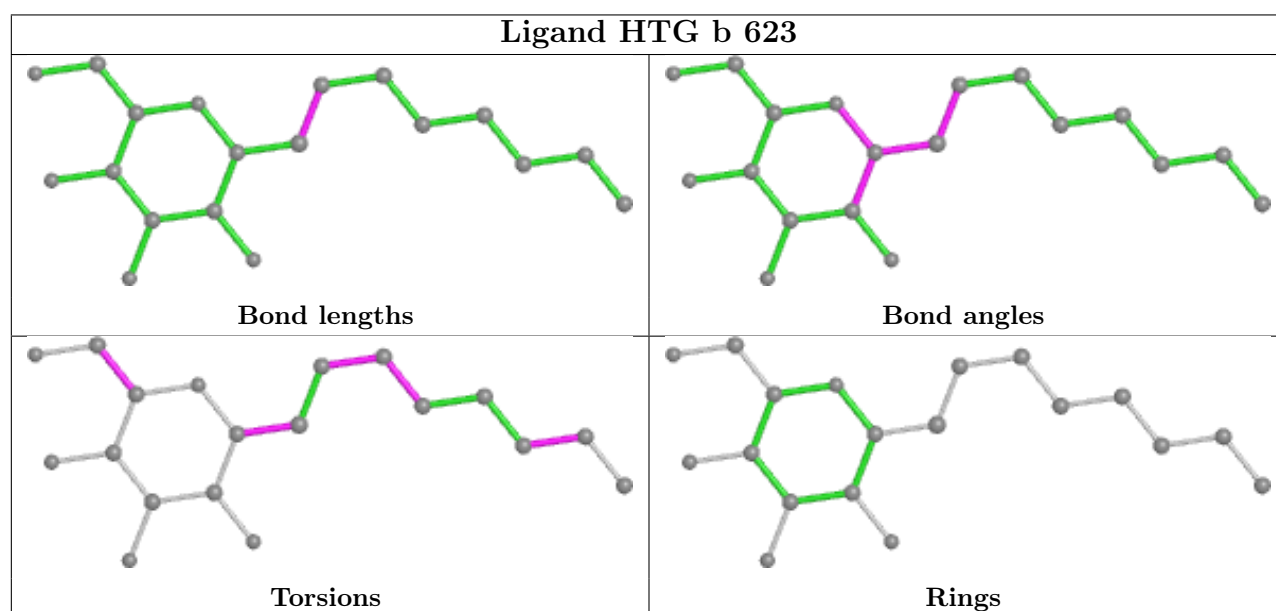
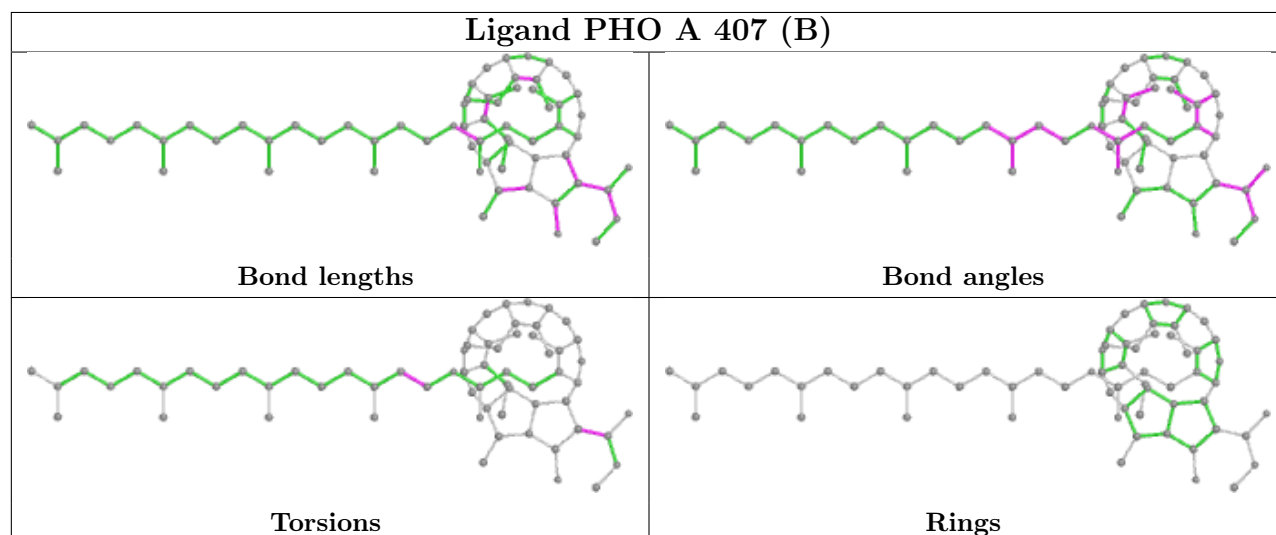
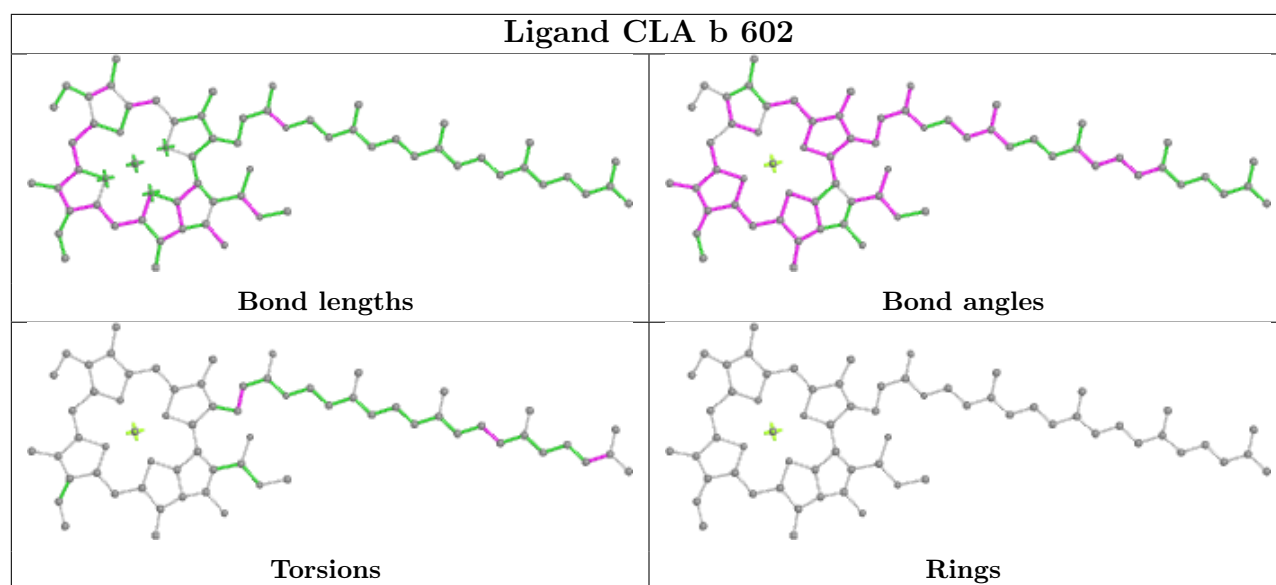


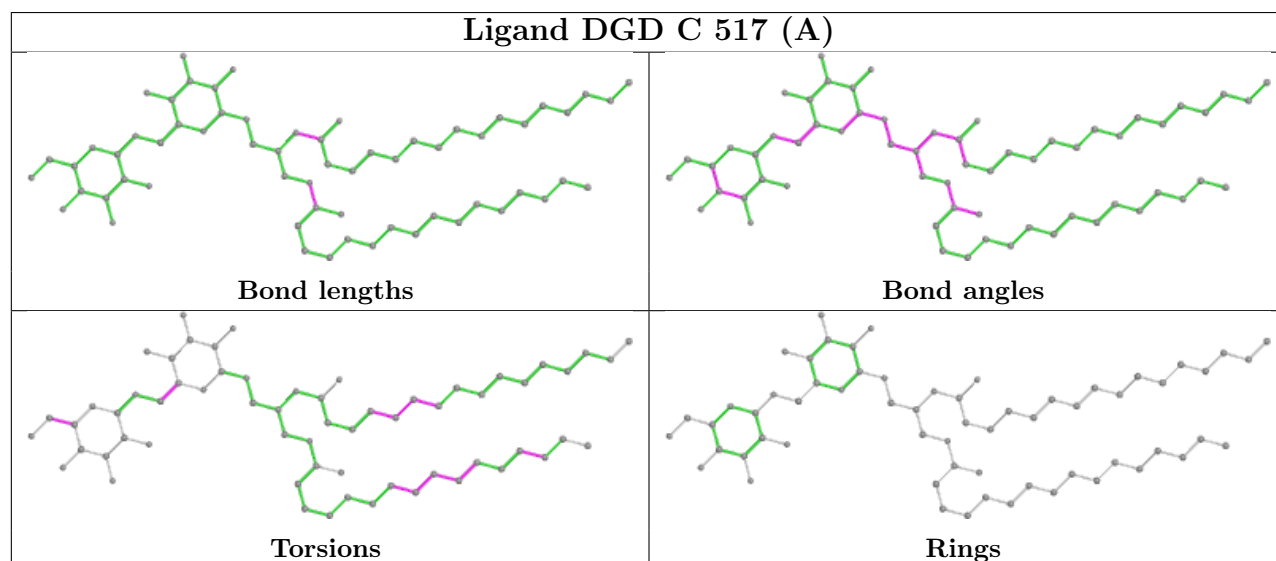
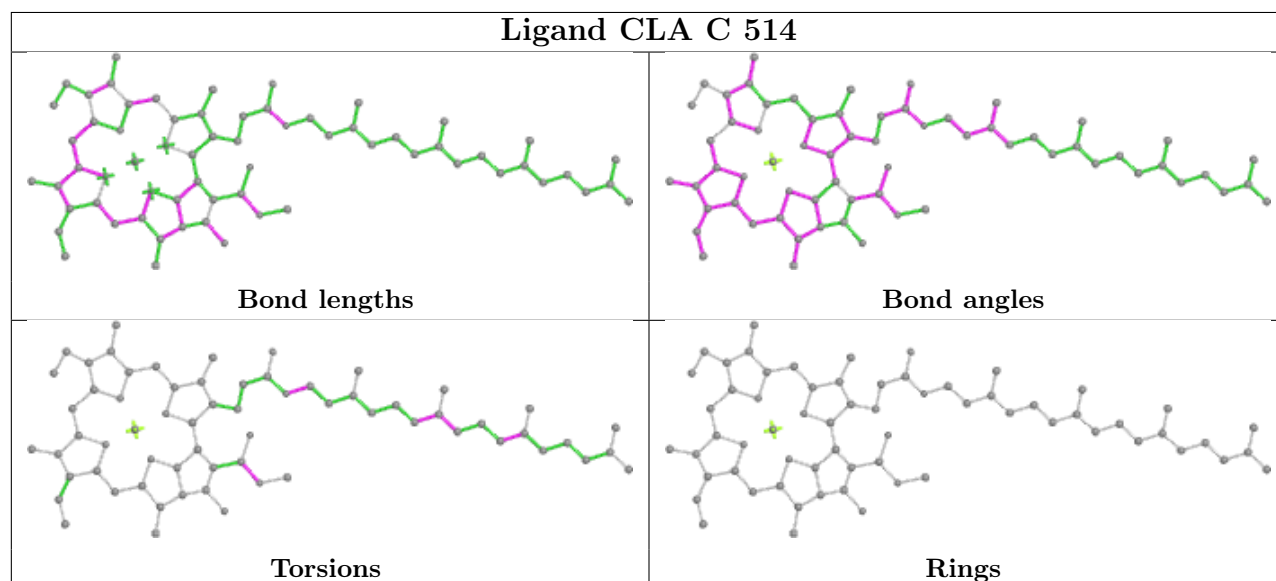
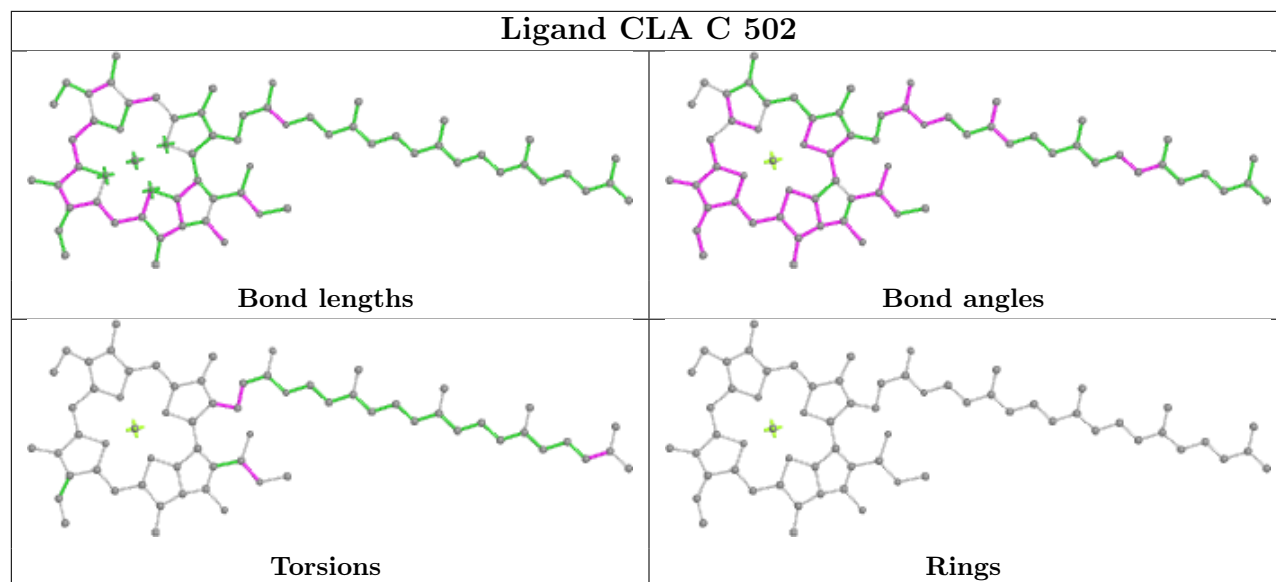


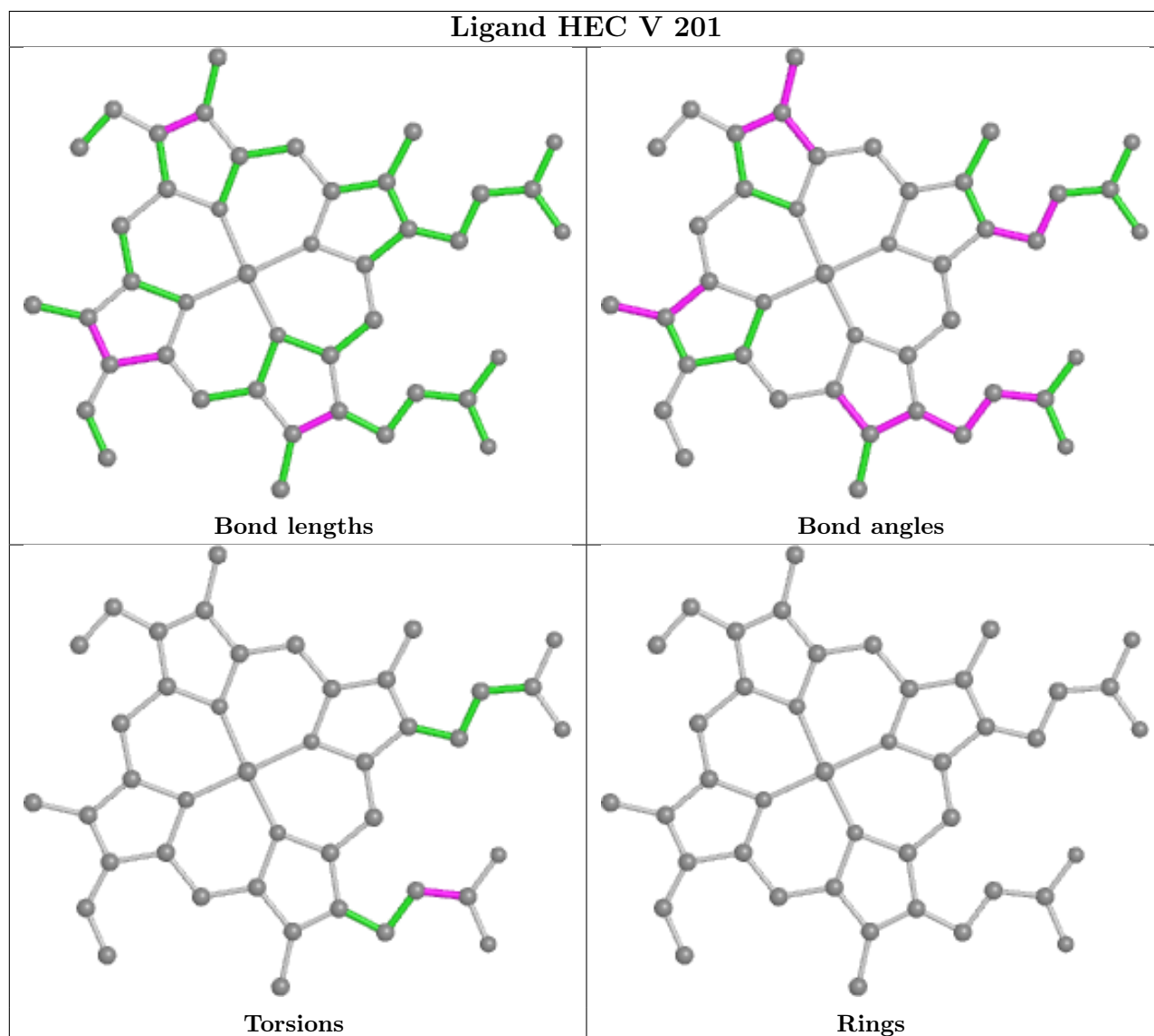
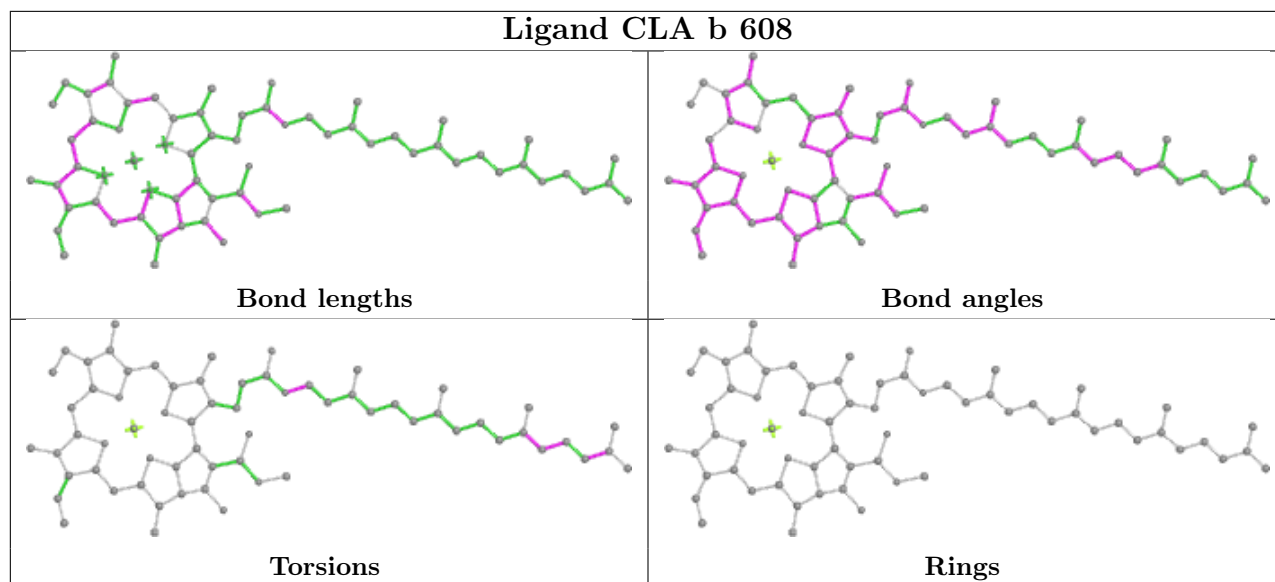


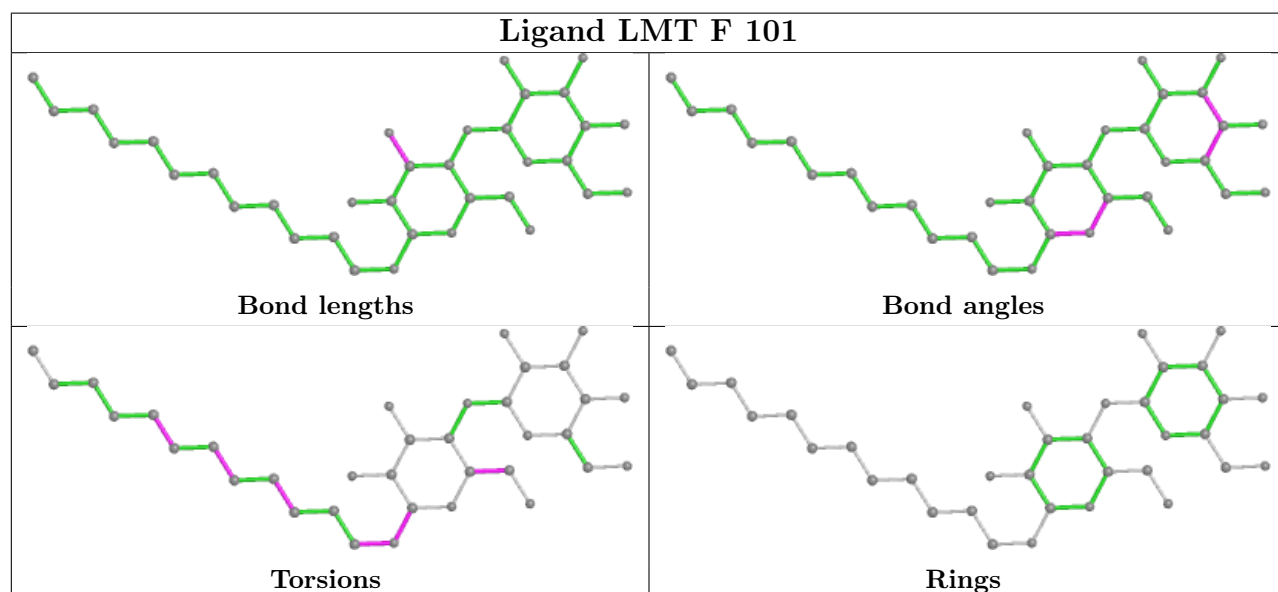
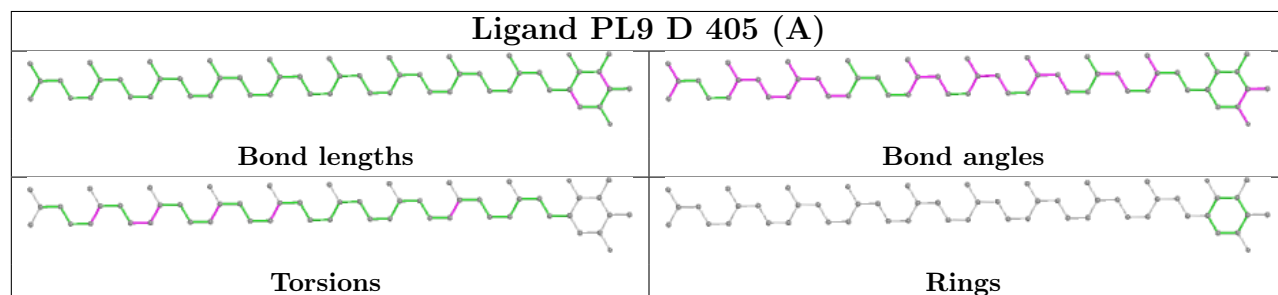
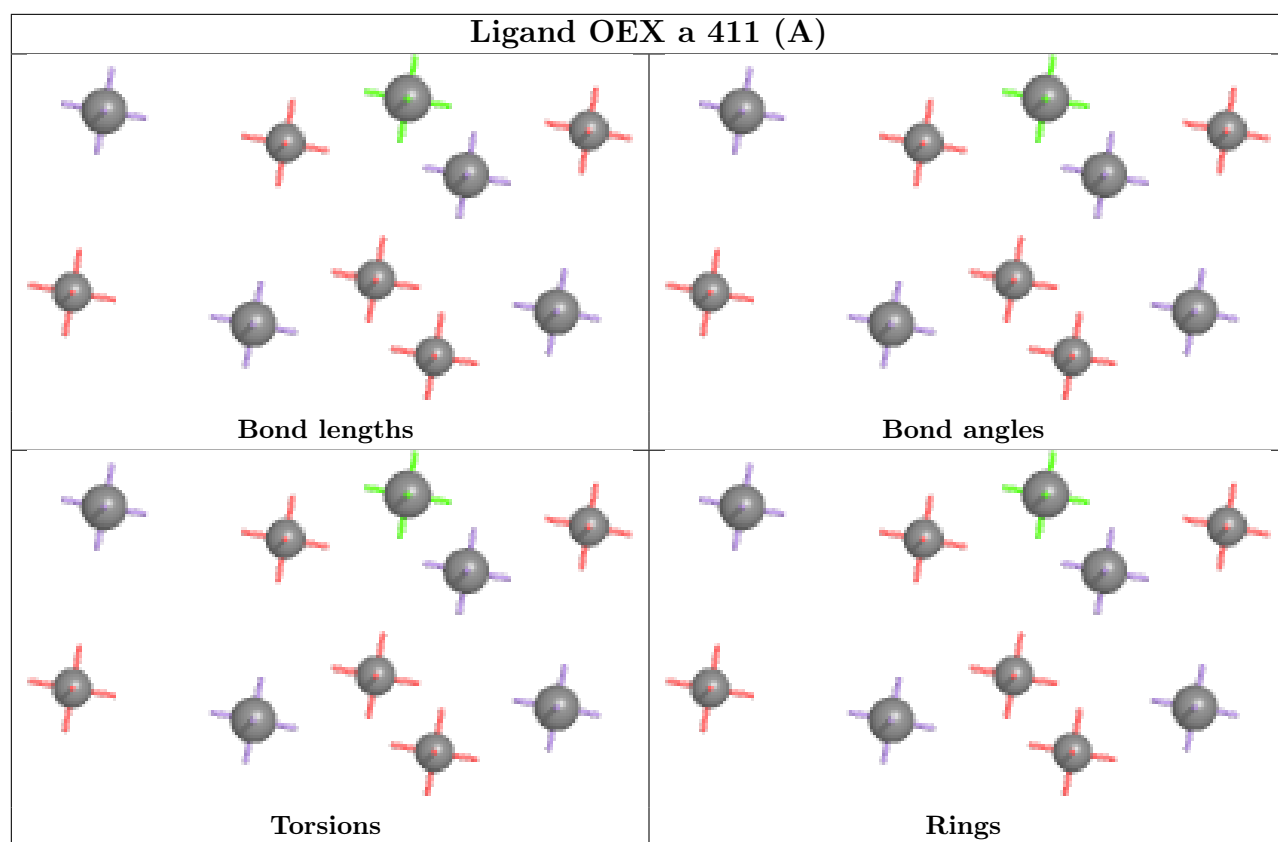


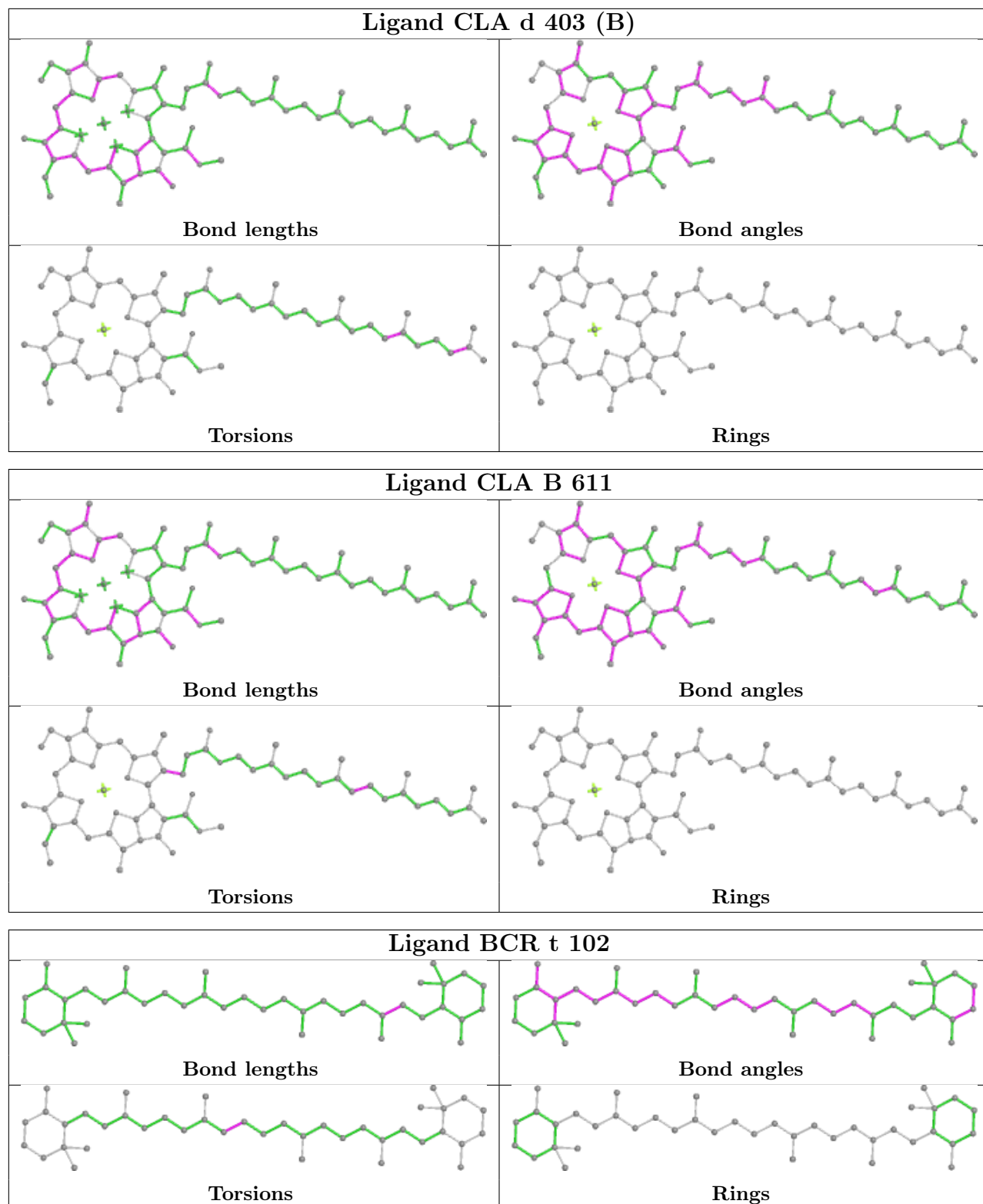


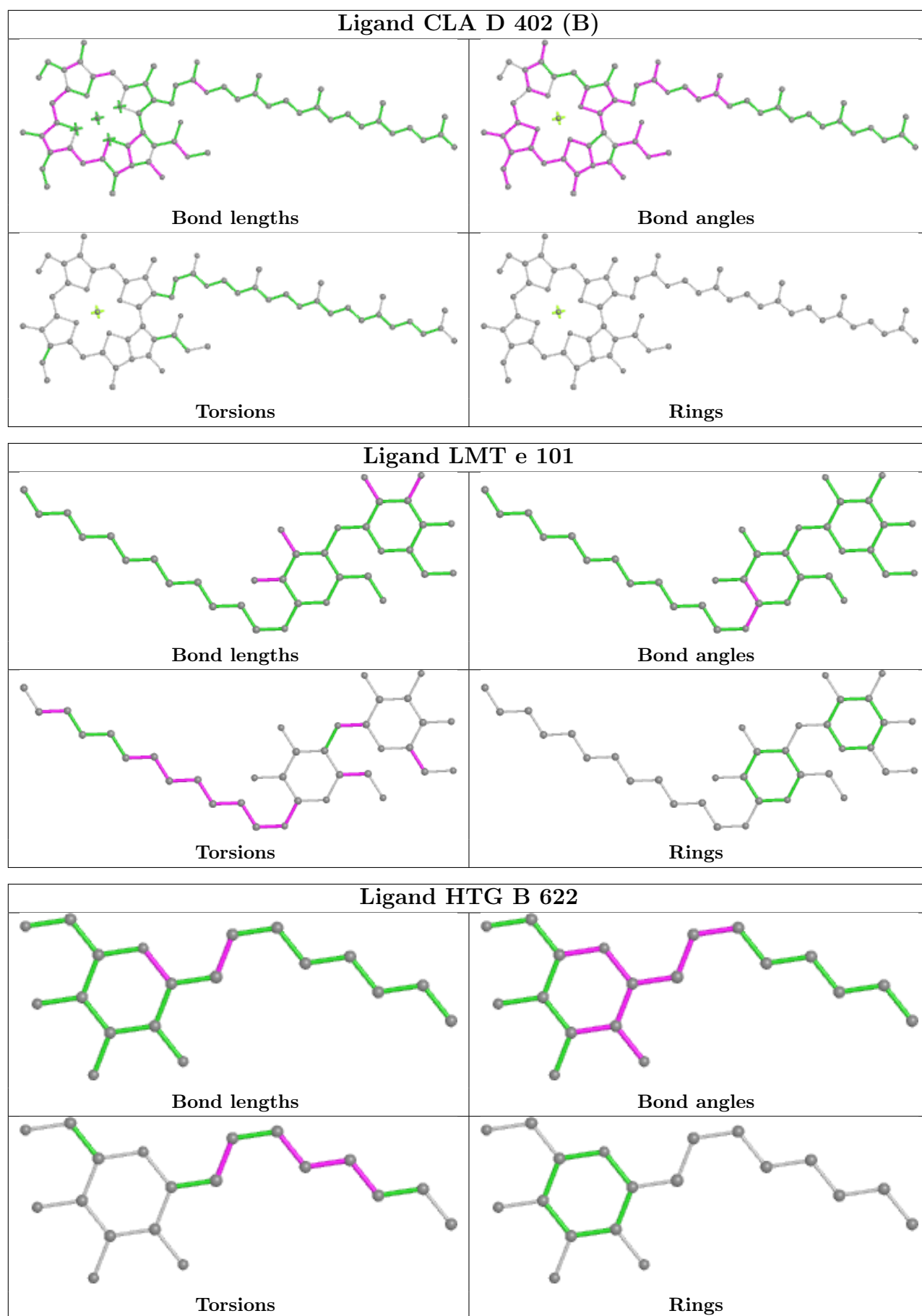


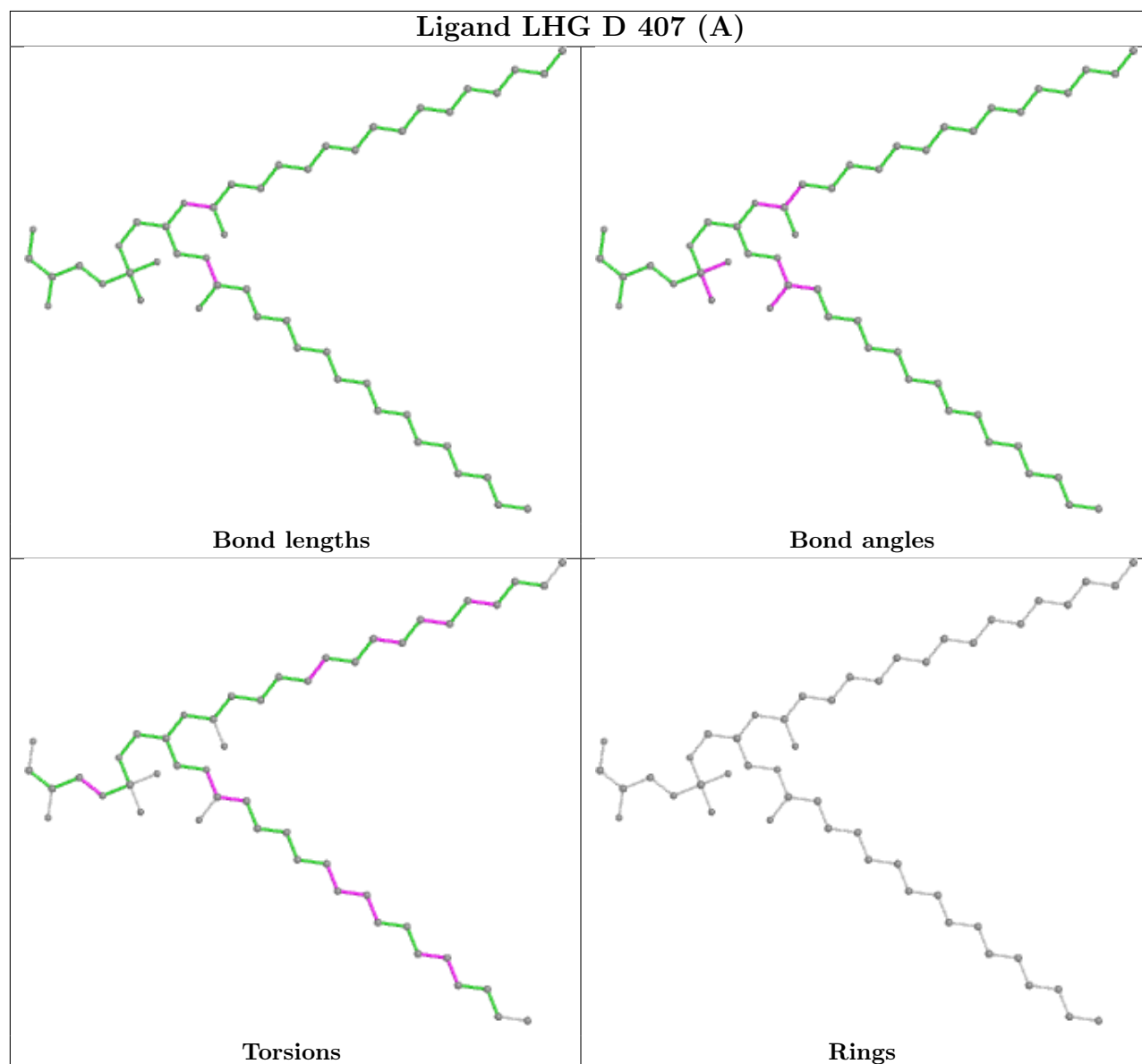
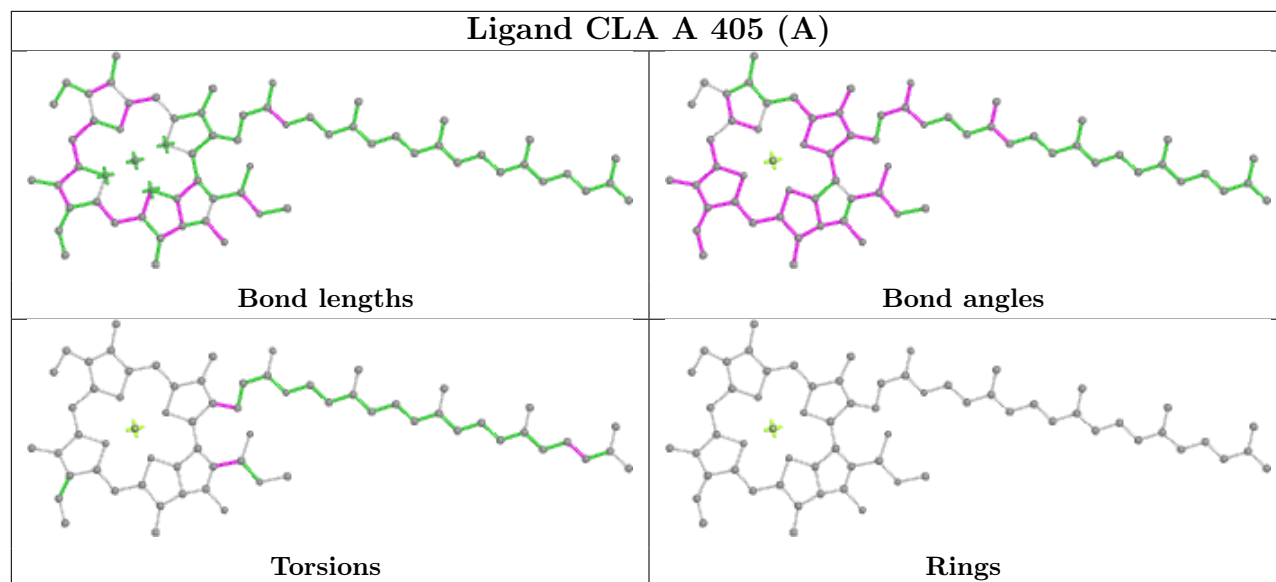


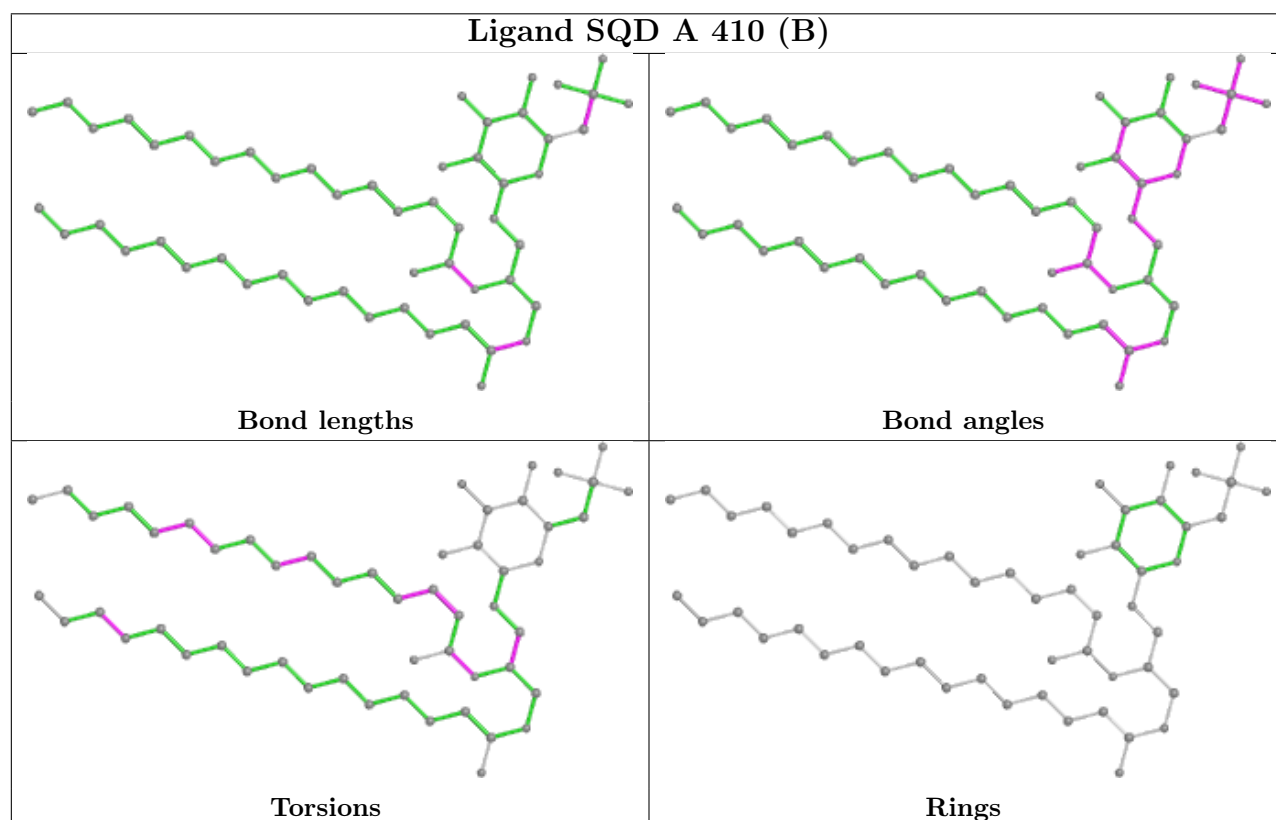
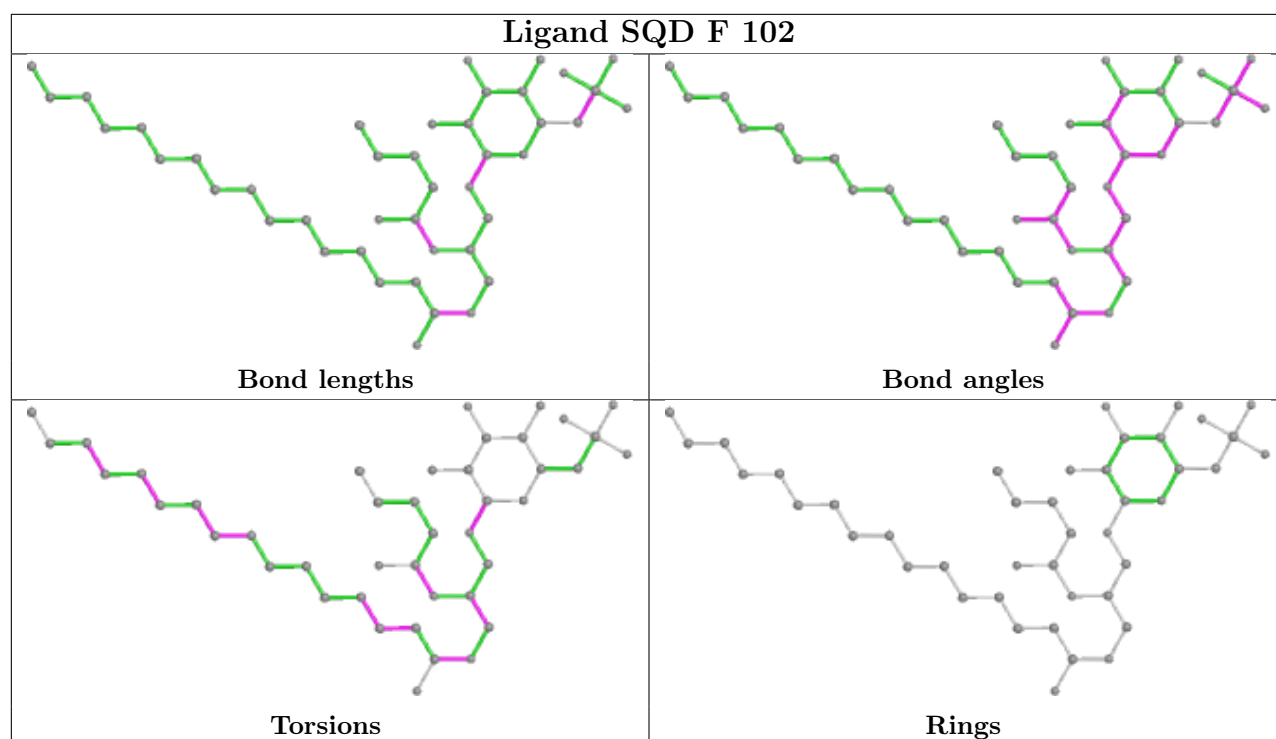


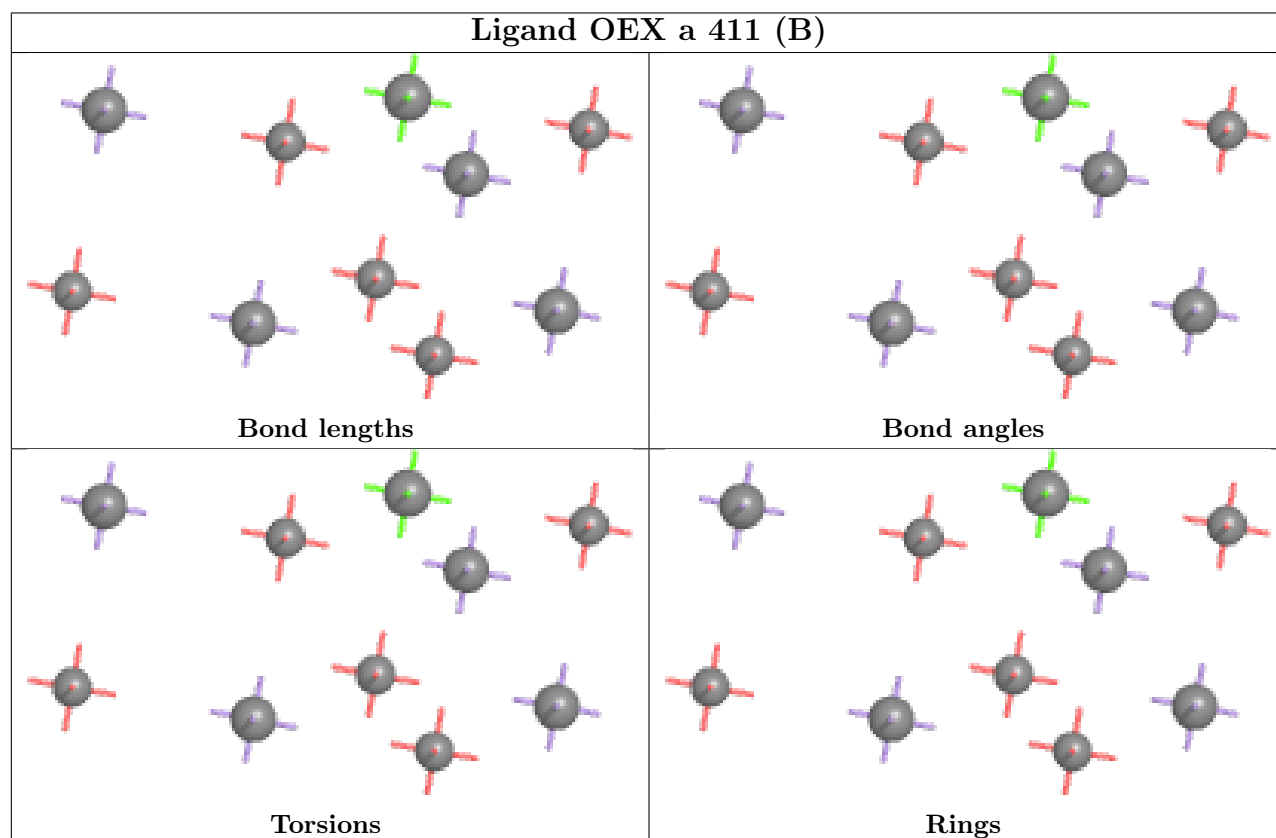
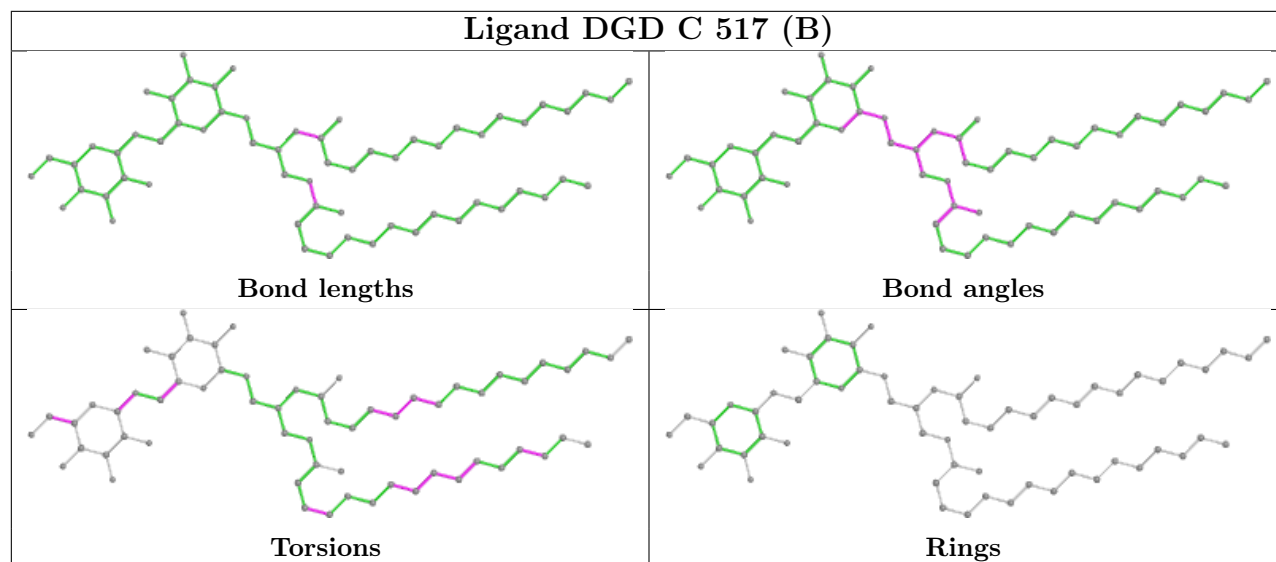
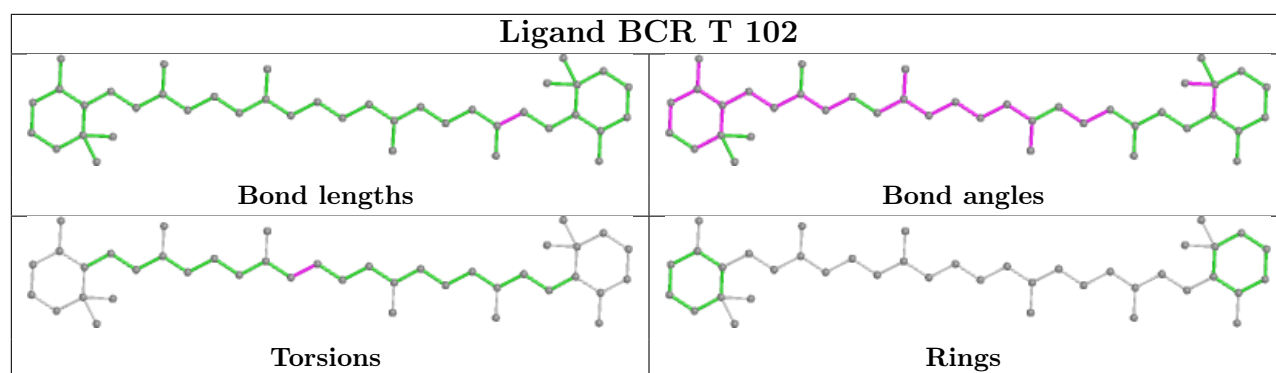


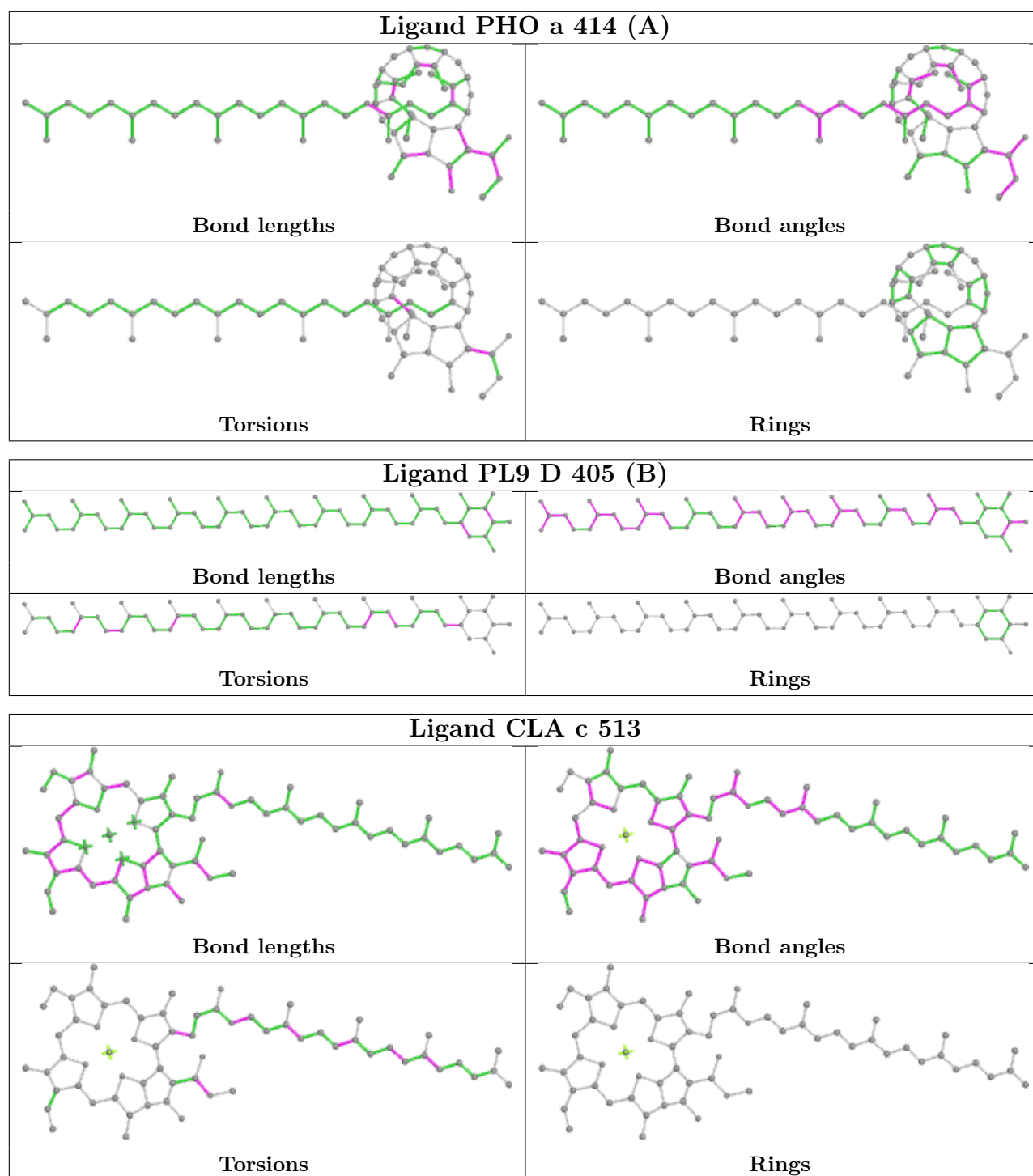


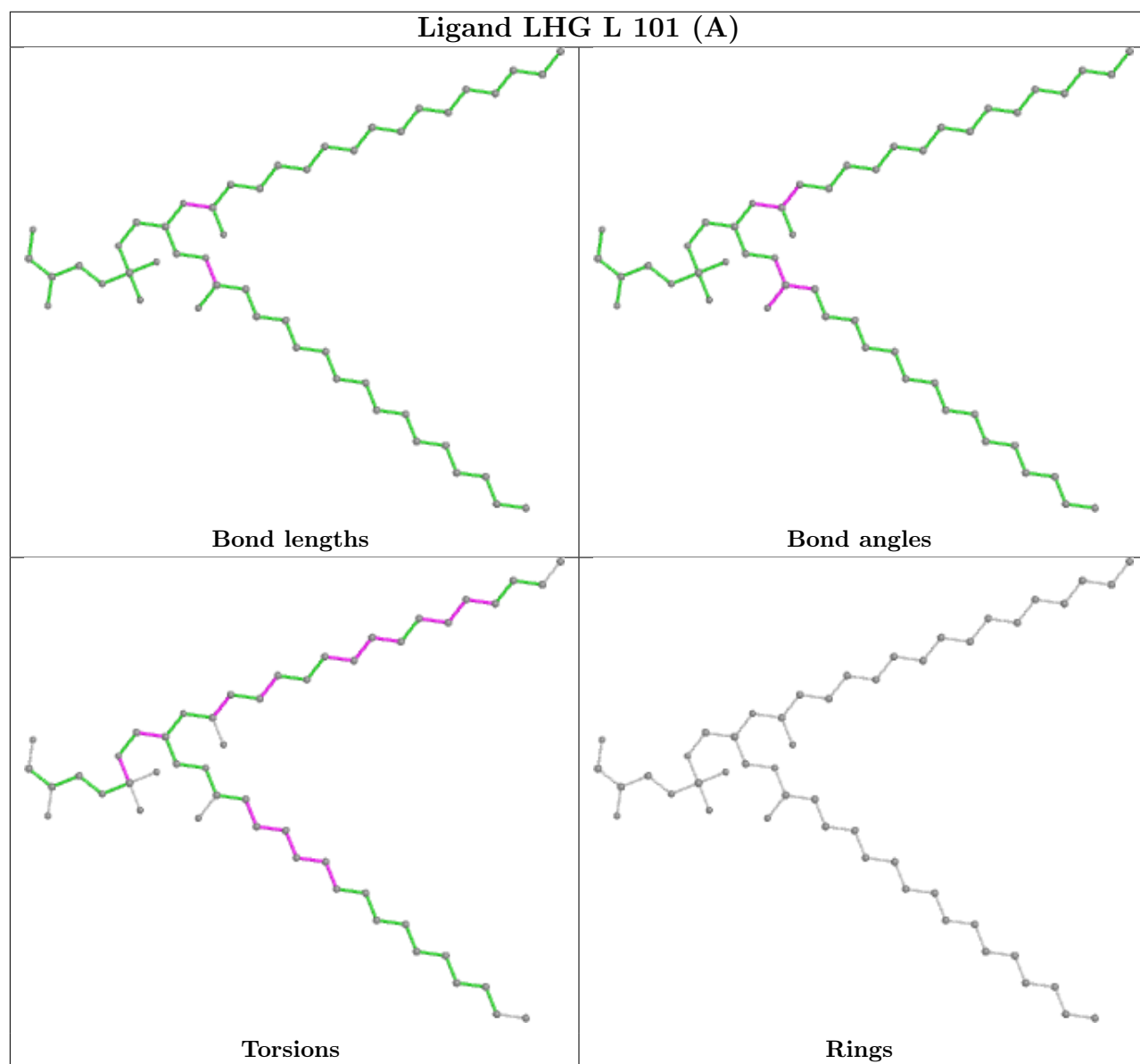
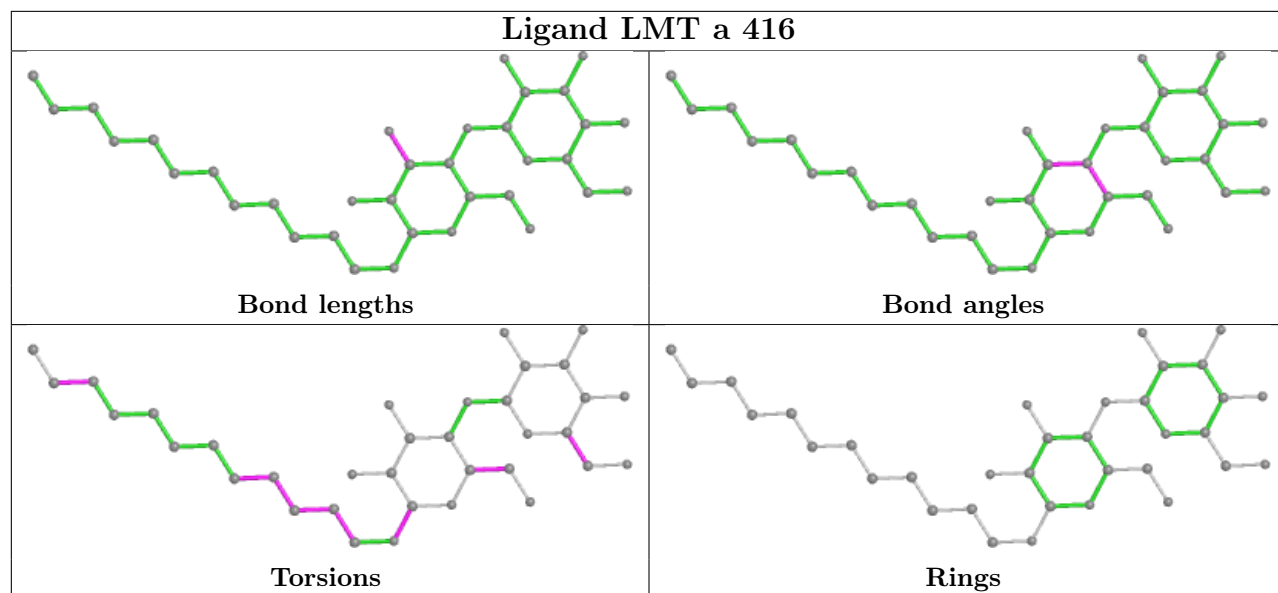


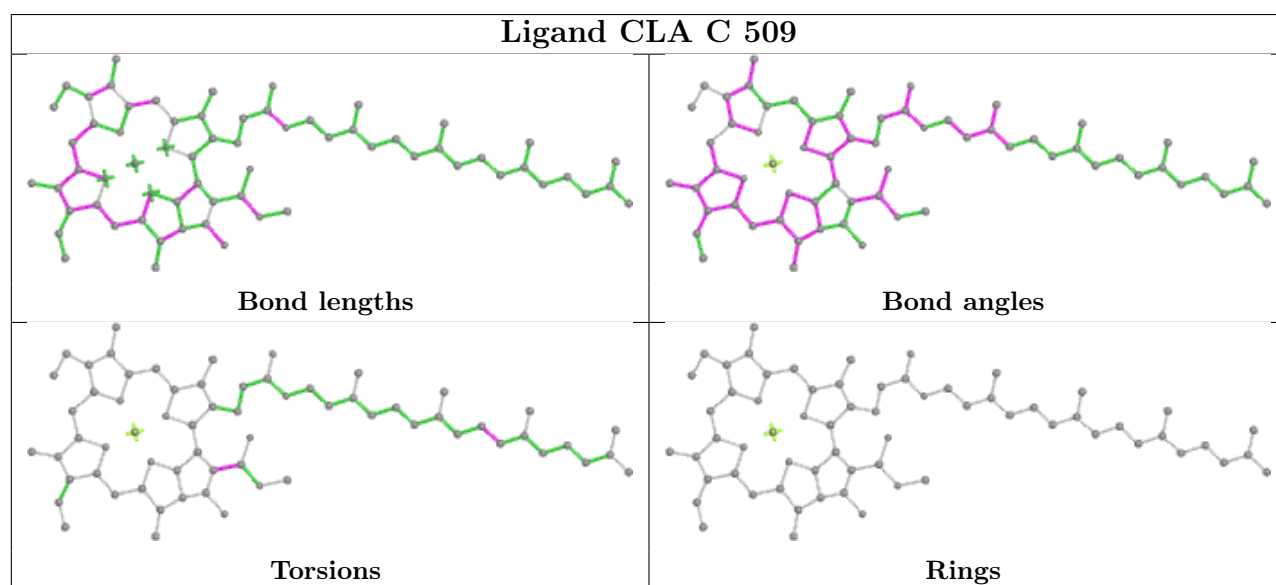
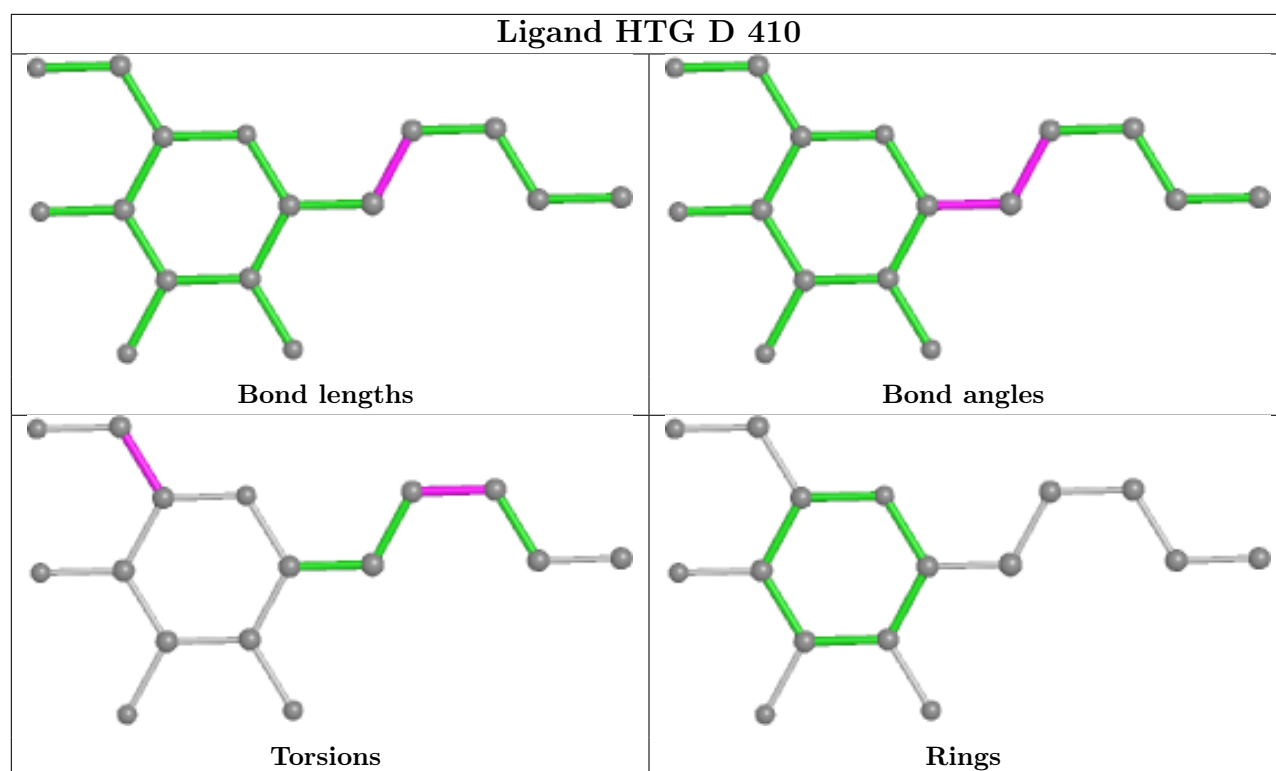


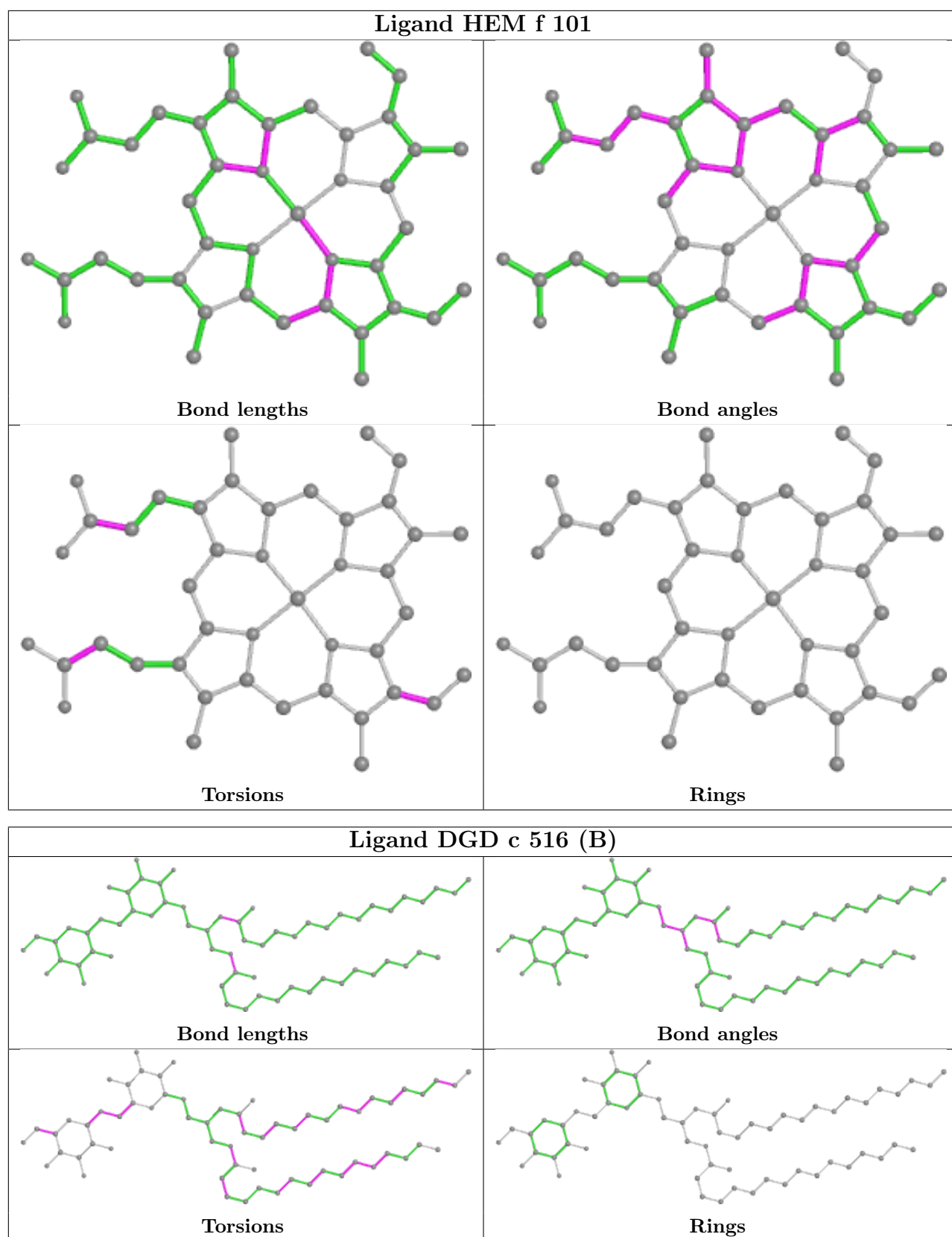


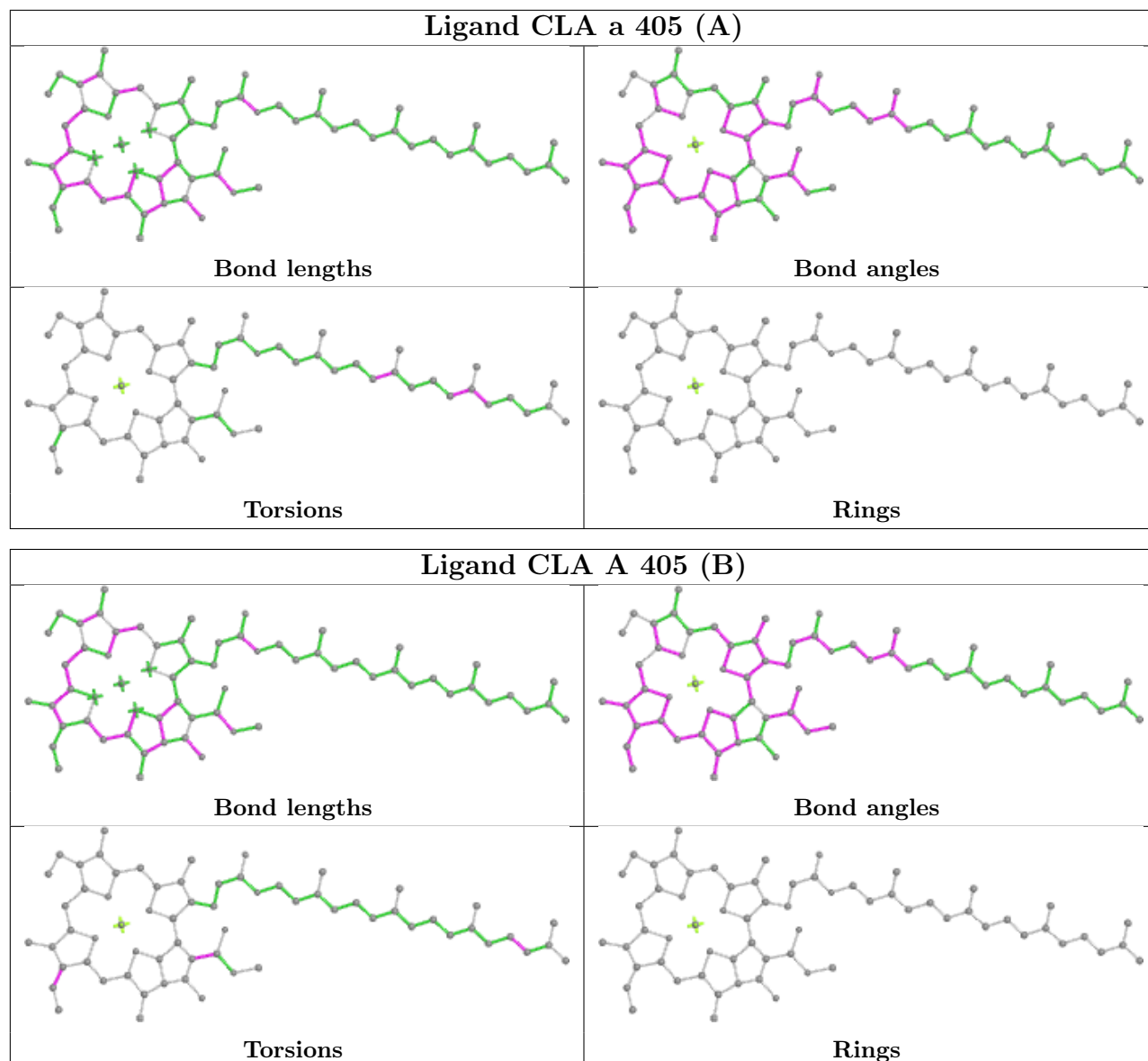


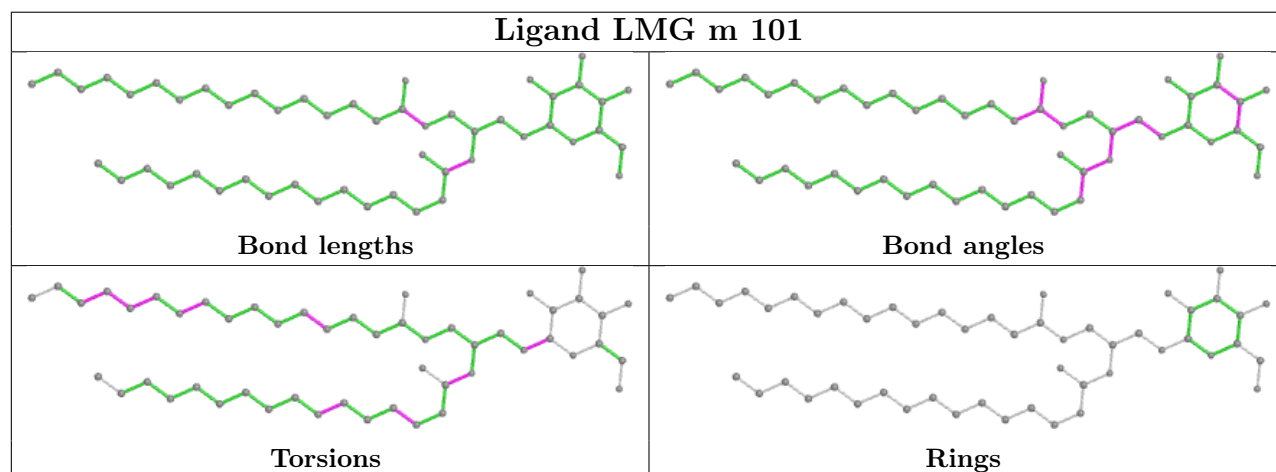
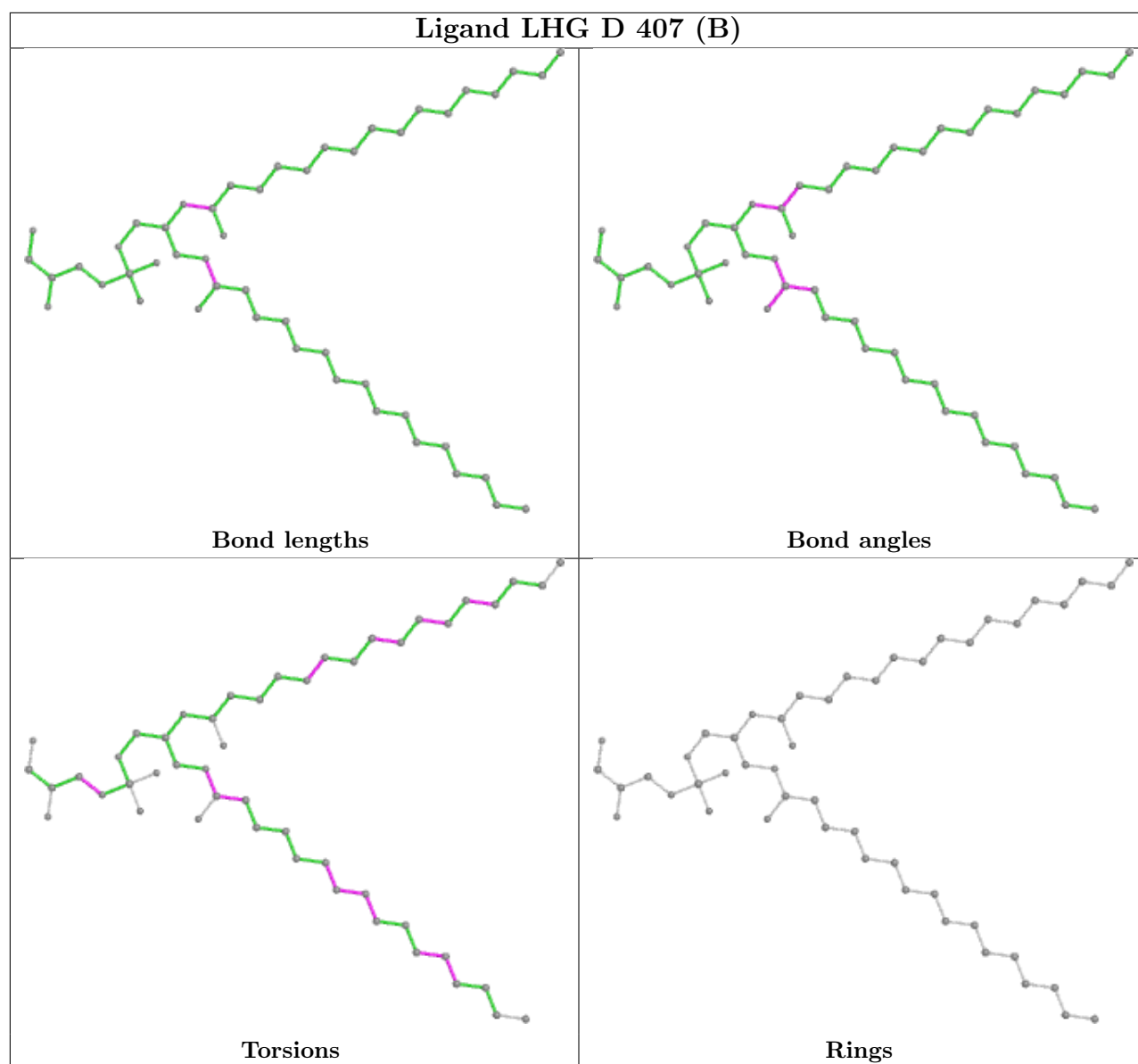


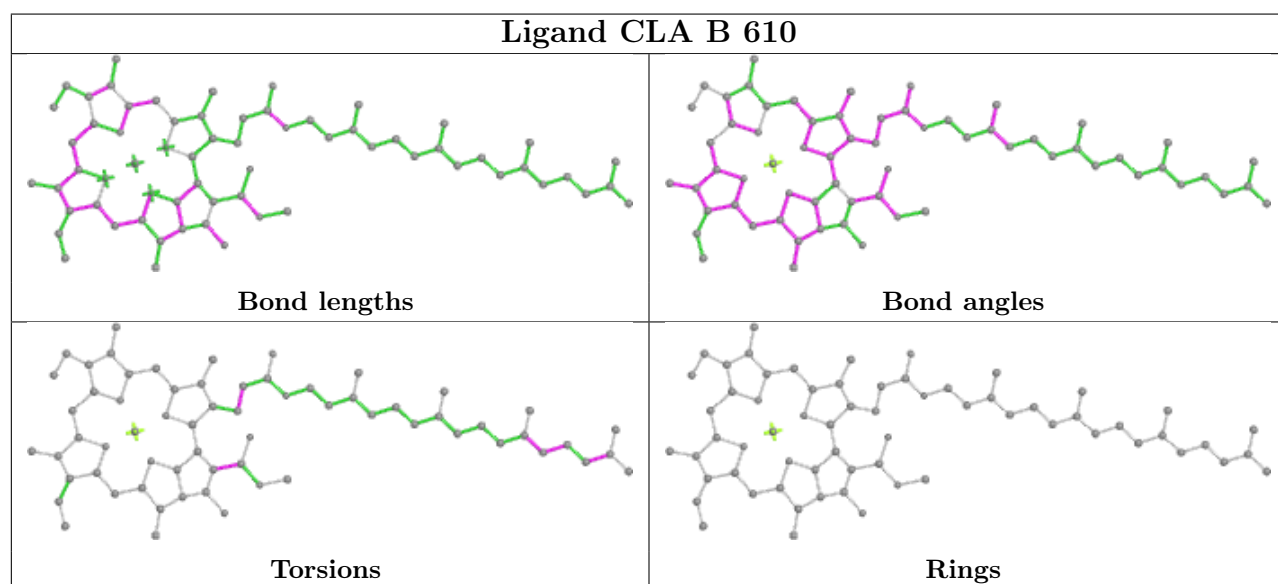
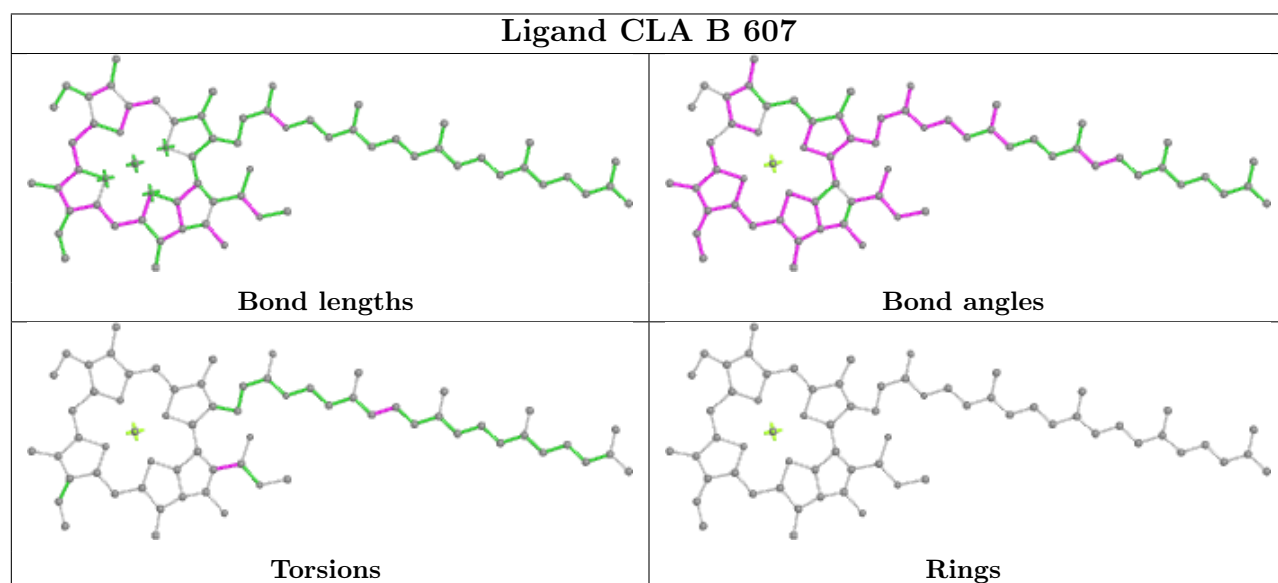
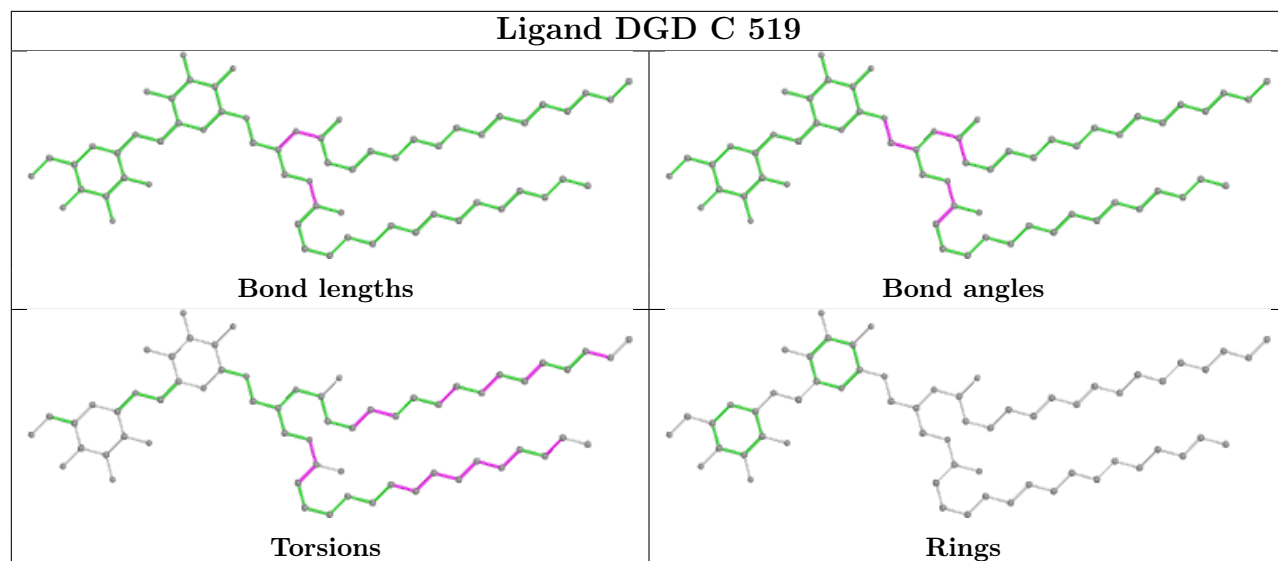


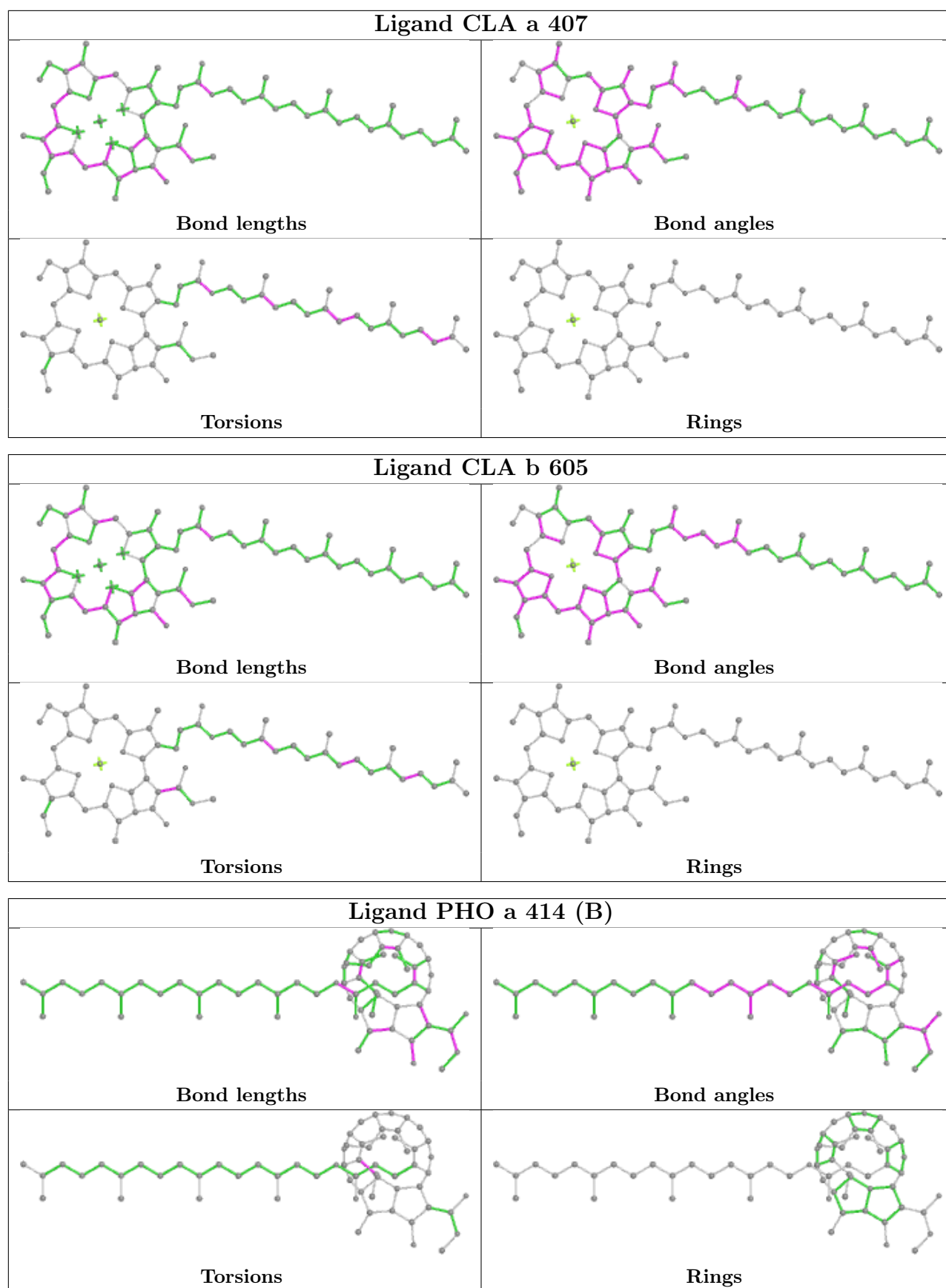


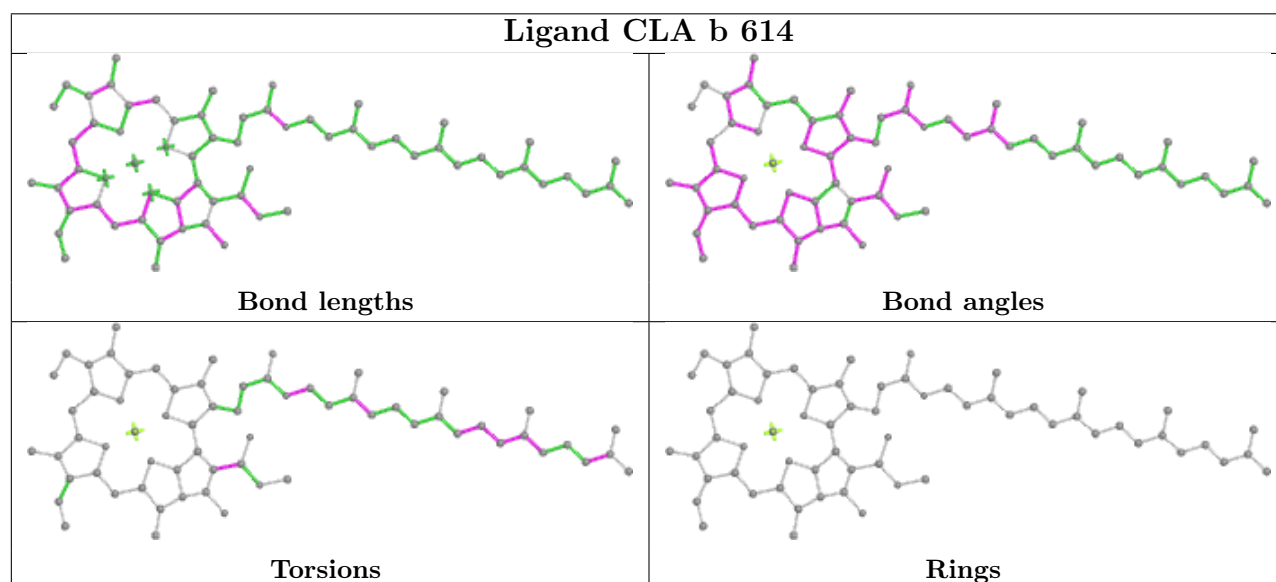
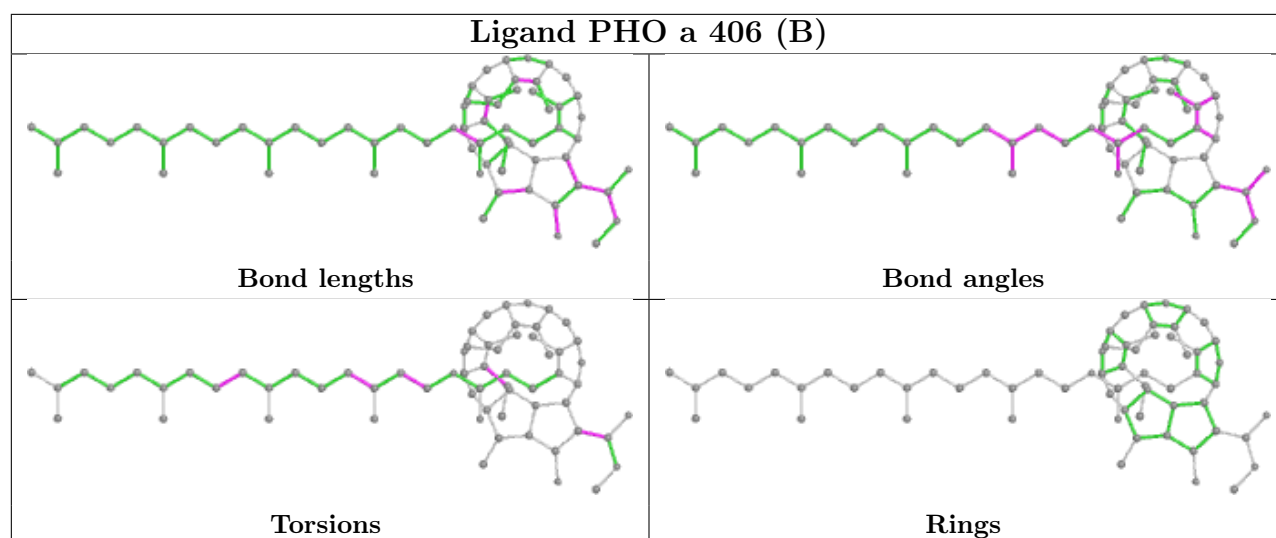


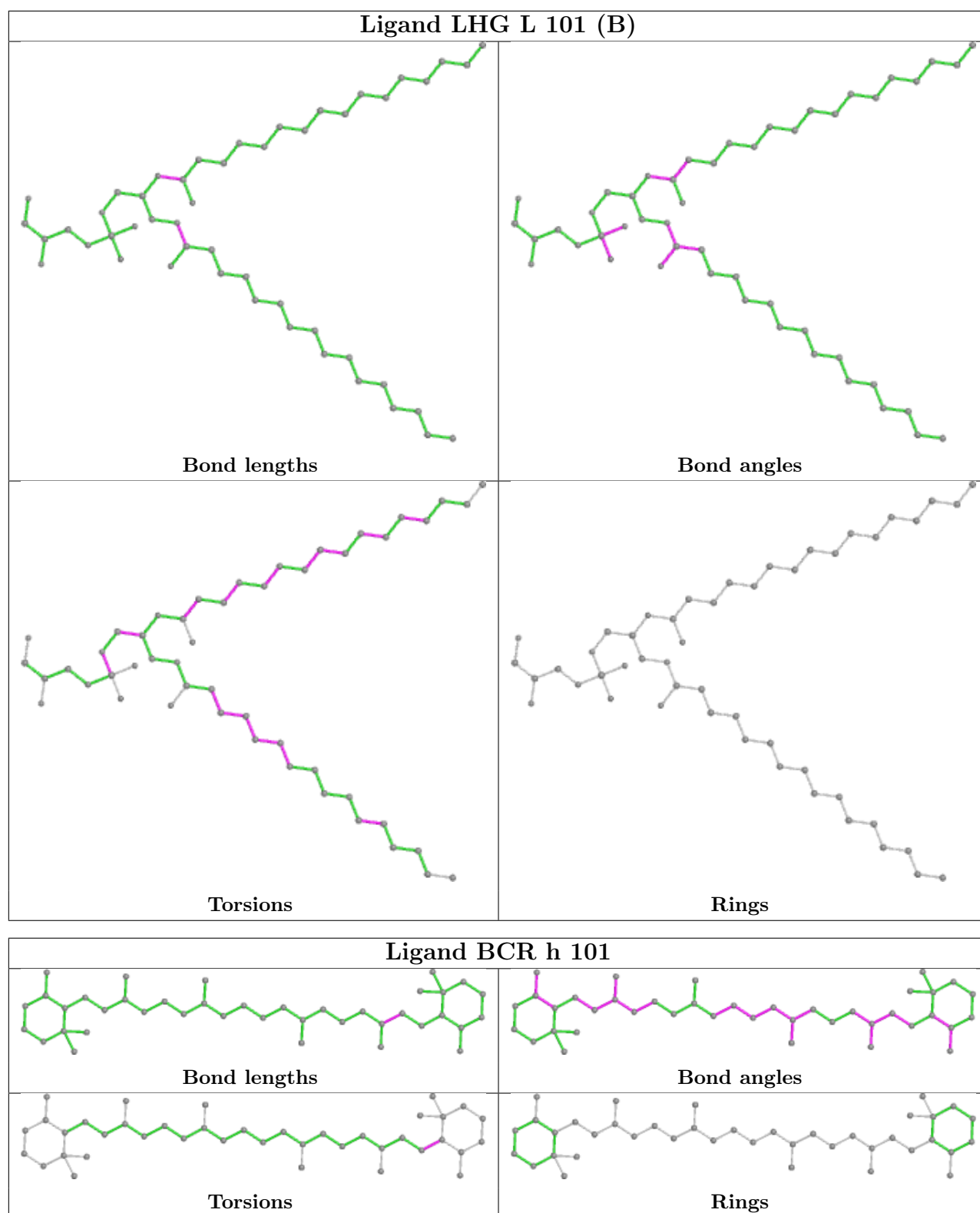


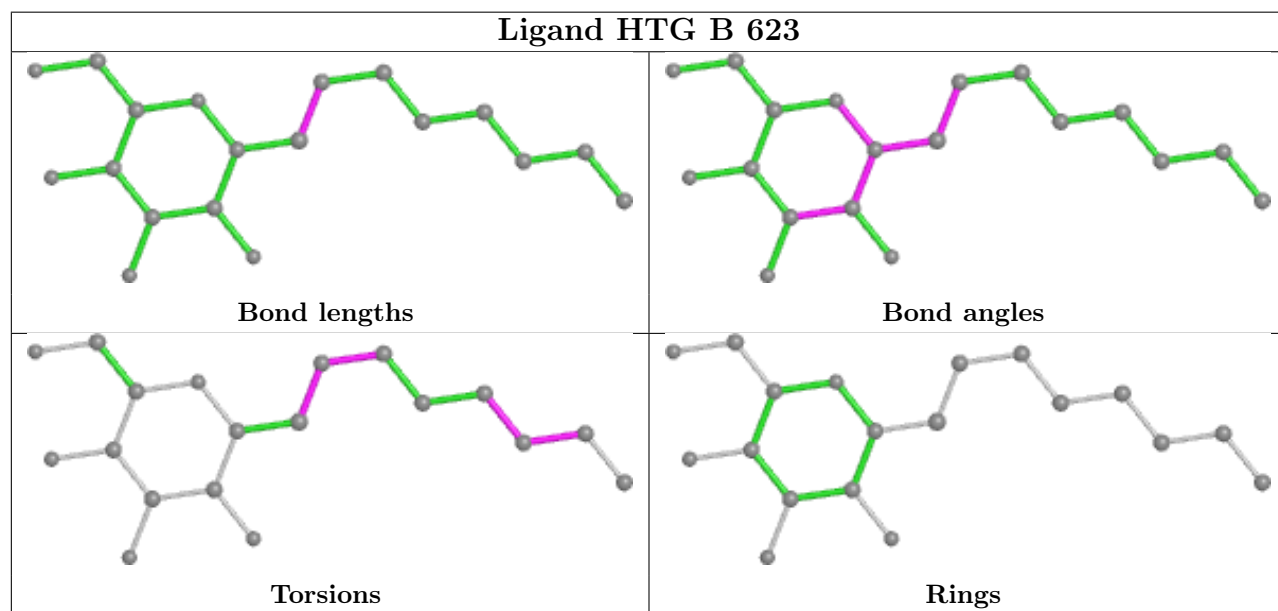
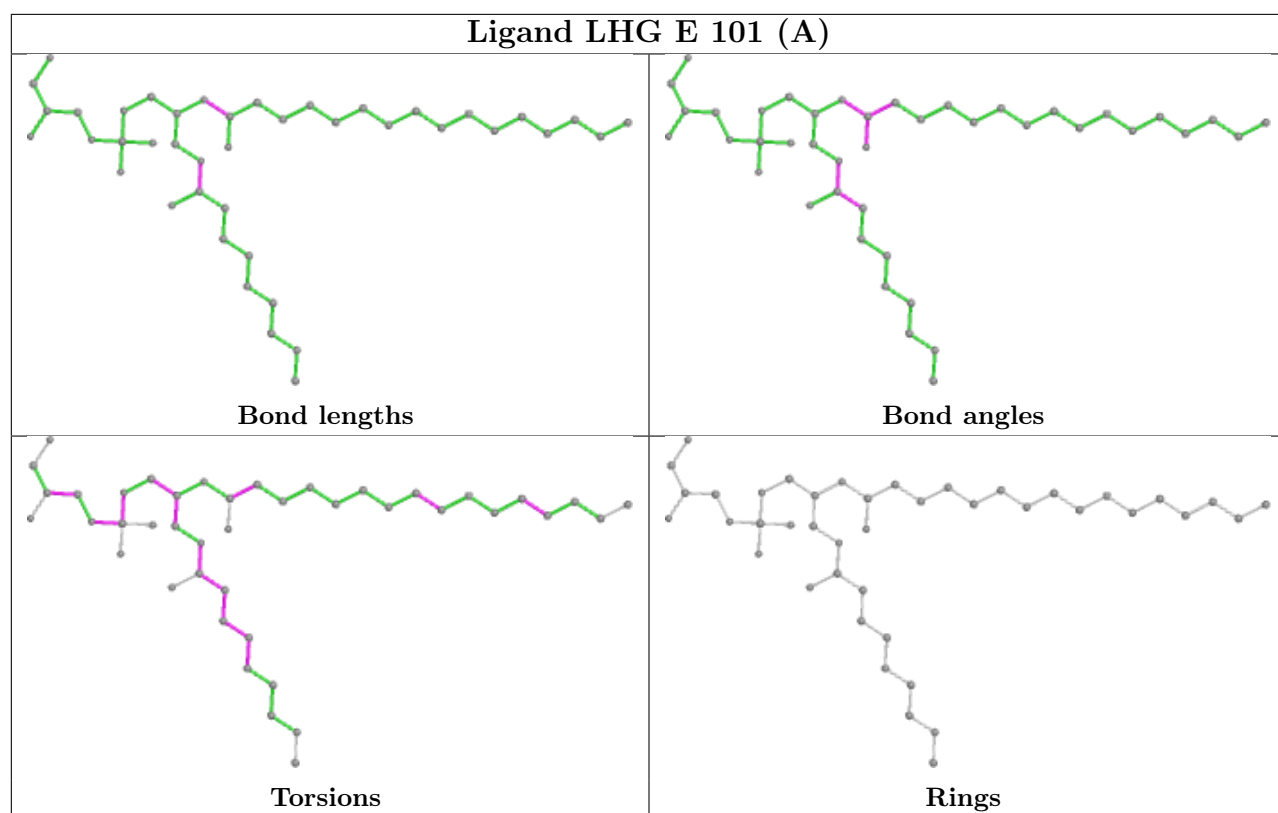


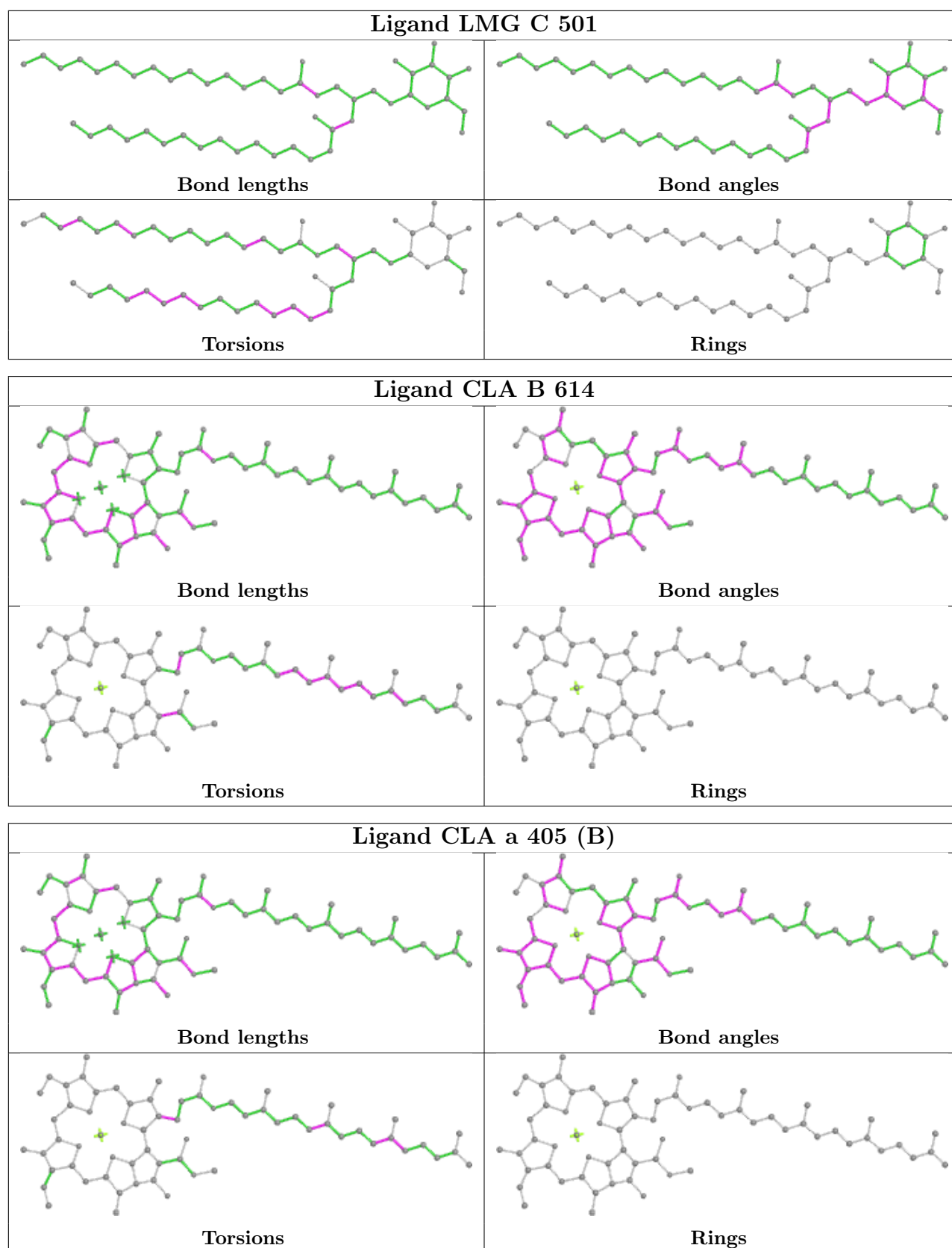


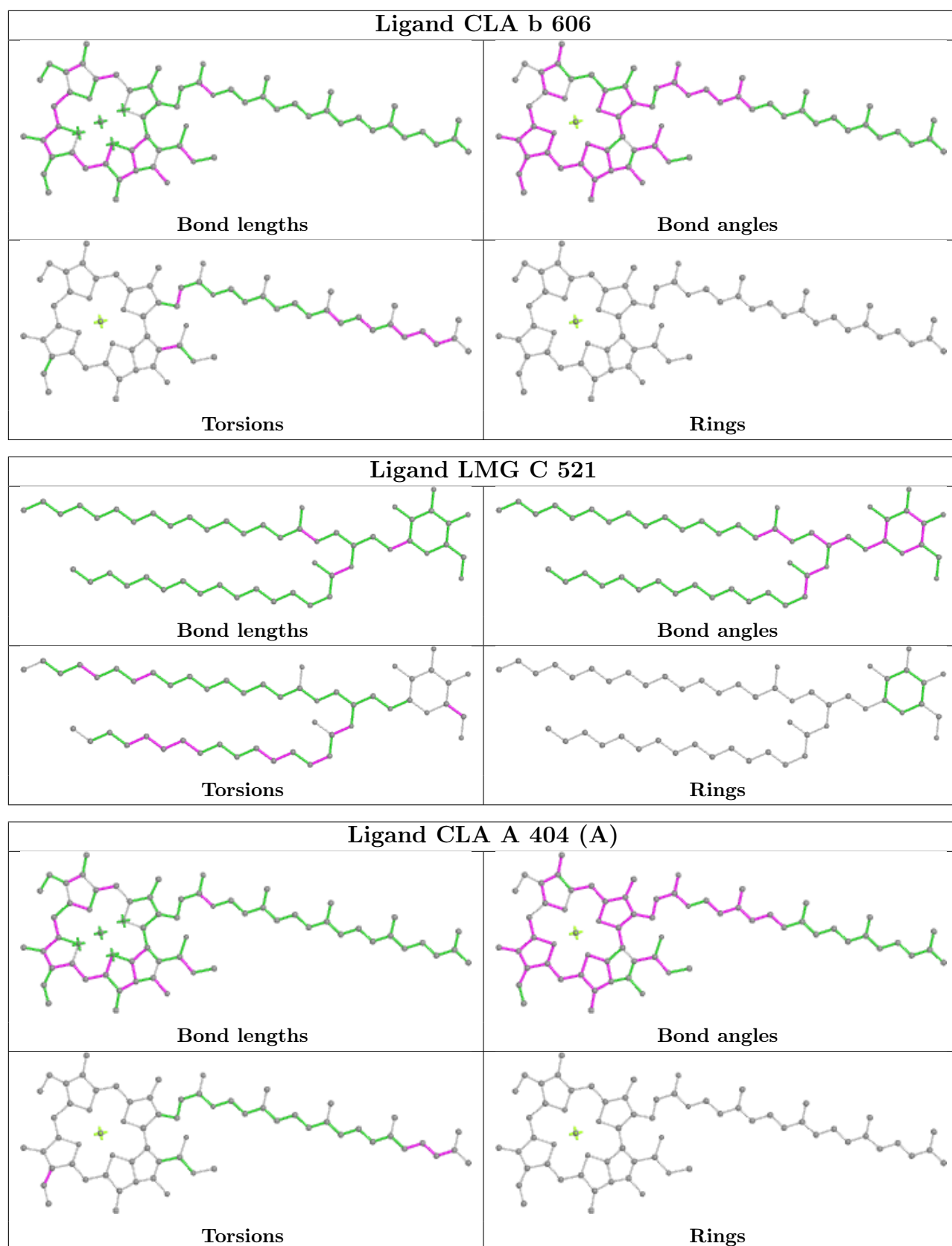


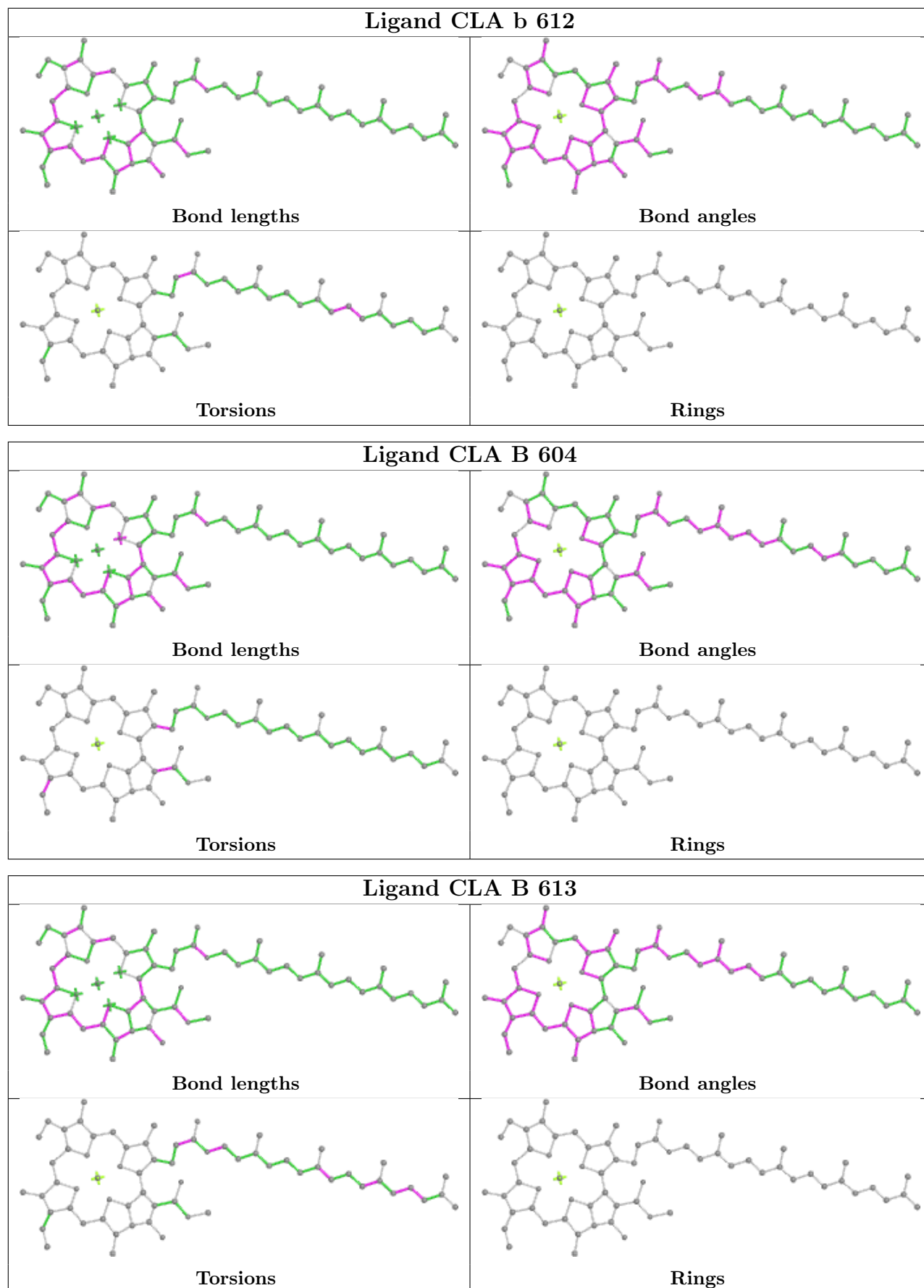


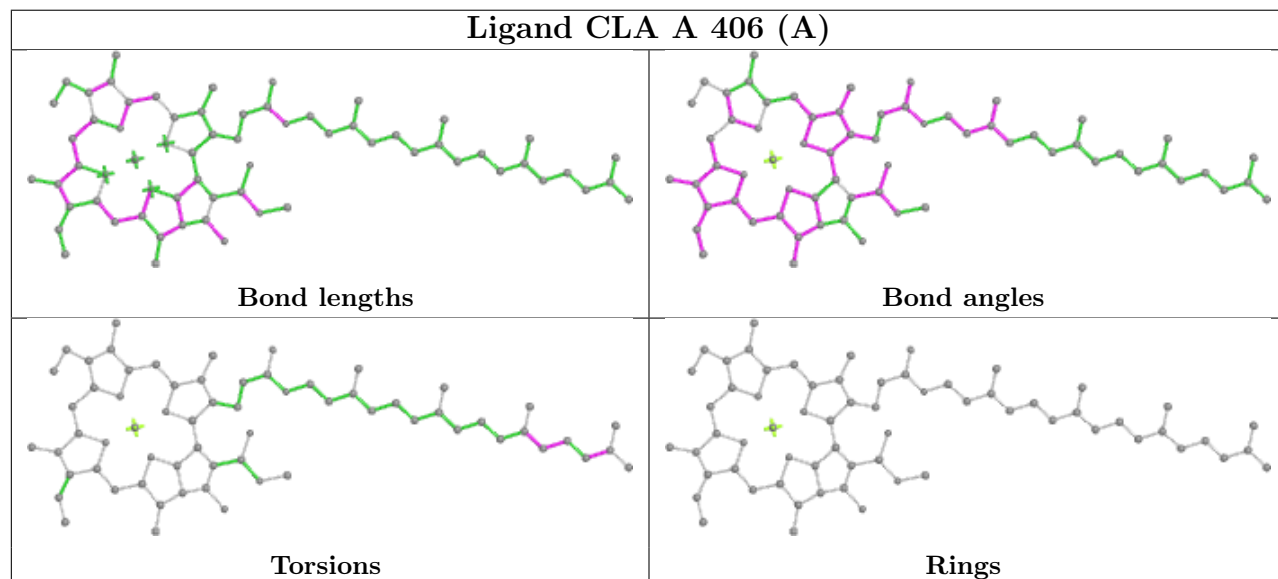
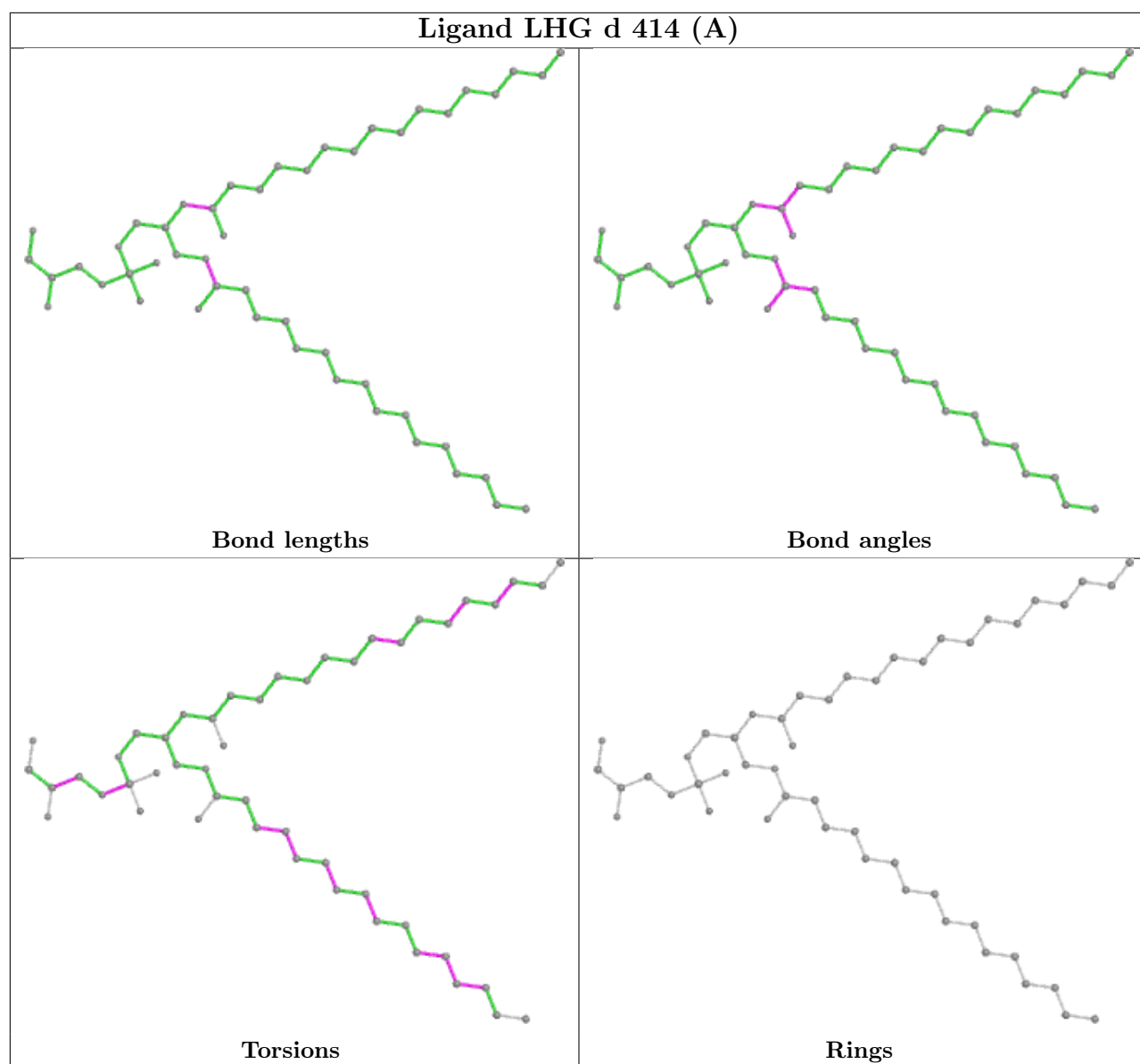


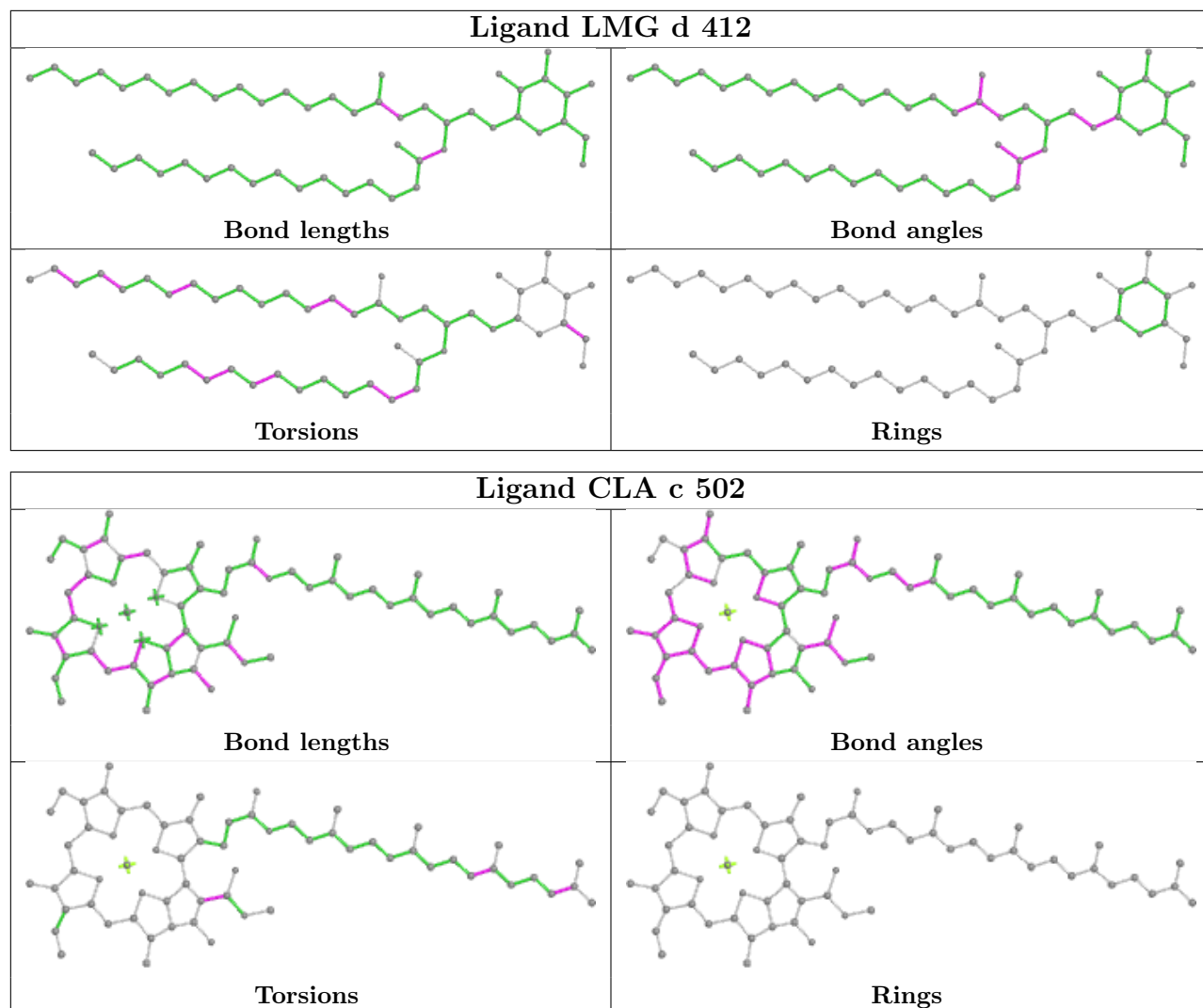


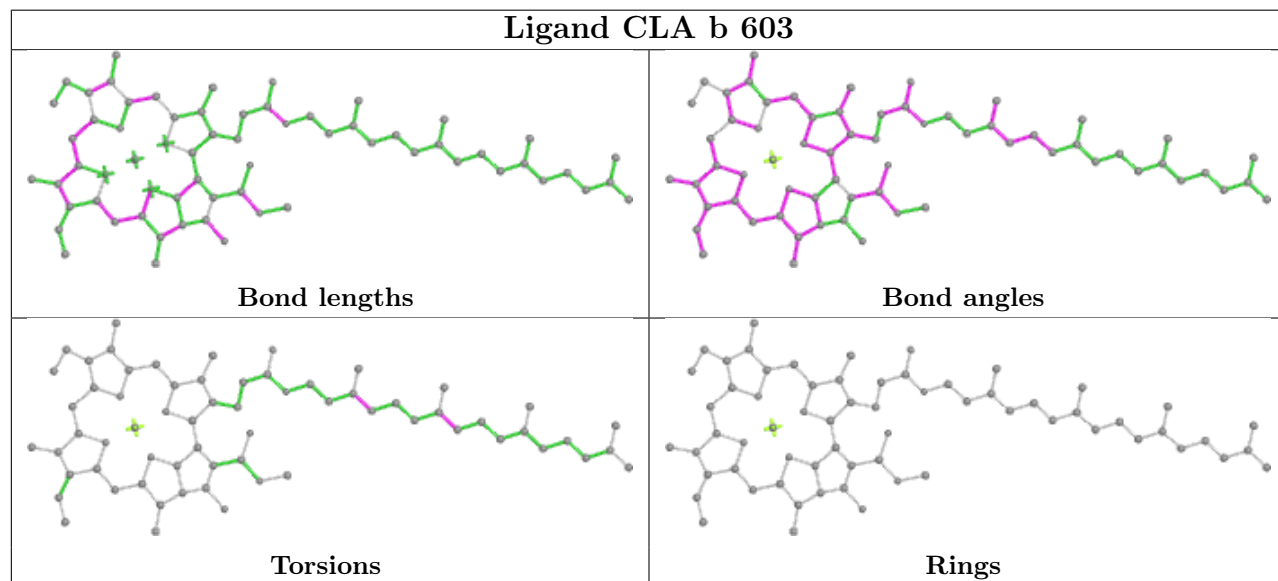
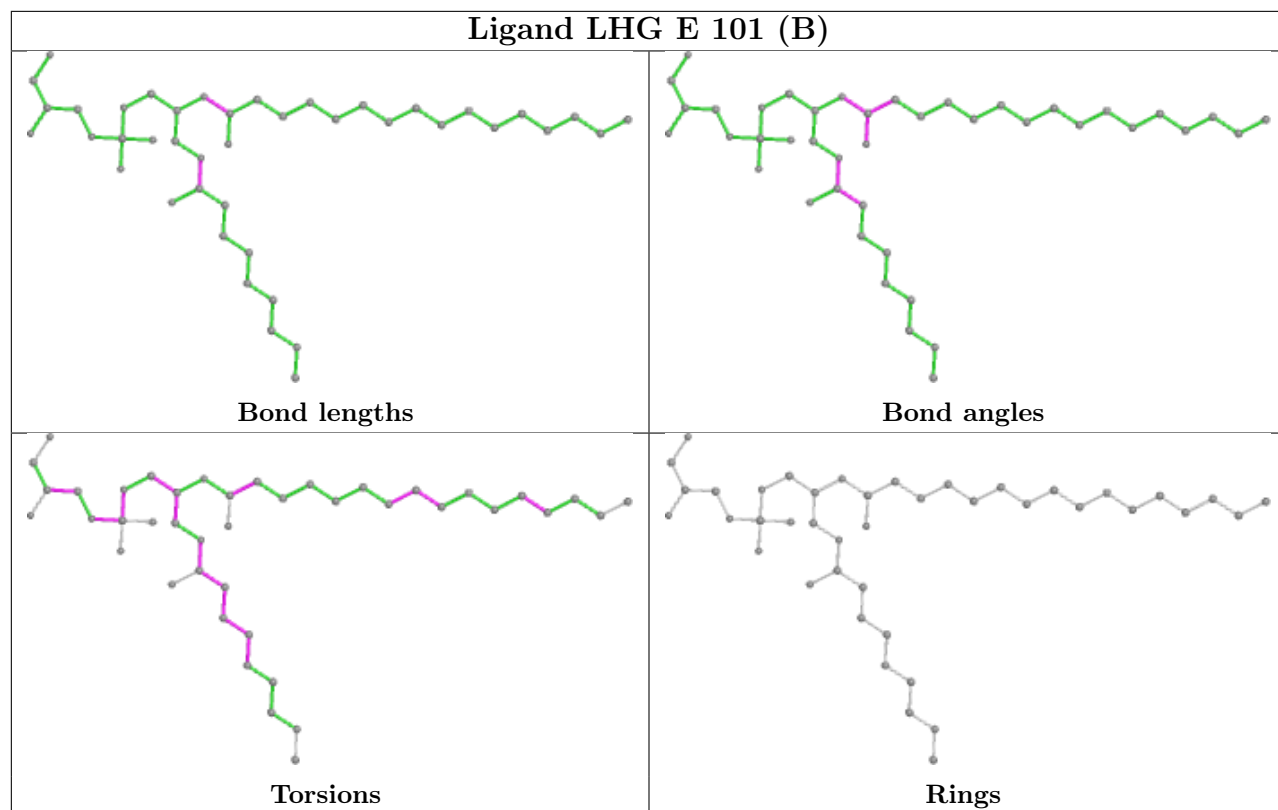


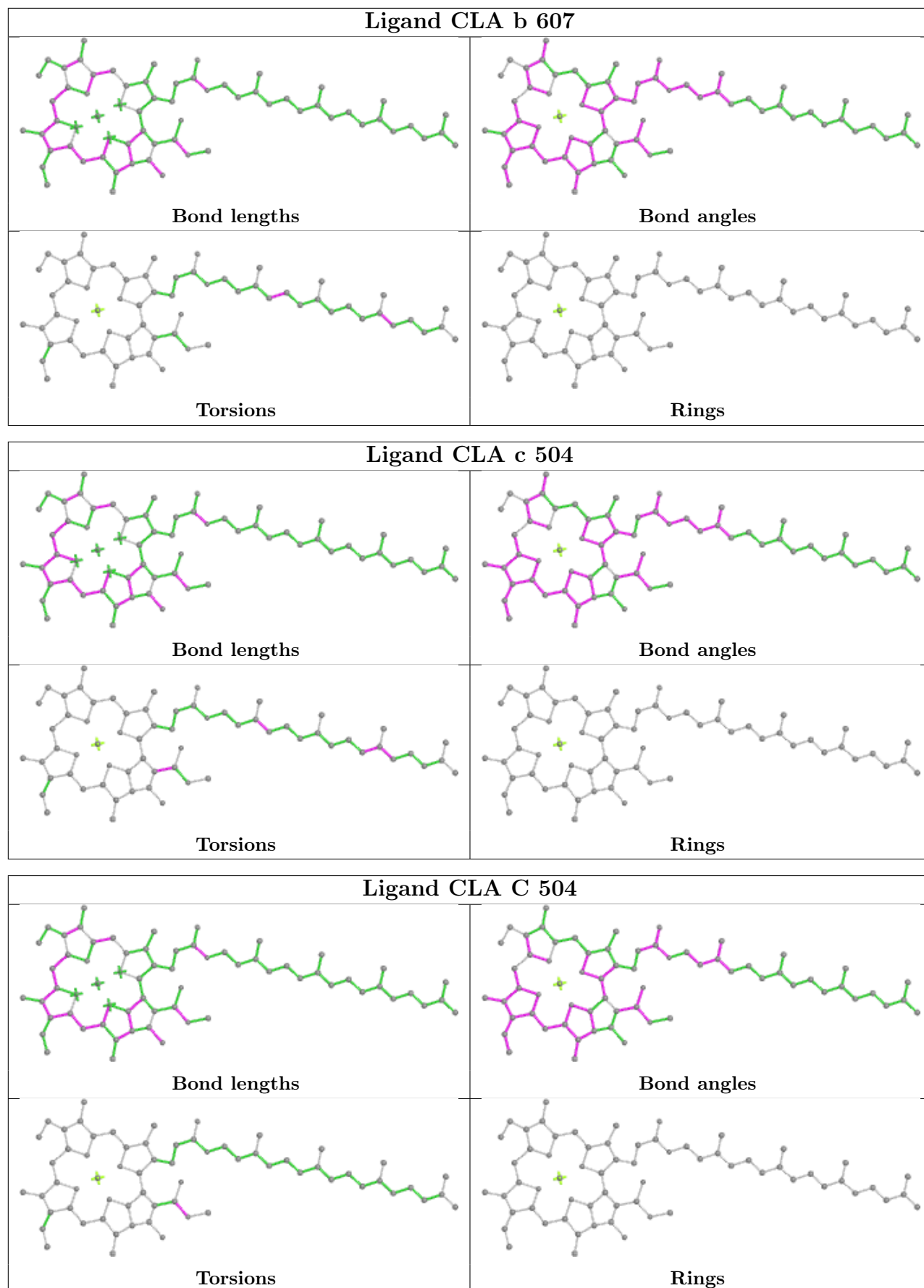


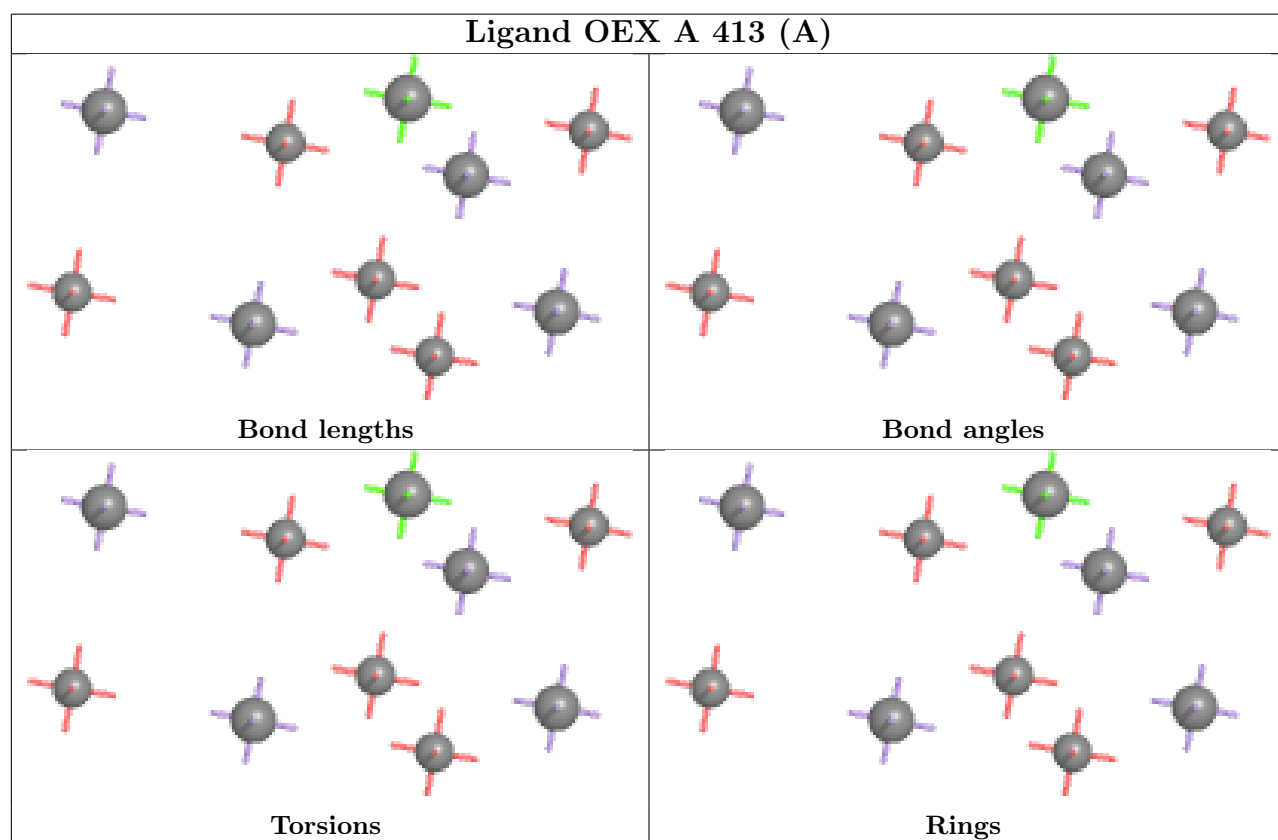
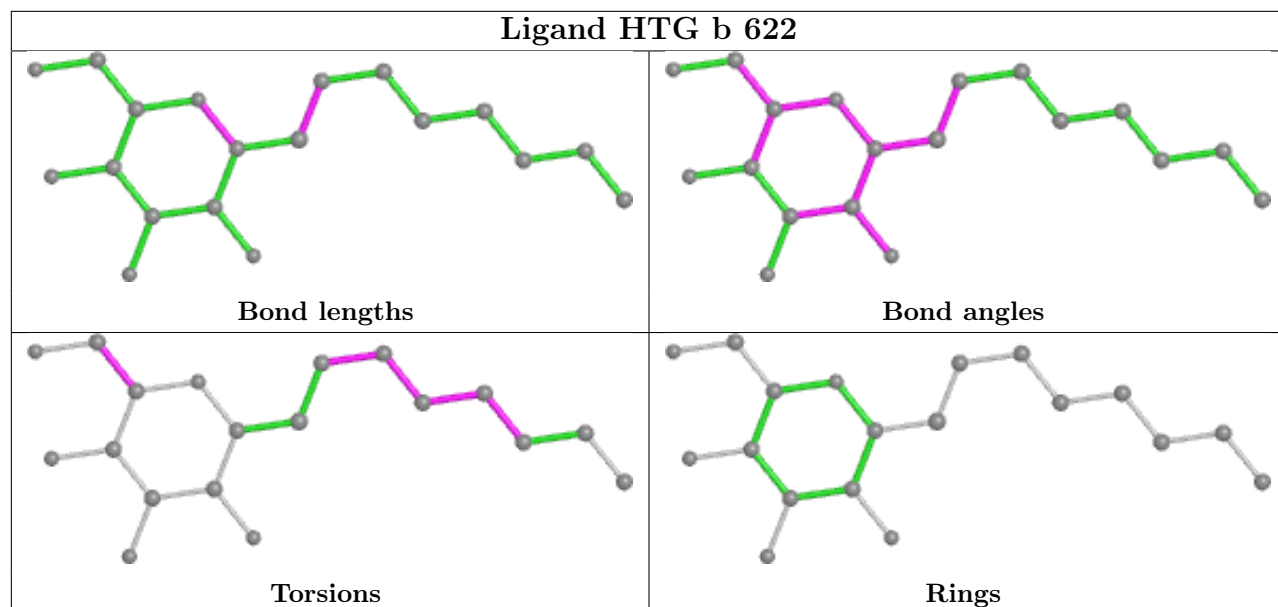


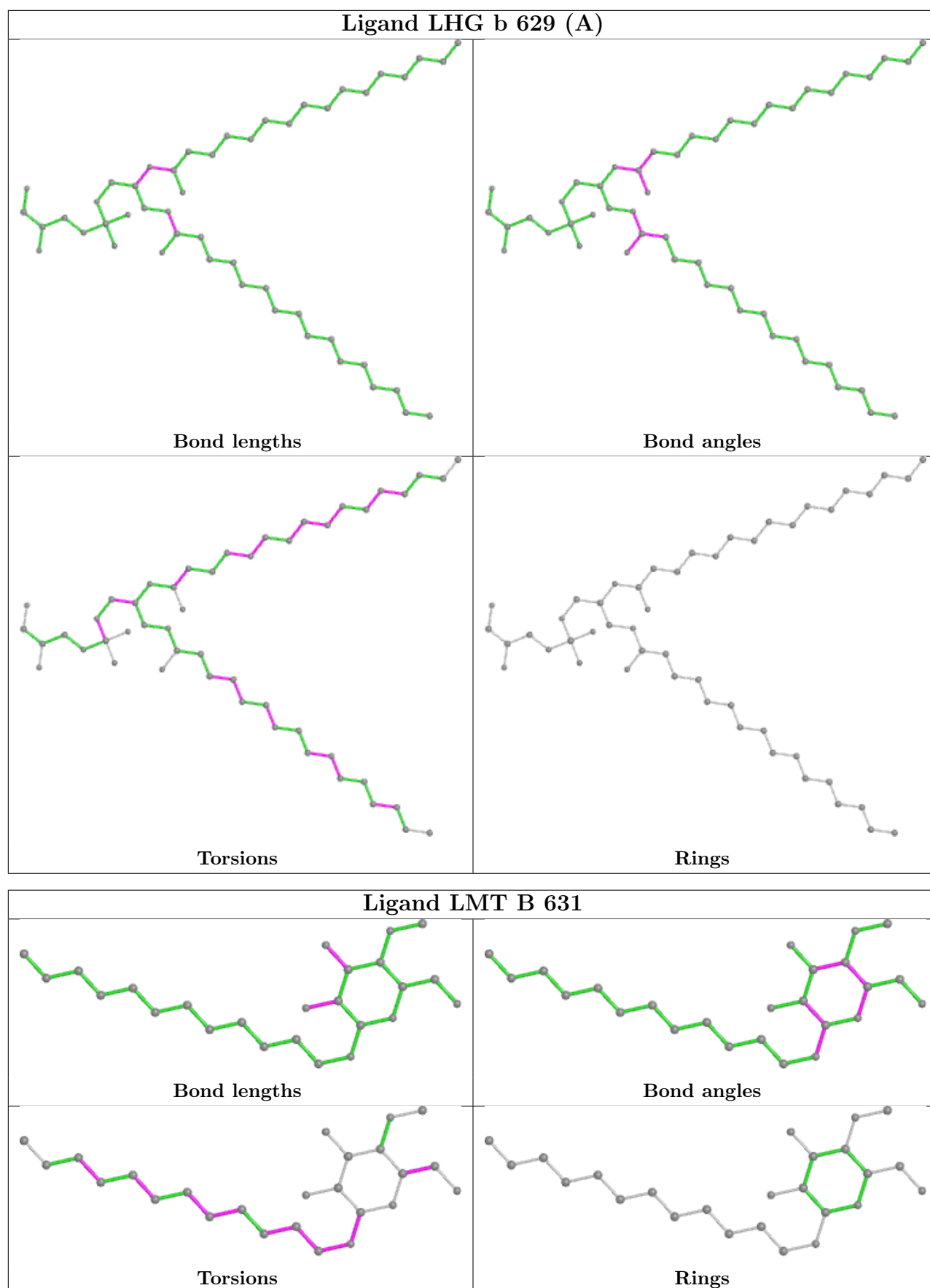


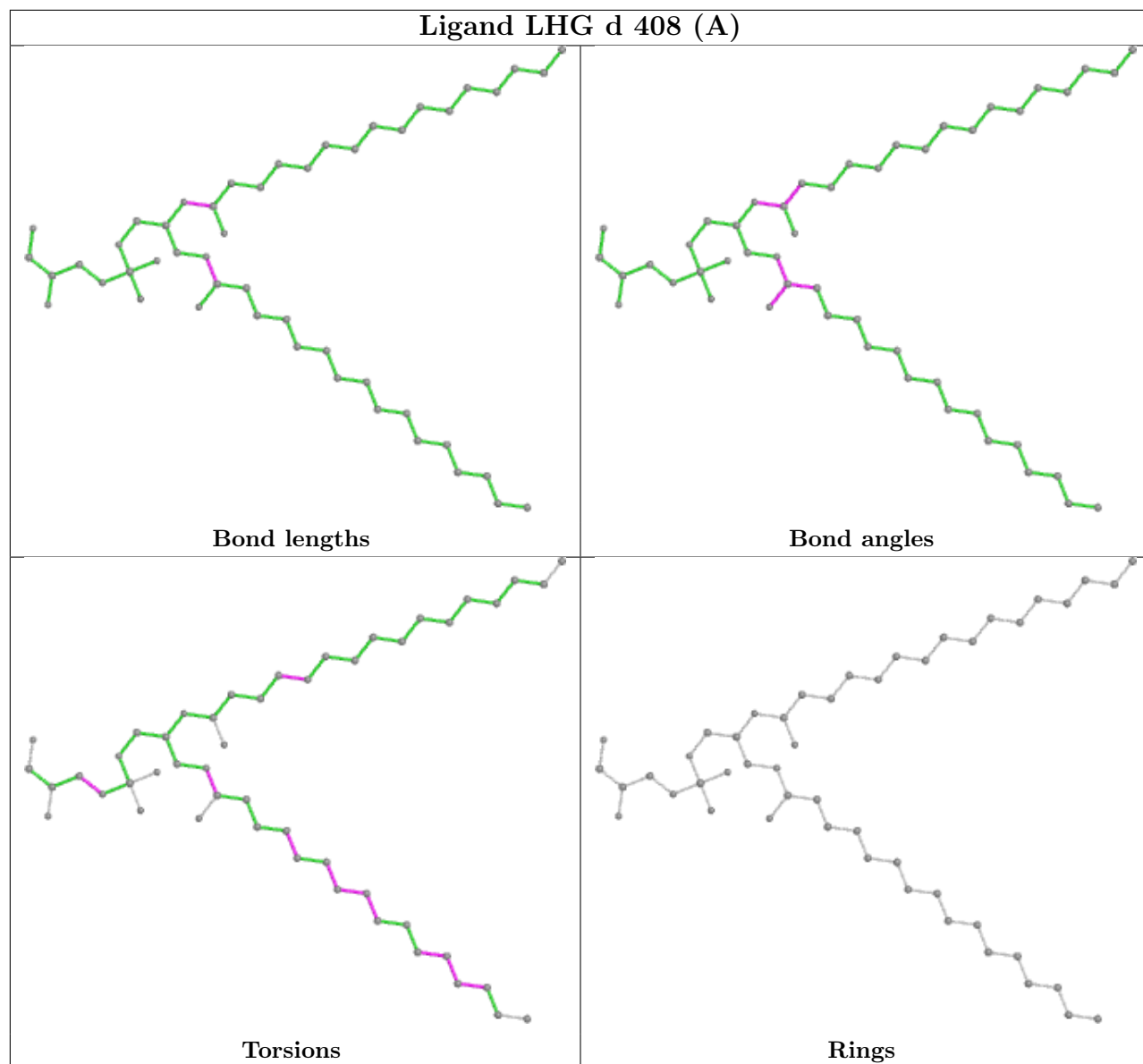


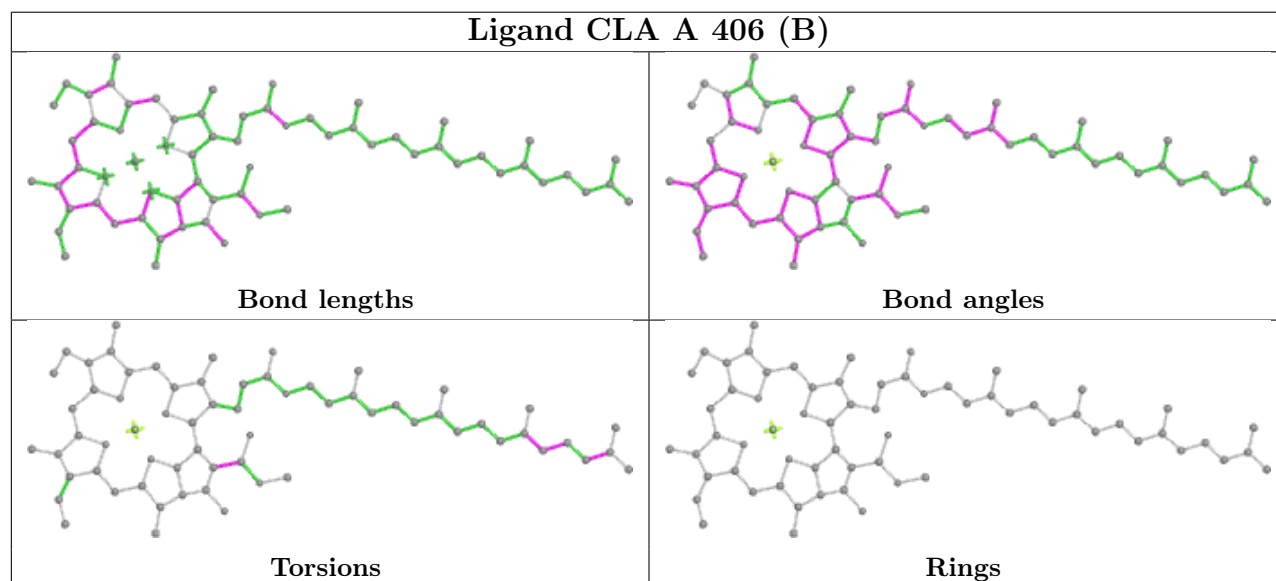
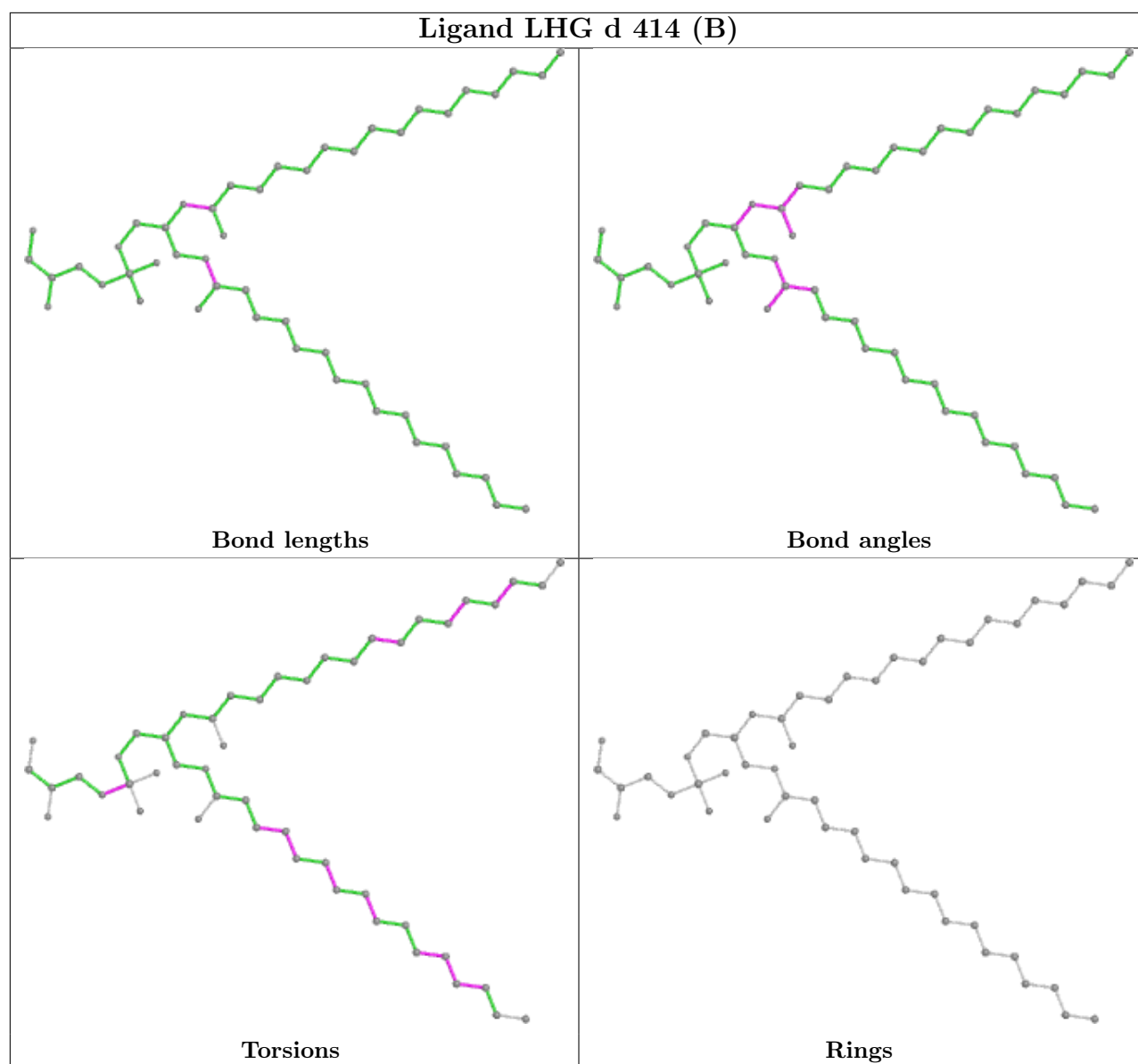


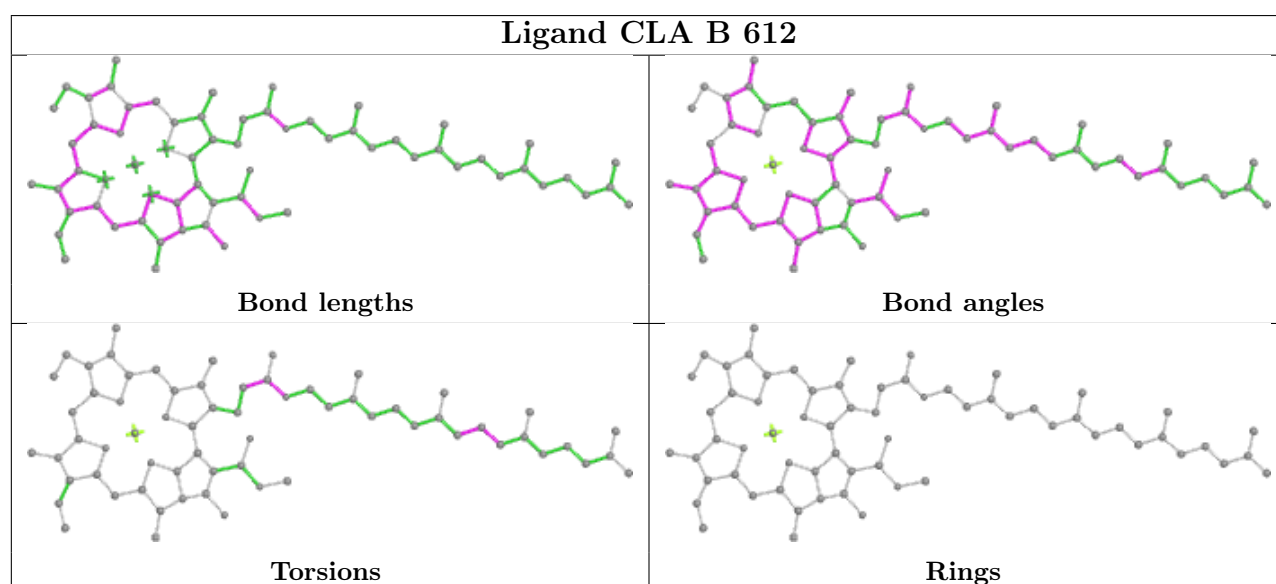
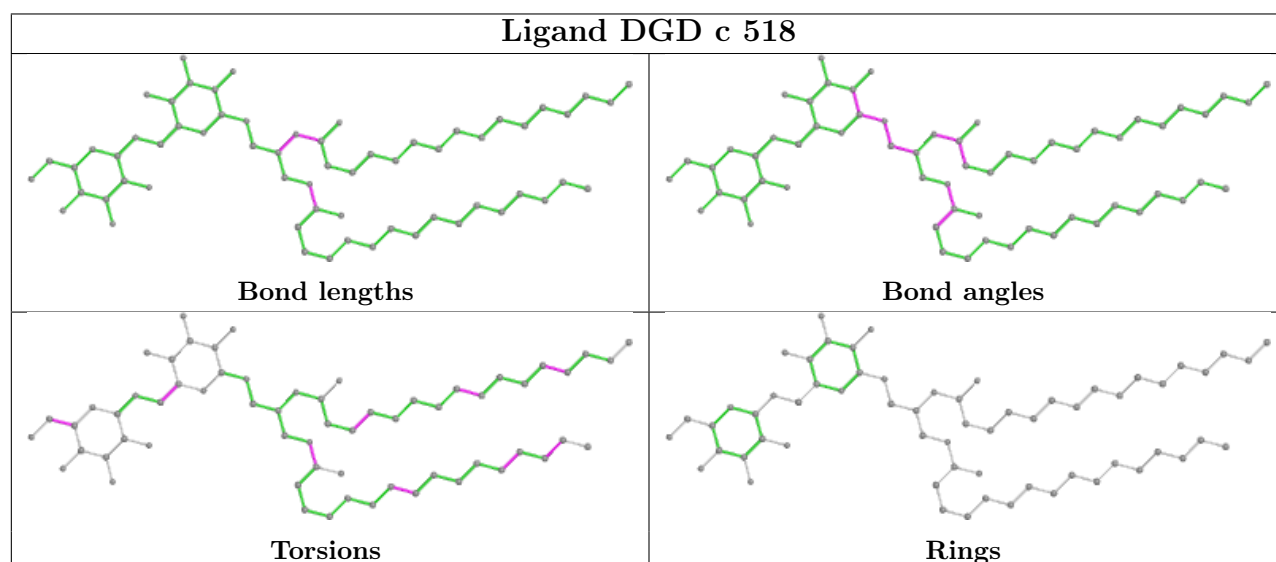
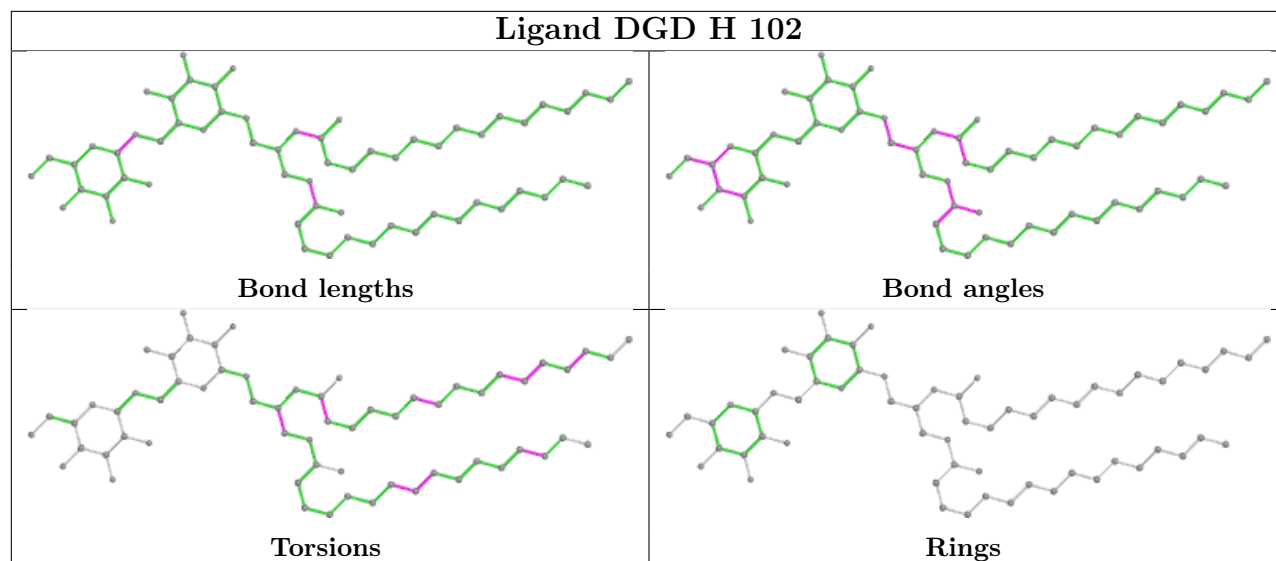


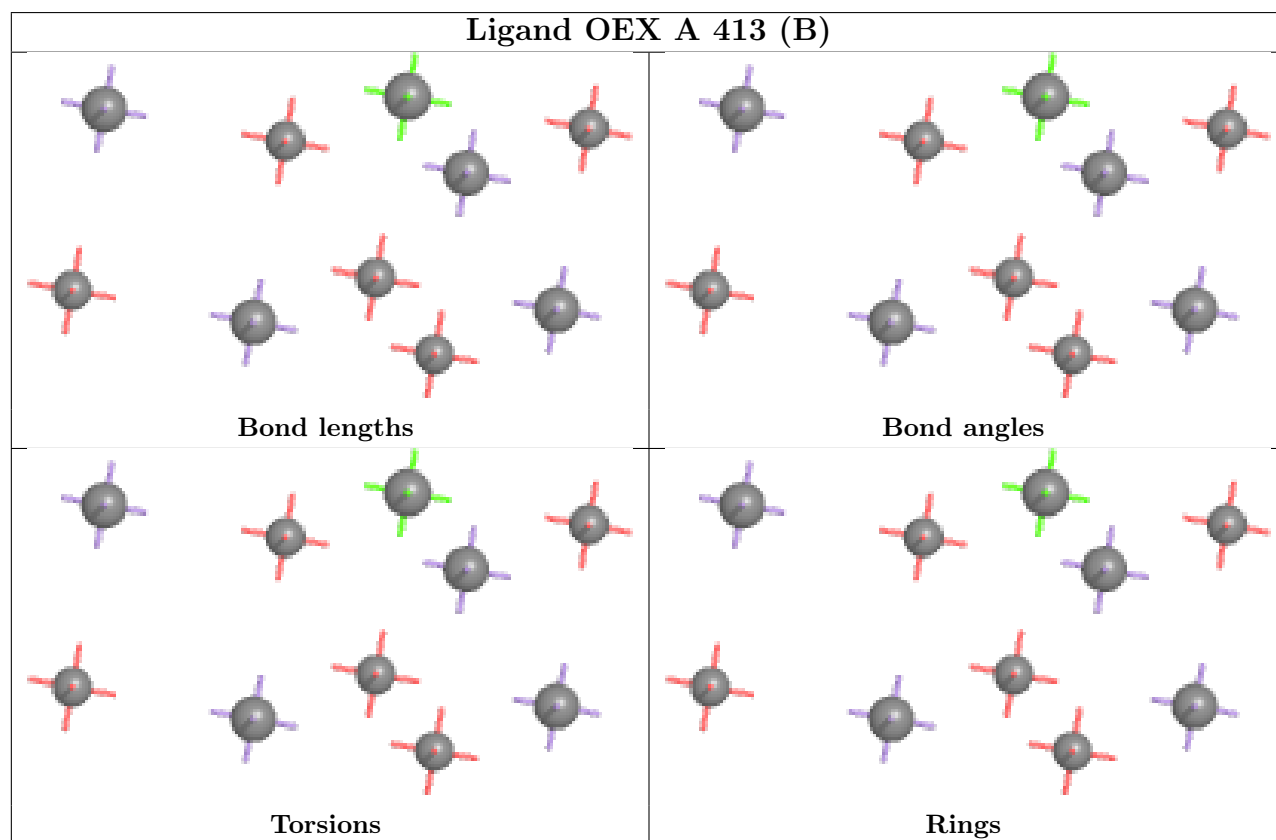
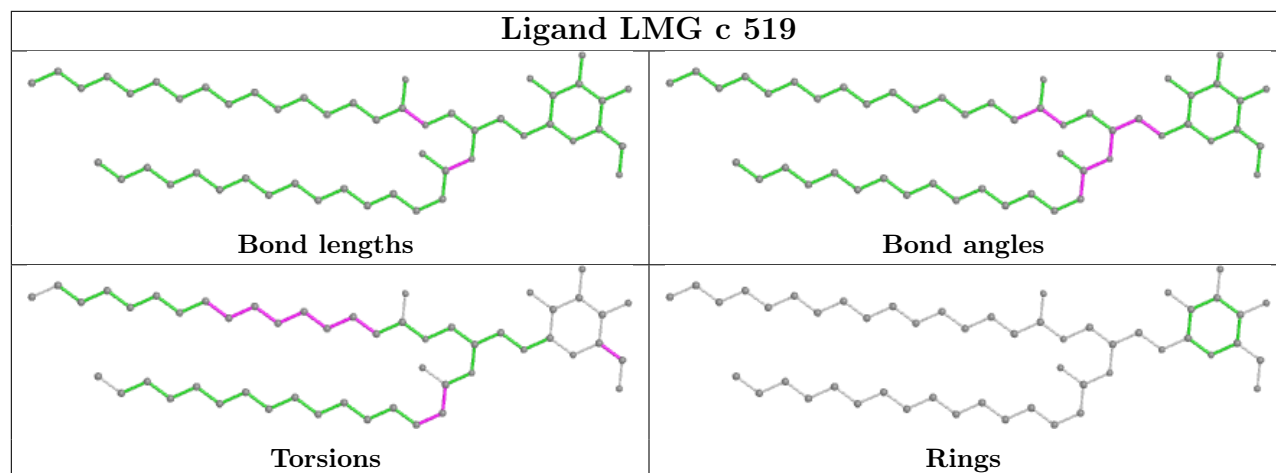
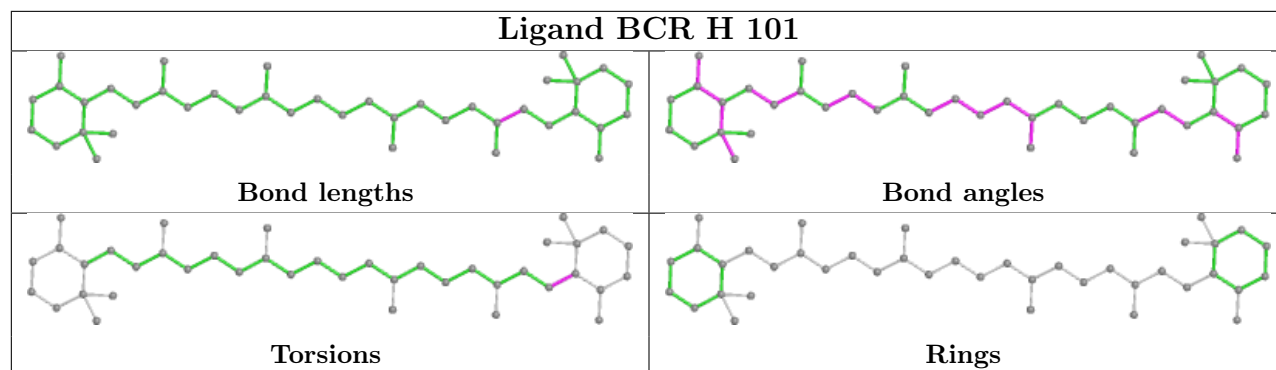


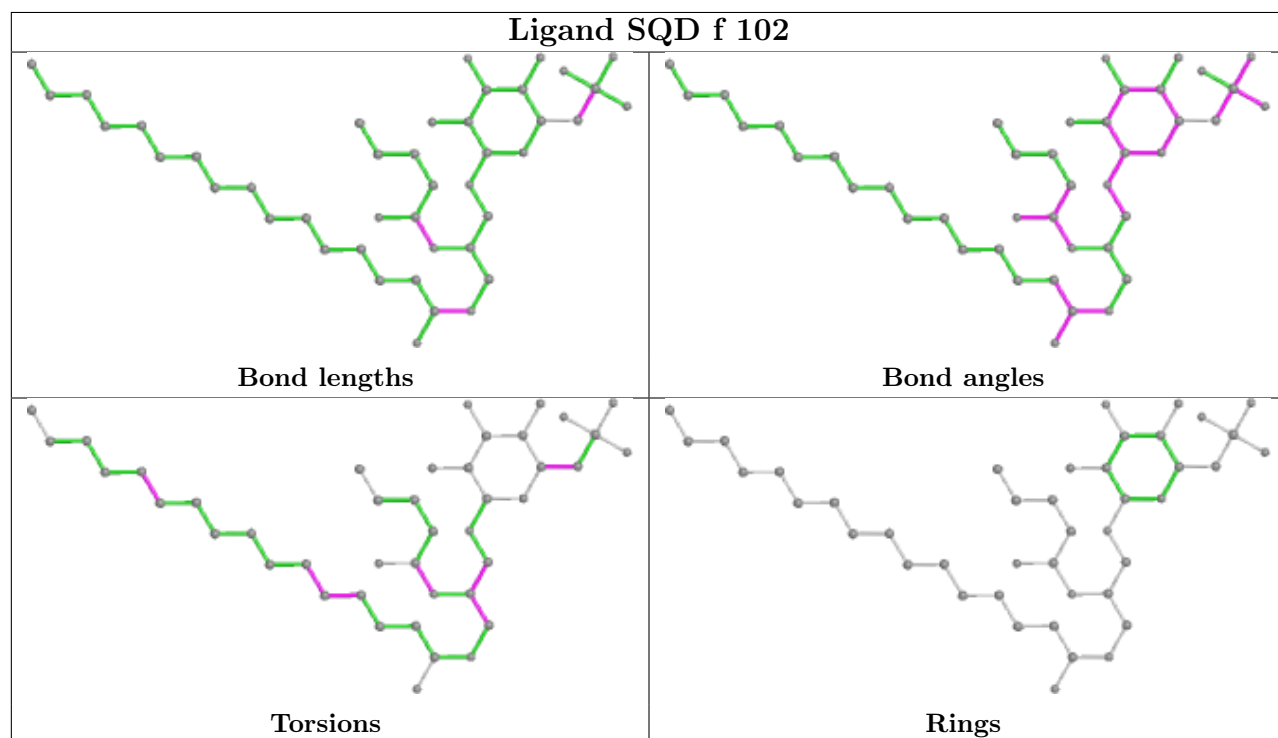
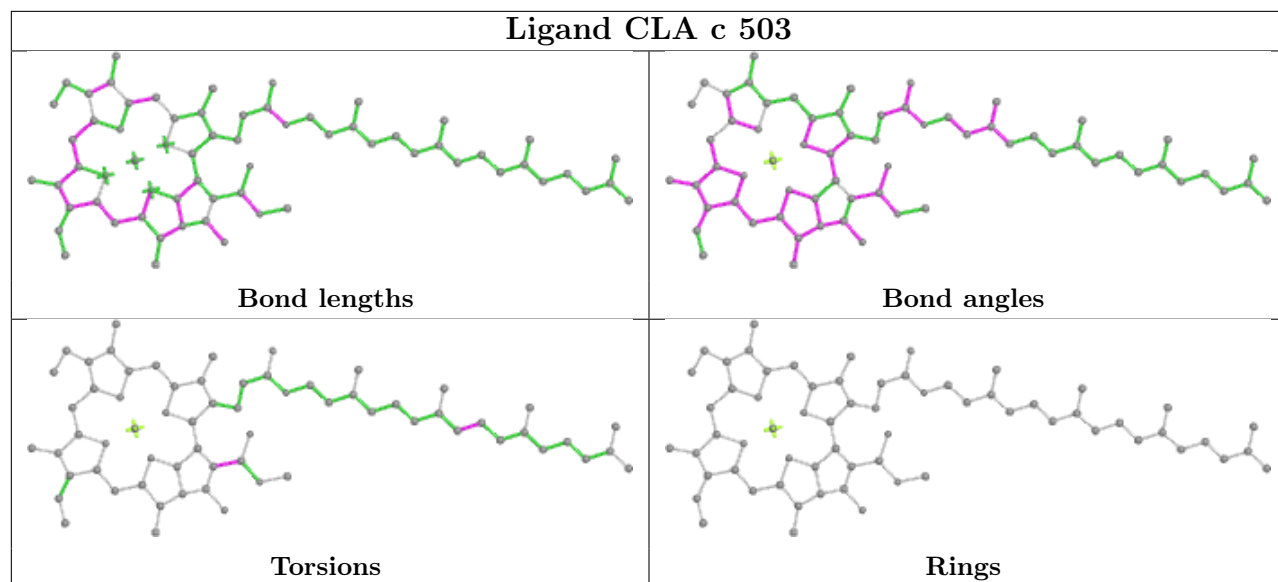


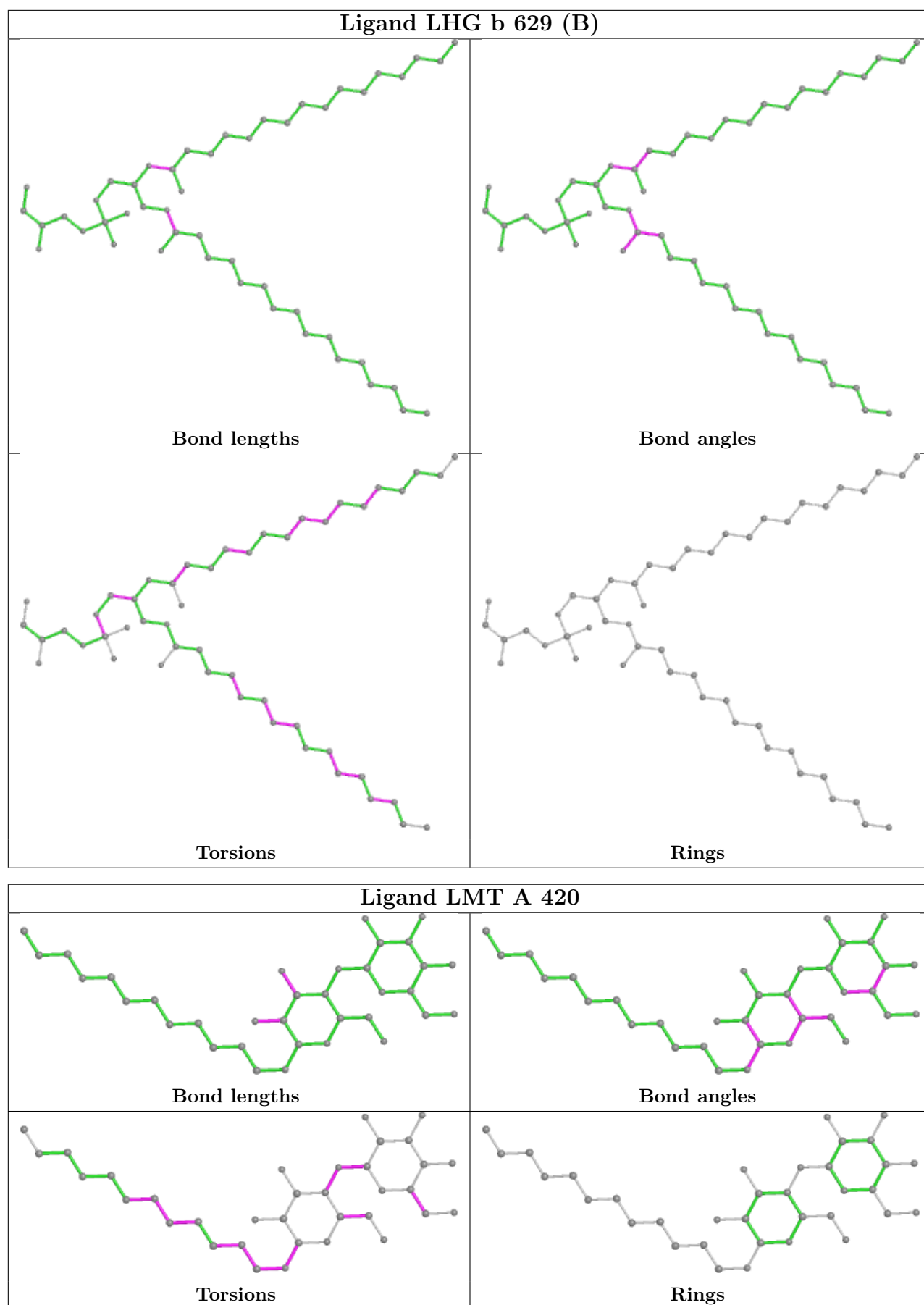


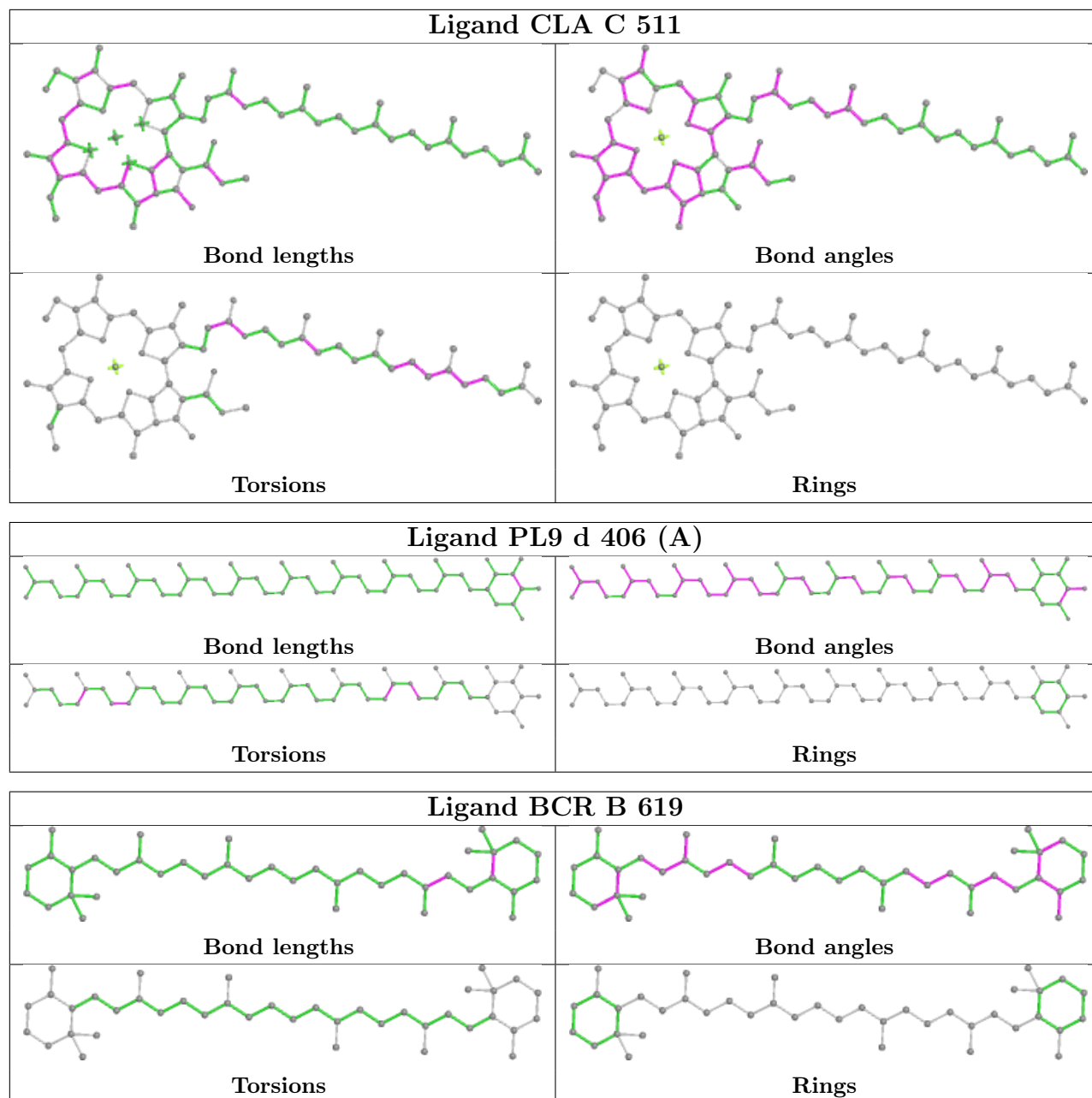


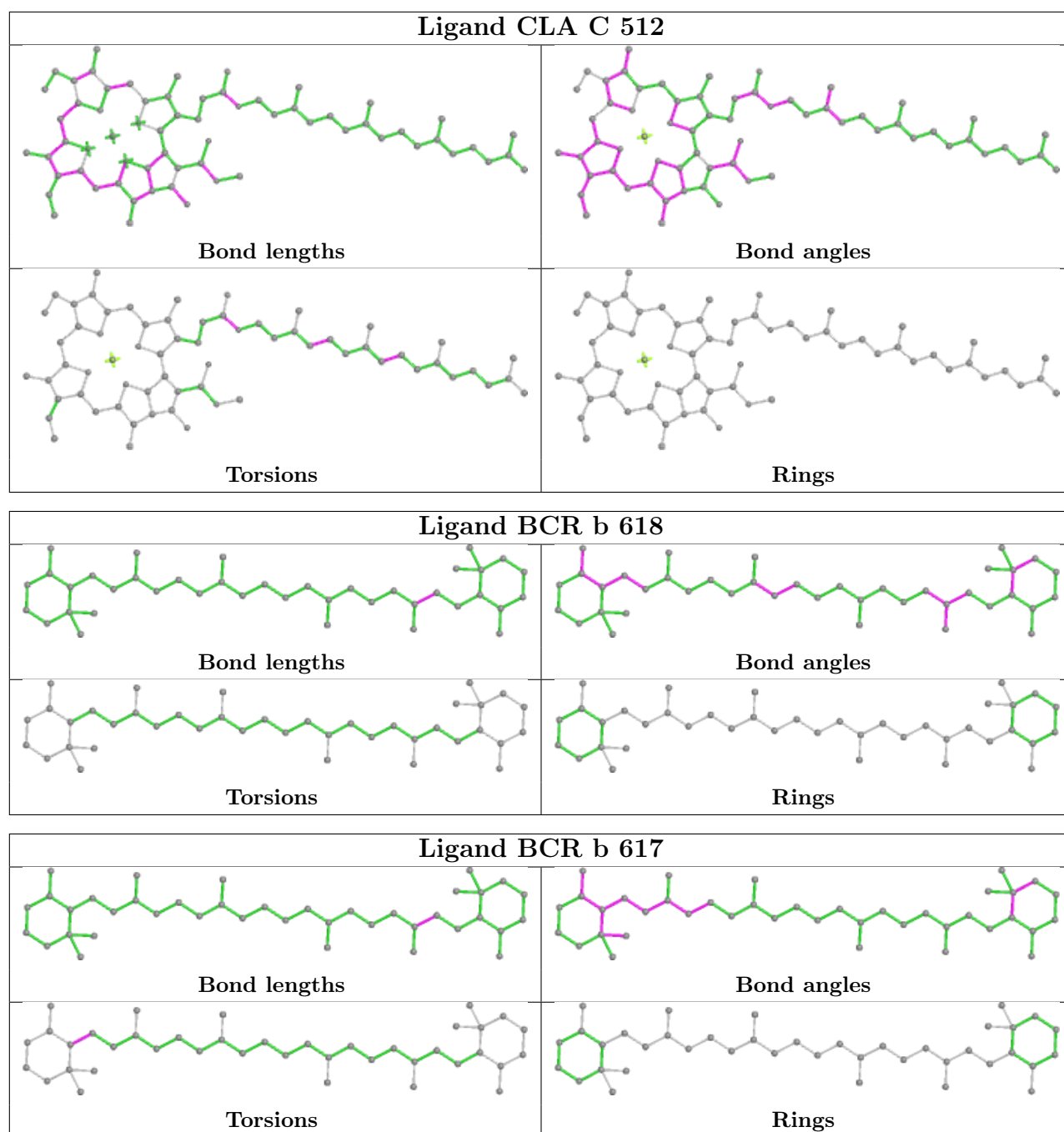


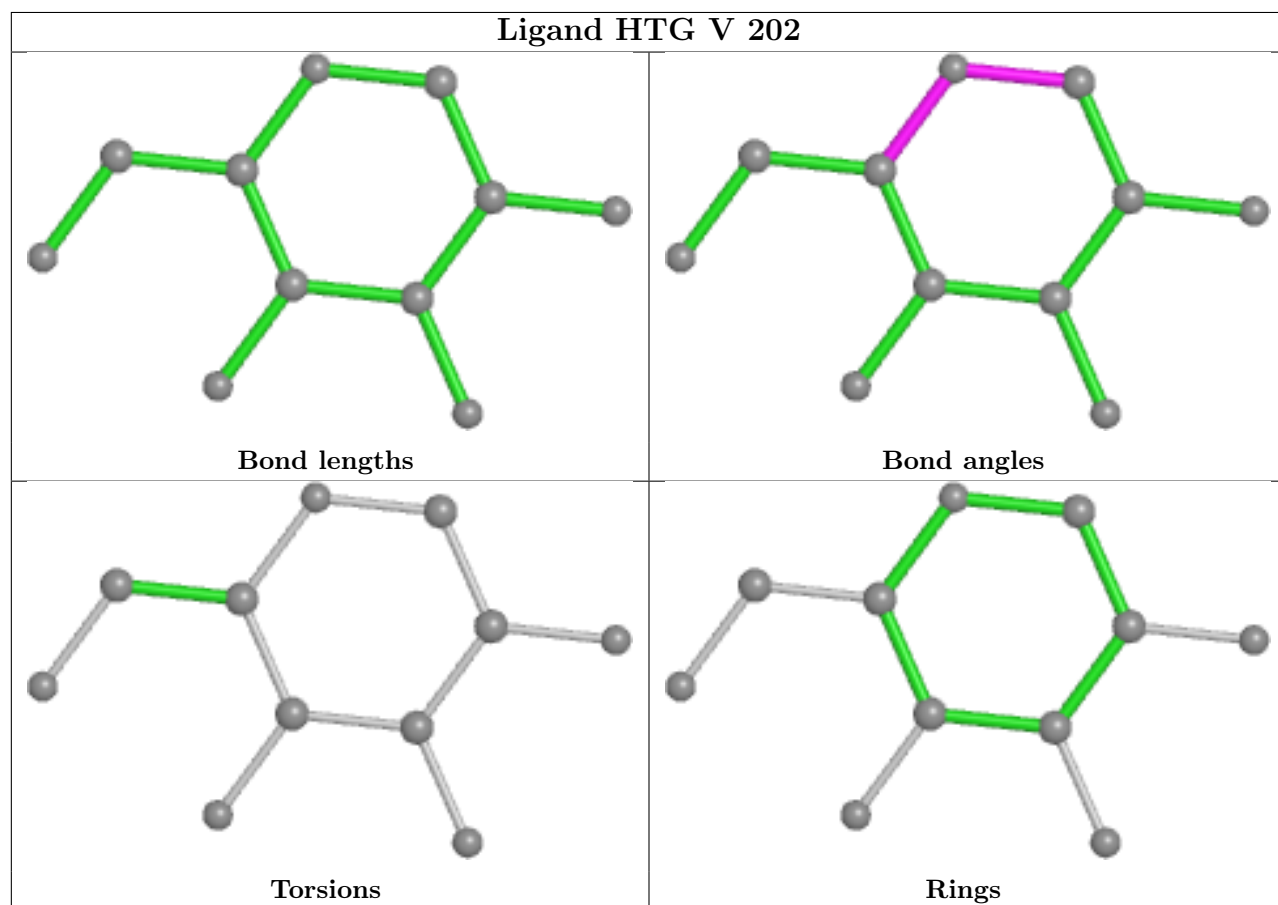
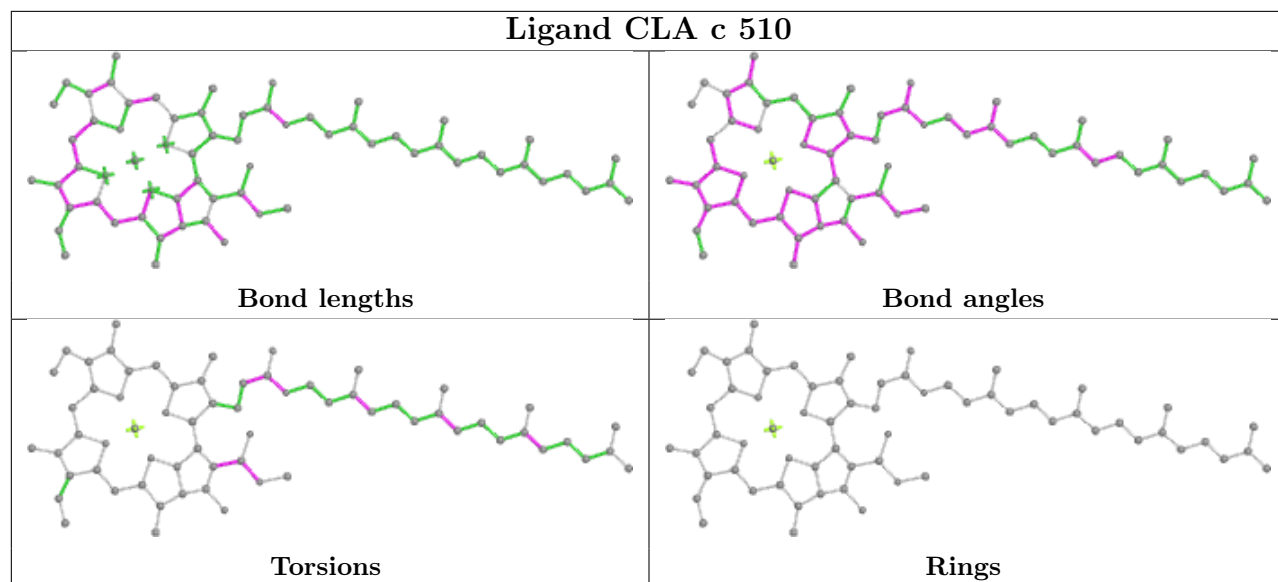


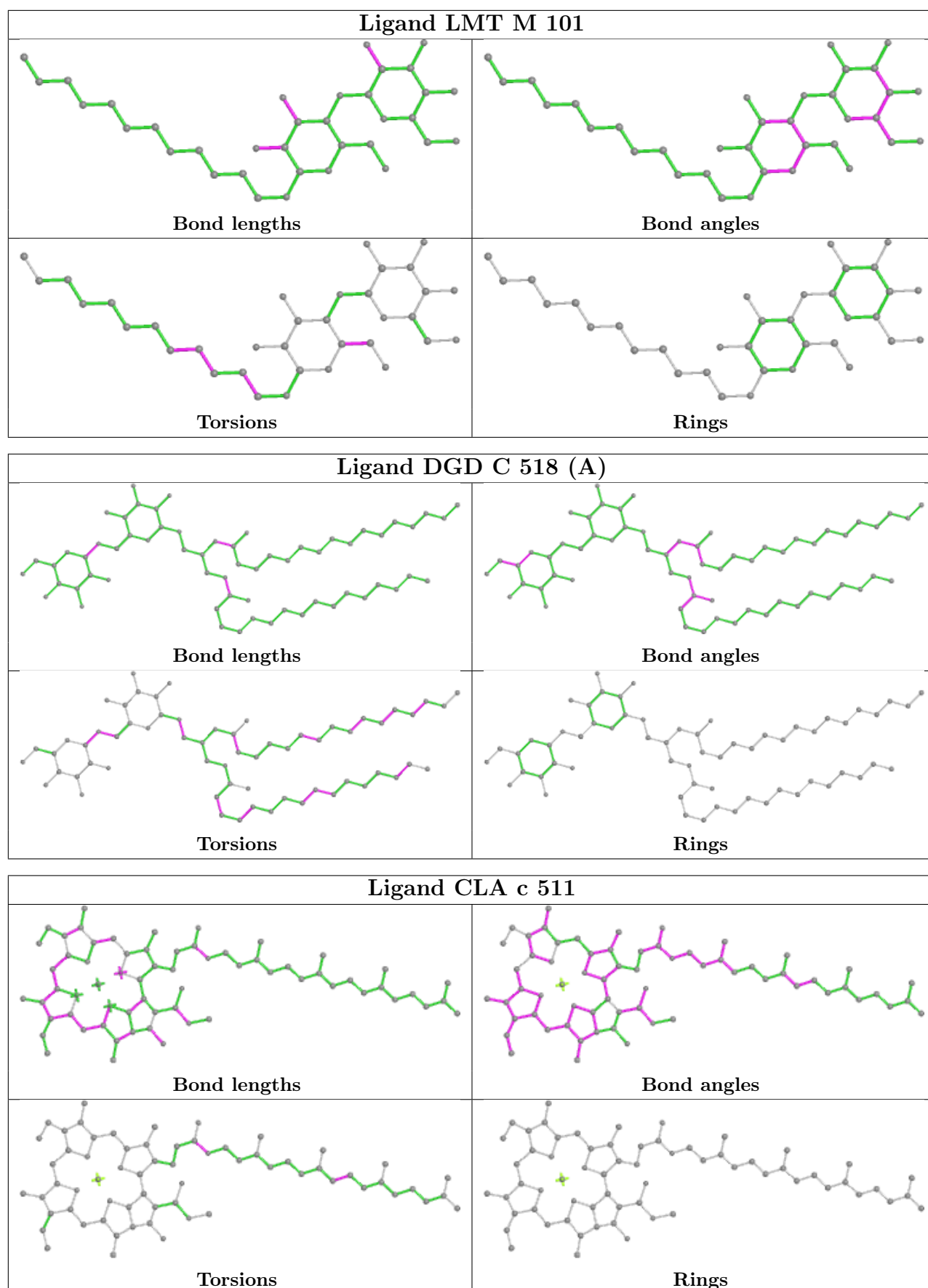












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 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%)	-0.77	6 (1%) 68 66	41, 48, 70, 126	0
1	a	334/344 (97%)	-0.64	3 (0%) 84 83	43, 52, 79, 132	0
2	B	504/505 (99%)	-0.47	11 (2%) 62 59	43, 54, 82, 116	0
2	b	504/505 (99%)	-0.31	26 (5%) 27 26	46, 58, 97, 167	1 (0%)
3	C	451/455 (99%)	-0.56	9 (1%) 65 63	45, 59, 79, 163	0
3	c	455/455 (100%)	-0.40	12 (2%) 56 53	48, 66, 85, 134	2 (0%)
4	D	342/342 (100%)	-0.68	2 (0%) 89 88	41, 50, 67, 141	0
4	d	341/342 (99%)	-0.67	2 (0%) 89 88	44, 54, 76, 133	0
5	E	81/84 (96%)	-0.11	4 (4%) 29 28	53, 70, 102, 166	0
5	e	79/84 (94%)	0.19	7 (8%) 9 8	63, 78, 116, 153	0
6	F	34/44 (77%)	-0.44	2 (5%) 22 21	54, 62, 84, 115	0
6	f	31/44 (70%)	-0.38	2 (6%) 18 17	59, 66, 96, 156	0
7	H	64/65 (98%)	-0.21	3 (4%) 31 30	51, 63, 86, 111	0
7	h	64/65 (98%)	-0.26	3 (4%) 31 30	57, 69, 94, 113	0
8	I	37/38 (97%)	-0.09	3 (8%) 12 10	57, 63, 124, 169	0
8	i	37/38 (97%)	-0.04	4 (10%) 5 5	54, 64, 122, 146	0
9	J	38/39 (97%)	-0.24	2 (5%) 26 25	52, 69, 117, 183	0
9	j	39/39 (100%)	0.13	6 (15%) 2 1	59, 77, 129, 165	0
10	K	37/37 (100%)	-0.58	1 (2%) 54 52	60, 68, 88, 105	0
10	k	37/37 (100%)	-0.48	0 100 100	68, 74, 95, 113	0
11	L	36/37 (97%)	-0.39	3 (8%) 11 10	41, 47, 103, 147	0
11	l	36/37 (97%)	-0.39	2 (5%) 24 23	44, 49, 100, 124	0
12	M	32/36 (88%)	-0.67	1 (3%) 49 47	45, 50, 77, 136	0
12	m	33/36 (91%)	-0.43	2 (6%) 21 20	44, 50, 72, 153	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	O	243/244 (99%)	-0.07	17 (6%) 16 15	43, 65, 120, 188	0
13	o	243/244 (99%)	0.05	26 (10%) 6 5	46, 66, 124, 171	0
14	T	29/32 (90%)	-0.63	2 (6%) 16 15	44, 49, 77, 124	0
14	t	29/32 (90%)	-0.70	1 (3%) 45 43	45, 51, 76, 126	0
15	U	96/104 (92%)	-0.42	1 (1%) 82 81	49, 59, 92, 102	0
15	u	97/104 (93%)	-0.37	2 (2%) 63 61	53, 63, 83, 137	0
16	V	137/137 (100%)	-0.56	0 100 100	48, 57, 83, 109	0
16	v	137/137 (100%)	-0.21	4 (2%) 51 49	54, 71, 102, 138	0
17	X	38/40 (95%)	-0.29	2 (5%) 26 25	61, 71, 90, 114	0
17	x	38/40 (95%)	0.18	4 (10%) 6 5	64, 77, 119, 164	0
18	Y	29/30 (96%)	0.94	7 (24%) 0 0	67, 84, 127, 131	0
18	y	29/30 (96%)	0.29	4 (13%) 2 2	75, 92, 112, 119	0
19	Z	62/62 (100%)	0.06	7 (11%) 5 4	67, 80, 132, 162	0
19	z	62/62 (100%)	0.30	10 (16%) 1 1	80, 94, 140, 206	0
20	R	34/34 (100%)	1.90	14 (41%) 0 0	79, 101, 130, 137	0
All	All	5283/5384 (98%)	-0.38	217 (4%) 37 35	41, 59, 100, 206	3 (0%)

The worst 5 of 217 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	c	20	SER	8.0
5	E	84	LYS	7.5
2	b	495	PHE	7.0
1	a	11	ALA	6.4
13	o	4	THR	6.4

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
8	FME	i	1	10/11	0.93	0.17	53,68,77,90	0
14	FME	T	1	10/11	0.94	0.10	45,55,64,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	FME	I	1	10/11	0.96	0.07	58,69,79,82	0
14	FME	t	1	10/11	0.96	0.09	44,51,65,75	0
12	FME	m	1	10/11	0.97	0.12	53,63,88,122	0
12	FME	M	1	10/11	0.97	0.11	52,60,89,108	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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(Å ²)	Q<0.9
30	UNL	b	626	33/-	0.47	0.36	68,97,161,173	0
30	UNL	I	101	40/-	0.48	0.35	73,111,158,166	0
30	UNL	B	626	33/-	0.49	0.37	54,117,145,149	0
31	LMT	T	101	35/35	0.49	0.31	77,131,185,192	0
30	UNL	j	101	10/-	0.50	0.29	80,93,103,106	0
31	LMT	b	621	25/35	0.55	0.29	84,112,164,173	0
27	GOL	a	417	6/6	0.58	0.54	78,98,110,112	0
30	UNL	i	101	40/-	0.59	0.30	73,110,160,171	0
30	UNL	A	415	28/-	0.60	0.35	93,117,135,155	0
31	LMT	B	630	35/35	0.60	0.36	66,117,148,156	0
30	UNL	K	101[A]	34/-	0.64	0.34	88,115,128,132	34
30	UNL	K	101[B]	34/-	0.64	0.34	88,115,128,133	34
33	LMG	C	521	51/55	0.64	0.30	63,117,164,179	0
30	UNL	c	524[B]	32/-	0.65	0.40	98,113,127,139	32
30	UNL	c	524[A]	32/-	0.65	0.40	98,113,127,139	32
31	LMT	M	101	35/35	0.65	0.26	63,96,120,125	0
31	LMT	A	417	35/35	0.66	0.32	65,116,144,148	0
31	LMT	F	101	35/35	0.68	0.52	102,138,184,189	0
33	LMG	c	520	51/55	0.68	0.28	73,135,172,190	0
34	HTG	D	410	16/19	0.68	0.29	84,104,134,149	0
31	LMT	B	631	25/35	0.69	0.24	63,87,150,170	0
30	UNL	d	410	36/-	0.70	0.20	65,93,136,146	0
34	HTG	b	623	19/19	0.70	0.50	84,135,161,168	0
31	LMT	B	628	35/35	0.71	0.28	67,102,138,150	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
33	LMG	Z	101	37/55	0.71	0.28	72,123,151,171	0
31	LMT	m	103	35/35	0.72	0.25	66,90,109,125	0
30	UNL	x	101	18/-	0.72	0.23	68,84,140,141	0
32	LHG	a	419[B]	42/49	0.73	0.35	94,140,157,165	42
31	LMT	A	420	35/35	0.73	0.36	100,135,156,170	0
32	LHG	a	419[A]	42/49	0.73	0.35	94,140,157,165	42
30	UNL	m	102	10/-	0.74	0.35	73,77,96,102	0
33	LMG	z	101	39/55	0.75	0.26	78,132,153,170	0
31	LMT	e	101	35/35	0.76	0.49	110,151,197,199	0
31	LMT	b	627	25/35	0.77	0.23	59,100,155,167	0
27	GOL	o	302	6/6	0.78	0.30	84,102,112,116	0
31	LMT	a	416	35/35	0.78	0.40	109,138,152,164	0
30	UNL	a	413	30/-	0.79	0.32	93,119,146,161	0
27	GOL	l	801[A]	6/6	0.79	0.87	73,104,107,111	6
27	GOL	l	801[B]	6/6	0.79	0.87	73,105,107,111	6
34	HTG	d	411	16/19	0.79	0.28	89,122,140,154	0
27	GOL	A	411	6/6	0.80	0.18	64,81,85,91	0
30	UNL	X	101	18/-	0.80	0.20	64,73,112,112	0
27	GOL	B	627	6/6	0.80	0.23	71,88,97,112	0
27	GOL	O	302	6/6	0.81	0.21	77,86,99,113	0
30	UNL	M	102	10/-	0.81	0.26	69,78,93,96	0
29	PL9	A	414[A]	55/55	0.82	0.23	74,100,115,120	55
32	LHG	E	101[A]	42/49	0.82	0.24	76,106,118,123	42
32	LHG	E	101[B]	42/49	0.82	0.24	76,106,118,124	42
34	HTG	C	522	19/19	0.82	0.34	112,130,148,148	0
29	PL9	A	414[B]	55/55	0.82	0.23	74,100,115,120	55
30	UNL	J	101	10/-	0.82	0.18	72,81,90,95	0
26	SQD	f	102	43/54	0.82	0.30	90,133,179,195	0
31	LMT	t	101	26/35	0.83	0.18	78,105,148,163	0
27	GOL	b	624	6/6	0.83	0.17	88,95,107,111	0
26	SQD	b	620	54/54	0.83	0.17	65,96,118,130	0
27	GOL	a	418	6/6	0.83	0.42	58,78,84,88	0
29	PL9	a	412[A]	55/55	0.83	0.23	82,109,121,129	55
29	PL9	a	412[B]	55/55	0.83	0.23	82,109,121,129	55
33	LMG	a	415	51/55	0.83	0.17	71,96,115,119	0
27	GOL	c	526	6/6	0.84	0.21	102,111,120,127	0
34	HTG	c	521	19/19	0.84	0.27	105,125,141,151	0
26	SQD	A	412	54/54	0.84	0.17	65,90,140,150	0
33	LMG	C	501	51/55	0.85	0.15	68,90,118,136	0
27	GOL	o	303	6/6	0.85	0.16	82,91,102,110	0
26	SQD	a	410	54/54	0.85	0.19	67,97,136,154	0
34	HTG	B	622	19/19	0.85	0.18	61,87,121,126	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
34	HTG	B	623	19/19	0.85	0.26	67,93,117,125	0
36	CA	f	103	1/1	0.85	0.06	120,120,120,120	0
27	GOL	A	418	6/6	0.86	0.48	51,82,88,93	0
34	HTG	b	622	19/19	0.86	0.18	58,80,121,125	0
36	CA	F	103	1/1	0.86	0.20	127,127,127,127	0
30	UNL	D	409	40/-	0.86	0.18	67,94,139,151	0
26	SQD	B	620	54/54	0.87	0.15	66,93,135,146	0
23	CLA	c	513	65/65	0.87	0.18	66,93,129,148	0
27	GOL	V	203[A]	6/6	0.87	0.19	60,70,77,77	6
27	GOL	V	203[B]	6/6	0.87	0.19	60,70,77,77	6
27	GOL	d	413	6/6	0.87	0.30	55,75,76,91	0
36	CA	o	301	1/1	0.87	0.07	103,103,103,103	0
25	BCR	K	102	40/40	0.88	0.18	56,65,76,82	0
33	LMG	d	412	51/55	0.88	0.18	54,72,124,155	0
25	BCR	C	515	40/40	0.88	0.13	55,75,91,93	0
33	LMG	D	411	51/55	0.88	0.18	50,72,124,138	0
27	GOL	O	303	6/6	0.88	0.25	82,95,107,108	0
23	CLA	b	601	65/65	0.89	0.17	59,84,128,166	0
23	CLA	b	616	65/65	0.89	0.17	48,62,133,146	0
27	GOL	v	202[A]	6/6	0.89	0.16	65,79,85,86	6
27	GOL	v	202[B]	6/6	0.89	0.16	65,79,85,87	6
25	BCR	h	101	40/40	0.89	0.15	55,70,91,97	0
27	GOL	B	629	6/6	0.89	0.27	74,79,93,97	0
23	CLA	C	514	65/65	0.89	0.14	59,83,115,120	0
27	GOL	D	412	6/6	0.90	0.23	51,68,73,94	0
23	CLA	c	512	65/65	0.90	0.17	60,81,126,140	0
23	CLA	B	616	65/65	0.90	0.18	48,59,132,147	0
23	CLA	d	404	65/65	0.90	0.14	52,67,130,157	0
33	LMG	c	519	51/55	0.90	0.18	62,91,136,161	0
34	HTG	b	625	19/19	0.91	0.11	68,79,97,110	0
33	LMG	C	520	51/55	0.91	0.17	55,85,123,134	0
23	CLA	B	601	65/65	0.91	0.14	57,78,114,156	0
25	BCR	Y	101	40/40	0.91	0.13	54,65,84,92	0
25	BCR	d	405	40/40	0.91	0.12	51,69,109,113	0
26	SQD	F	102	43/54	0.91	0.18	69,107,131,145	0
30	UNL	D	408	17/-	0.92	0.14	62,78,99,122	0
23	CLA	B	606	65/65	0.92	0.14	44,56,114,130	0
23	CLA	C	507	65/65	0.92	0.14	53,71,125,144	0
23	CLA	b	606	65/65	0.92	0.13	43,58,117,132	0
35	DGD	c	517[A]	62/66	0.92	0.12	56,69,123,138	62
35	DGD	c	517[B]	62/66	0.92	0.12	56,69,123,139	62
35	DGD	h	102	62/66	0.92	0.12	52,65,79,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
36	CA	C	524	1/1	0.92	0.07	72,72,72,72	0
23	CLA	C	513	65/65	0.92	0.14	54,72,117,136	0
33	LMG	B	621	51/55	0.92	0.12	55,72,95,116	0
23	CLA	c	506	65/65	0.92	0.15	54,72,126,142	0
25	BCR	c	514	40/40	0.93	0.11	71,83,93,98	0
33	LMG	m	101	51/55	0.93	0.13	63,76,98,115	0
35	DGD	c	518	62/66	0.93	0.12	50,67,106,131	0
30	UNL	d	409	17/-	0.93	0.12	69,79,114,116	0
23	CLA	B	609	65/65	0.93	0.16	47,59,72,83	0
34	HTG	V	202	11/19	0.93	0.39	83,111,123,130	0
35	DGD	C	519	62/66	0.93	0.12	45,61,103,122	0
35	DGD	H	102	62/66	0.93	0.12	47,63,75,90	0
25	BCR	H	101	40/40	0.94	0.10	53,68,90,93	0
23	CLA	a	407	65/65	0.94	0.16	42,57,141,161	0
23	CLA	c	507	65/65	0.94	0.12	50,67,85,92	0
25	BCR	b	618	40/40	0.94	0.10	47,57,76,94	0
27	GOL	C	523[A]	6/6	0.94	0.13	59,62,67,72	6
27	GOL	C	523[B]	6/6	0.94	0.13	59,63,67,72	6
35	DGD	C	518[A]	62/66	0.94	0.12	49,63,114,118	62
35	DGD	C	518[B]	62/66	0.94	0.12	49,63,114,118	62
23	CLA	c	511	65/65	0.94	0.12	56,68,87,107	0
23	CLA	A	408	65/65	0.94	0.12	43,54,128,149	0
23	CLA	C	509	65/65	0.94	0.10	47,56,122,147	0
25	BCR	k	101	40/40	0.94	0.14	59,75,85,87	0
23	CLA	b	612	65/65	0.94	0.11	41,54,65,76	0
25	BCR	A	409	40/40	0.94	0.10	40,52,67,71	0
25	BCR	B	618	40/40	0.94	0.09	43,55,73,80	0
25	BCR	B	619	40/40	0.94	0.10	47,60,90,101	0
23	CLA	D	403	65/65	0.94	0.13	47,60,132,138	0
25	BCR	D	404	40/40	0.94	0.09	44,62,108,115	0
32	LHG	b	629[B]	49/49	0.95	0.13	51,60,72,95	49
32	LHG	d	408[A]	49/49	0.95	0.16	52,64,117,134	49
32	LHG	d	408[B]	49/49	0.95	0.16	52,64,117,134	49
23	CLA	C	505	65/65	0.95	0.10	42,58,106,131	0
26	SQD	a	409[A]	54/54	0.95	0.14	61,83,121,123	54
26	SQD	a	409[B]	54/54	0.95	0.14	61,83,121,123	54
23	CLA	B	611	65/65	0.95	0.10	38,46,65,74	0
25	BCR	b	619	40/40	0.95	0.09	48,64,90,95	0
23	CLA	c	508	65/65	0.95	0.12	46,63,133,152	0
23	CLA	b	609	65/65	0.95	0.13	49,65,77,90	0
25	BCR	C	516	40/40	0.95	0.12	51,61,76,90	0
35	DGD	c	516[A]	62/66	0.95	0.11	48,64,103,113	62

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
35	DGD	c	516[B]	62/66	0.95	0.11	47,64,103,114	62
23	CLA	C	508	65/65	0.95	0.11	47,61,83,93	0
25	BCR	t	102	40/40	0.95	0.09	44,59,80,89	0
26	SQD	A	410[A]	54/54	0.95	0.12	57,81,115,119	54
26	SQD	A	410[B]	54/54	0.95	0.12	57,81,115,119	54
23	CLA	C	502	65/65	0.95	0.09	49,60,74,81	0
23	CLA	c	504	65/65	0.95	0.10	53,64,107,142	0
36	CA	O	301	1/1	0.95	0.08	104,104,104,104	0
34	HTG	B	625	19/19	0.95	0.10	68,82,98,105	0
32	LHG	b	629[A]	49/49	0.95	0.13	51,60,72,95	49
32	LHG	d	414[B]	49/49	0.96	0.14	51,69,82,94	49
25	BCR	c	515	40/40	0.96	0.11	57,65,78,86	0
23	CLA	a	405[A]	65/65	0.96	0.10	43,55,126,133	65
23	CLA	a	405[B]	65/65	0.96	0.10	42,55,126,133	65
23	CLA	c	509	65/65	0.96	0.10	46,62,90,101	0
23	CLA	B	603	65/65	0.96	0.11	43,54,73,83	0
25	BCR	y	101	40/40	0.96	0.08	59,71,89,100	0
23	CLA	B	610	65/65	0.96	0.12	42,55,68,84	0
23	CLA	b	602	65/65	0.96	0.12	47,61,80,92	0
23	CLA	b	604	65/65	0.96	0.12	42,52,106,121	0
24	PHO	a	414[A]	64/64	0.96	0.12	44,56,64,72	64
24	PHO	a	414[B]	64/64	0.96	0.12	44,56,64,72	64
23	CLA	b	605	65/65	0.96	0.11	38,52,73,83	0
23	CLA	C	510	65/65	0.96	0.11	50,59,83,94	0
23	CLA	b	607	65/65	0.96	0.08	38,48,81,94	0
29	PL9	D	405[A]	55/55	0.96	0.11	38,50,57,72	55
29	PL9	D	405[B]	55/55	0.96	0.11	38,50,58,72	55
23	CLA	C	511	65/65	0.96	0.09	48,59,81,89	0
23	CLA	b	611	65/65	0.96	0.09	41,51,72,81	0
29	PL9	d	406[A]	55/55	0.96	0.11	41,52,63,72	55
29	PL9	d	406[B]	55/55	0.96	0.11	40,52,63,72	55
23	CLA	C	512	65/65	0.96	0.13	49,64,80,84	0
23	CLA	b	614	65/65	0.96	0.09	42,53,102,117	0
27	GOL	B	624	6/6	0.96	0.19	70,73,86,91	0
35	DGD	C	517[A]	62/66	0.96	0.10	47,57,103,109	62
35	DGD	C	517[B]	62/66	0.96	0.10	47,57,103,109	62
32	LHG	A	419[A]	49/49	0.96	0.13	50,66,89,93	49
32	LHG	A	419[B]	49/49	0.96	0.13	50,66,89,93	49
32	LHG	D	407[A]	49/49	0.96	0.14	49,61,110,113	49
32	LHG	D	407[B]	49/49	0.96	0.14	49,61,110,114	49
23	CLA	b	615	65/65	0.96	0.10	48,59,83,95	0
25	BCR	T	102	40/40	0.96	0.08	45,57,73,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	CLA	C	504	65/65	0.96	0.08	46,62,72,88	0
25	BCR	a	408	40/40	0.96	0.08	45,53,67,69	0
25	BCR	b	617	40/40	0.96	0.09	43,53,64,69	0
23	CLA	c	501	65/65	0.96	0.11	55,67,80,93	0
32	LHG	d	407[A]	49/49	0.96	0.15	49,57,72,79	49
32	LHG	d	407[B]	49/49	0.96	0.15	49,58,72,79	49
23	CLA	B	602	65/65	0.96	0.11	46,56,74,88	0
36	CA	c	522	1/1	0.96	0.13	73,73,73,73	0
23	CLA	B	614	65/65	0.96	0.10	39,50,104,118	0
32	LHG	d	414[A]	49/49	0.96	0.14	51,69,81,93	49
38	HEM	f	101	43/43	0.96	0.13	61,80,114,135	0
23	CLA	b	603	65/65	0.97	0.08	43,56,80,101	0
23	CLA	B	607	65/65	0.97	0.10	38,48,72,85	0
24	PHO	A	416[A]	64/64	0.97	0.10	39,51,56,63	64
24	PHO	A	416[B]	64/64	0.97	0.10	38,51,56,64	64
24	PHO	a	406[A]	64/64	0.97	0.09	43,50,55,60	64
24	PHO	a	406[B]	64/64	0.97	0.09	43,50,56,60	64
23	CLA	A	406[B]	65/65	0.97	0.09	41,48,114,125	65
21	FE2	a	401[A]	1/1	0.97	0.06	55,55,55,55	1
21	FE2	a	401[B]	1/1	0.97	0.06	55,55,55,55	1
25	BCR	B	617	40/40	0.97	0.09	42,55,65,69	0
23	CLA	B	612	65/65	0.97	0.07	38,50,63,72	0
23	CLA	b	610	65/65	0.97	0.09	46,57,68,71	0
23	CLA	B	613	65/65	0.97	0.08	39,48,100,109	0
23	CLA	A	404[A]	65/65	0.97	0.12	37,45,63,71	65
32	LHG	D	406[A]	49/49	0.97	0.14	46,57,70,80	49
32	LHG	D	406[B]	49/49	0.97	0.14	46,57,71,80	49
23	CLA	b	613	65/65	0.97	0.08	43,50,88,108	0
23	CLA	B	615	65/65	0.97	0.10	45,55,78,96	0
23	CLA	D	402[A]	65/65	0.97	0.11	36,45,69,80	65
23	CLA	D	402[B]	65/65	0.97	0.11	36,45,69,80	65
32	LHG	L	101[A]	49/49	0.97	0.12	49,58,71,94	49
32	LHG	L	101[B]	49/49	0.97	0.12	48,58,71,94	49
23	CLA	A	404[B]	65/65	0.97	0.12	37,45,63,71	65
23	CLA	c	502	65/65	0.97	0.09	46,60,92,112	0
23	CLA	c	503	65/65	0.97	0.09	49,70,86,93	0
23	CLA	a	404[A]	65/65	0.97	0.13	41,46,64,77	65
23	CLA	c	505	65/65	0.97	0.09	51,64,92,97	0
23	CLA	a	404[B]	65/65	0.97	0.13	41,46,65,78	65
23	CLA	B	604	65/65	0.97	0.09	37,49,118,134	0
27	GOL	b	628	6/6	0.97	0.21	78,88,92,92	0
27	GOL	c	525[A]	6/6	0.97	0.20	65,72,77,77	6

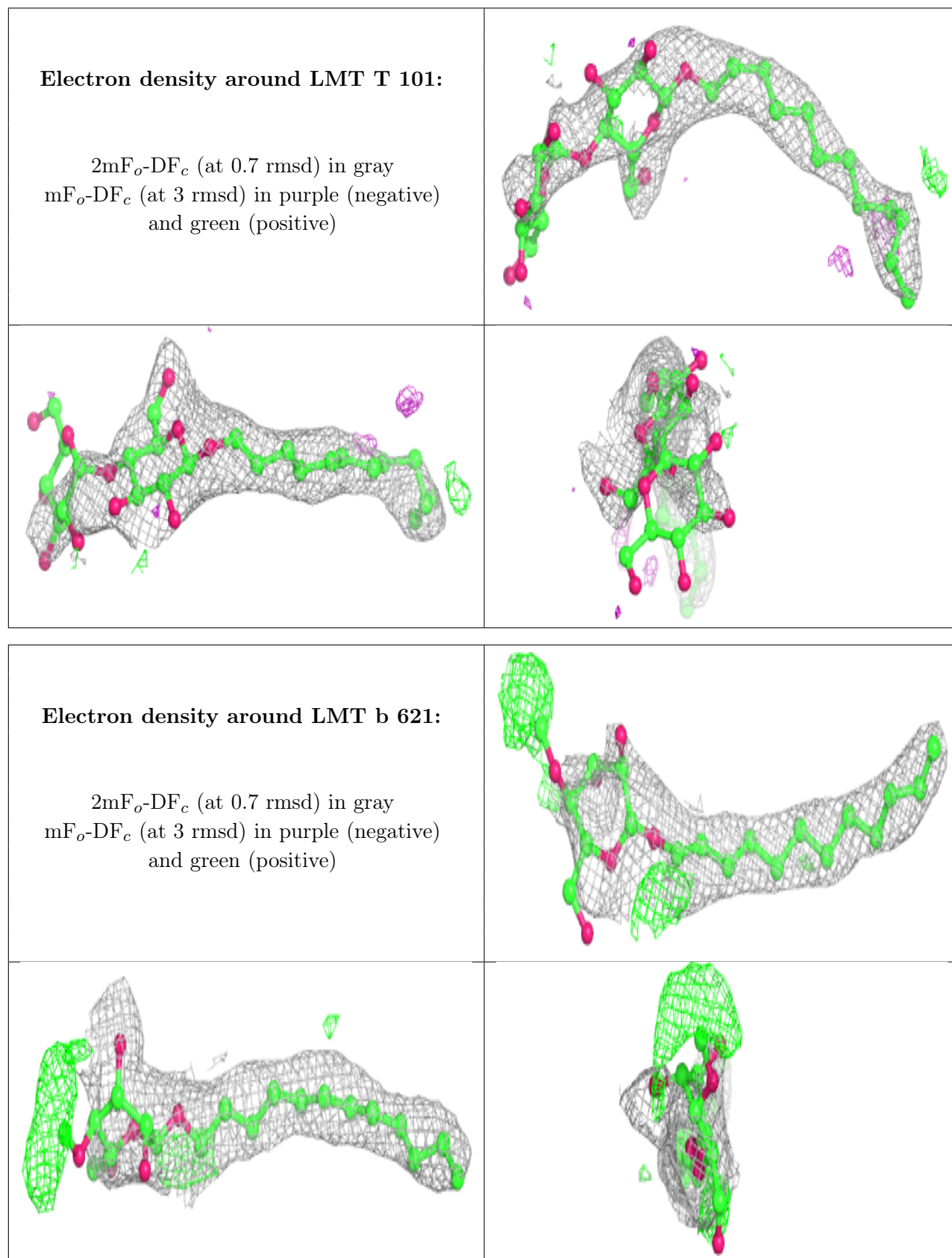
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
27	GOL	c	525[B]	6/6	0.97	0.20	65,73,77,78	6
23	CLA	C	503	65/65	0.97	0.08	43,55,84,91	0
23	CLA	B	605	65/65	0.97	0.11	39,49,69,86	0
36	CA	c	523	1/1	0.97	0.06	77,77,77,77	0
23	CLA	c	510	65/65	0.97	0.10	51,62,80,95	0
23	CLA	A	406[A]	65/65	0.97	0.09	41,48,114,125	65
38	HEM	E	102	43/43	0.97	0.11	53,69,82,94	0
23	CLA	C	506	65/65	0.97	0.09	46,60,96,109	0
40	HEC	V	201	43/43	0.97	0.13	40,51,58,62	0
40	HEC	v	201	43/43	0.97	0.12	50,62,67,75	0
22	CL	a	403[B]	1/1	0.98	0.03	54,54,54,54	1
22	CL	a	402[A]	1/1	0.98	0.05	50,50,50,50	1
22	CL	a	402[B]	1/1	0.98	0.05	50,50,50,50	1
23	CLA	d	402[A]	65/65	0.98	0.08	40,46,64,73	65
23	CLA	d	402[B]	65/65	0.98	0.08	40,46,64,73	65
23	CLA	d	403[A]	65/65	0.98	0.11	38,48,76,95	65
23	CLA	d	403[B]	65/65	0.98	0.11	37,48,76,95	65
23	CLA	B	608	65/65	0.98	0.08	40,50,69,83	0
24	PHO	A	407[A]	64/64	0.98	0.09	38,47,53,59	64
24	PHO	A	407[B]	64/64	0.98	0.09	38,47,53,60	64
37	BCT	D	401[A]	4/4	0.98	0.13	54,55,61,68	4
37	BCT	D	401[B]	4/4	0.98	0.13	54,55,62,69	4
37	BCT	d	401[A]	4/4	0.98	0.10	59,61,69,78	4
37	BCT	d	401[B]	4/4	0.98	0.10	60,61,69,80	4
23	CLA	A	405[A]	65/65	0.98	0.09	37,45,58,74	65
23	CLA	b	608	65/65	0.98	0.08	41,57,79,95	0
39	MG	J	102	1/1	0.98	0.03	57,57,57,57	0
39	MG	j	102	1/1	0.98	0.08	62,62,62,62	0
23	CLA	A	405[B]	65/65	0.98	0.09	37,45,58,75	65
22	CL	a	403[A]	1/1	0.98	0.03	54,54,54,54	1
22	CL	A	402[A]	1/1	0.99	0.03	44,44,44,44	1
22	CL	A	402[B]	1/1	0.99	0.03	44,44,44,44	1
28	OEX	A	413[A]	10/10	0.99	0.05	42,44,48,50	10
28	OEX	A	413[B]	10/10	0.99	0.05	42,45,49,50	10
28	OEX	a	411[A]	10/10	0.99	0.06	48,51,52,56	10
28	OEX	a	411[B]	10/10	0.99	0.06	48,50,52,54	10
22	CL	A	403[A]	1/1	0.99	0.08	49,49,49,49	1
22	CL	A	403[B]	1/1	0.99	0.08	49,49,49,49	1
21	FE2	A	401[A]	1/1	0.99	0.06	51,51,51,51	1
21	FE2	A	401[B]	1/1	0.99	0.06	51,51,51,51	1

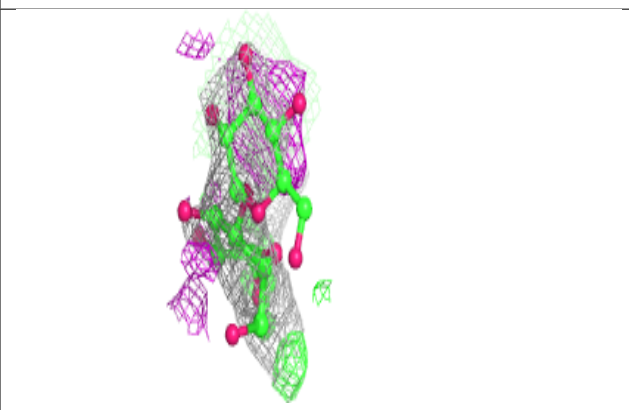
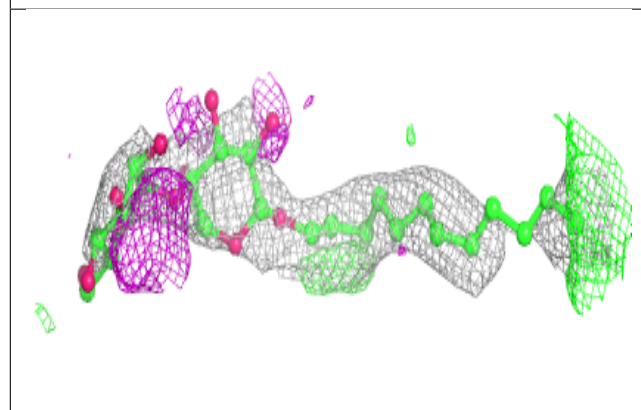
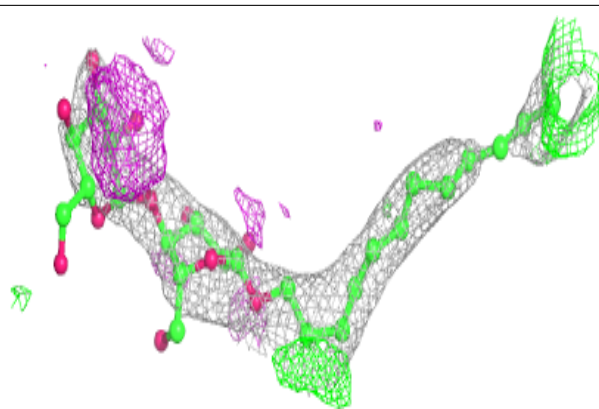
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

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

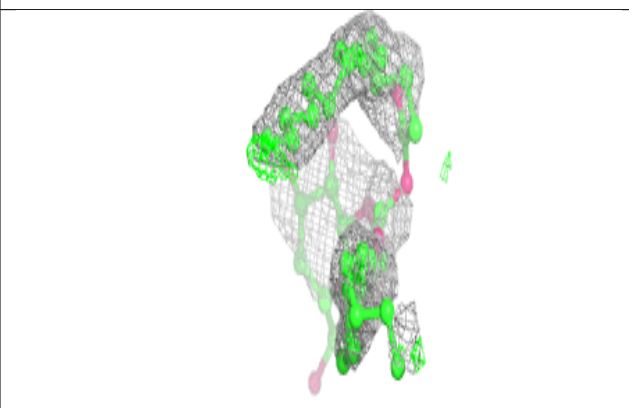
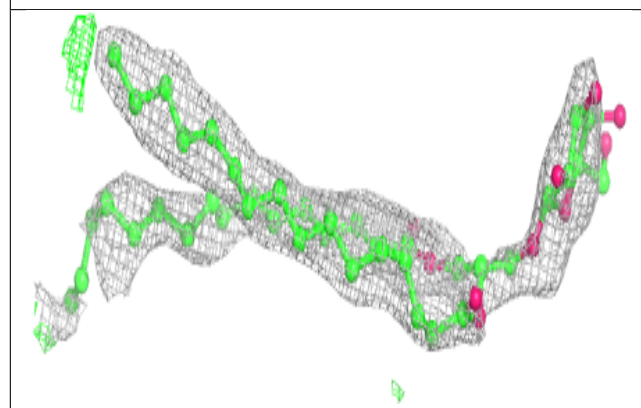
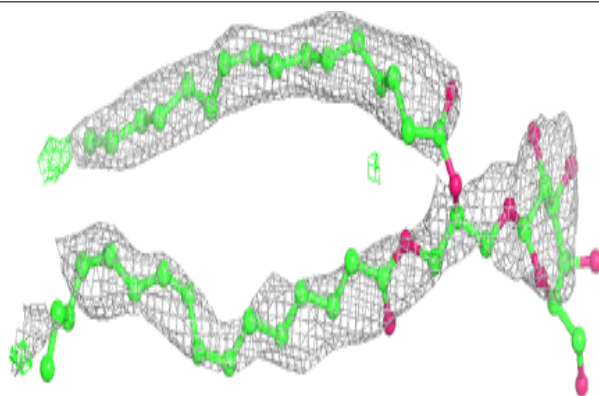


Electron density around LMT B 630:

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

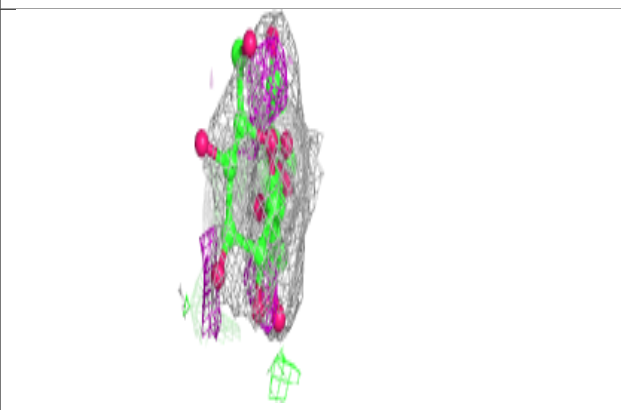
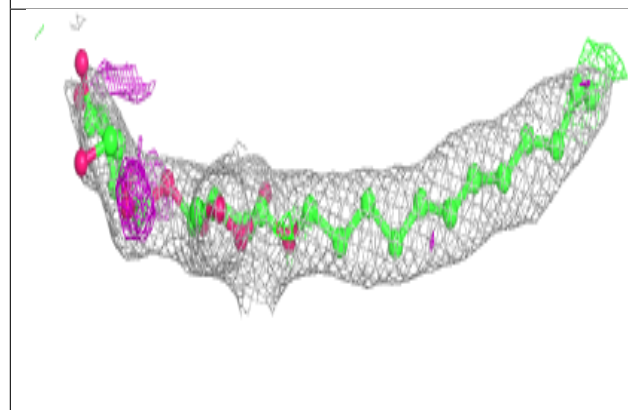
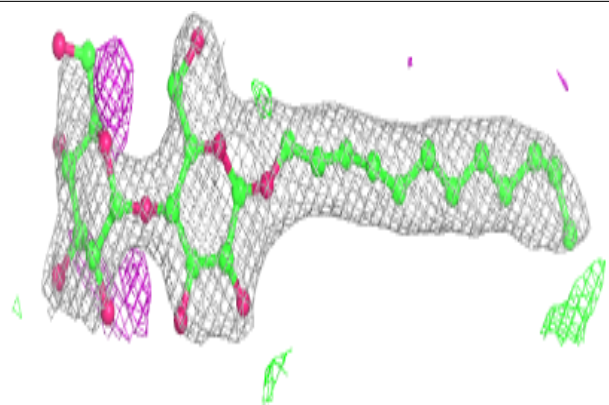
**Electron density around LMG C 521:**

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

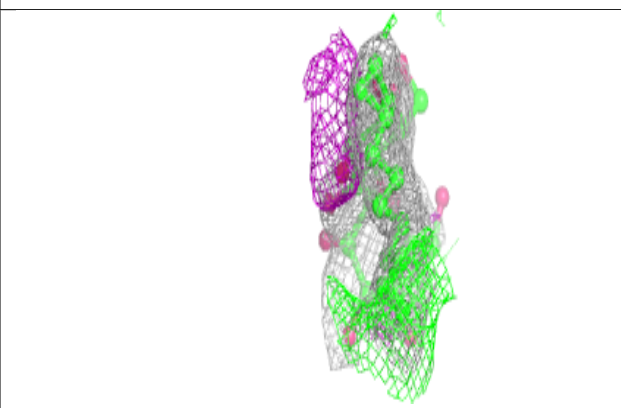
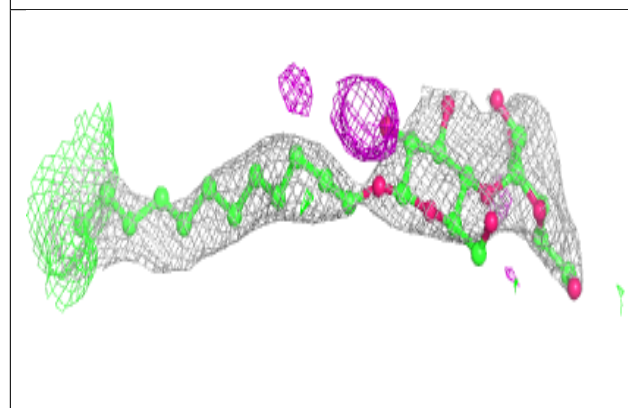
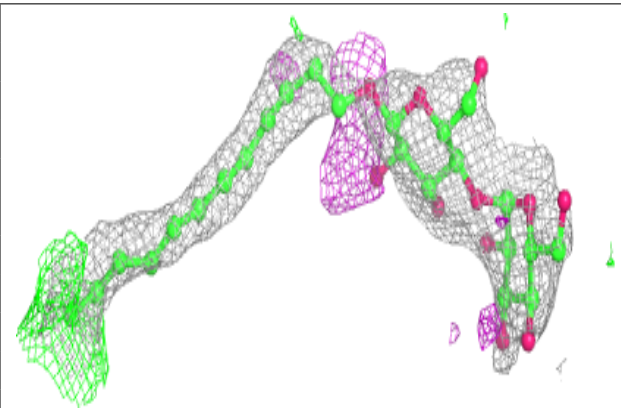


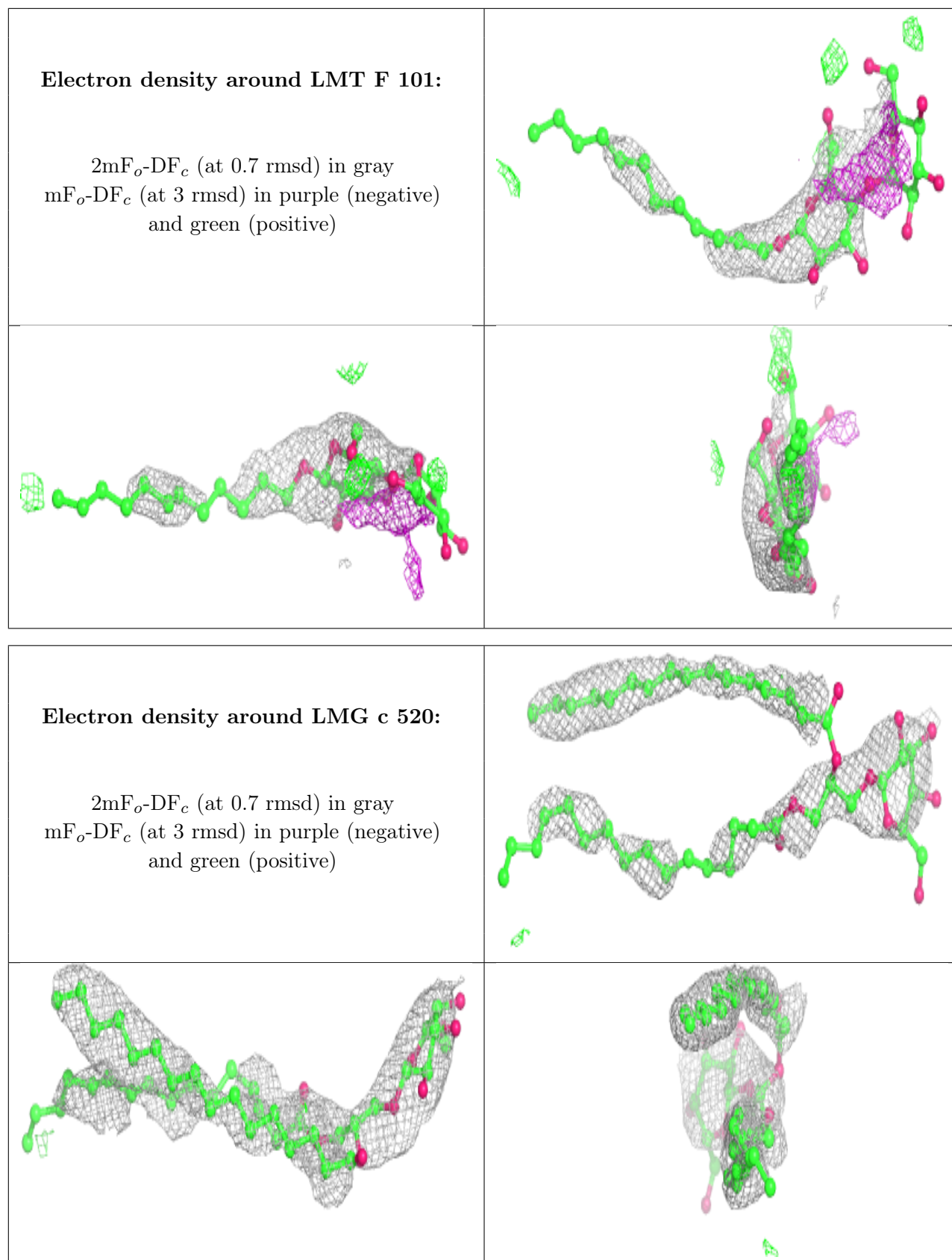
Electron density around LMT M 101:

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

**Electron density around LMT A 417:**

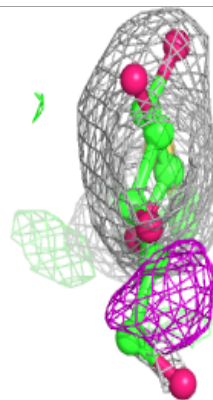
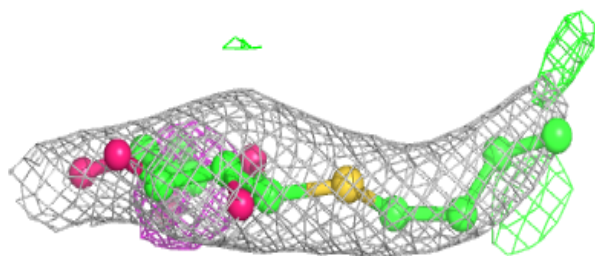
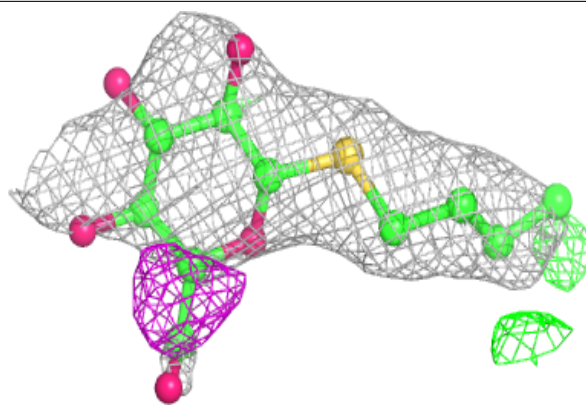
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



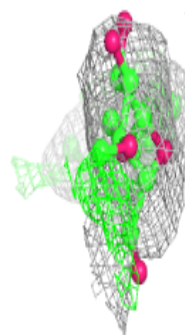
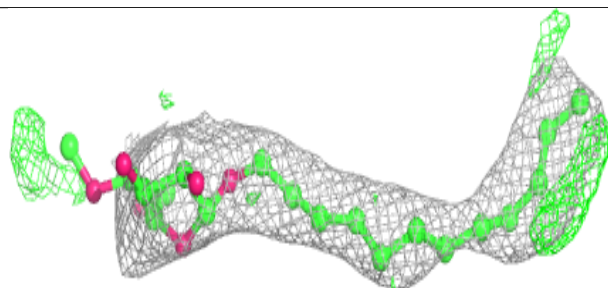
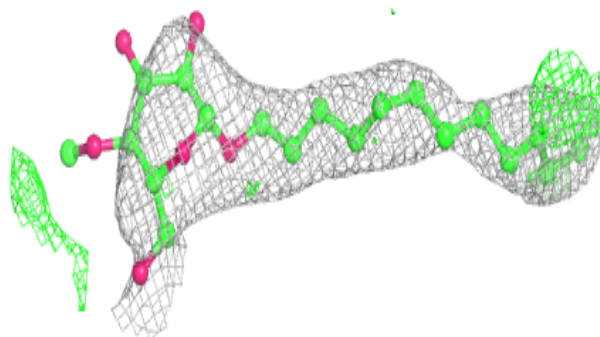


Electron density around HTG D 410:

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

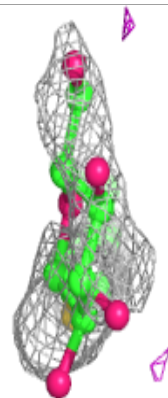
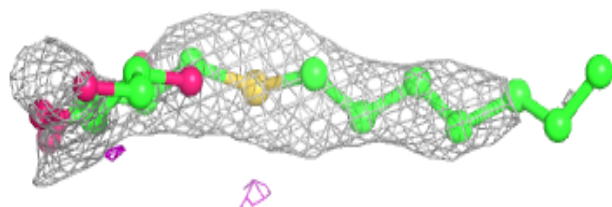
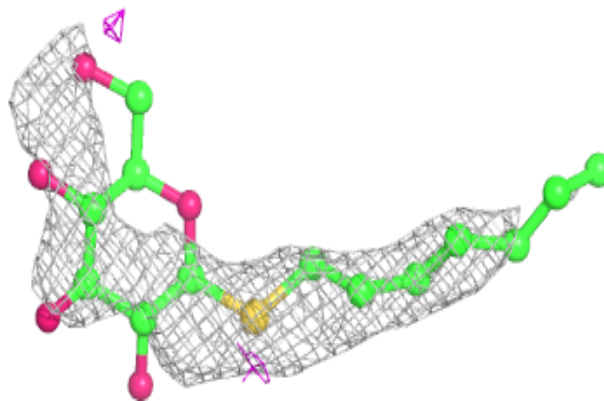
**Electron density around LMT B 631:**

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

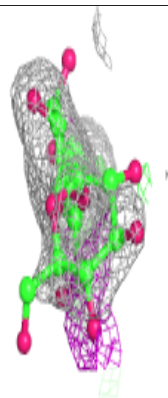
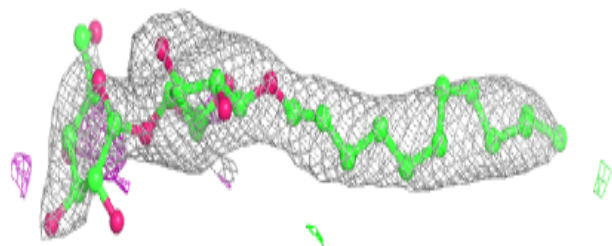
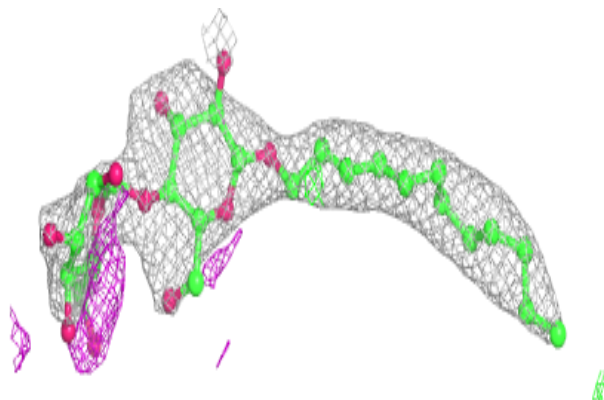


Electron density around HTG b 623:

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

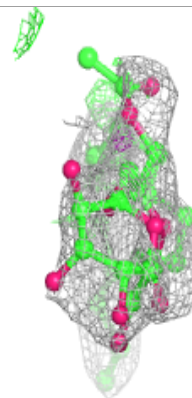
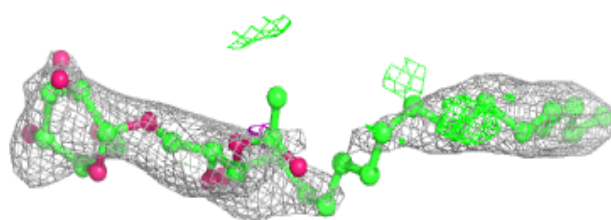
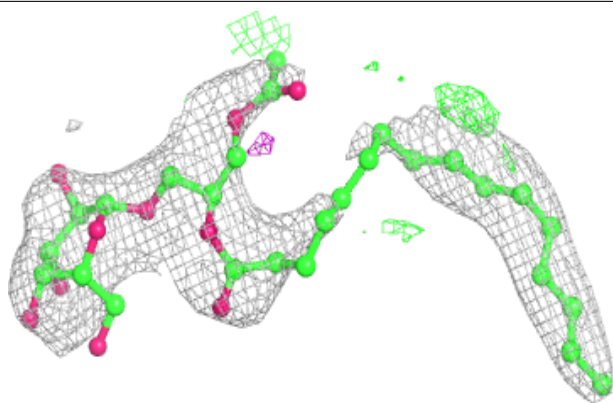
**Electron density around LMT B 628:**

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

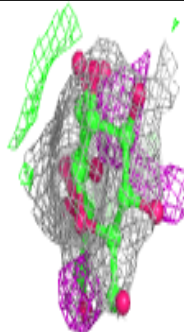
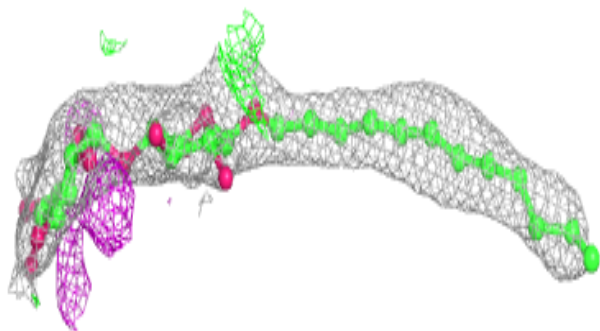
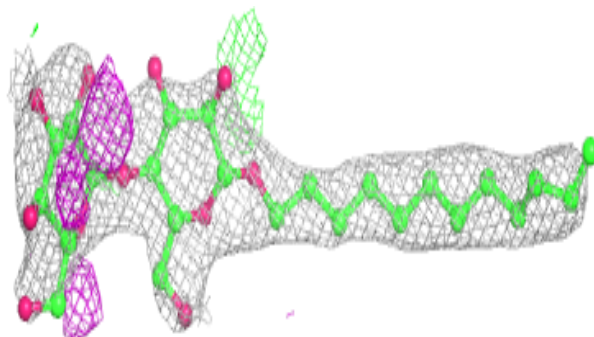


Electron density around LMG Z 101:

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

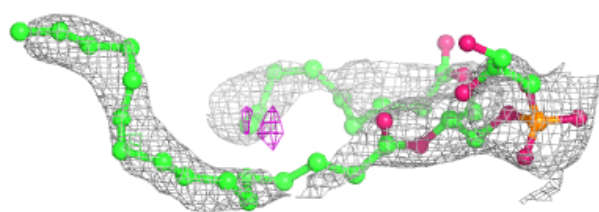
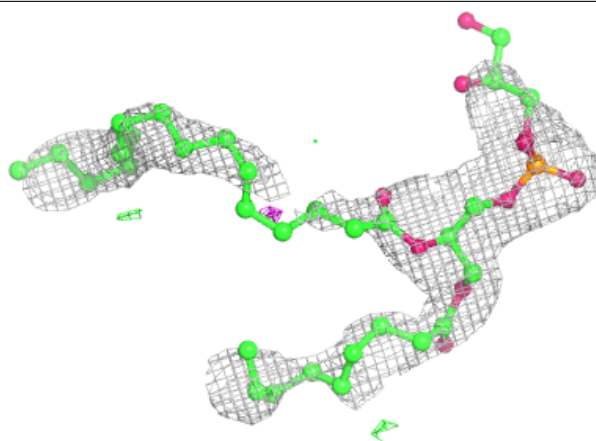
**Electron density around LMT m 103:**

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

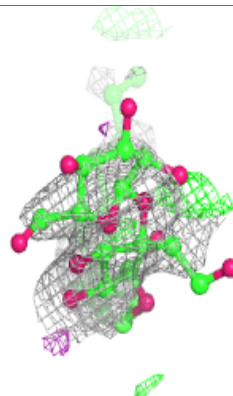
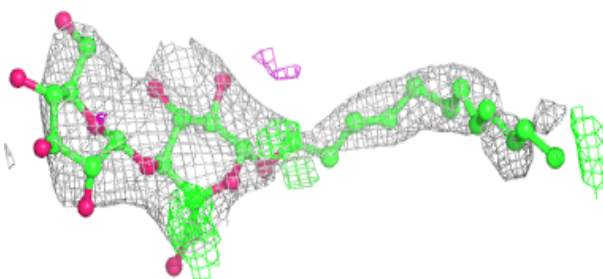
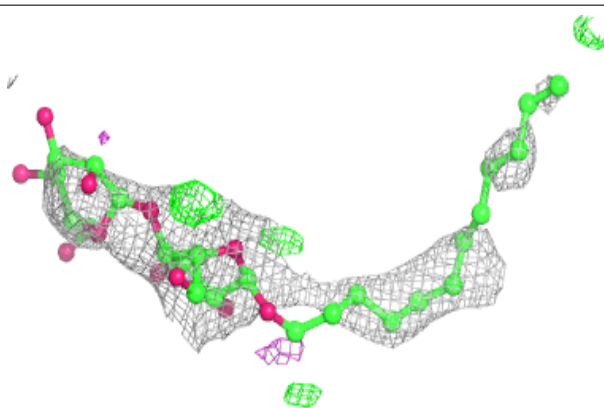


Electron density around LHG a 419 (B):

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

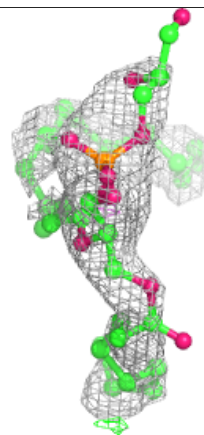
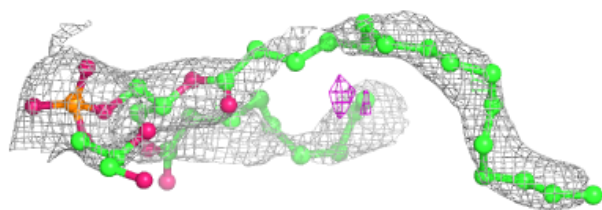
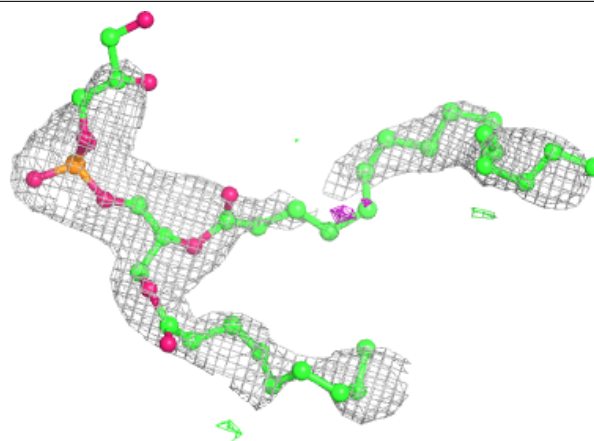
**Electron density around LMT A 420:**

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

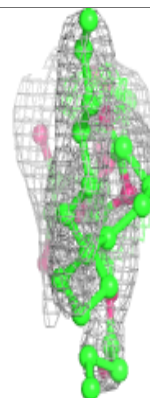
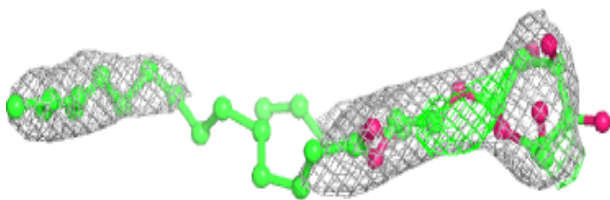
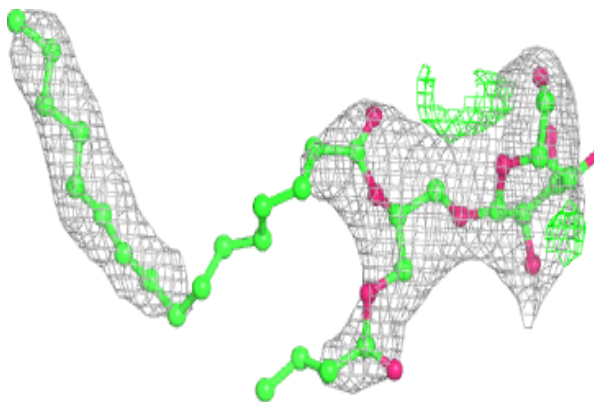


Electron density around LHG a 419 (A):

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

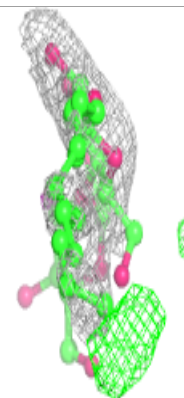
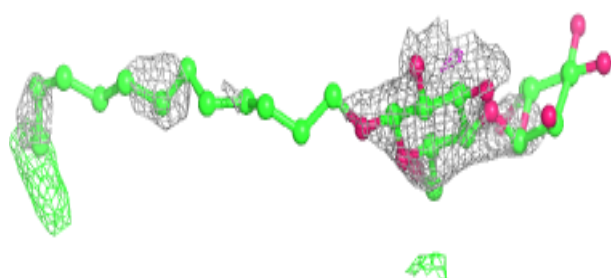
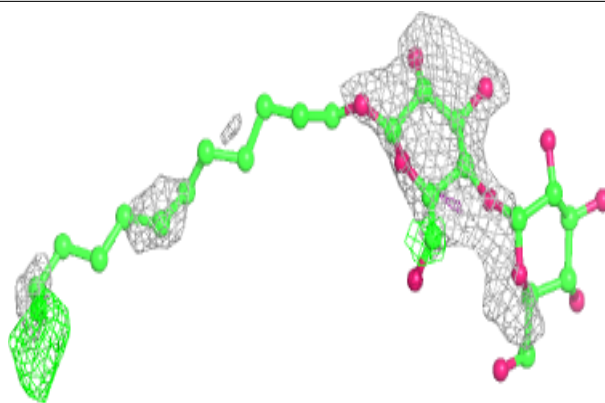
**Electron density around LMG z 101:**

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

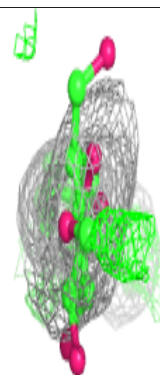
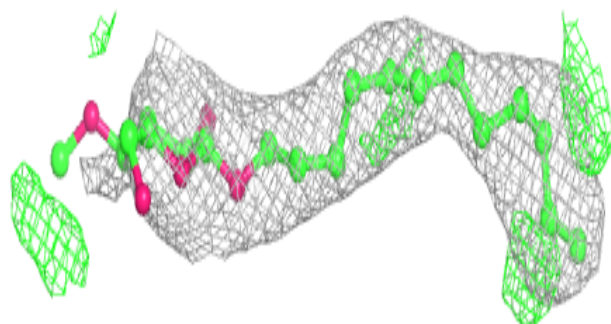
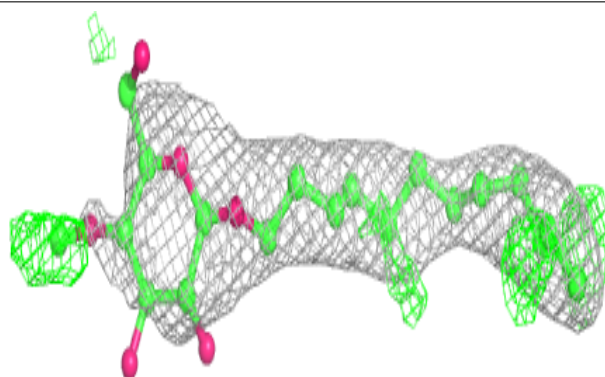


Electron density around LMT e 101:

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

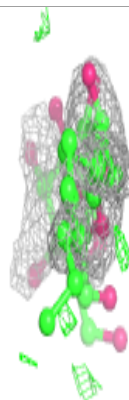
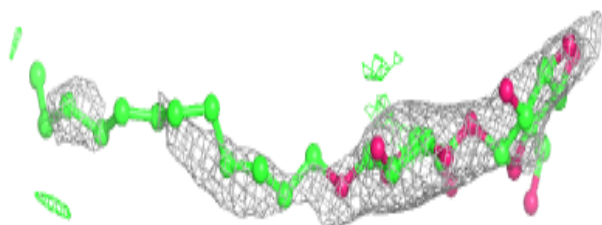
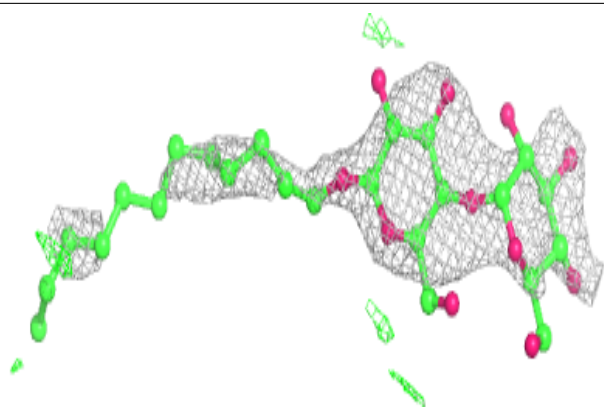
**Electron density around LMT b 627:**

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

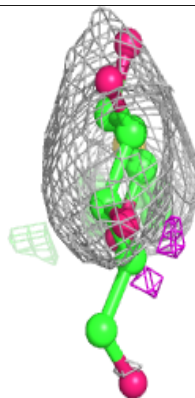
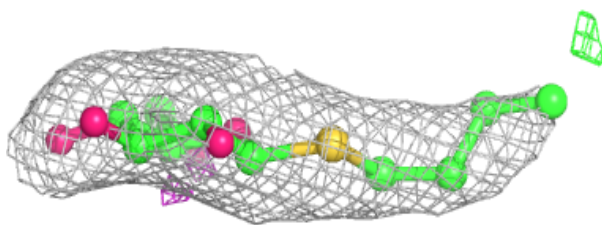
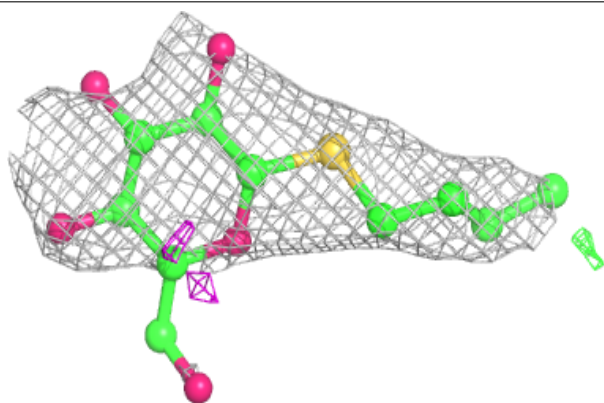


Electron density around LMT a 416:

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

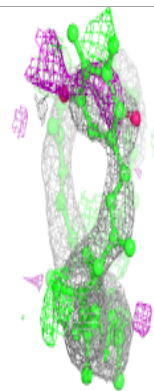
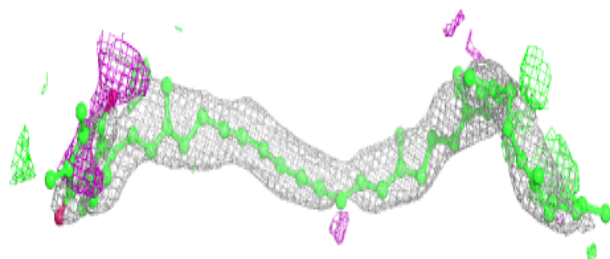
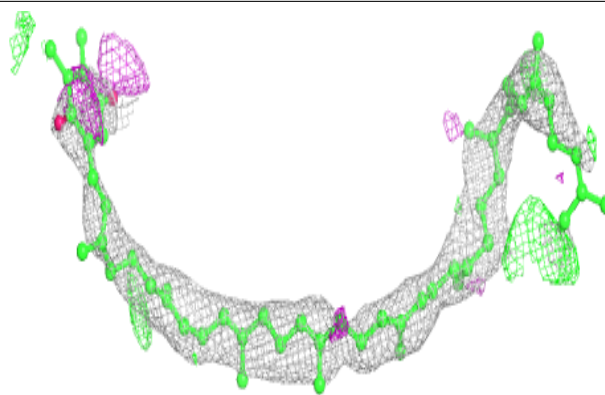
**Electron density around HTG d 411:**

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

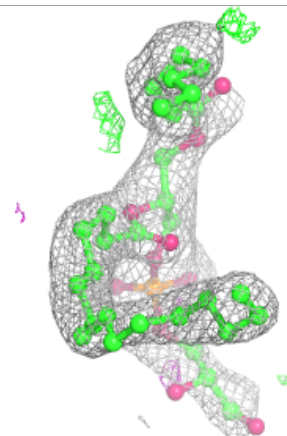
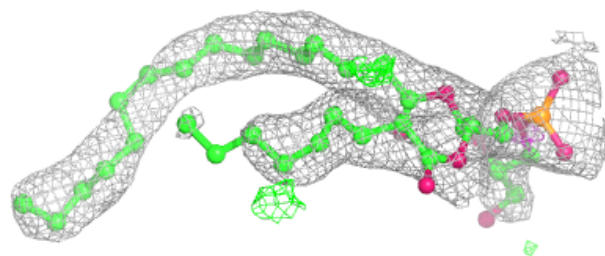
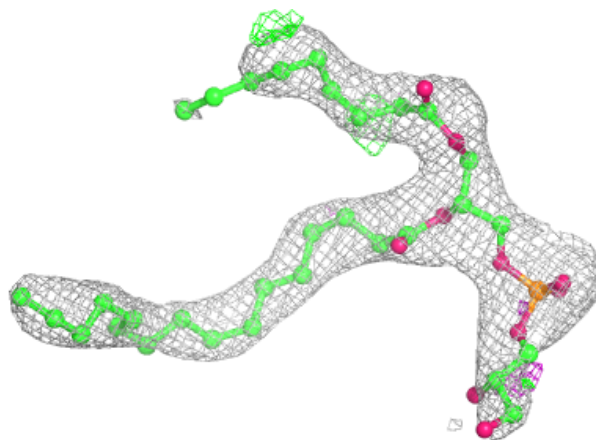


Electron density around PL9 A 414 (A):

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

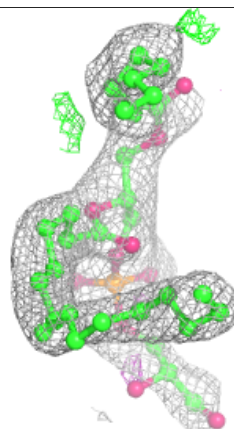
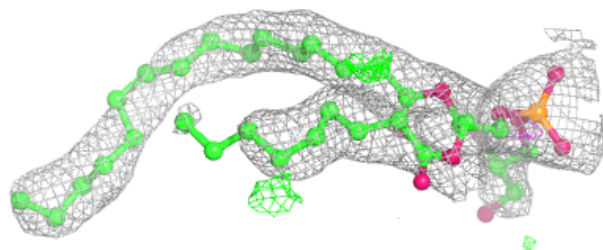
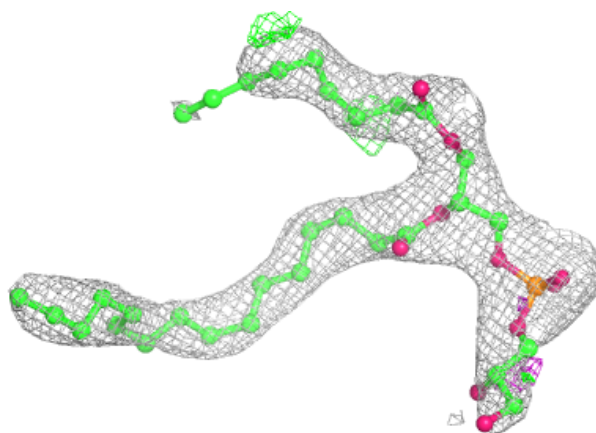
**Electron density around LHG E 101 (A):**

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

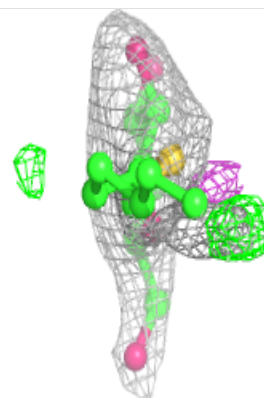
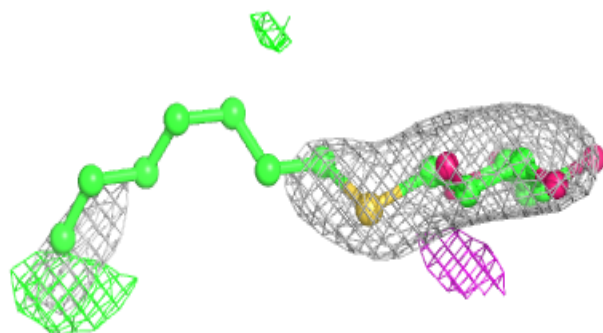
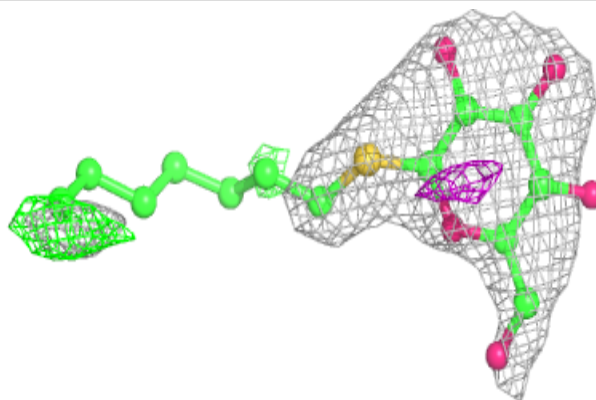


Electron density around LHG E 101 (B):

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

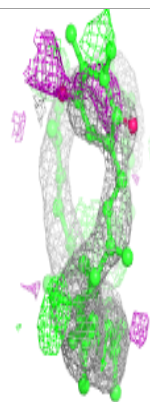
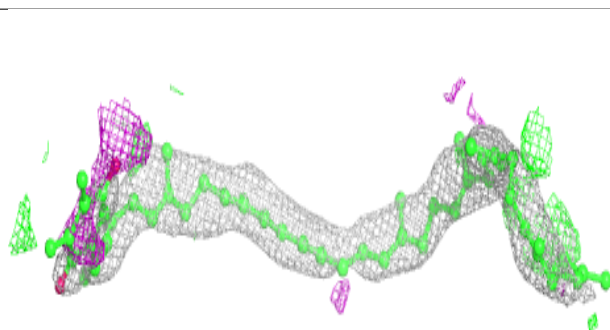
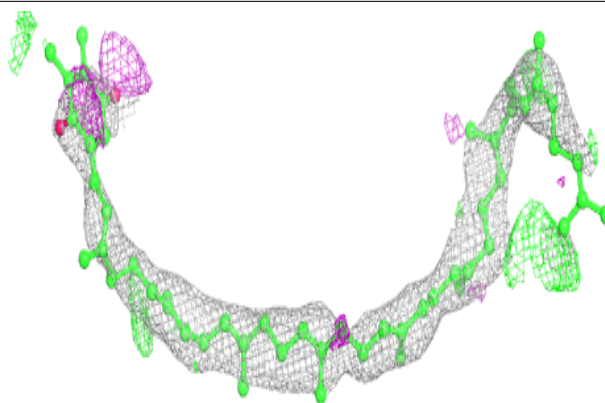
**Electron density around HTG C 522:**

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

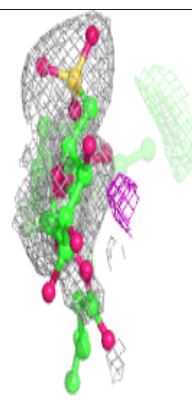
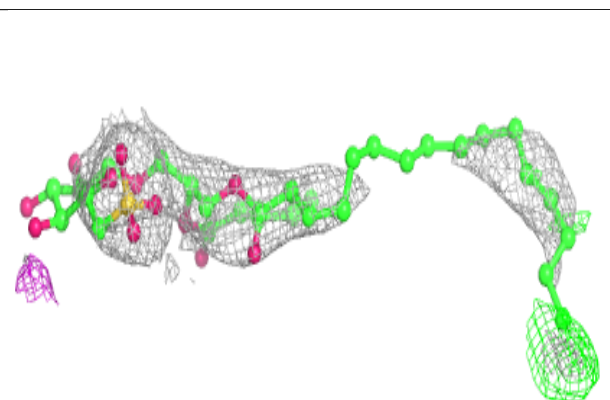
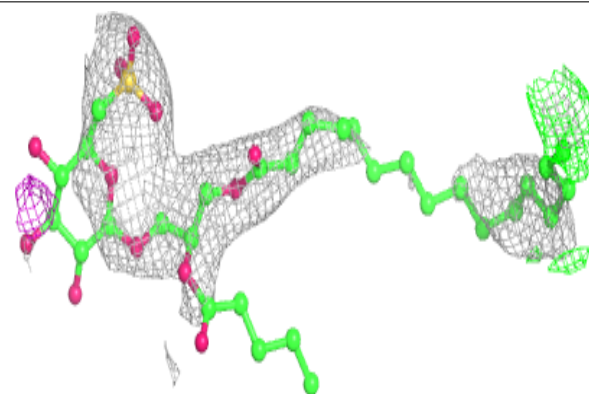


Electron density around PL9 A 414 (B):

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

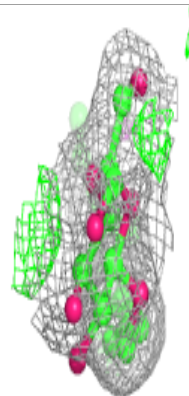
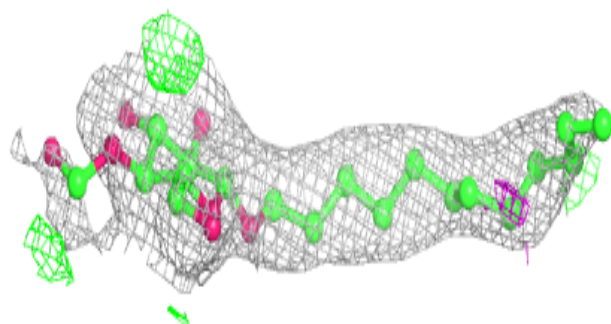
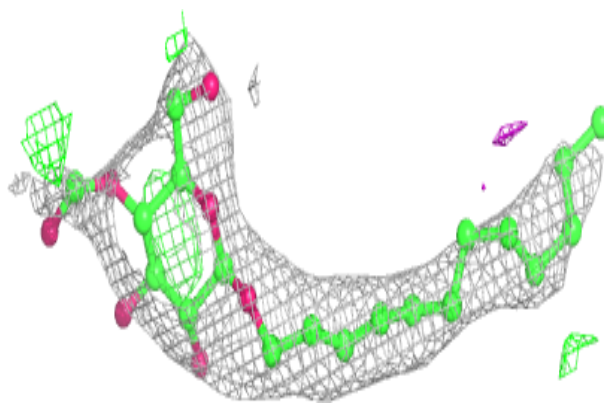
**Electron density around SQD f 102:**

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

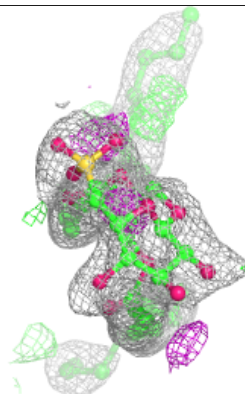
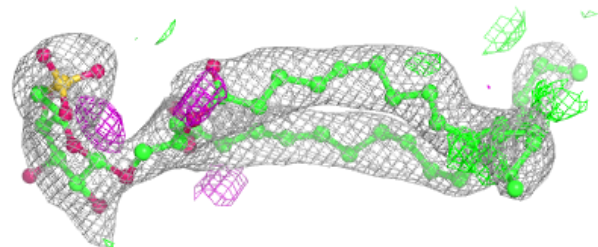
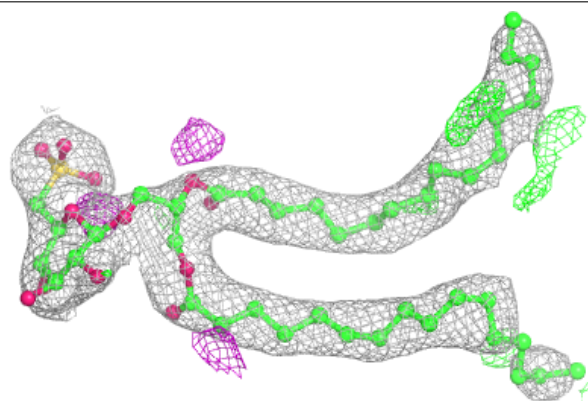


Electron density around LMT t 101:

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

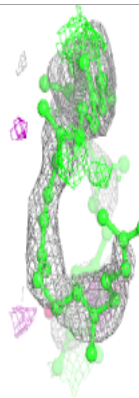
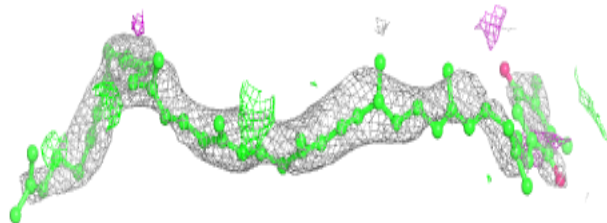
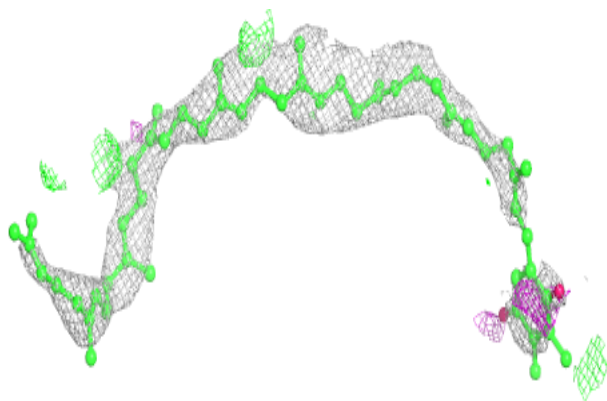
**Electron density around SQD b 620:**

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

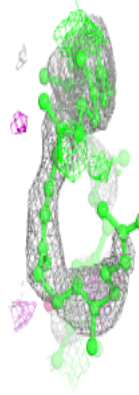
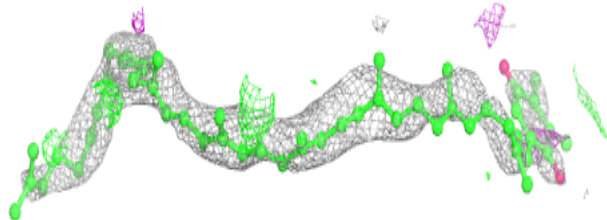
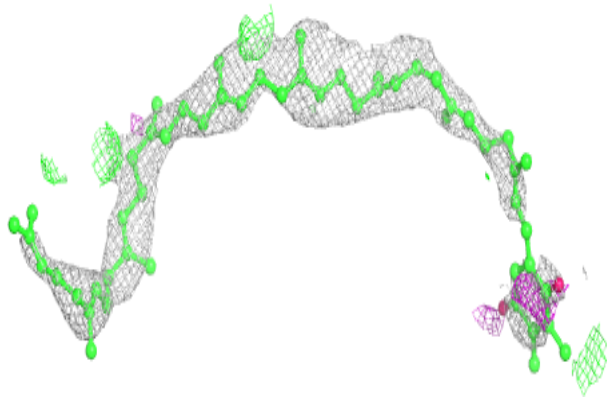


Electron density around PL9 a 412 (A):

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

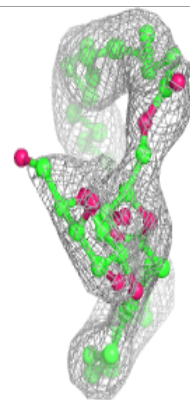
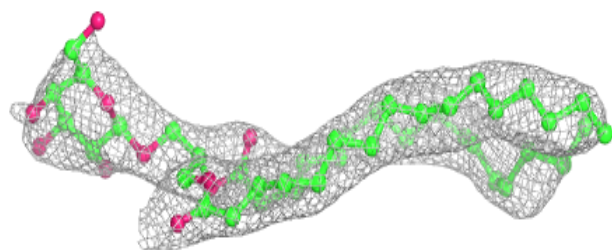
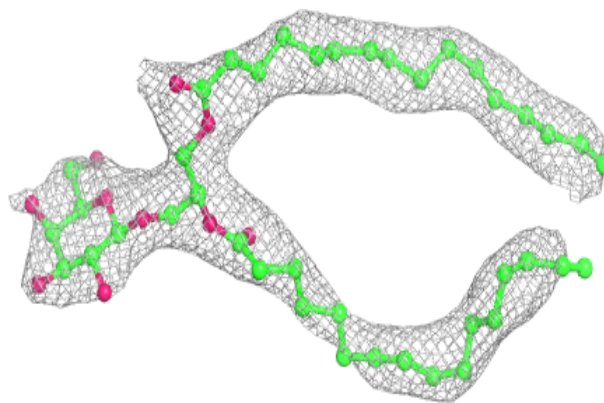
**Electron density around PL9 a 412 (B):**

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

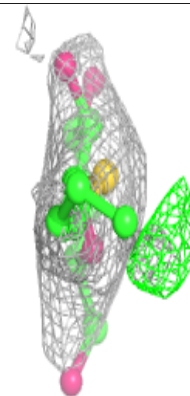
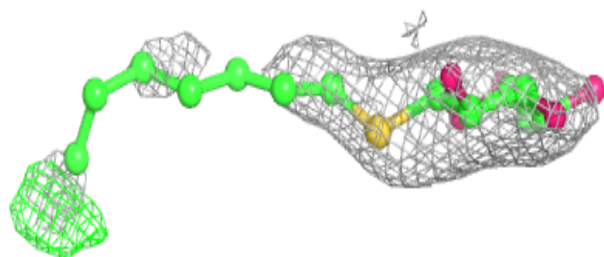
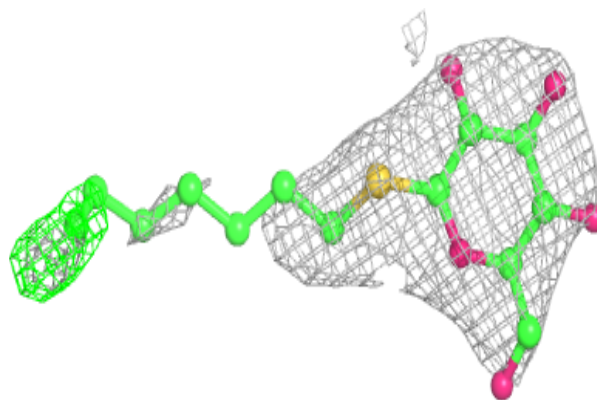


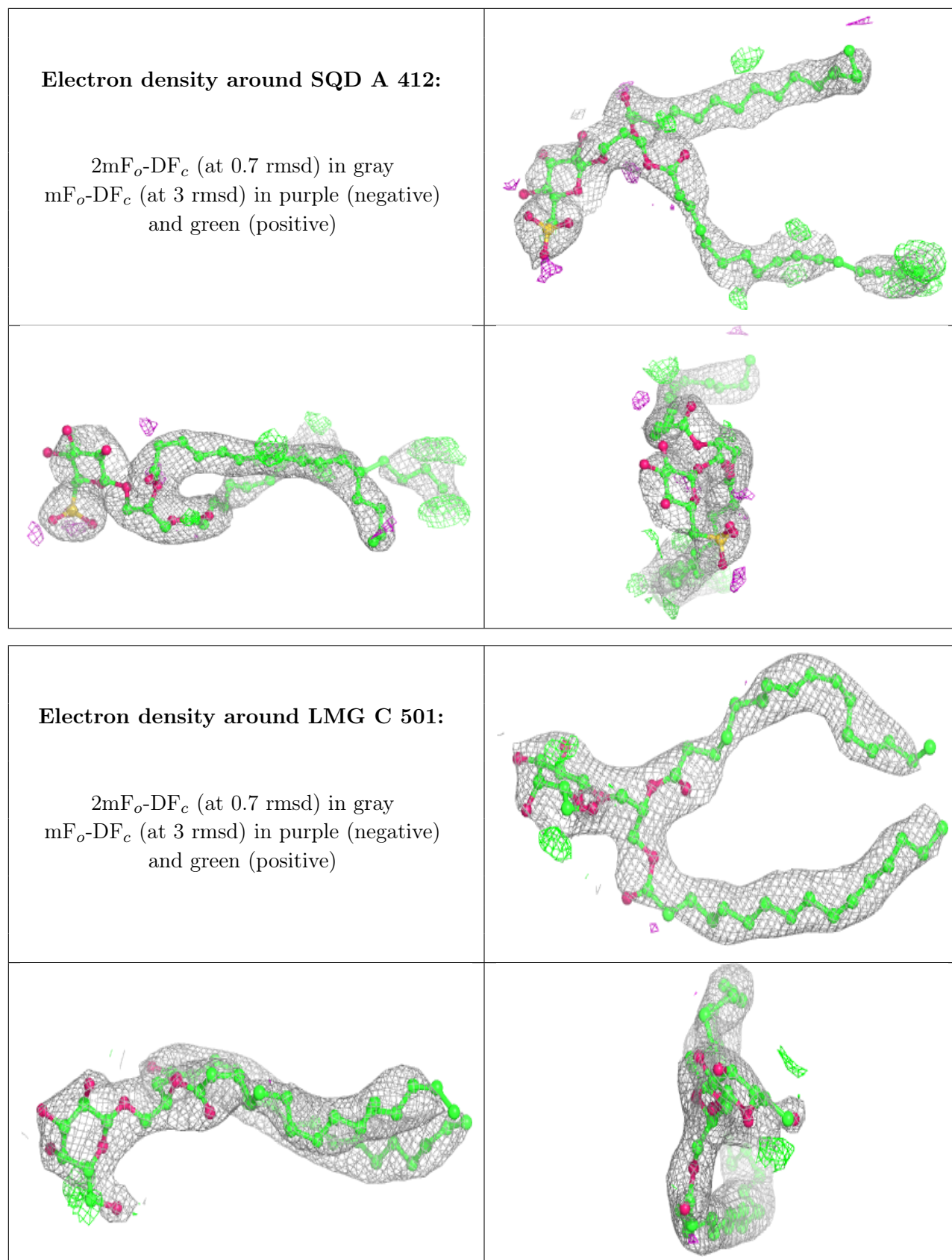
Electron density around LMG a 415:

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

**Electron density around HTG c 521:**

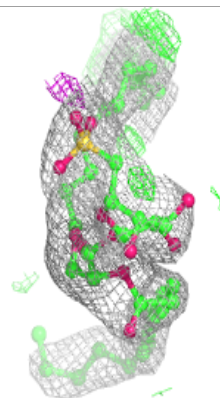
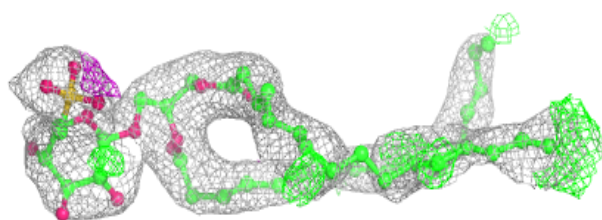
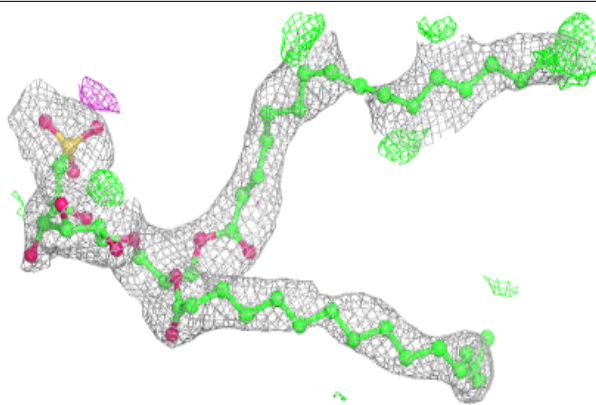
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



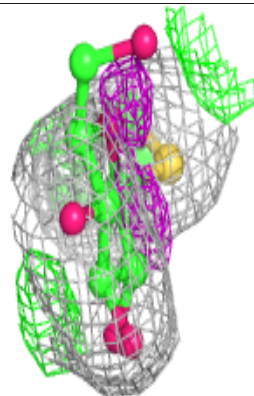
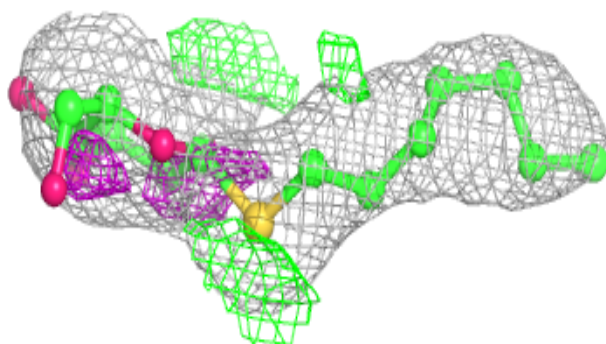
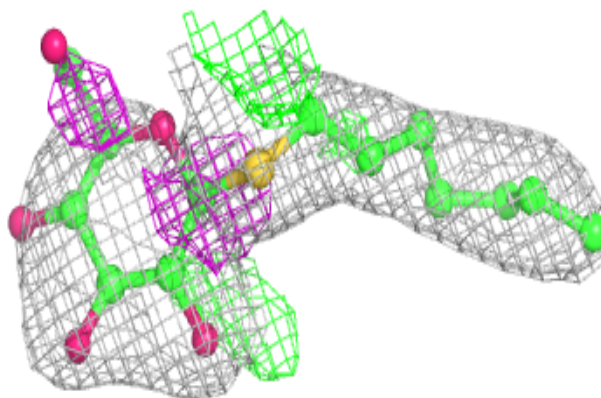


Electron density around SQD a 410:

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

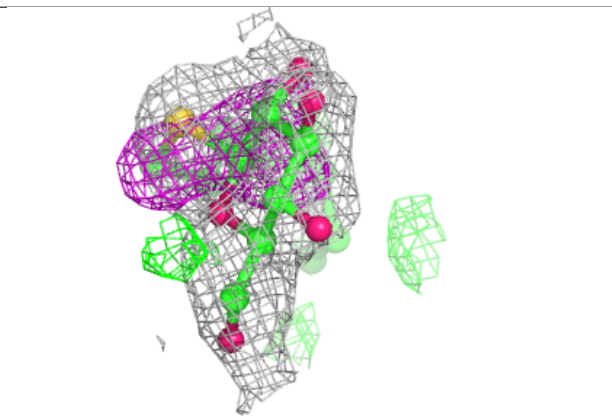
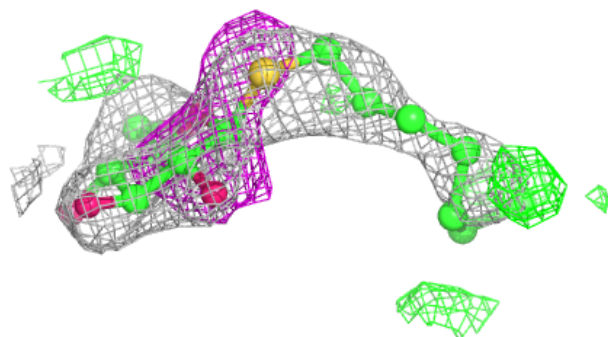
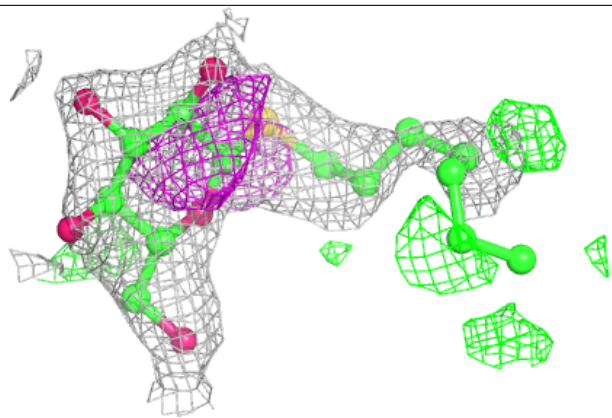
**Electron density around HTG B 622:**

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

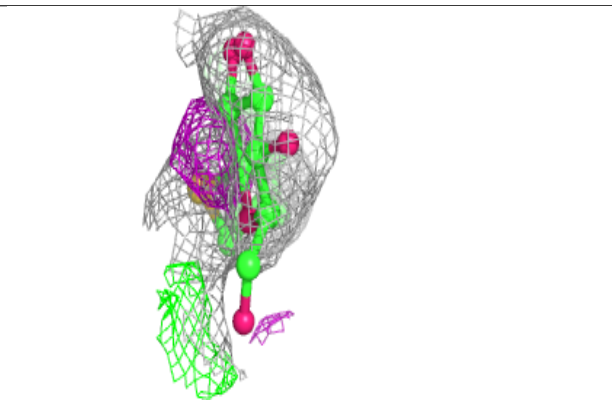
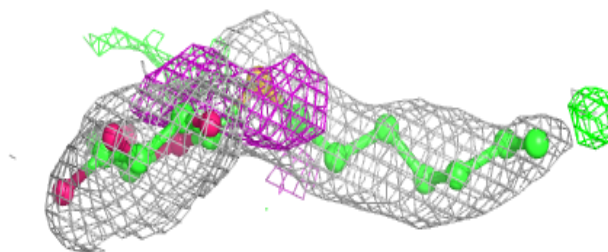
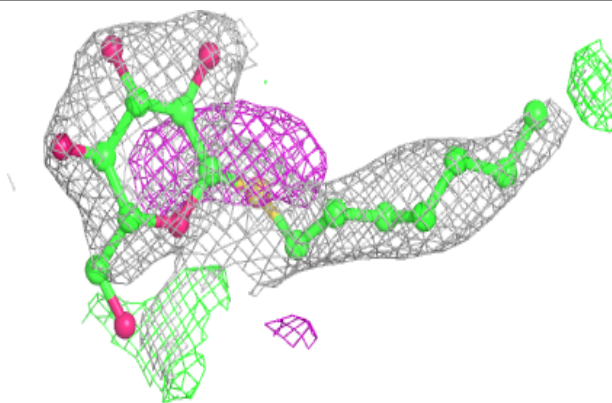


Electron density around HTG B 623:

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

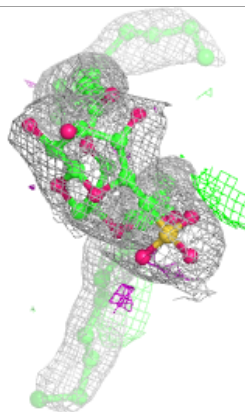
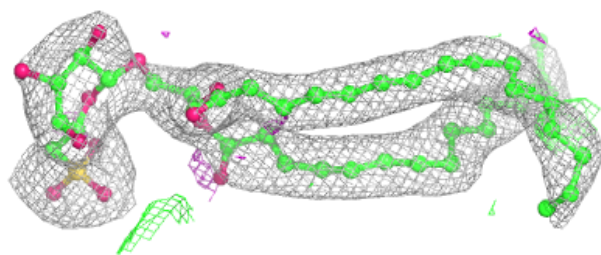
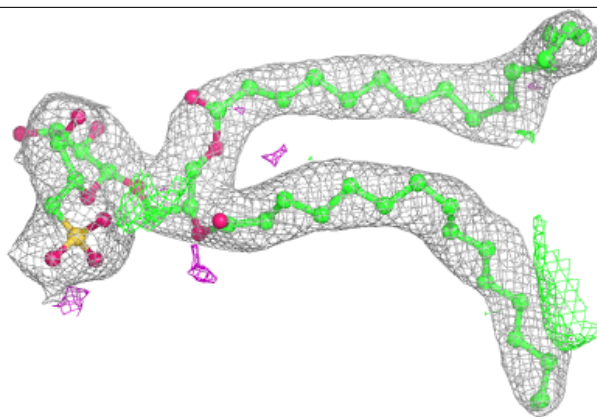
**Electron density around HTG b 622:**

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

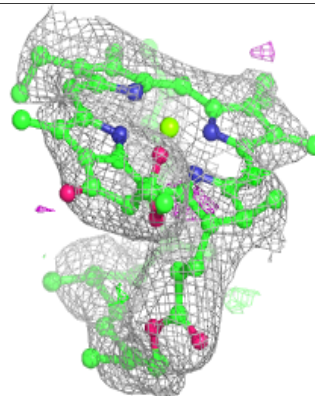
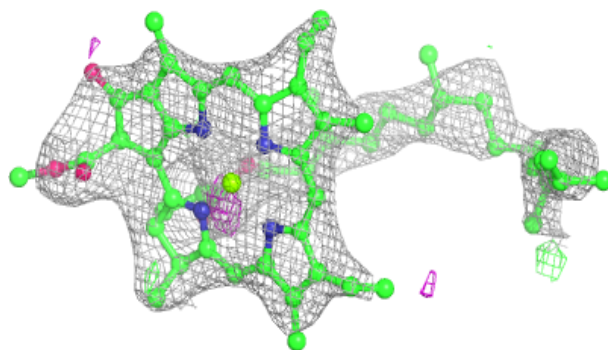
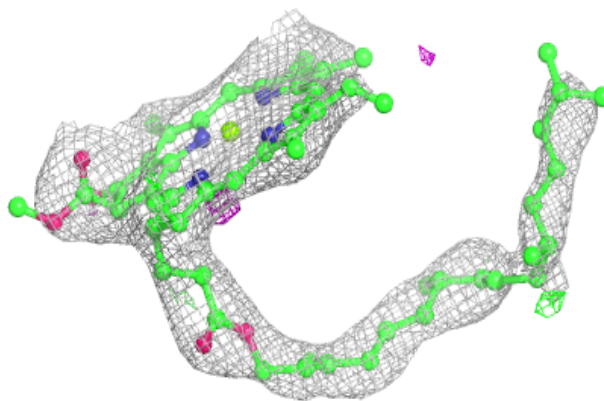


Electron density around SQD B 620:

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

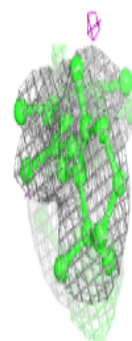
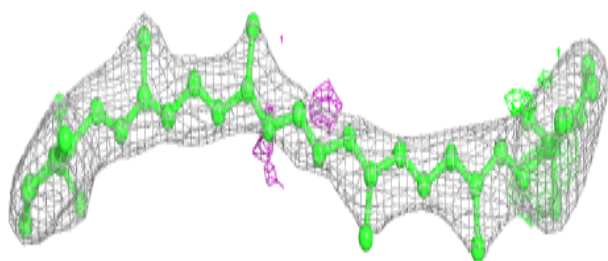
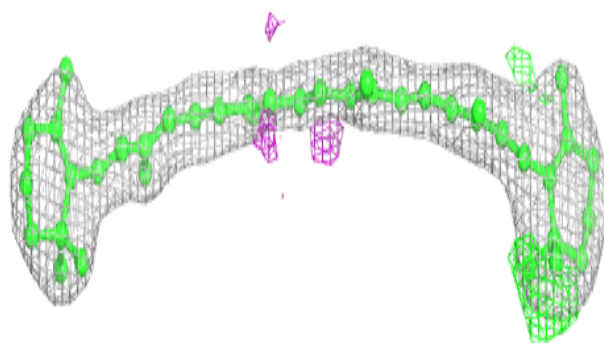
**Electron density around CLA c 513:**

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

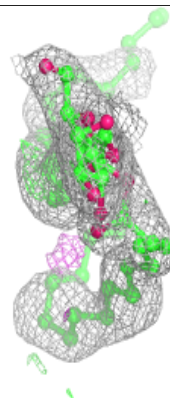
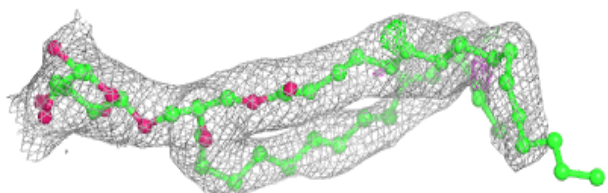
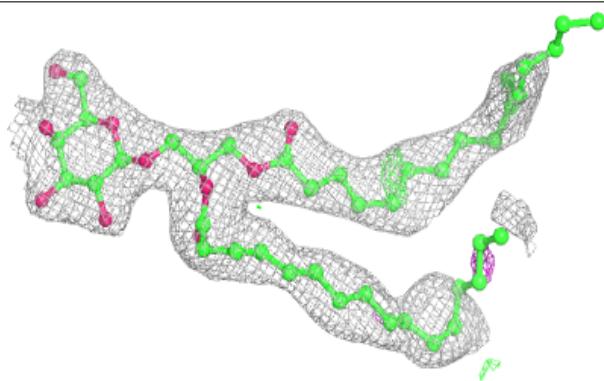


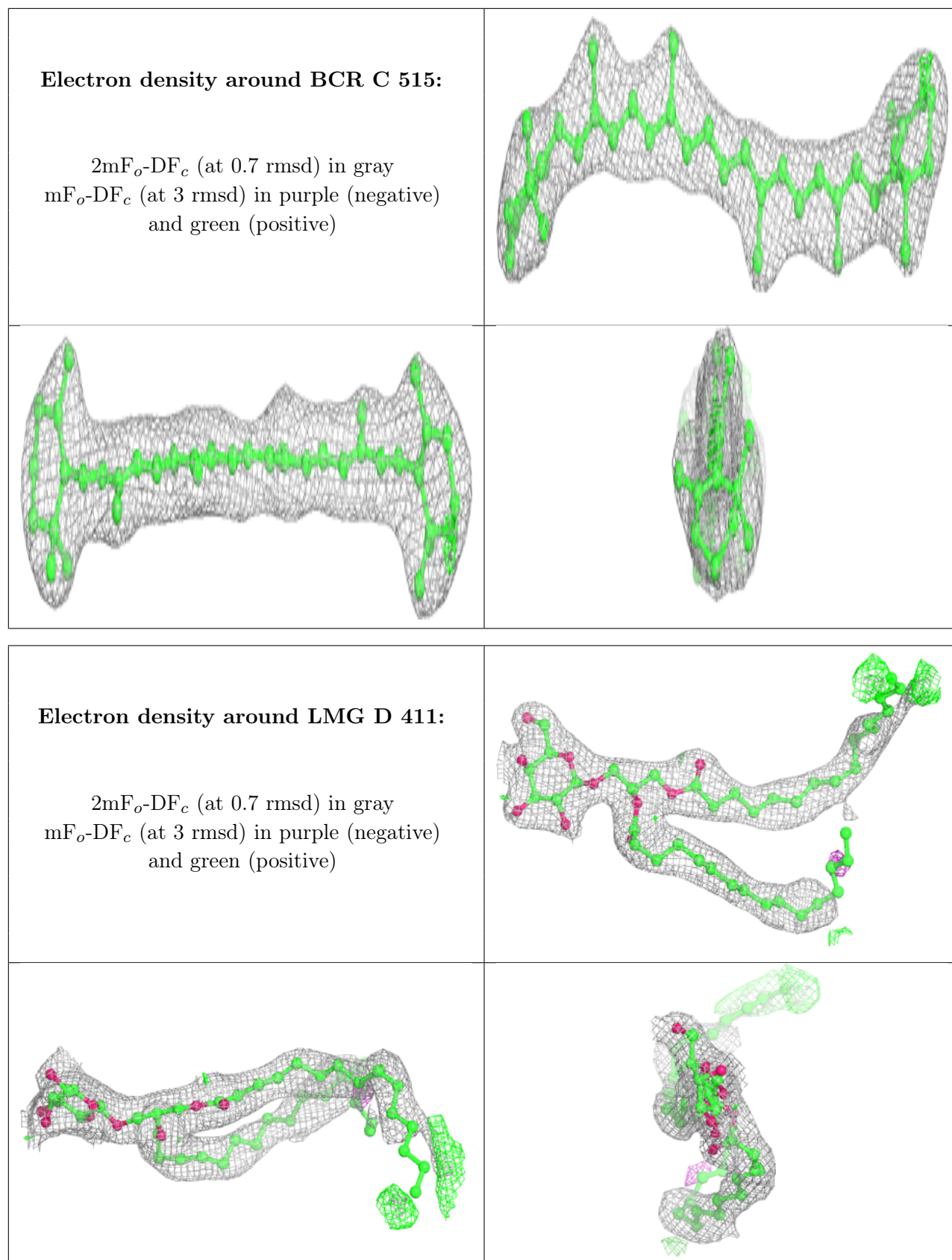
Electron density around BCR K 102:

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

**Electron density around LMG d 412:**

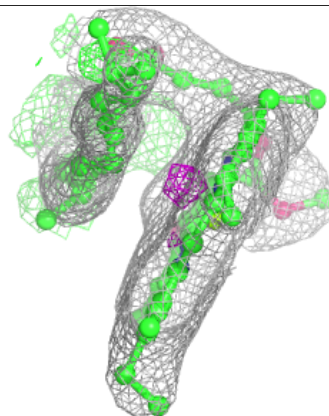
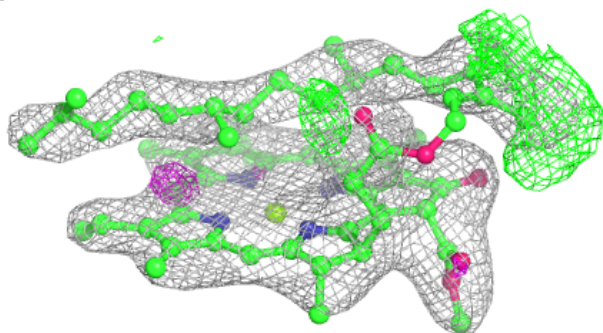
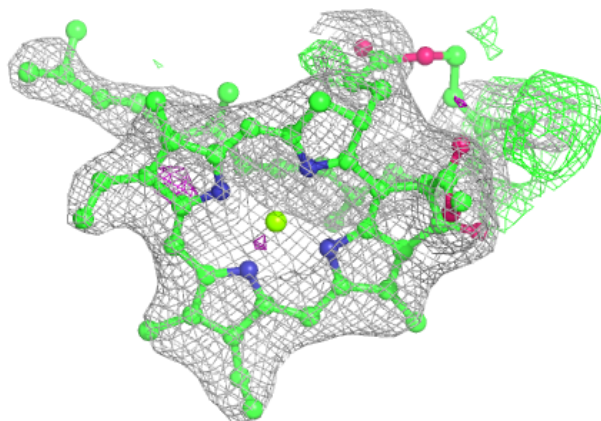
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





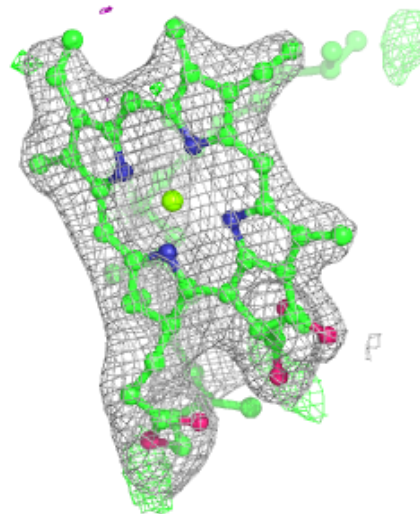
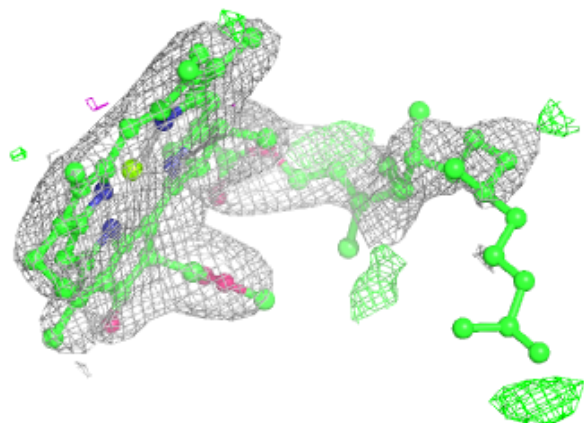
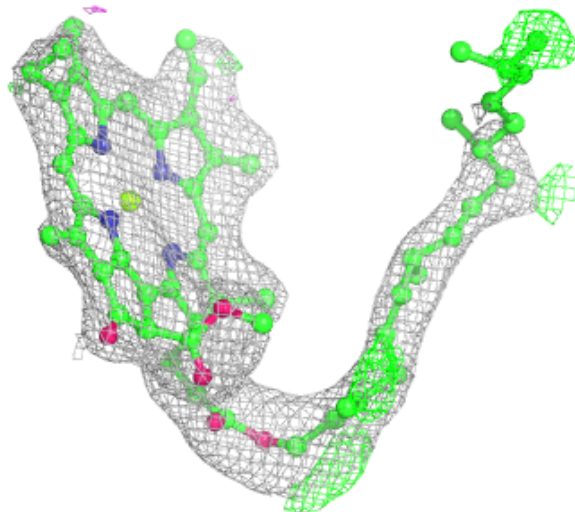
Electron density around CLA b 601:

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



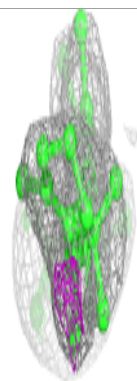
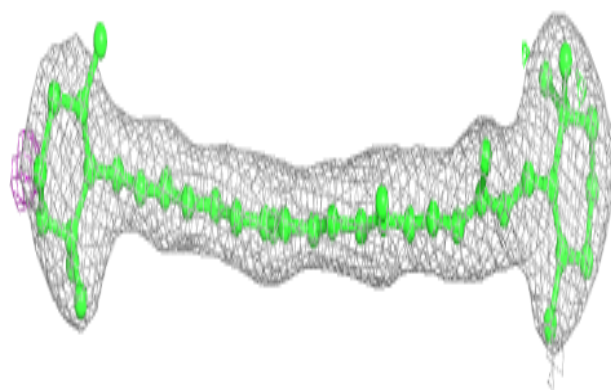
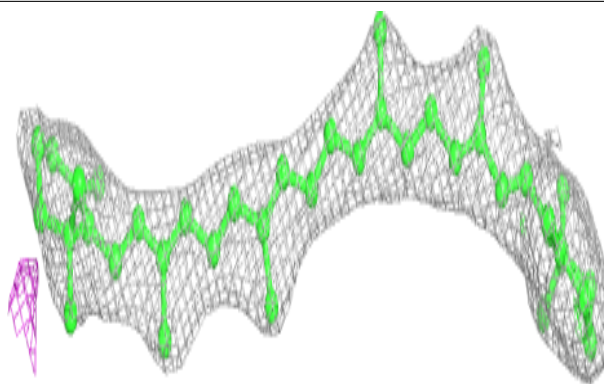
Electron density around CLA b 616:

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

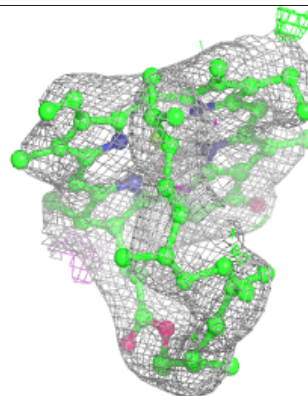
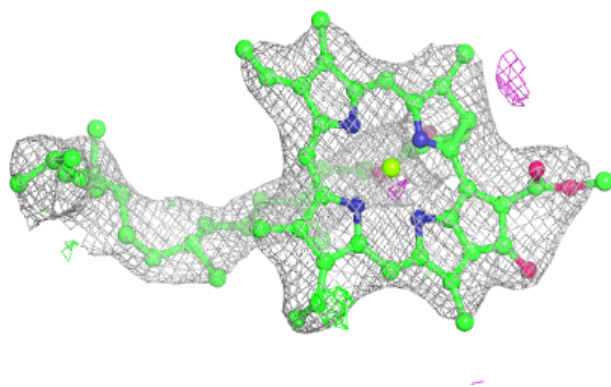
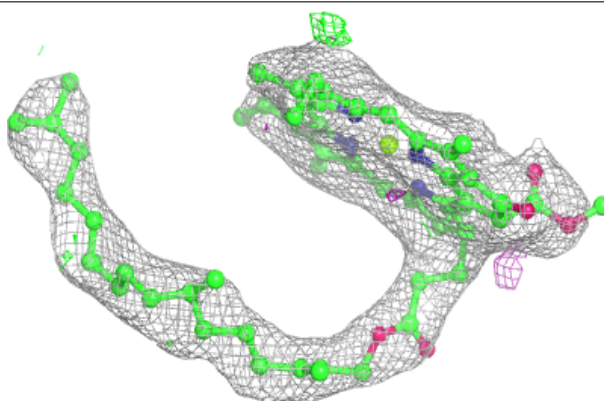


Electron density around BCR h 101:

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

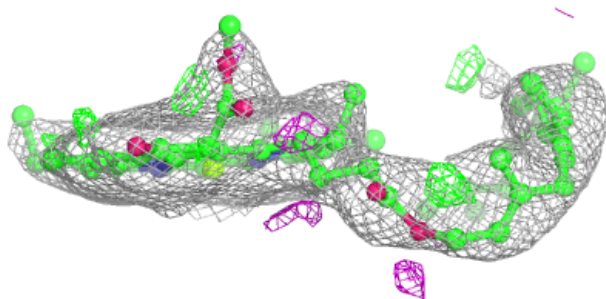
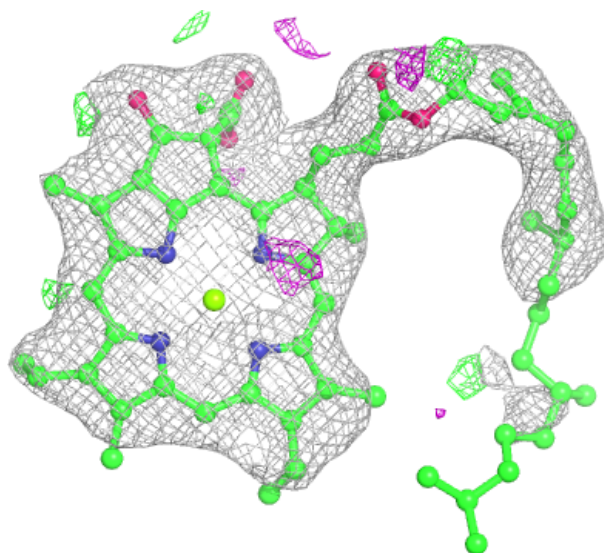
**Electron density around CLA C 514:**

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



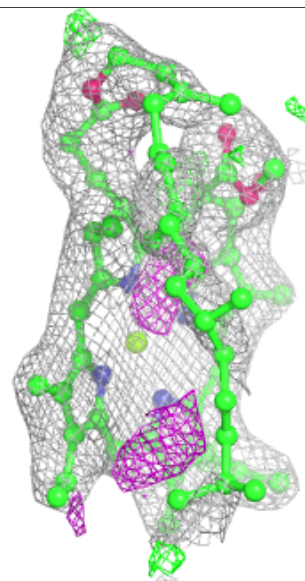
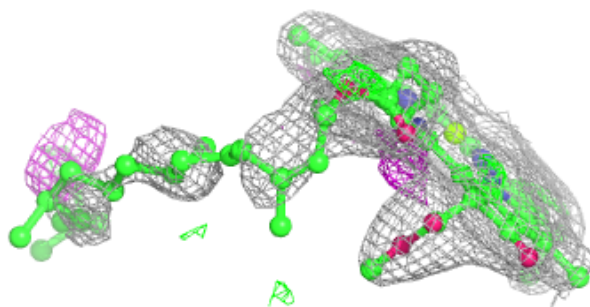
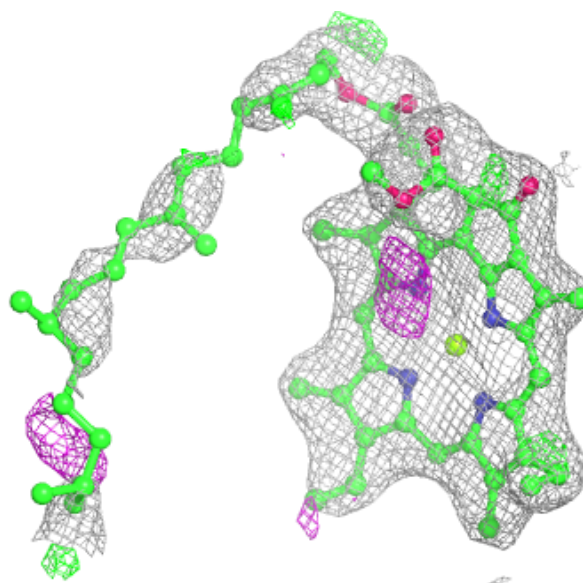
Electron density around CLA c 512:

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



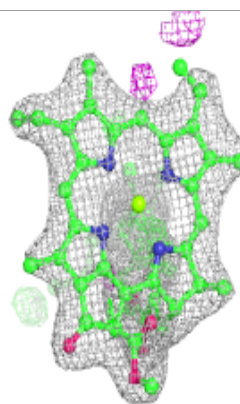
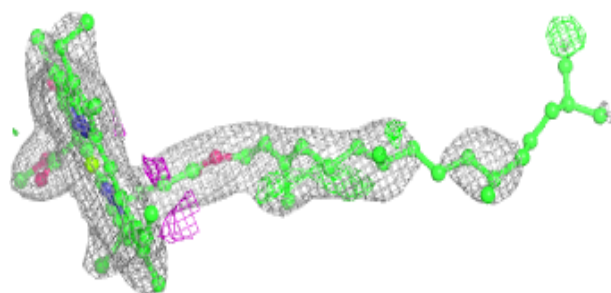
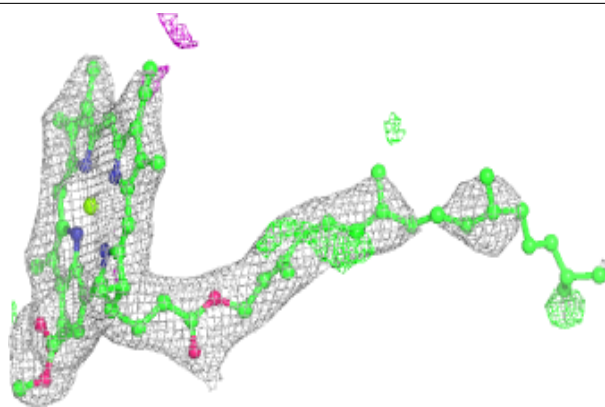
Electron density around CLA B 616:

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

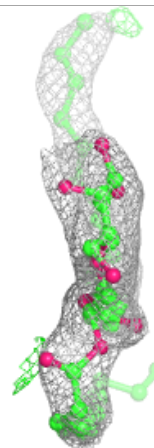
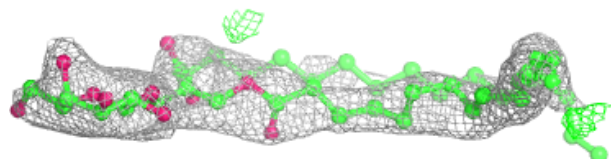
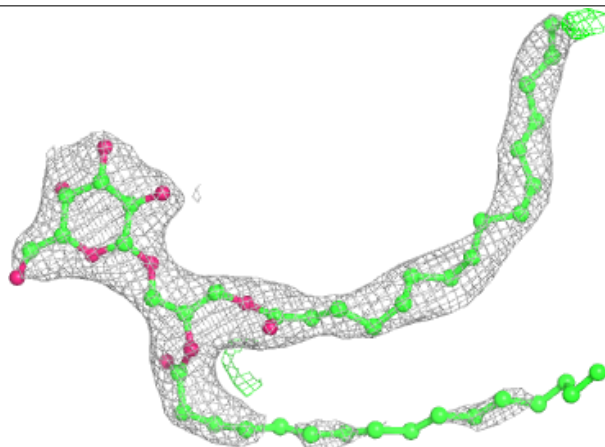


Electron density around CLA d 404:

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

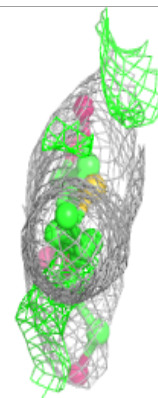
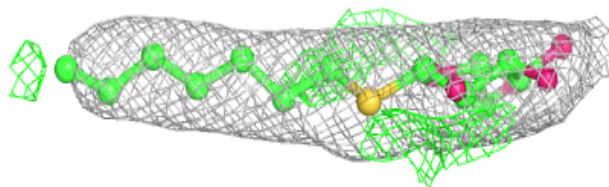
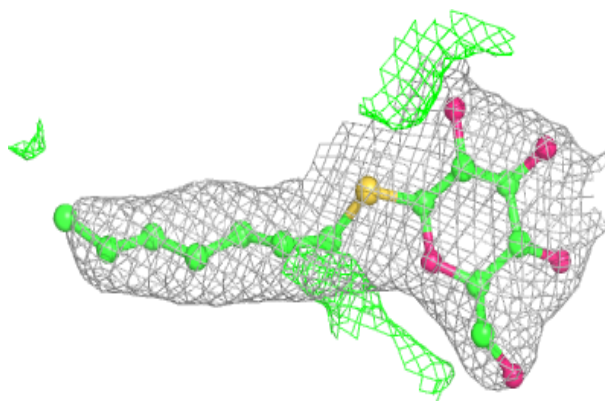
**Electron density around LMG c 519:**

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

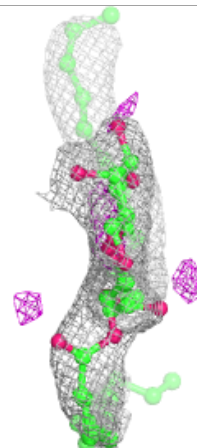
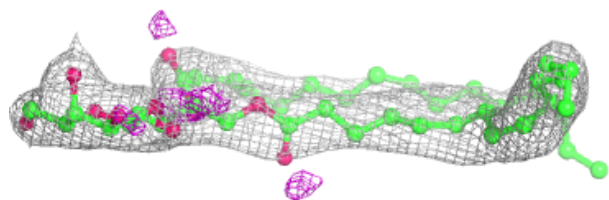
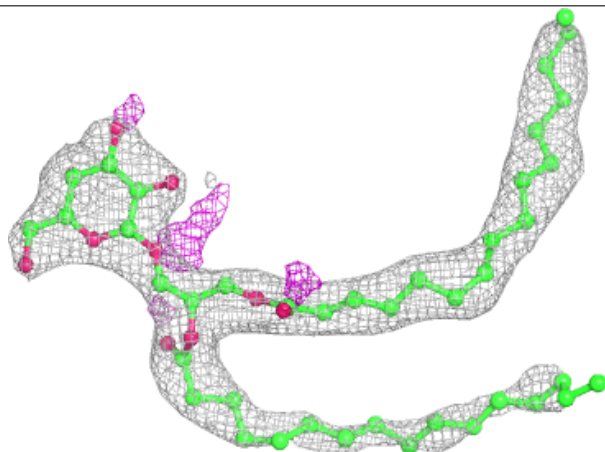


Electron density around HTG b 625:

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

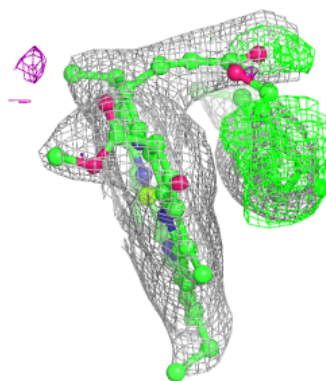
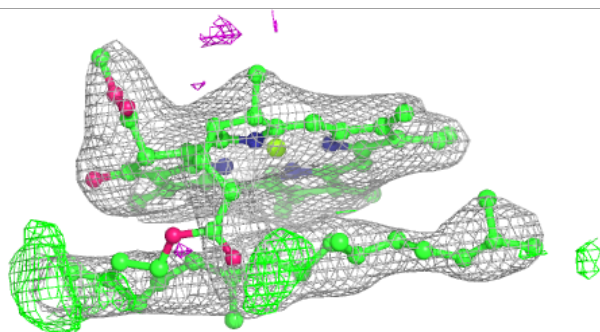
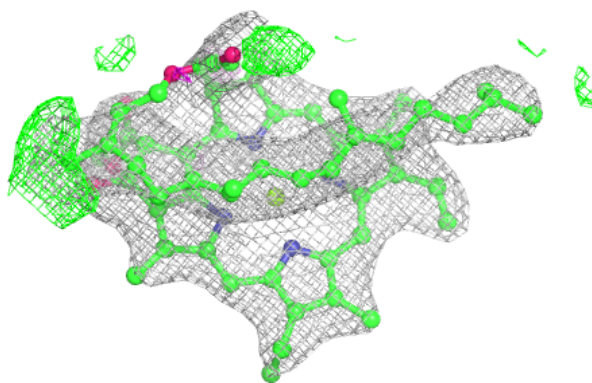
**Electron density around LMG C 520:**

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

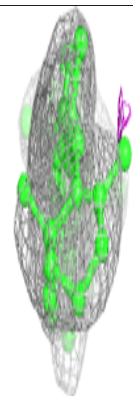
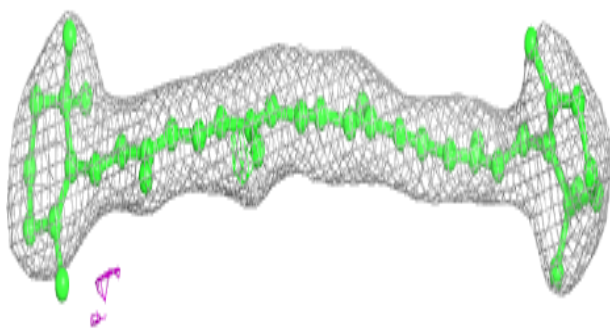
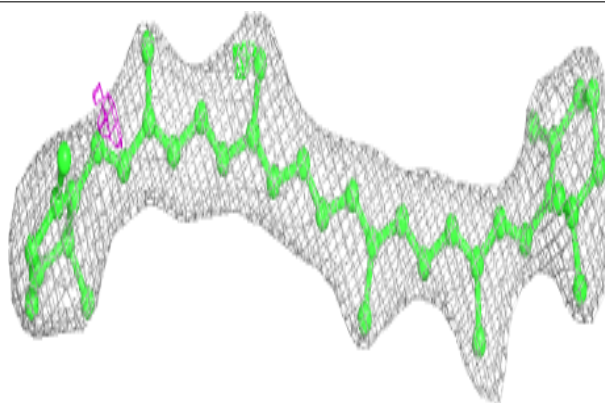


Electron density around CLA B 601:

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

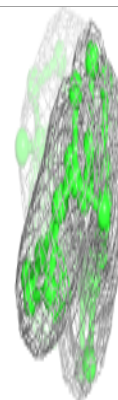
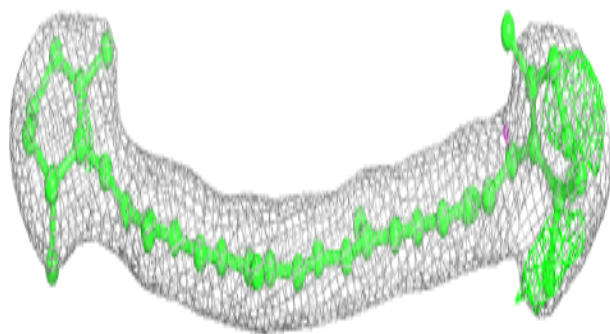
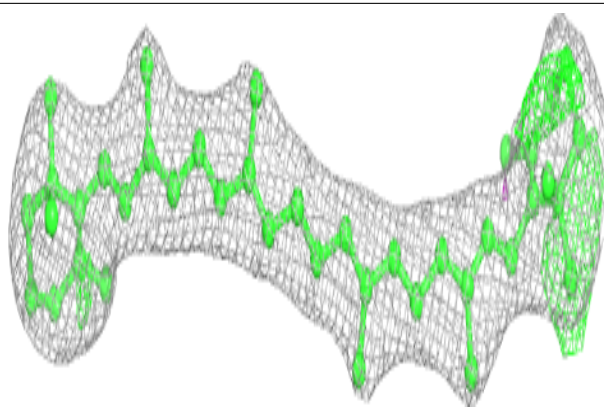
**Electron density around BCR Y 101:**

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

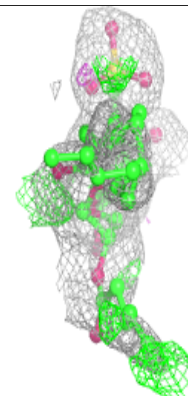
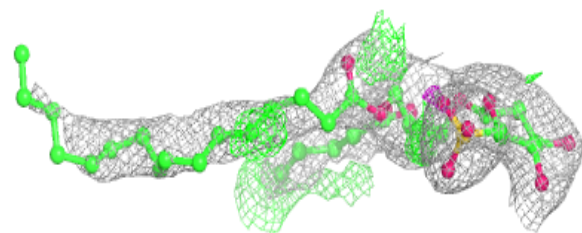
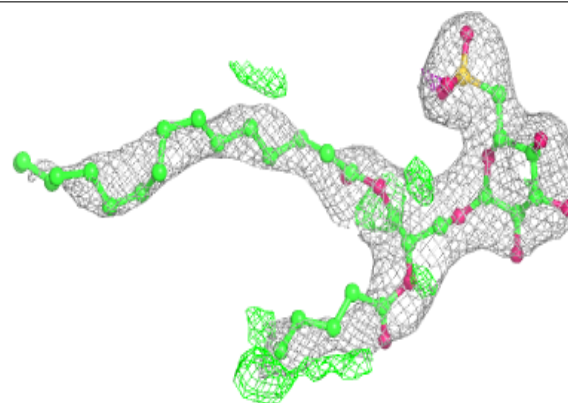


Electron density around BCR d 405:

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

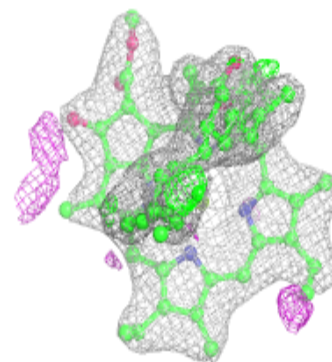
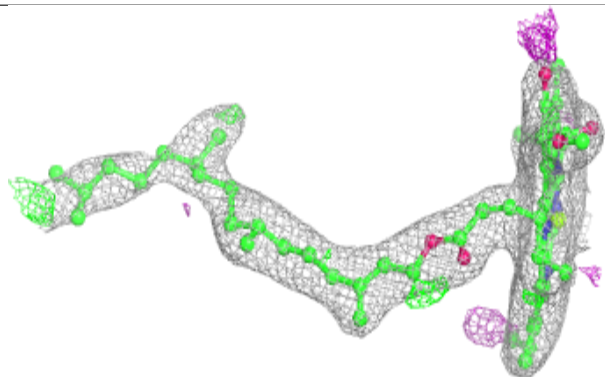
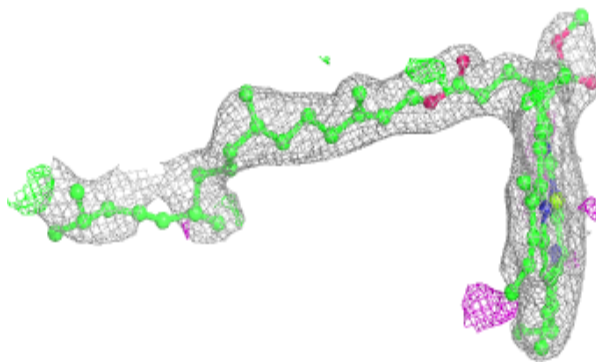
**Electron density around SQD F 102:**

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

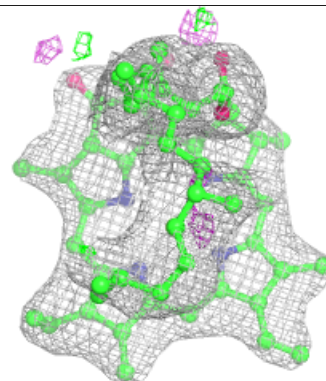
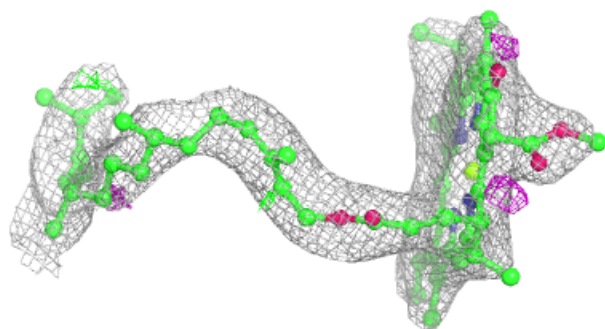
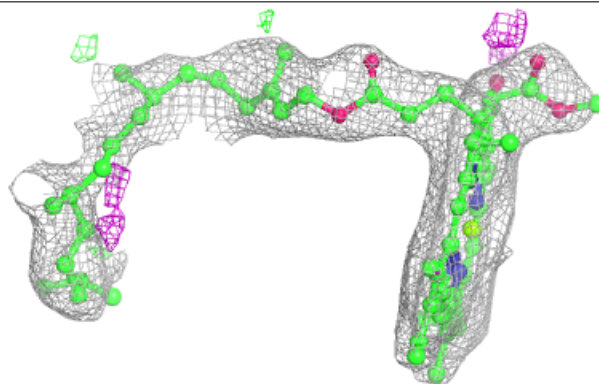


Electron density around CLA B 606:

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

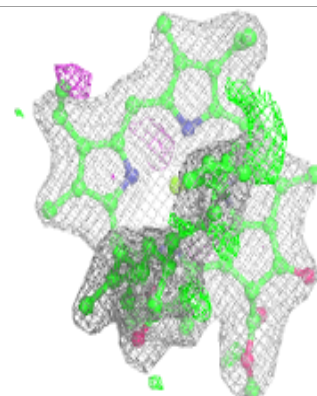
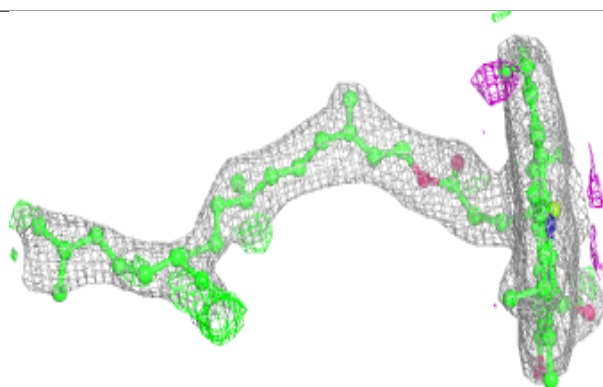
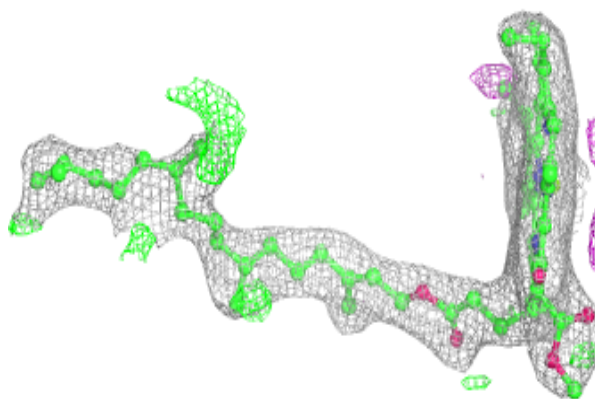
**Electron density around CLA C 507:**

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

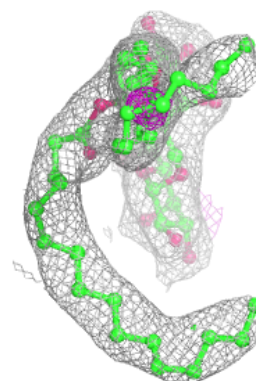
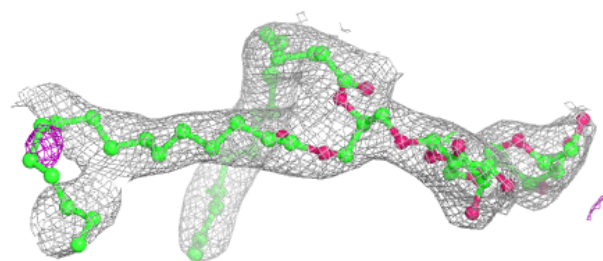
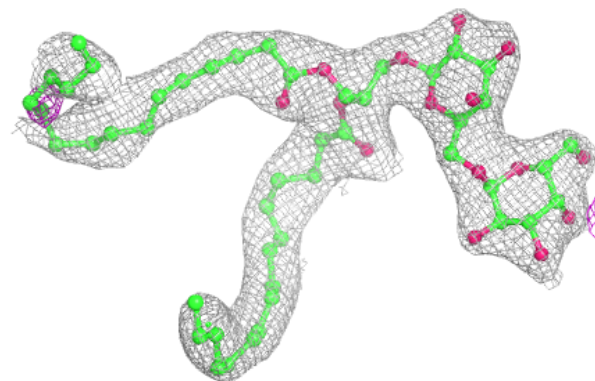


Electron density around CLA b 606:

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

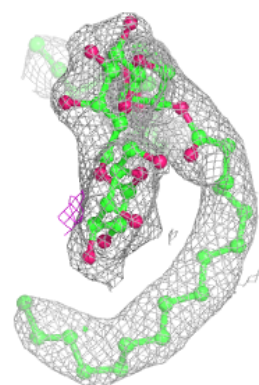
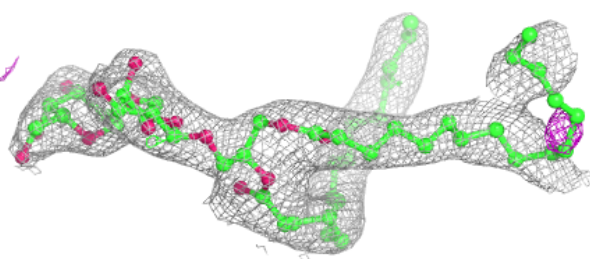
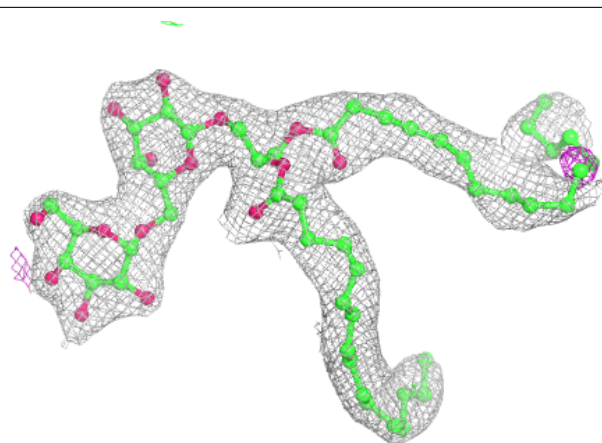
**Electron density around DGD c 517 (A):**

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

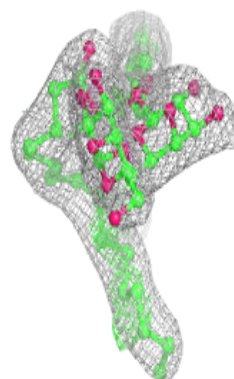
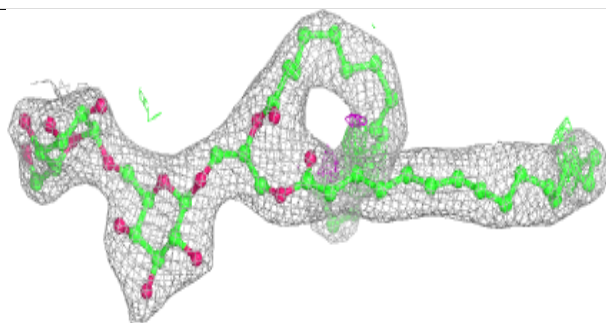
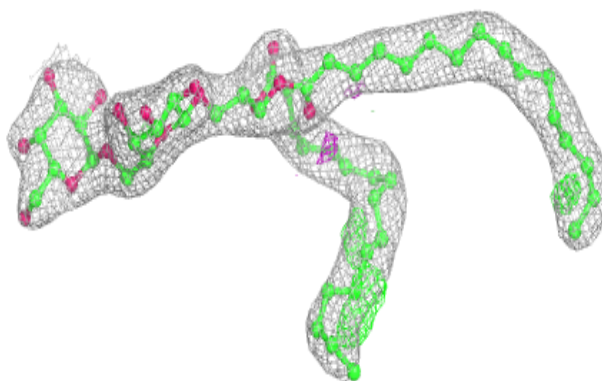


Electron density around DGD c 517 (B):

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

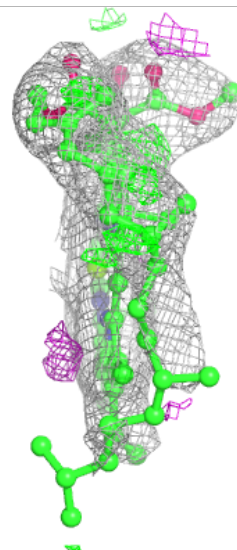
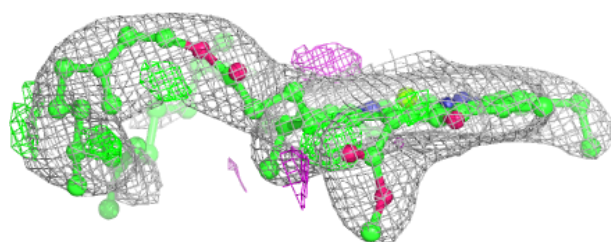
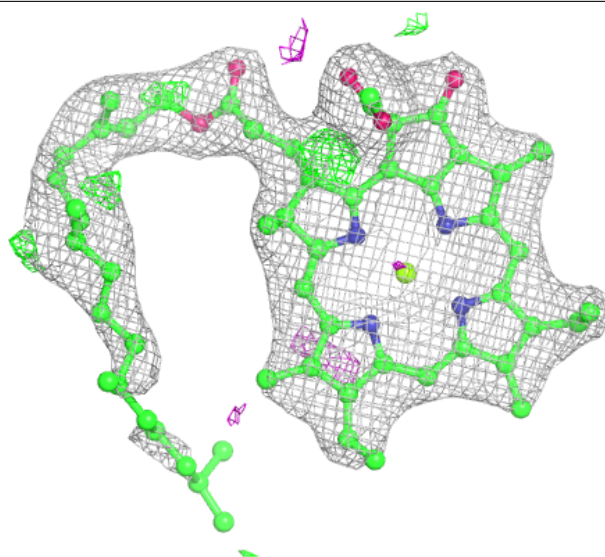
**Electron density around DGD h 102:**

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



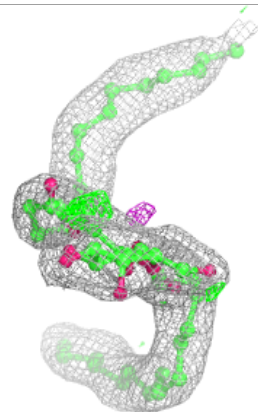
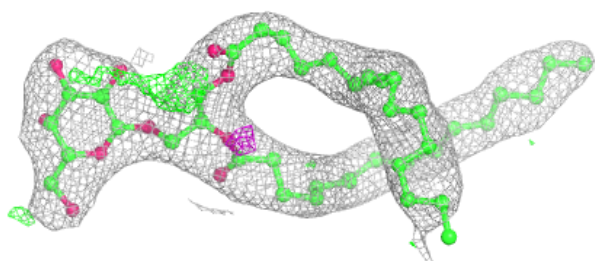
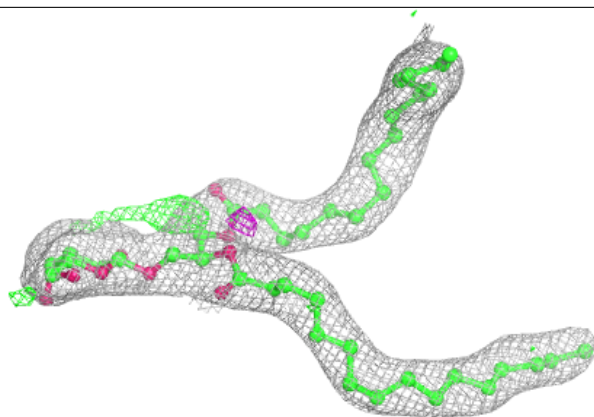
Electron density around CLA C 513:

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

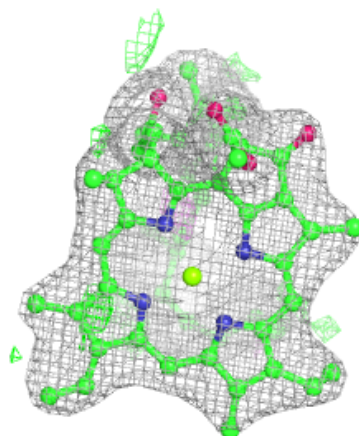
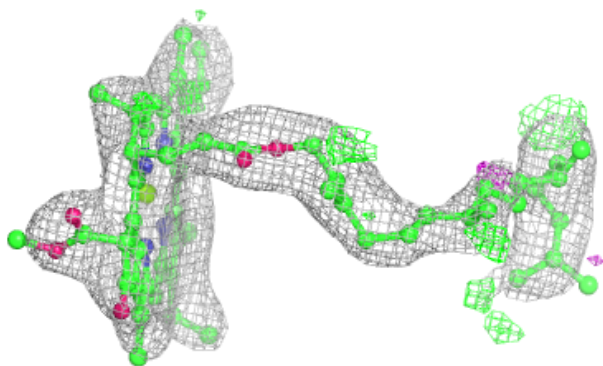
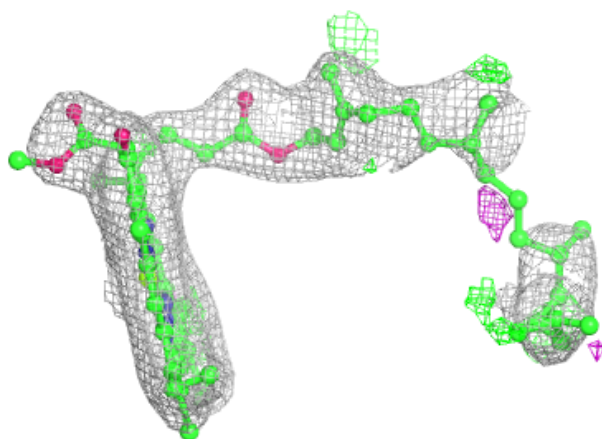


Electron density around LMG B 621:

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

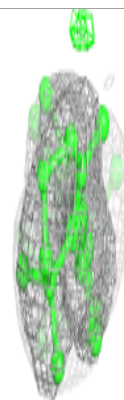
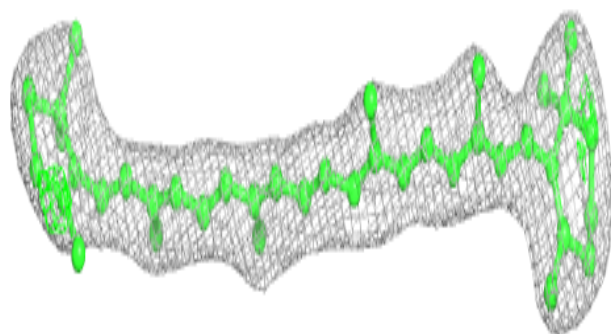
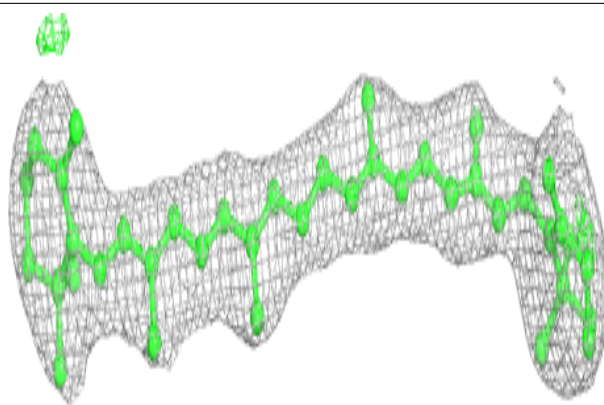
**Electron density around CLA c 506:**

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

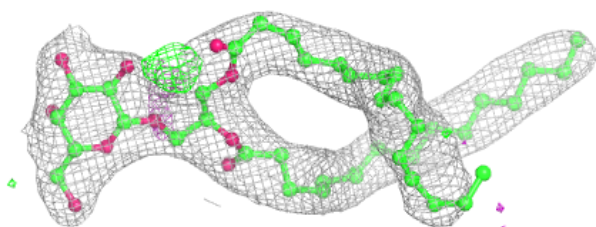
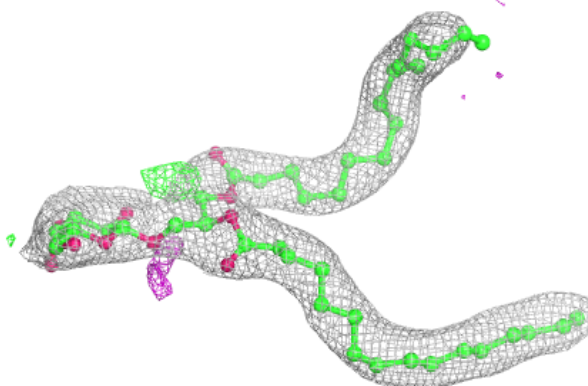


Electron density around BCR c 514:

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

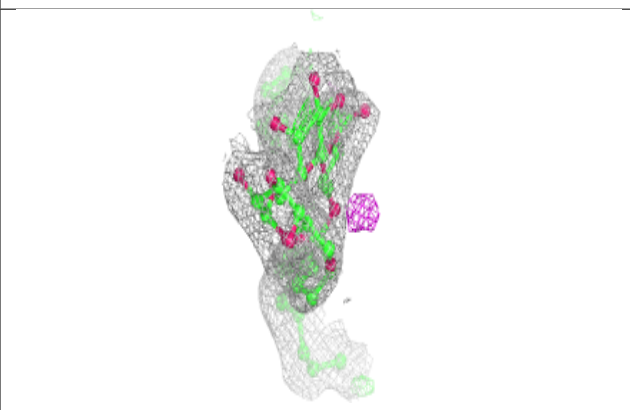
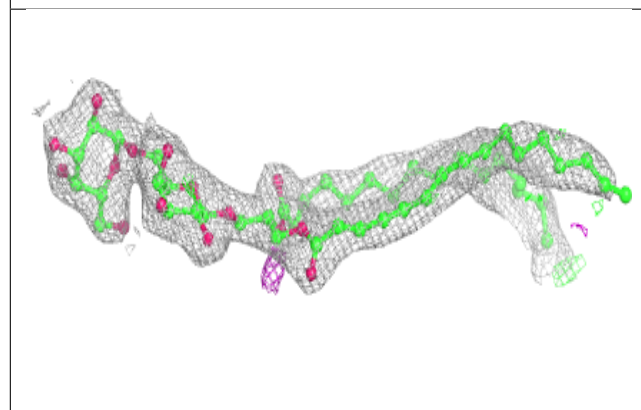
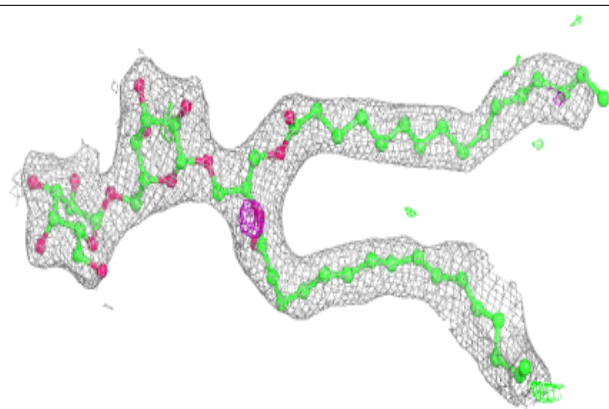
**Electron density around LMG m 101:**

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

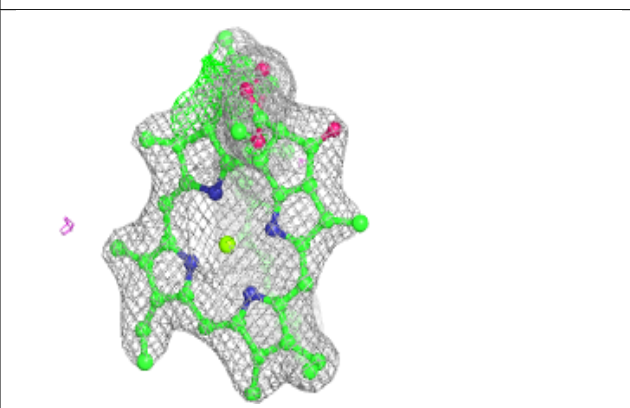
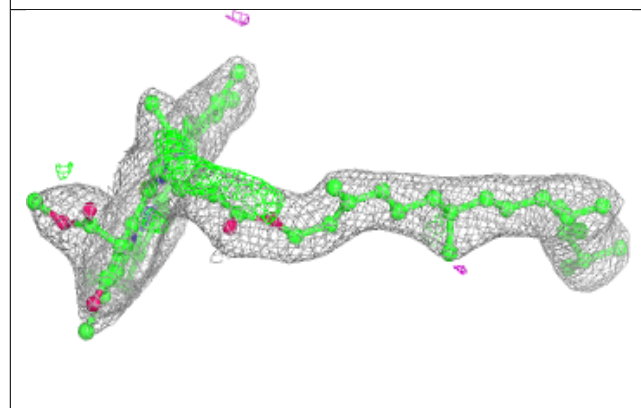
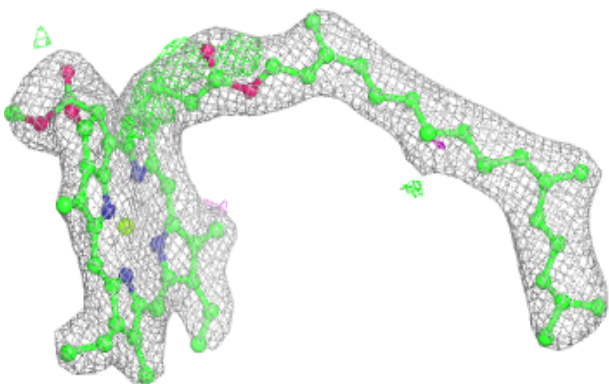


Electron density around DGD c 518:

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

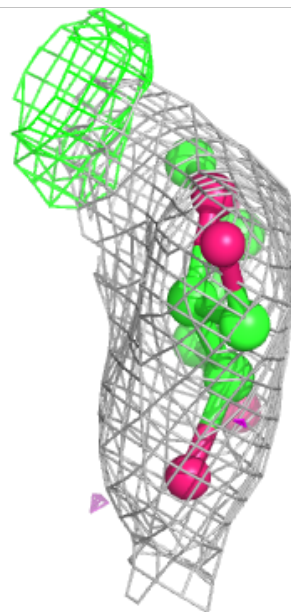
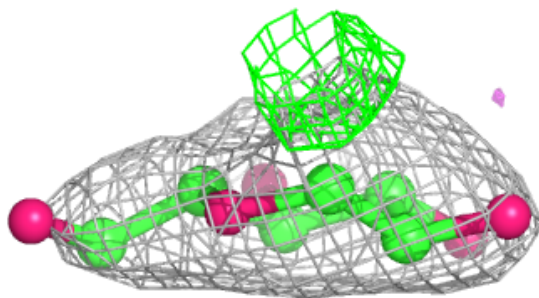
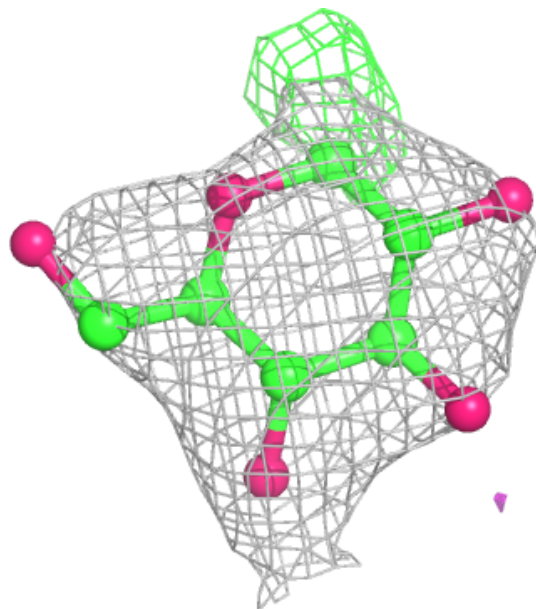
**Electron density around CLA B 609:**

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



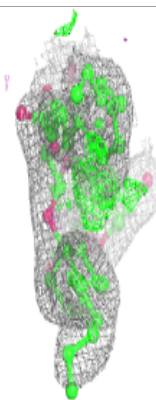
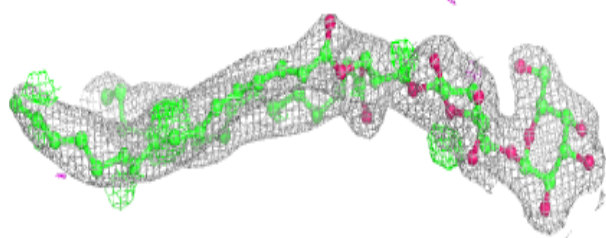
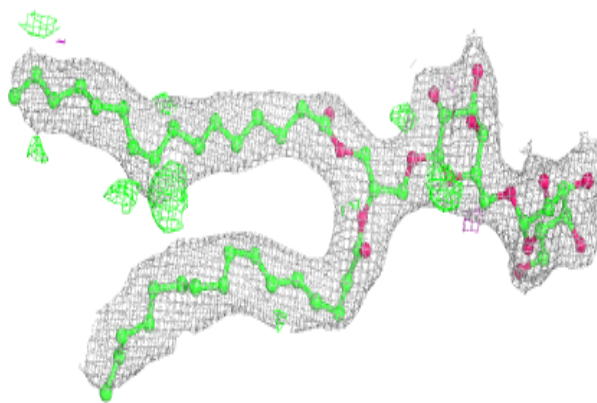
Electron density around HTG V 202:

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

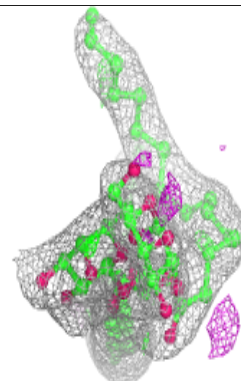
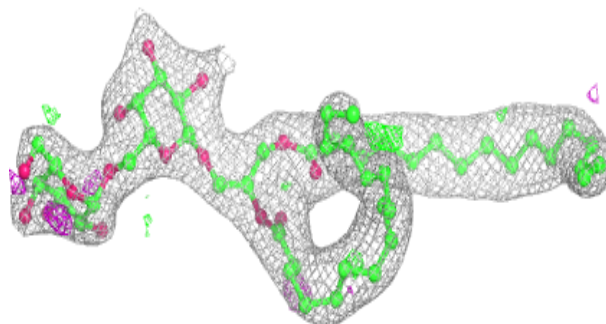
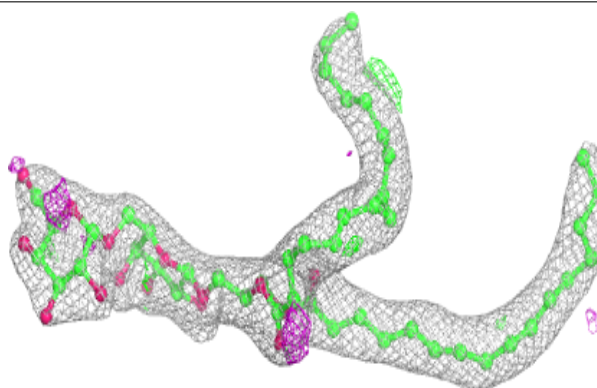


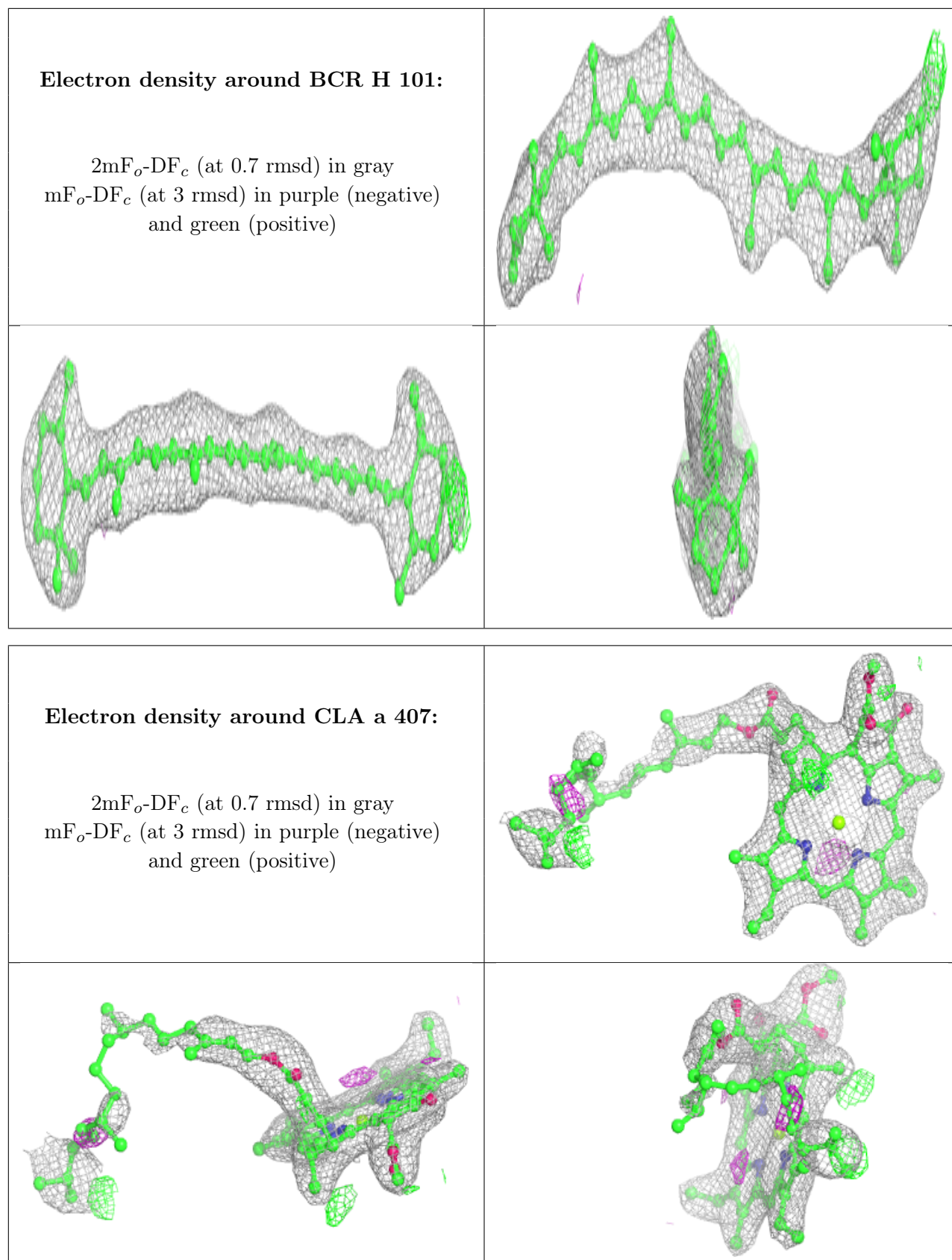
Electron density around DGD C 519:

$2mF_o-DF_c$ (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:**

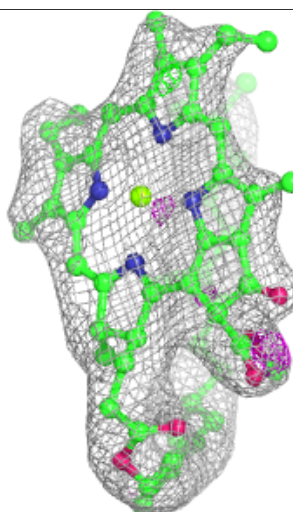
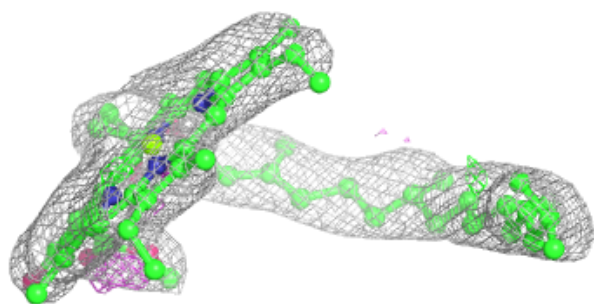
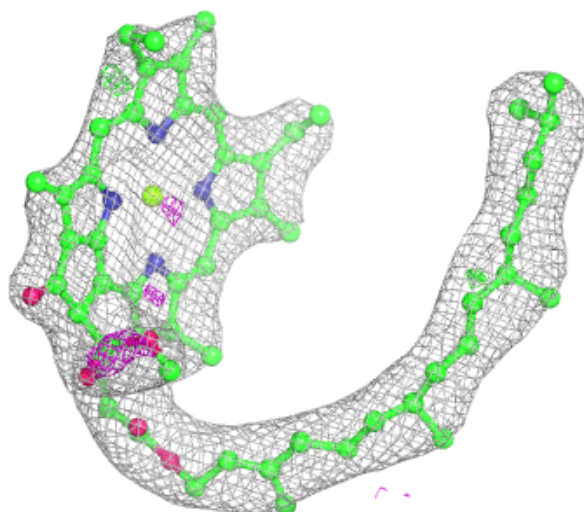
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





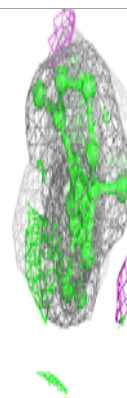
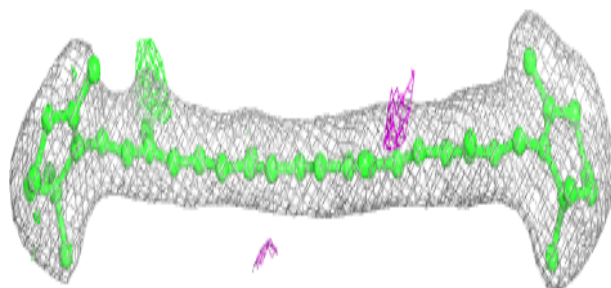
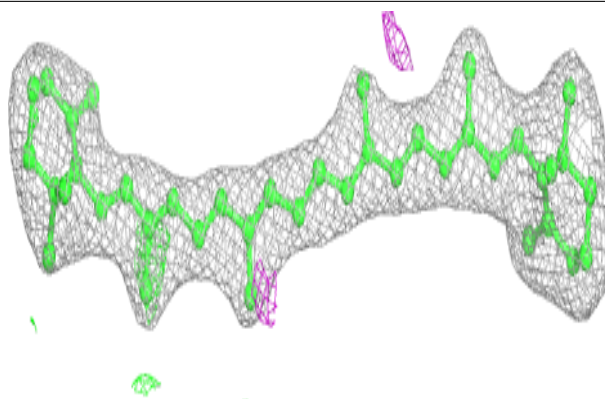
Electron density around CLA c 507:

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

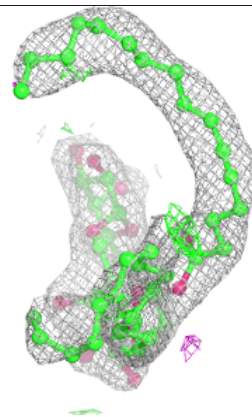
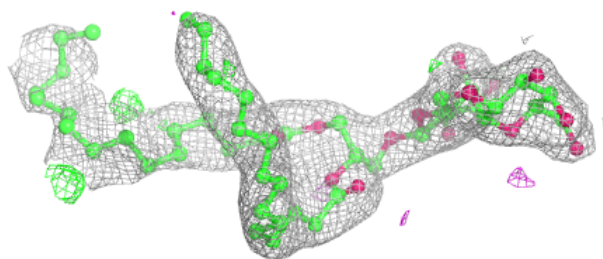
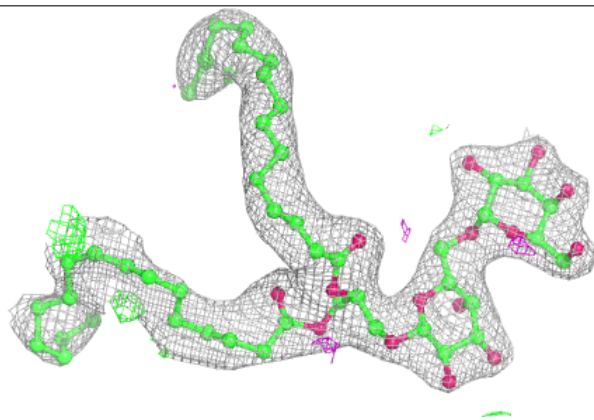


Electron density around BCR b 618:

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

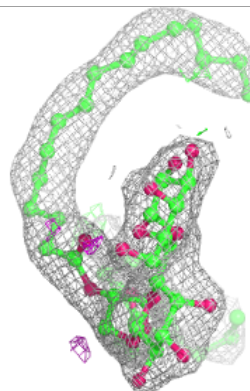
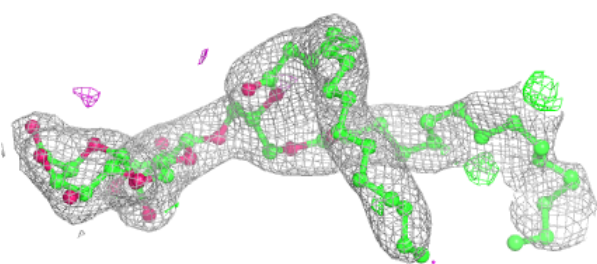
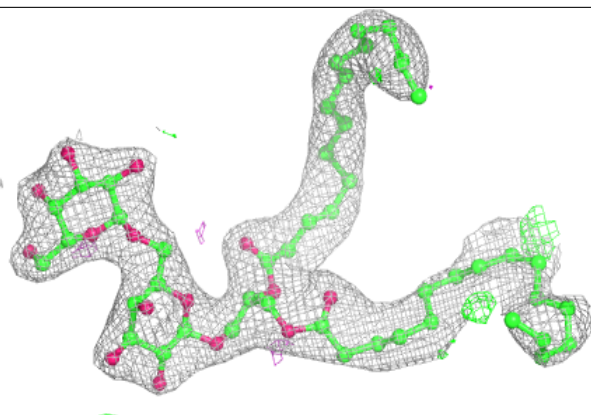
**Electron density around DGD C 518 (A):**

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

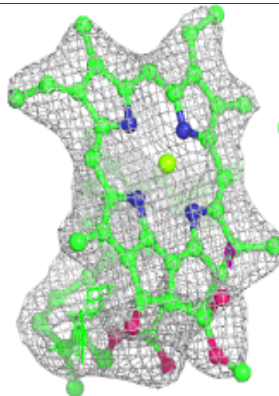
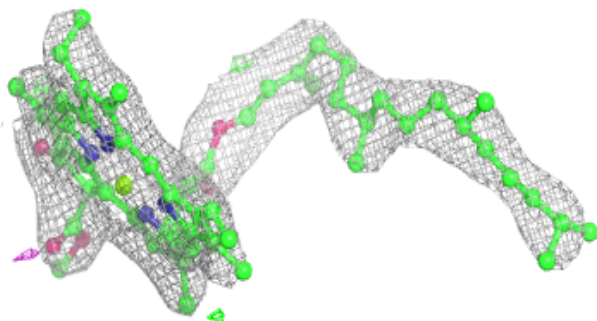
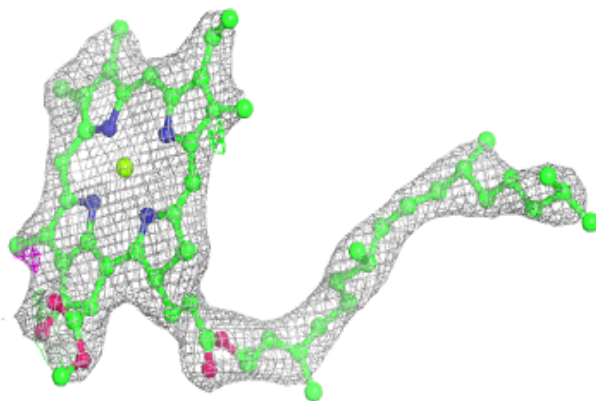


Electron density around DGD C 518 (B):

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

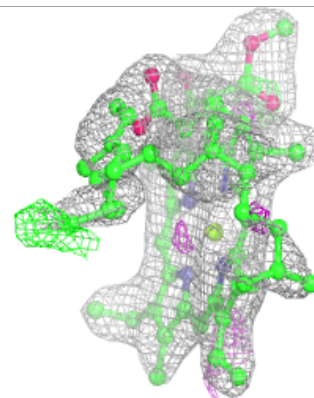
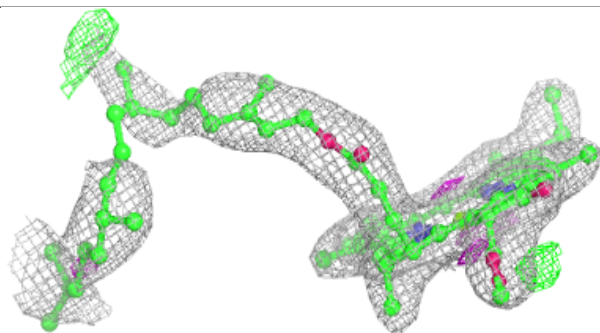
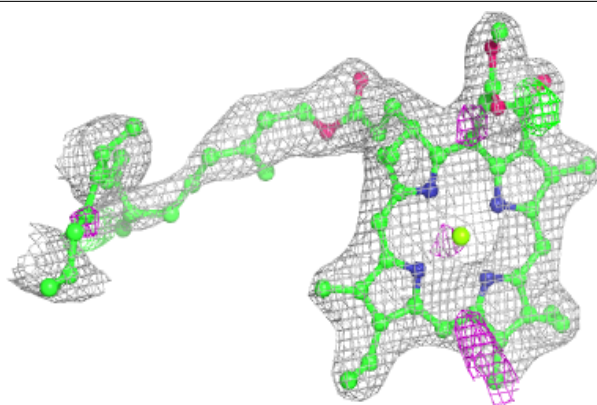
**Electron density around CLA c 511:**

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

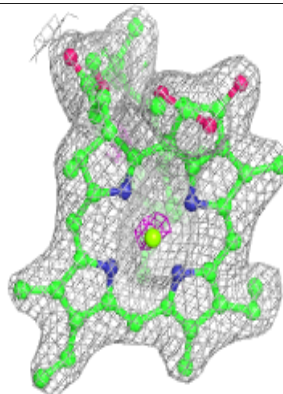
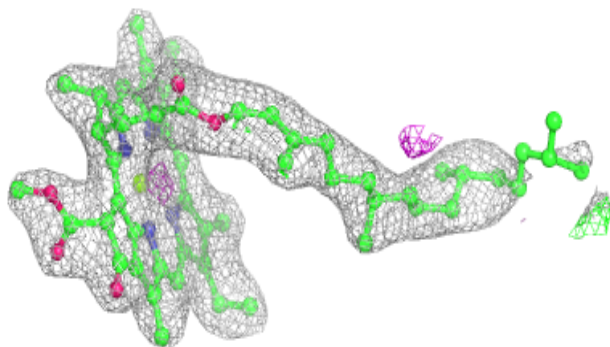
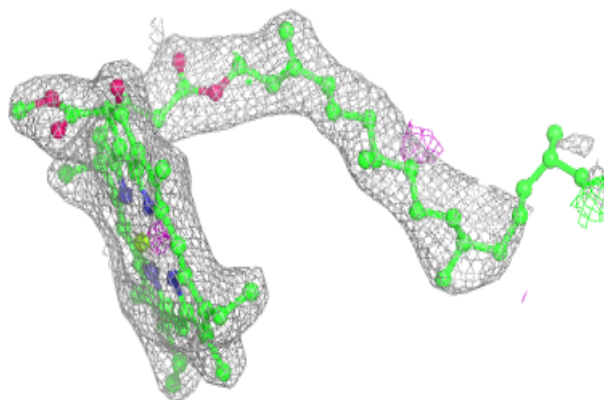


Electron density around CLA A 408:

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

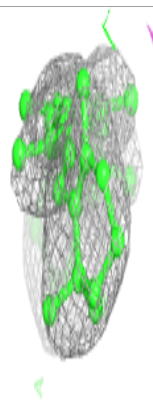
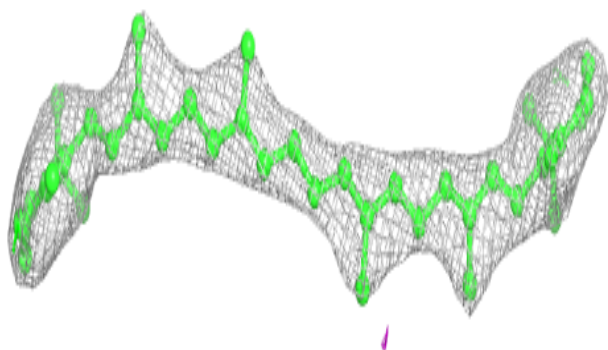
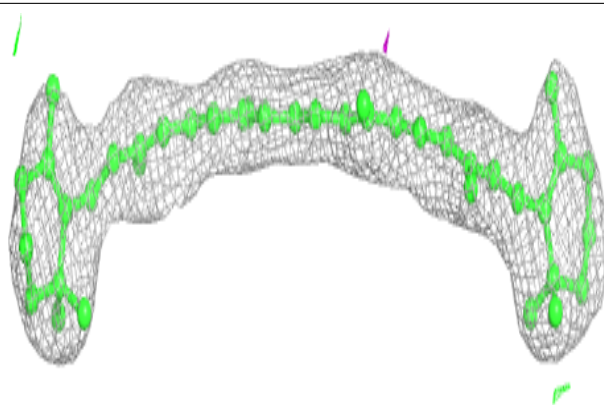
**Electron density around CLA C 509:**

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

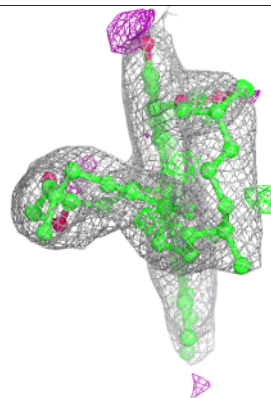
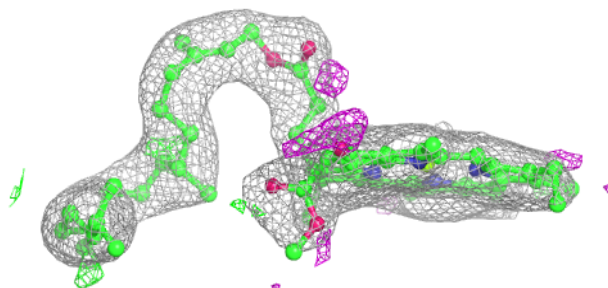
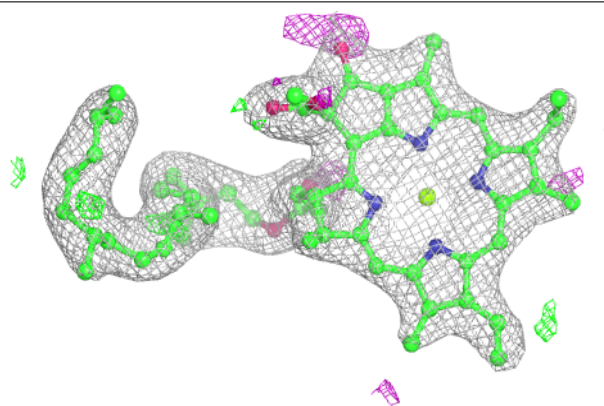


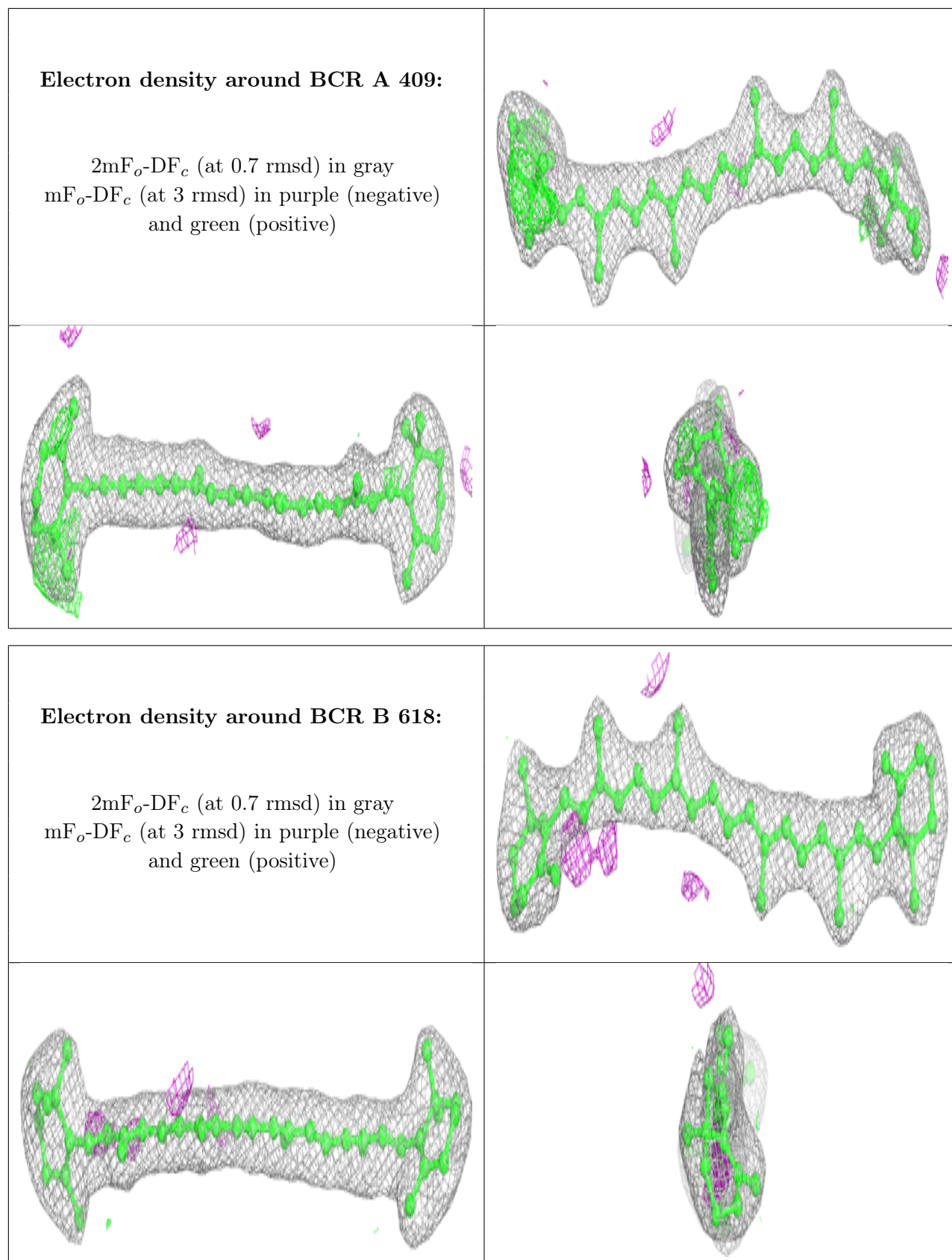
Electron density around BCR k 101:

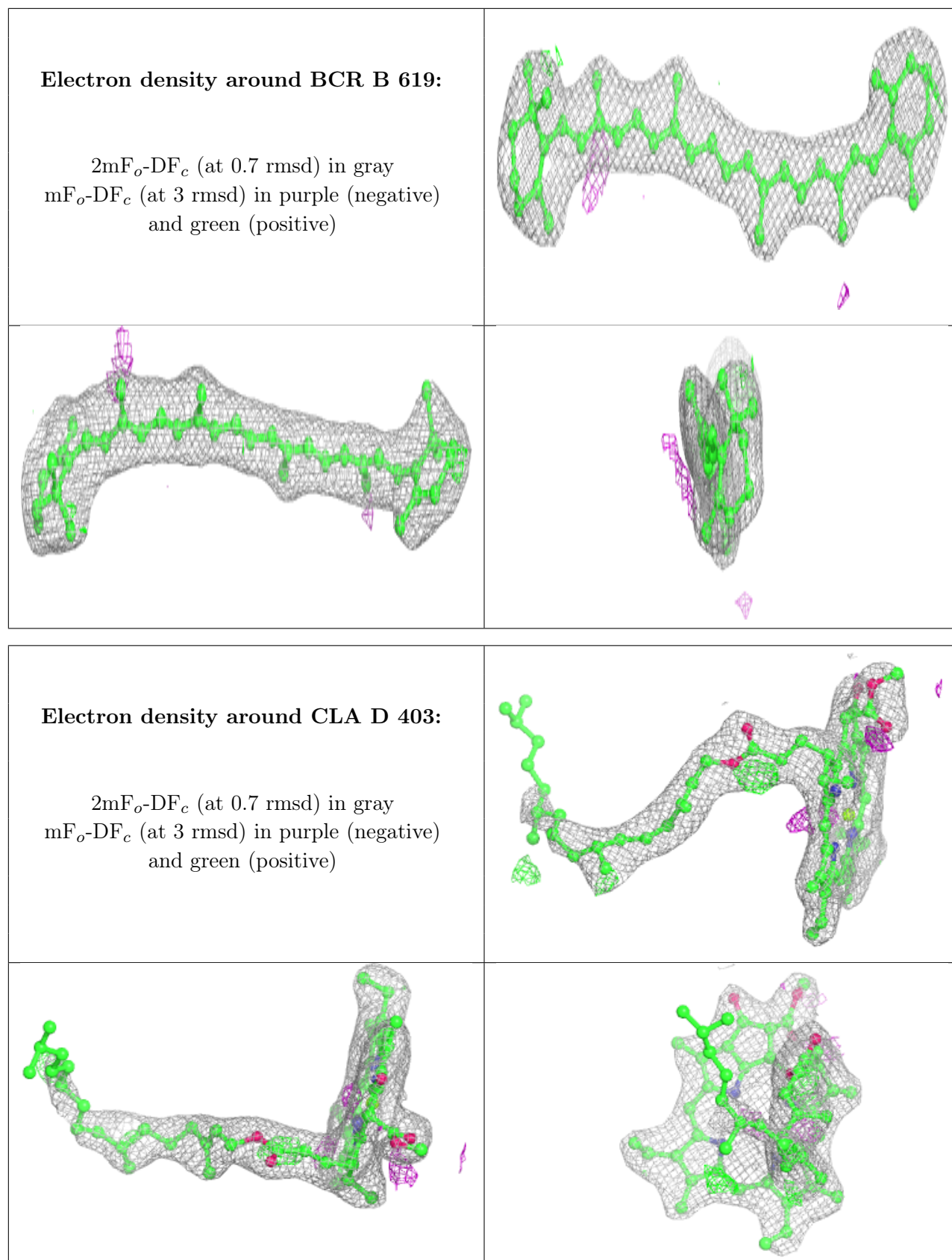
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

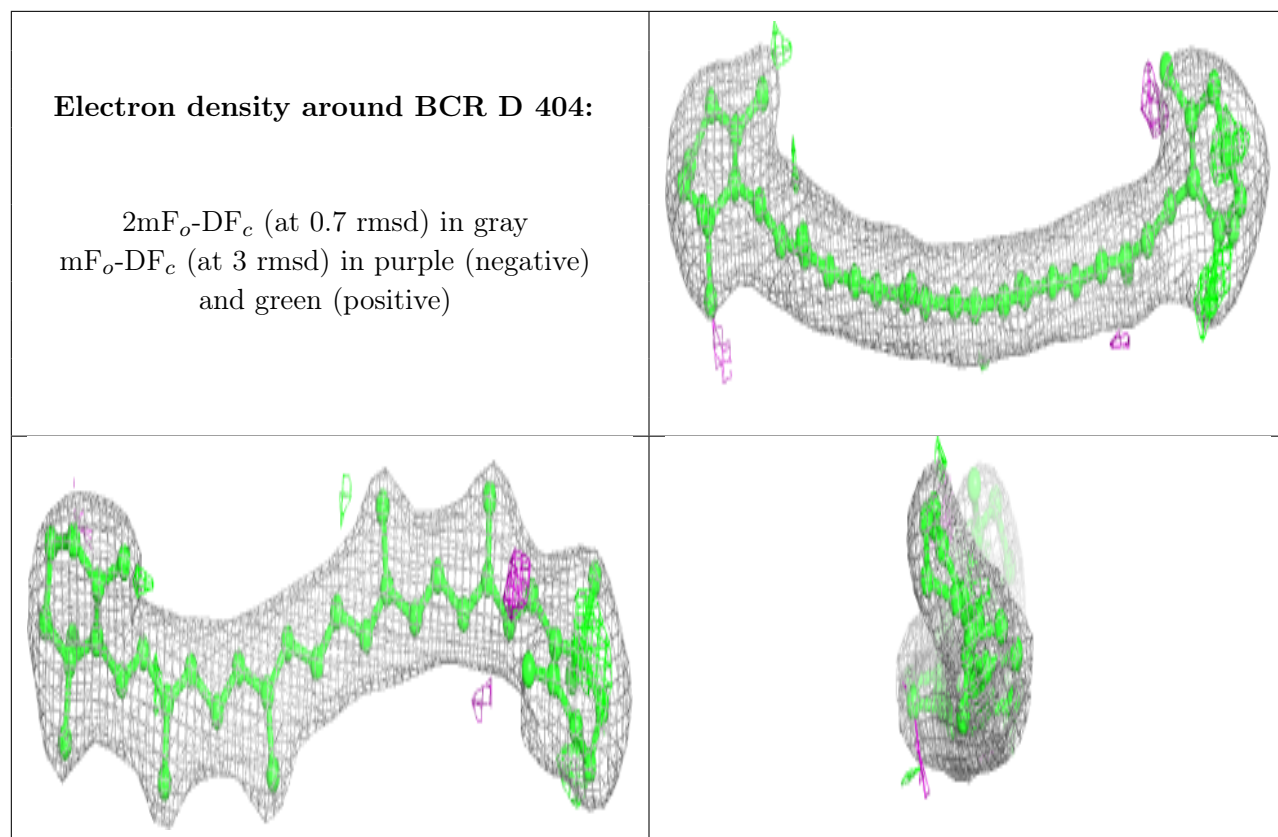
**Electron density around CLA b 612:**

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



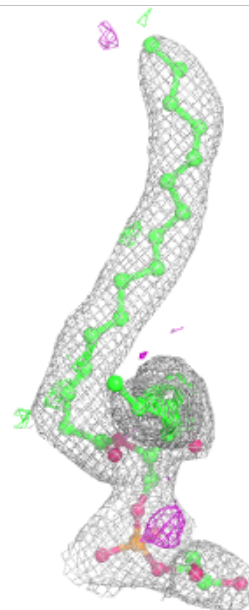
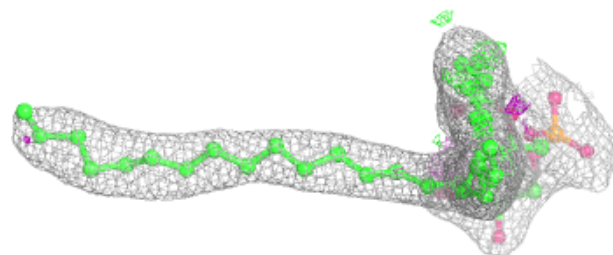
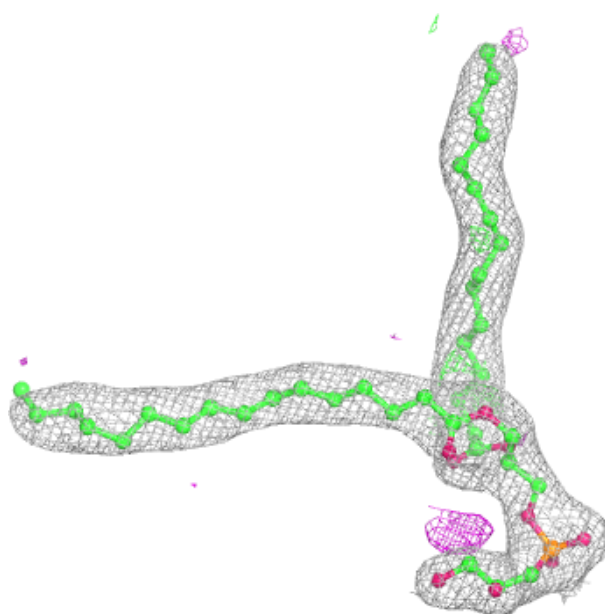






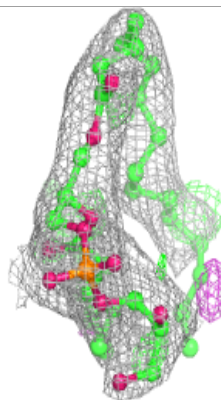
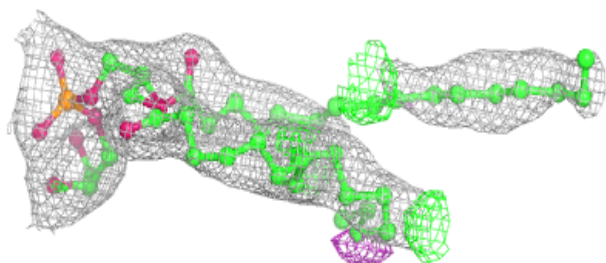
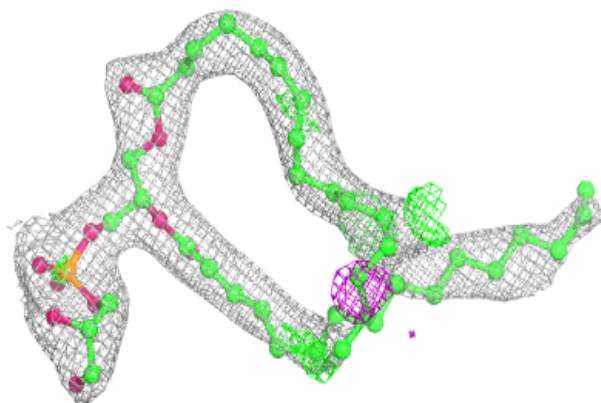
Electron density around LHG b 629 (B):

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

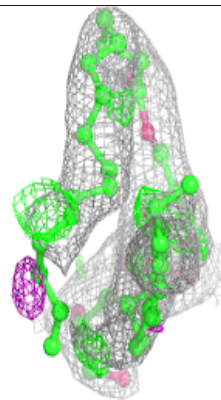
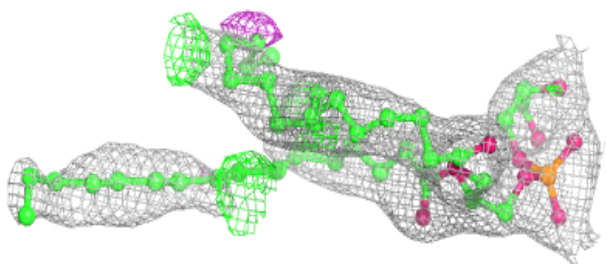
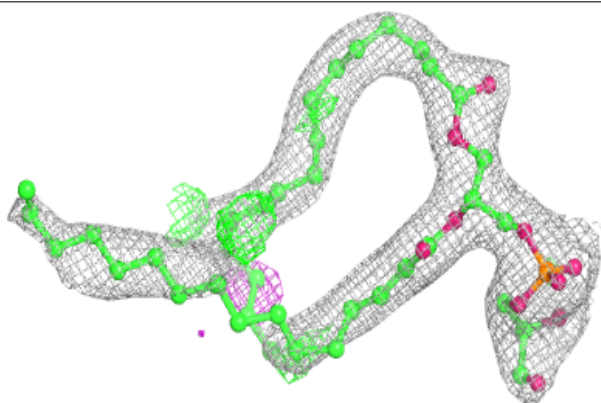


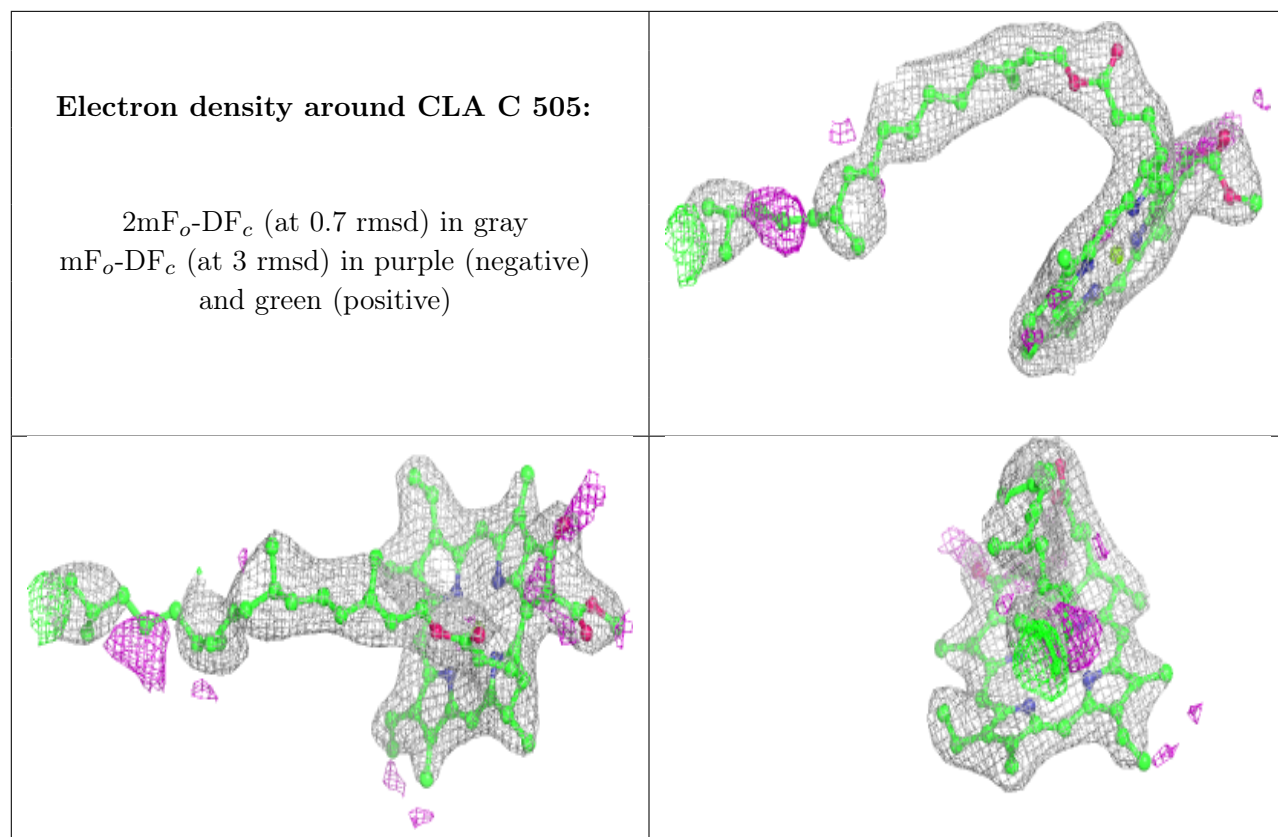
Electron density around LHG d 408 (A):

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

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

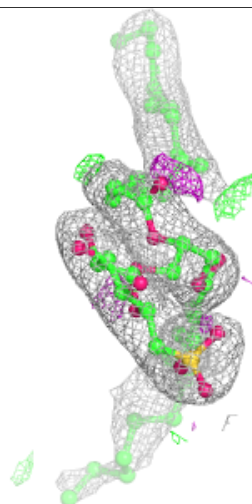
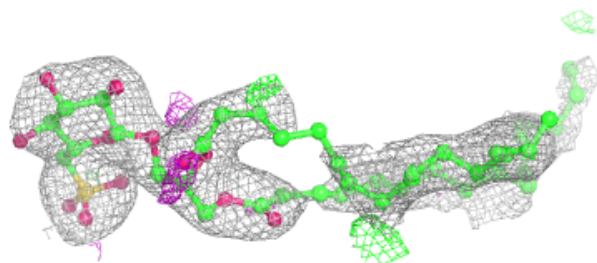
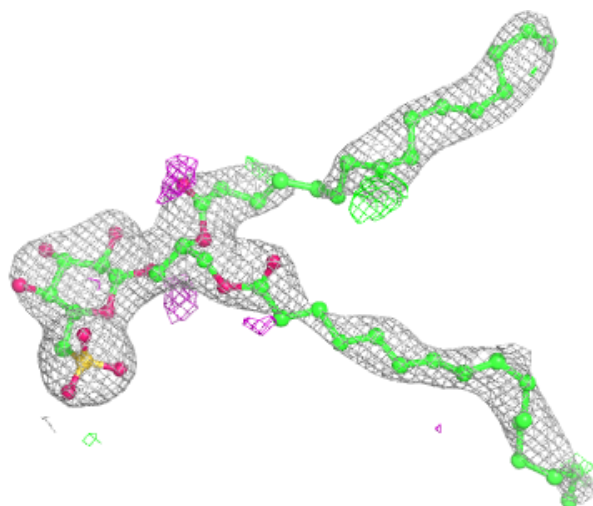
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





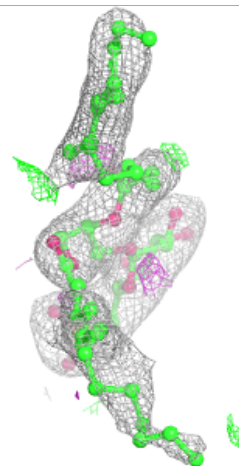
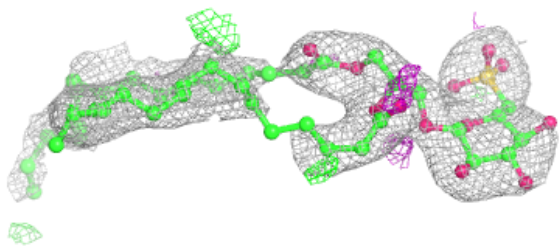
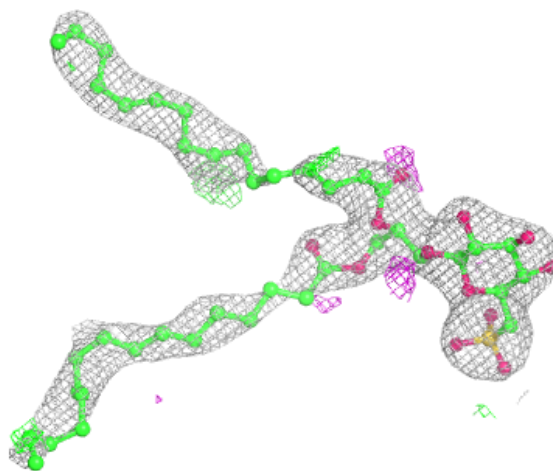
Electron density around SQD a 409 (A):

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



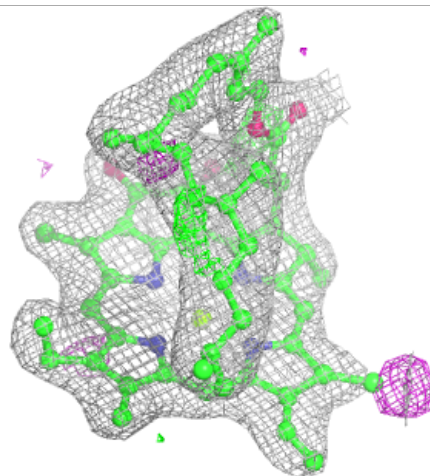
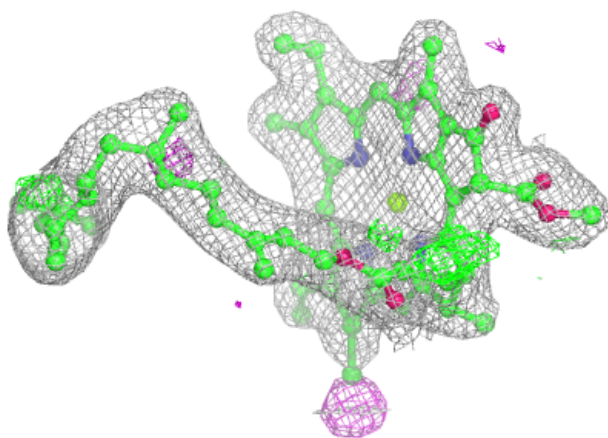
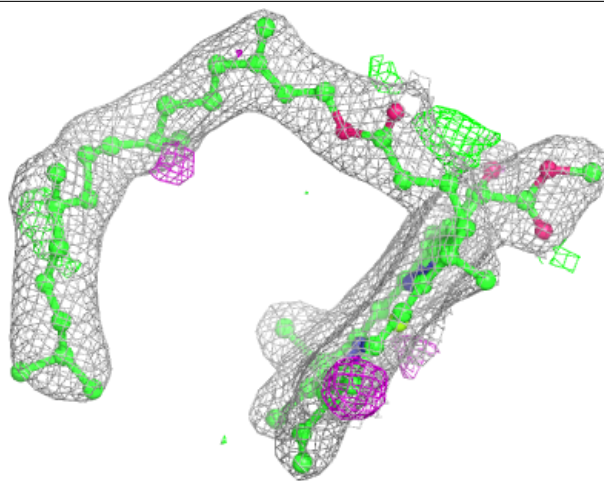
Electron density around SQD a 409 (B):

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



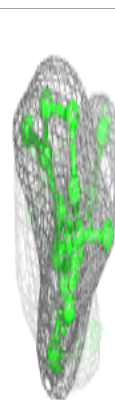
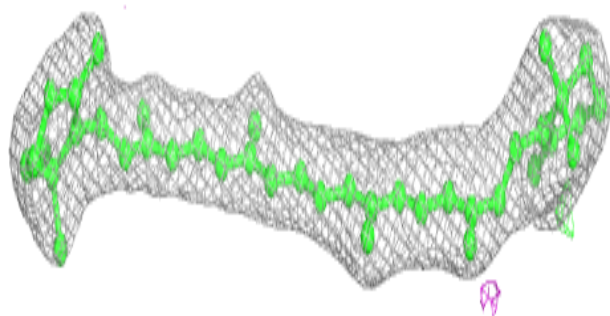
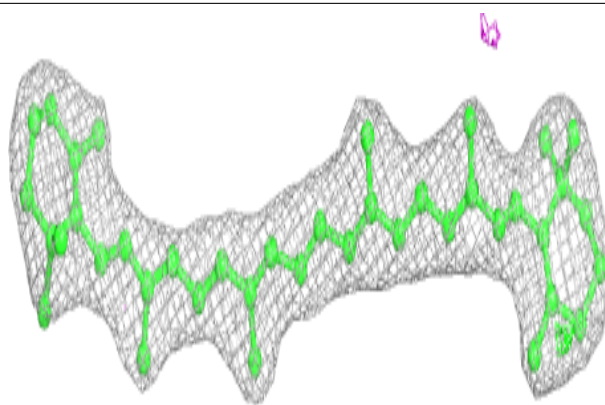
Electron density around CLA B 611:

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

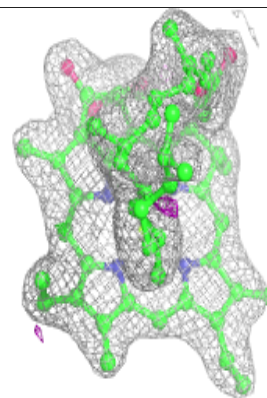
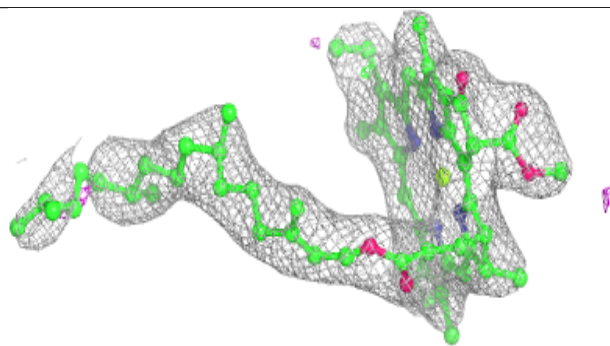
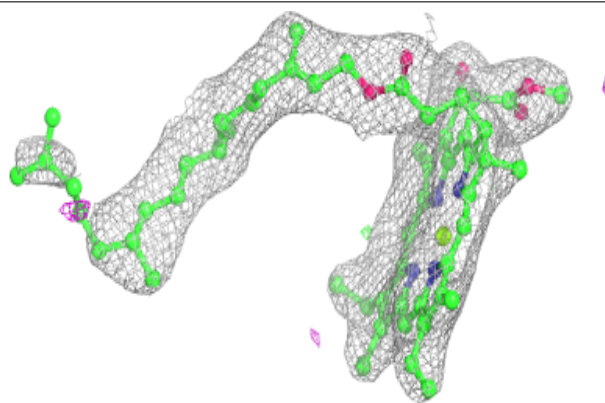


Electron density around BCR b 619:

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

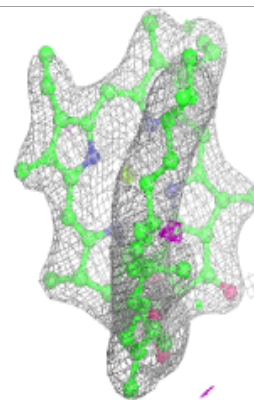
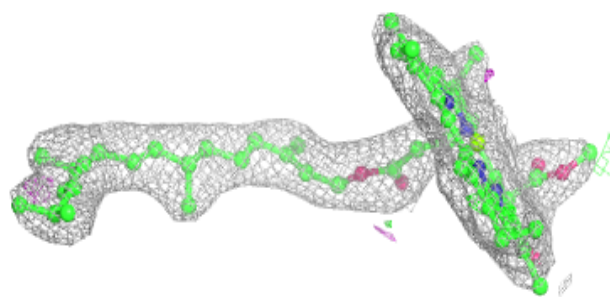
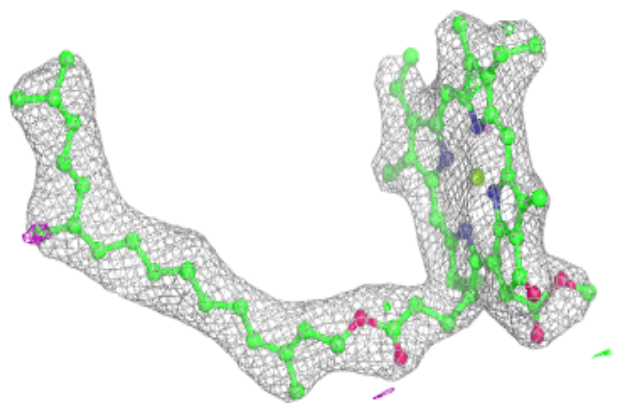
**Electron density around CLA c 508:**

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

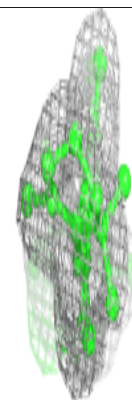
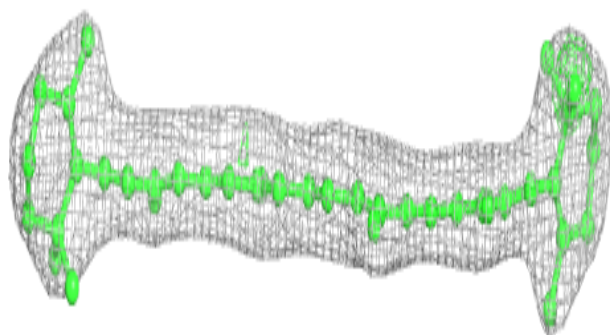
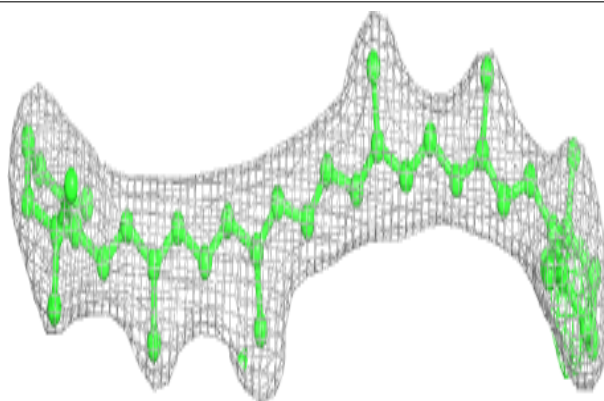


Electron density around CLA b 609:

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

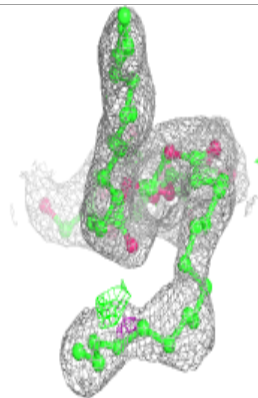
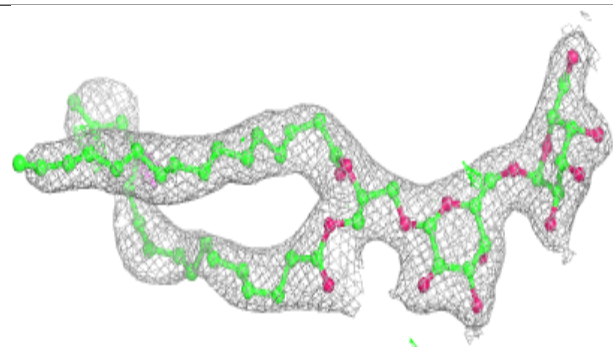
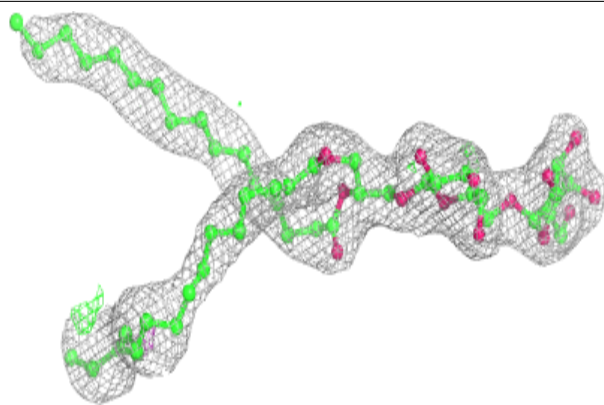
**Electron density around BCR C 516:**

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

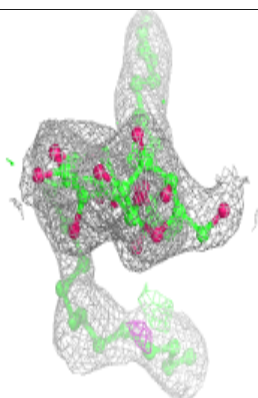
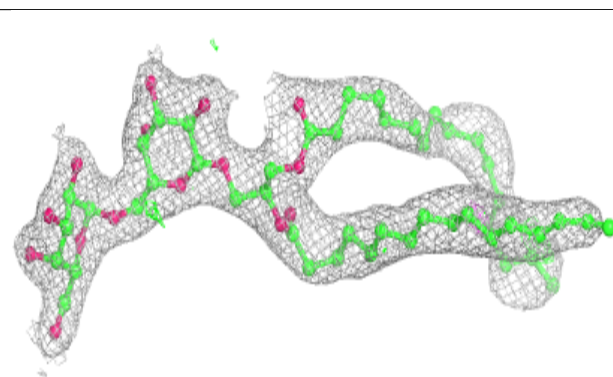
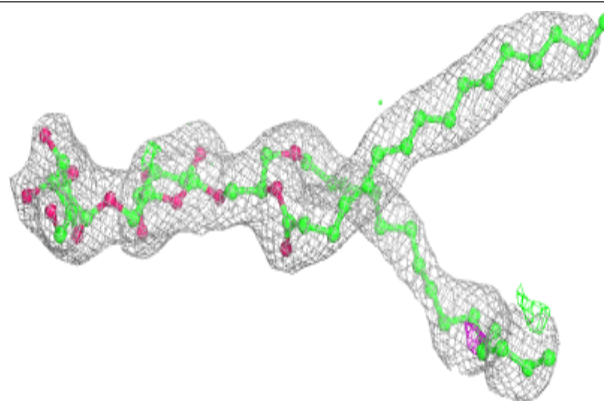


Electron density around DGD c 516 (A):

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

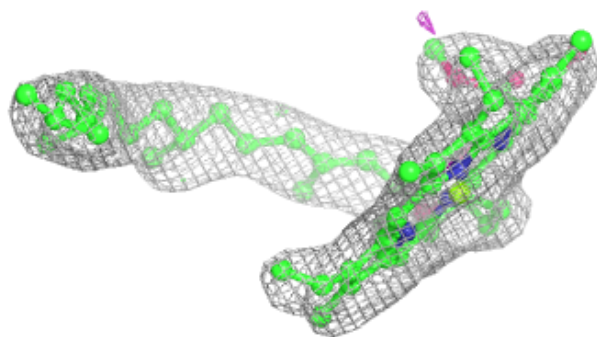
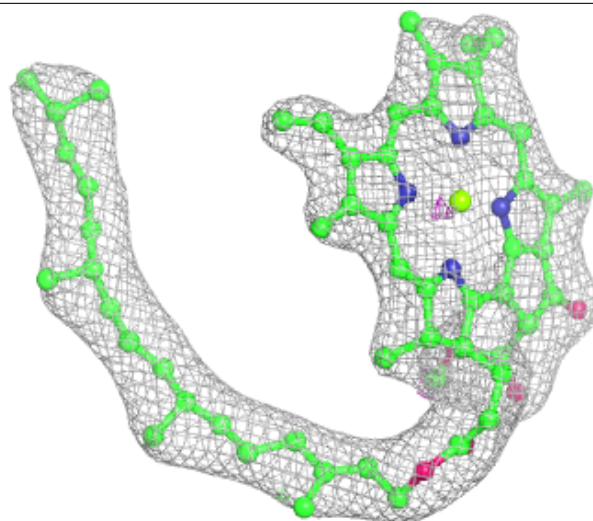
**Electron density around DGD c 516 (B):**

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



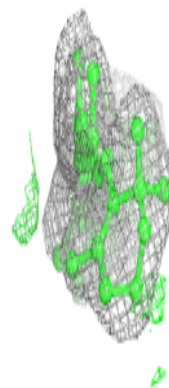
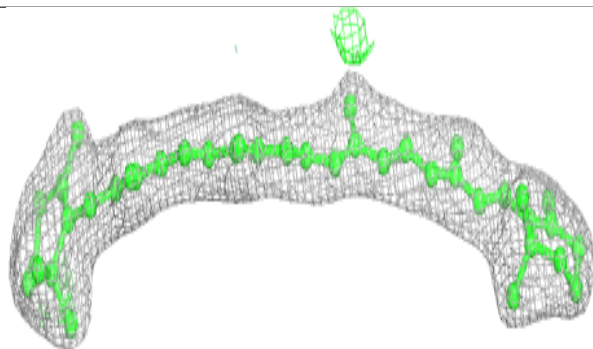
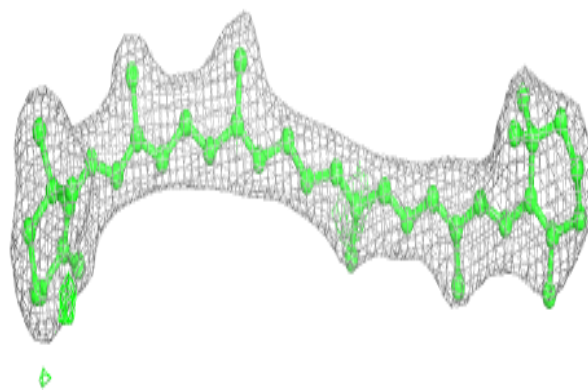
Electron density around CLA C 508:

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



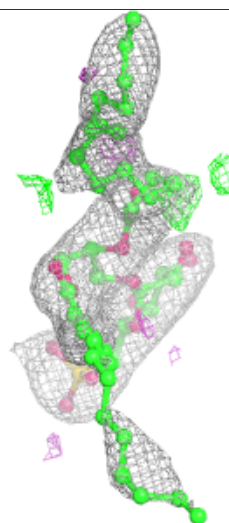
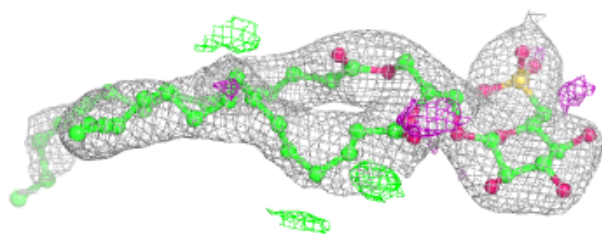
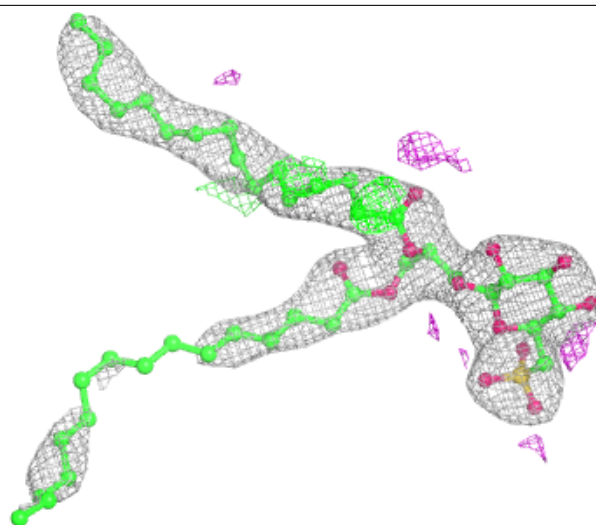
Electron density around BCR t 102:

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



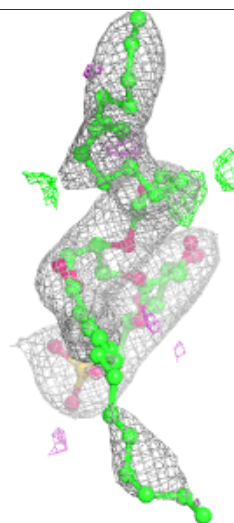
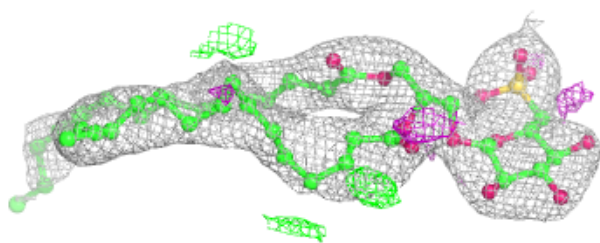
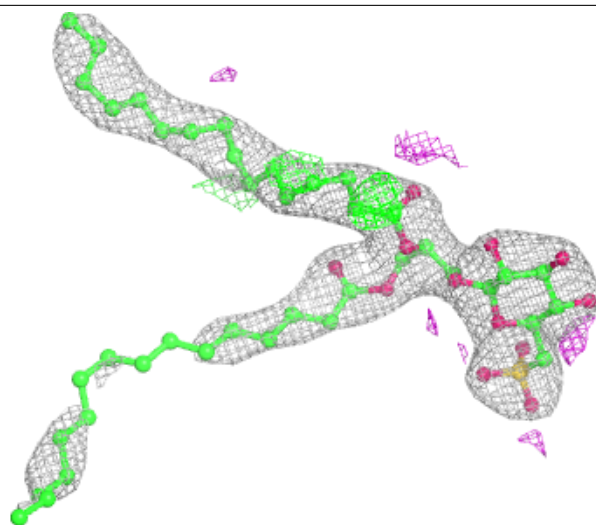
Electron density around SQD A 410 (A):

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



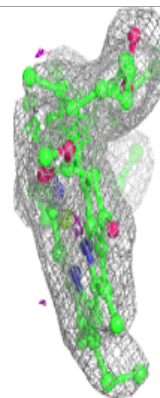
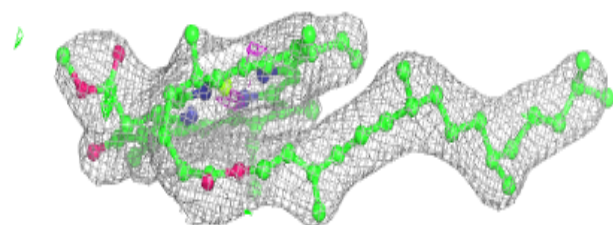
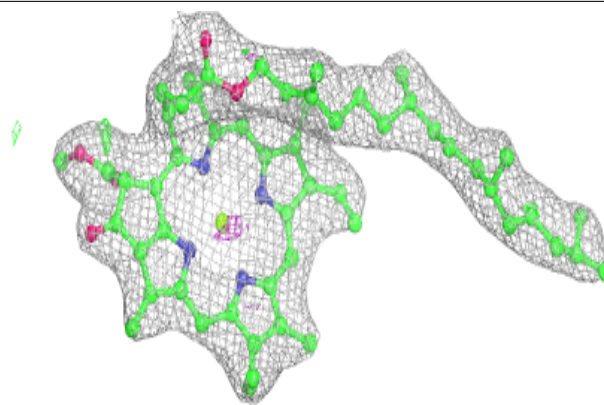
Electron density around SQD A 410 (B):

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

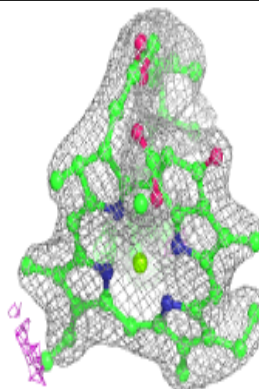
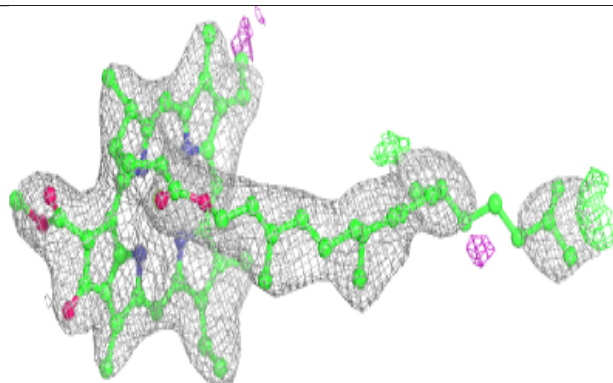
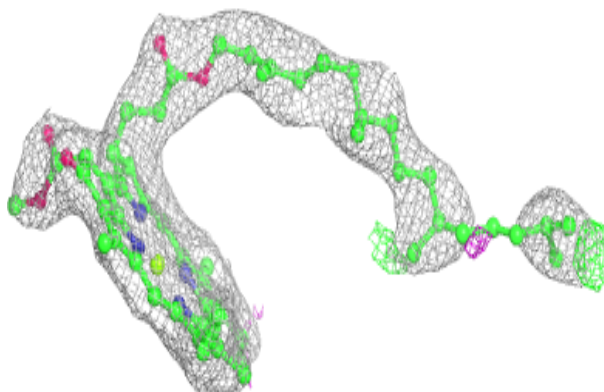


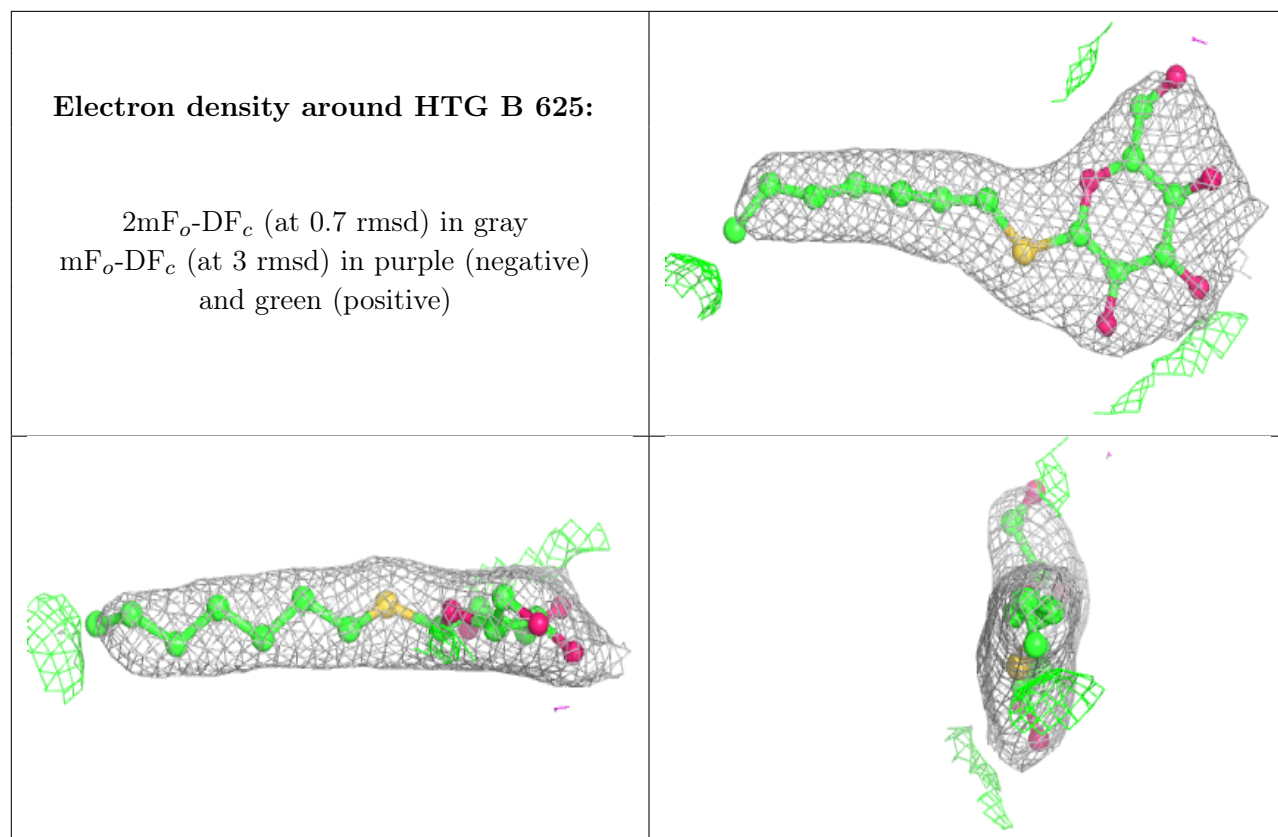
Electron density around CLA C 502:

$2mF_o-DF_c$ (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:**

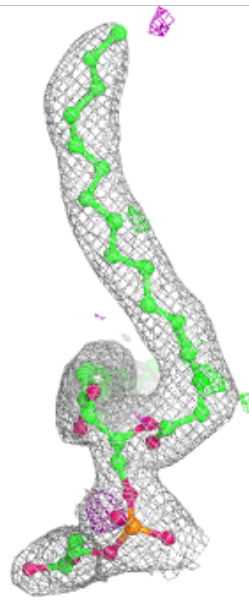
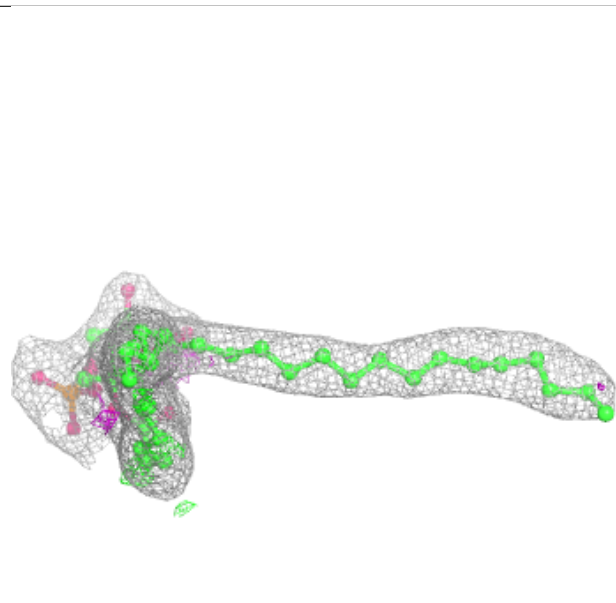
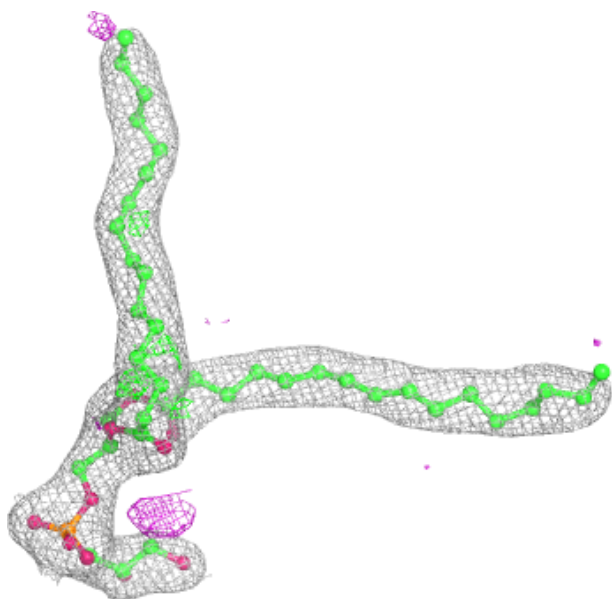
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





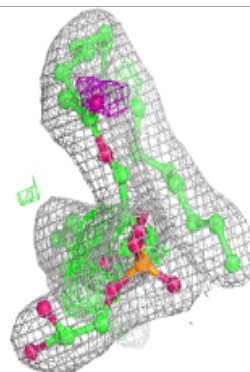
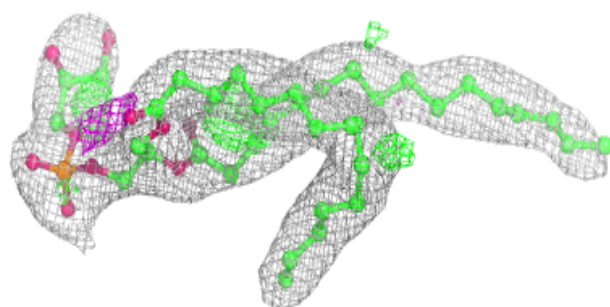
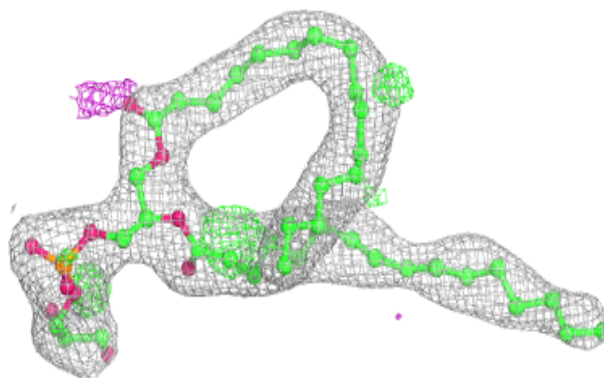
Electron density around LHG b 629 (A):

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

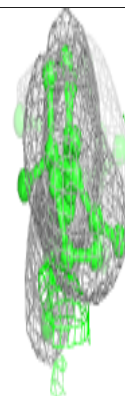
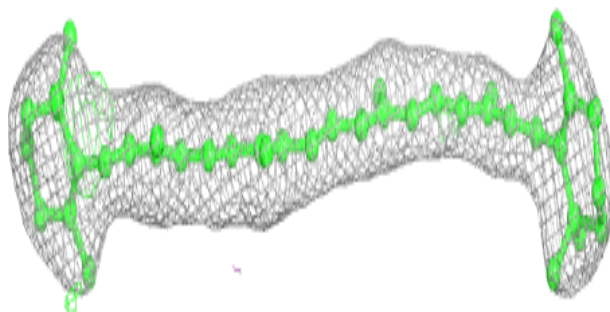
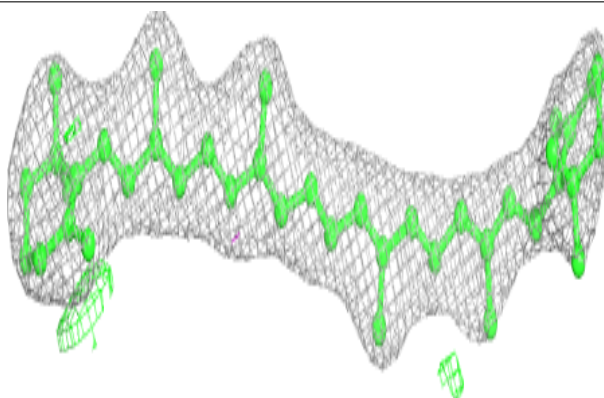


Electron density around LHG d 414 (B):

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

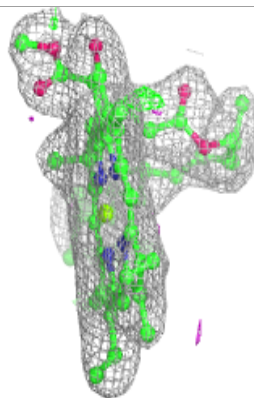
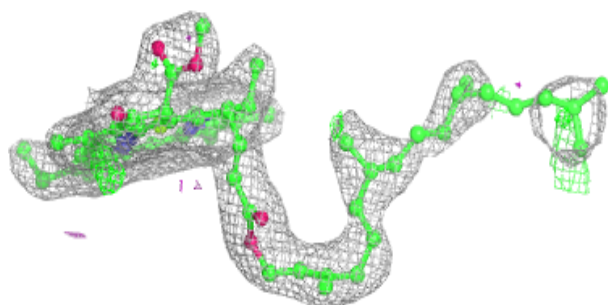
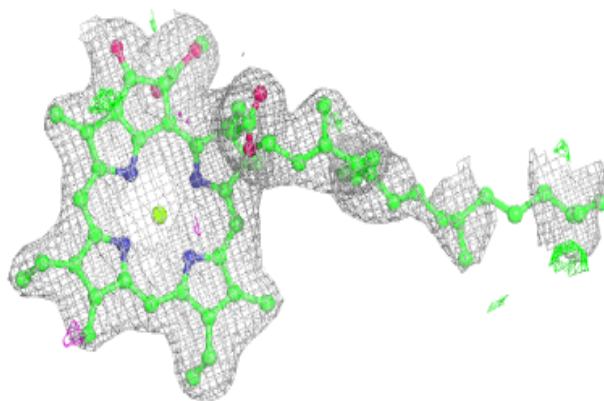
**Electron density around BCR c 515:**

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

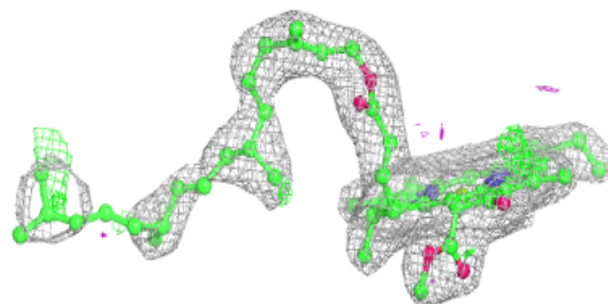
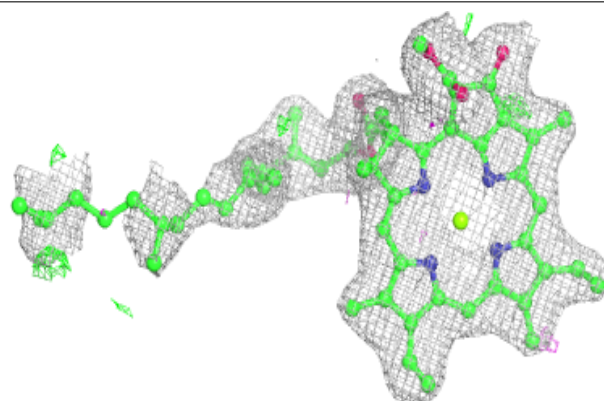


Electron density around CLA a 405 (A):

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

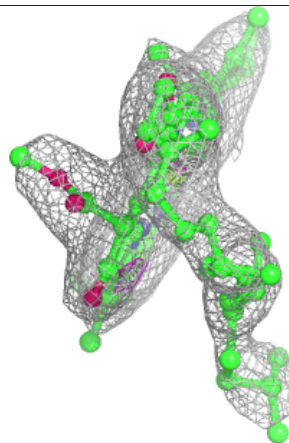
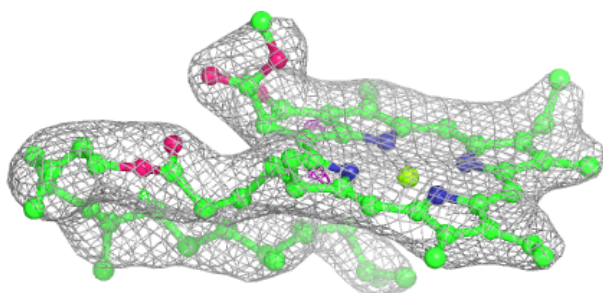
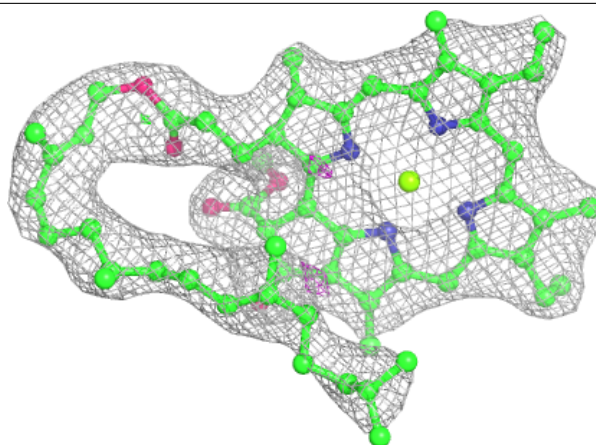
**Electron density around CLA a 405 (B):**

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

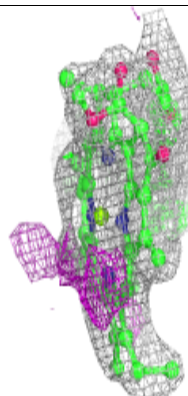
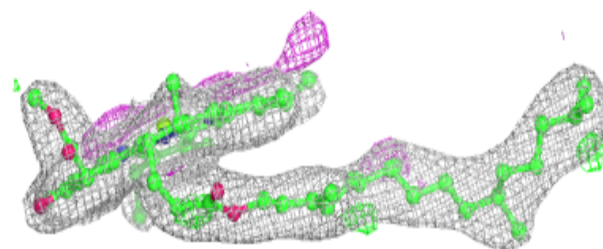
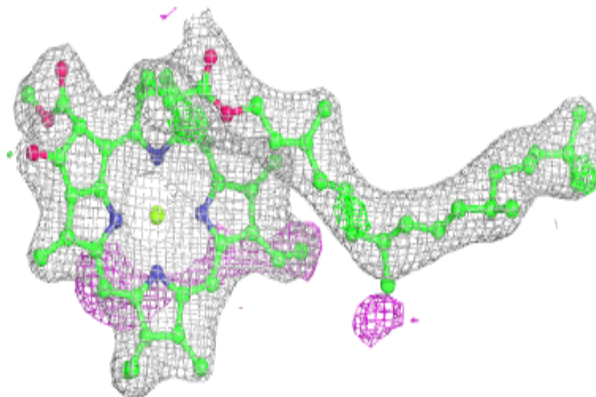


Electron density around CLA c 509:

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

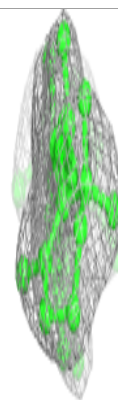
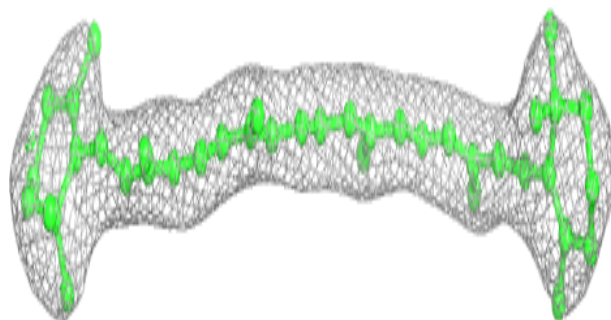
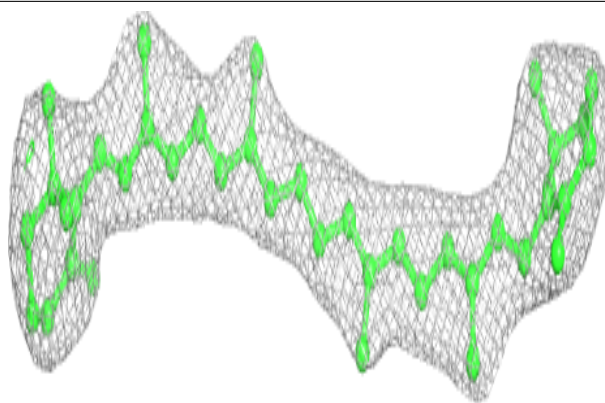
**Electron density around CLA B 603:**

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

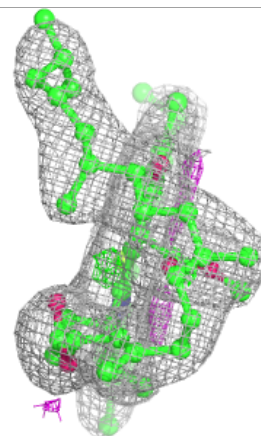
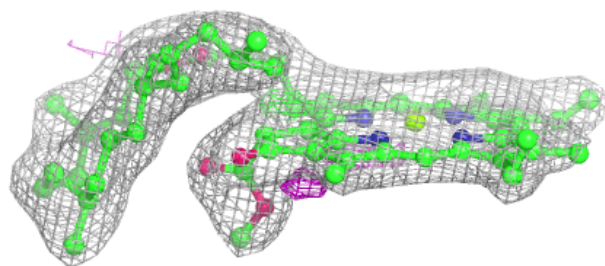
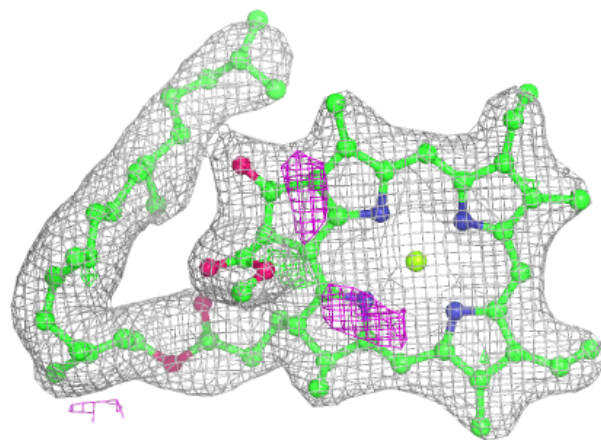


Electron density around BCR y 101:

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

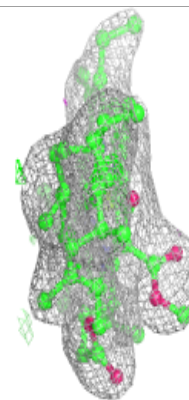
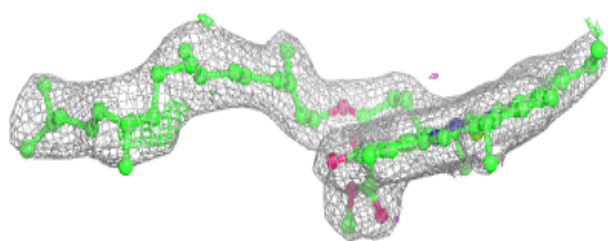
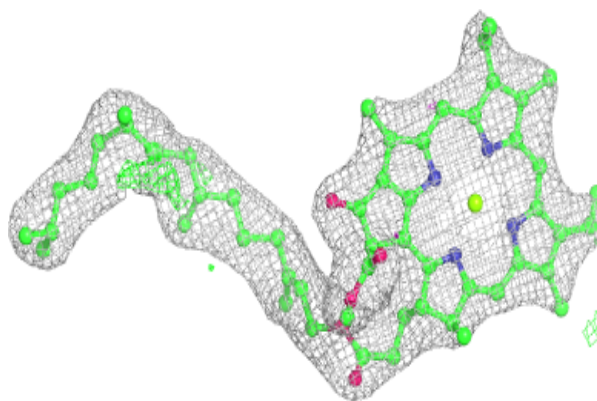
**Electron density around CLA B 610:**

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

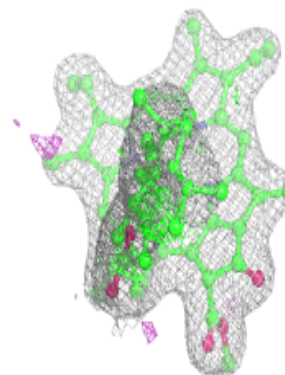
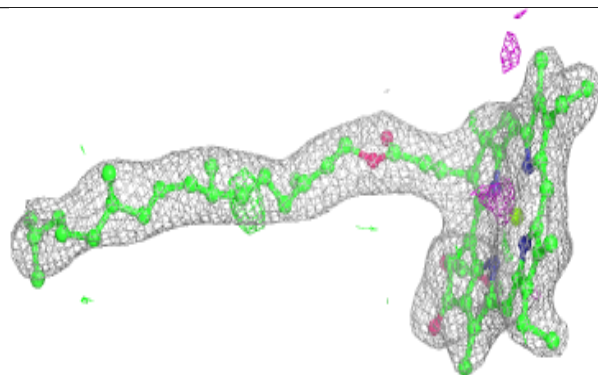
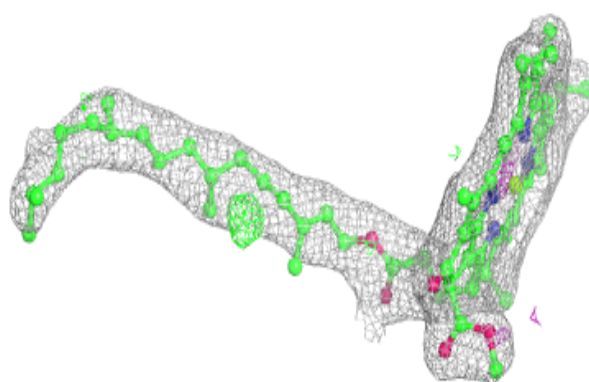


Electron density around CLA b 602:

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

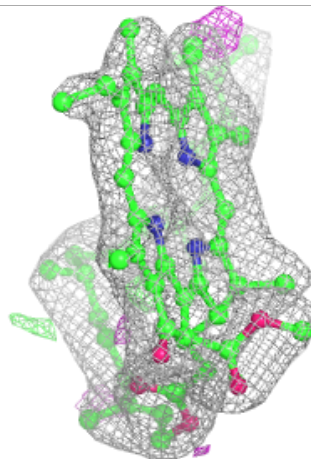
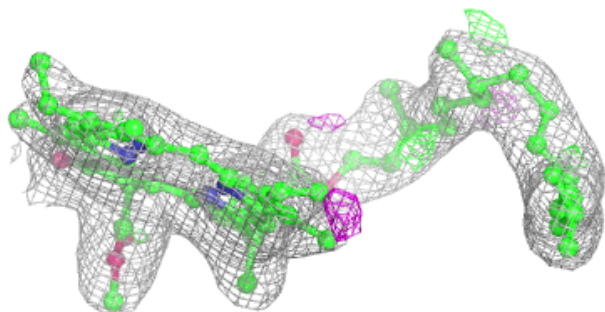
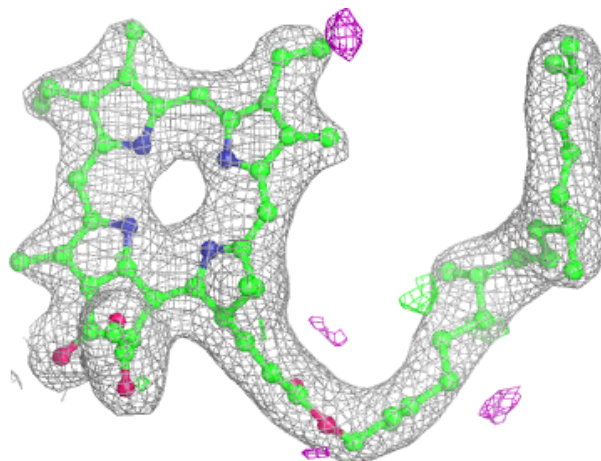
**Electron density around CLA b 604:**

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



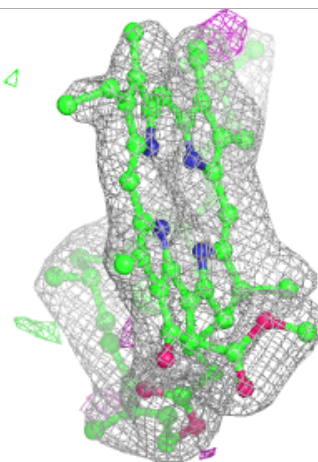
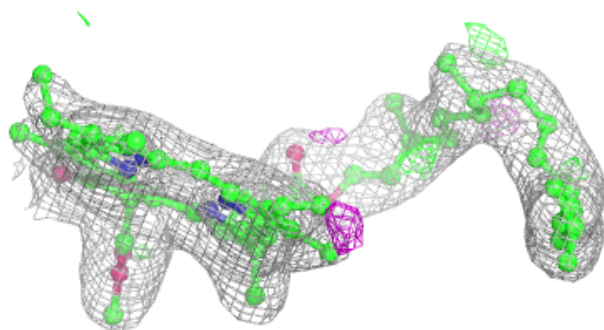
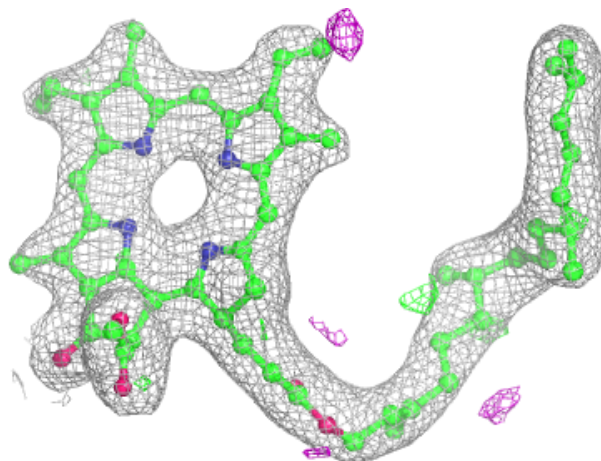
Electron density around PHO a 414 (A):

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



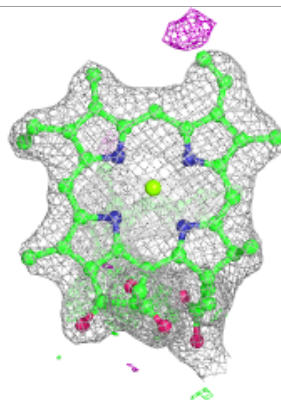
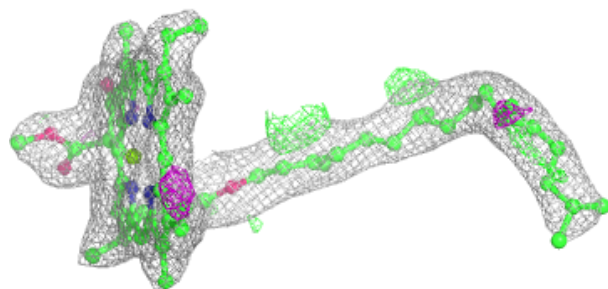
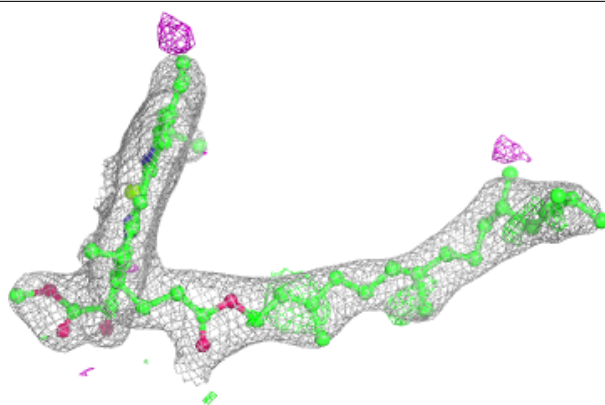
Electron density around PHO a 414 (B):

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

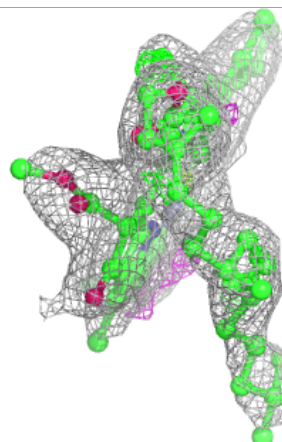
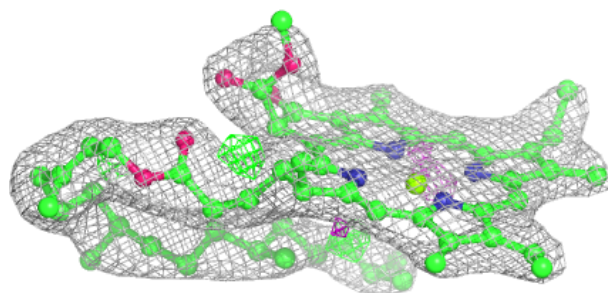
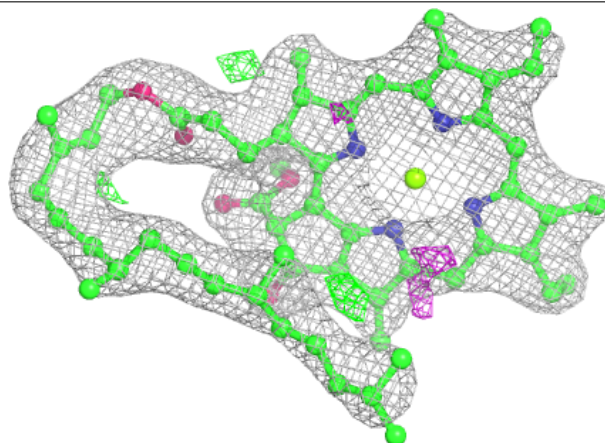


Electron density around CLA b 605:

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

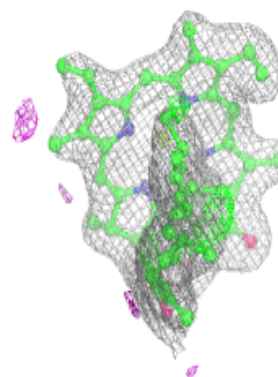
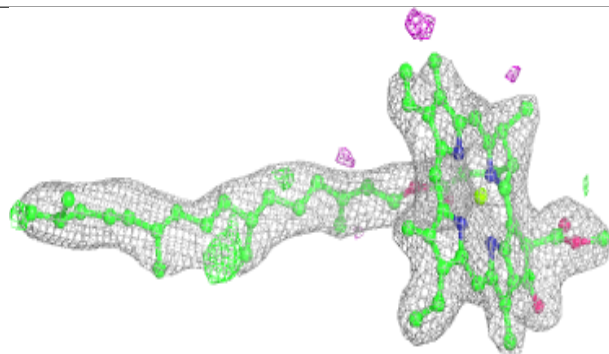
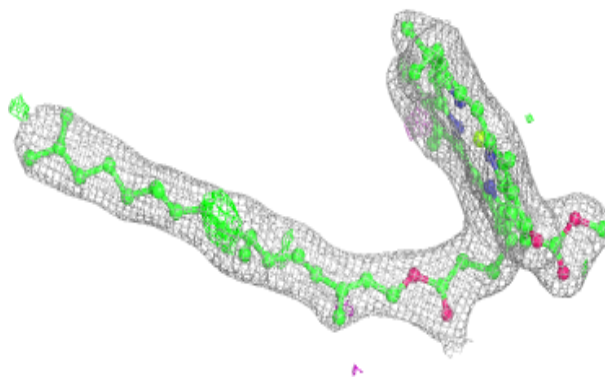
**Electron density around CLA C 510:**

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

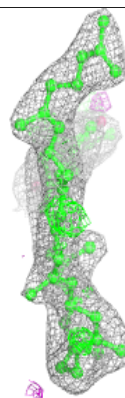
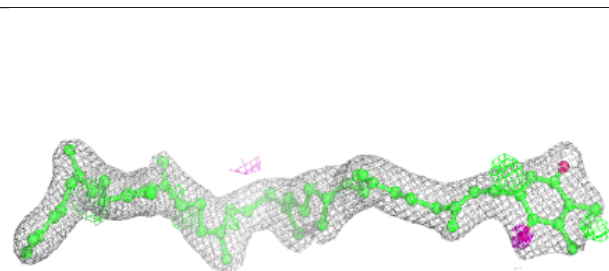
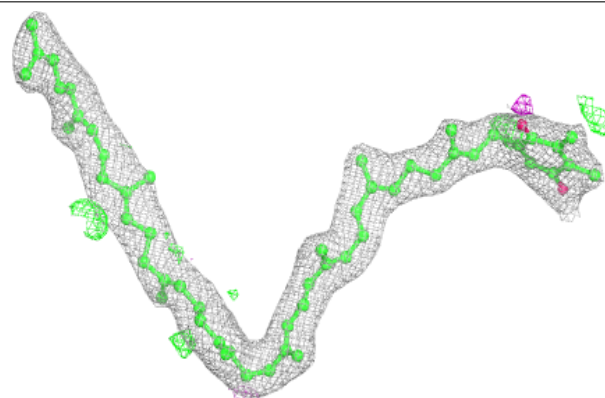


Electron density around CLA b 607:

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

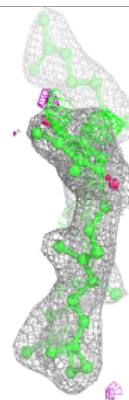
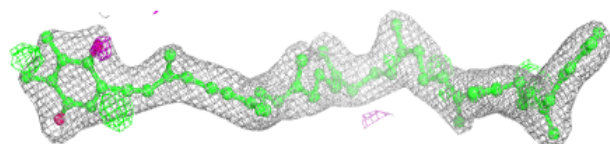
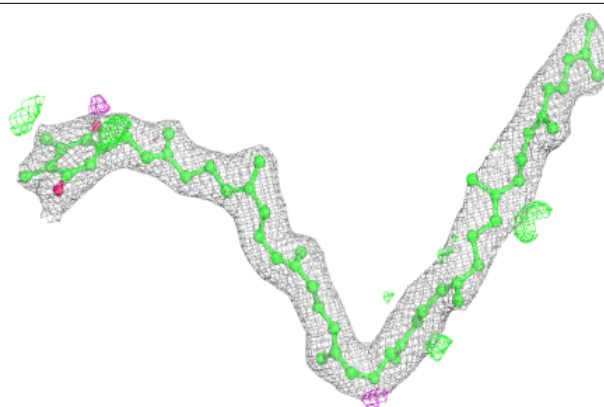
**Electron density around PL9 D 405 (A):**

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



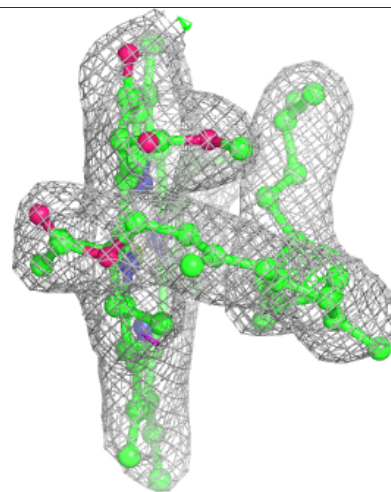
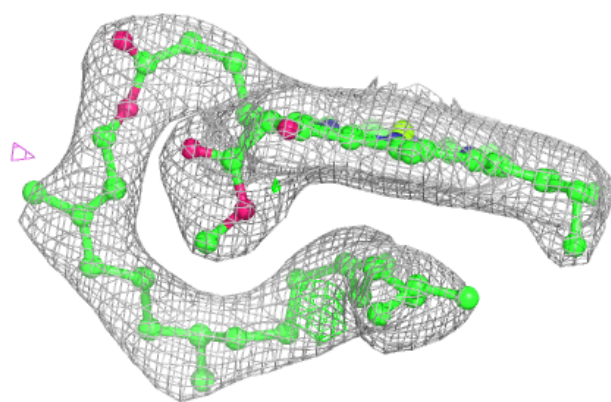
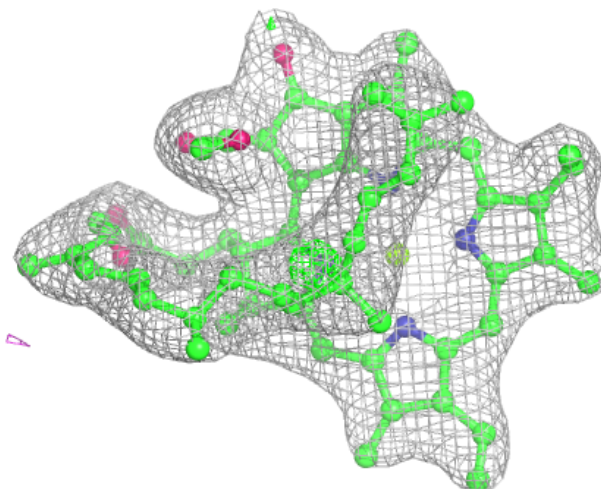
Electron density around PL9 D 405 (B):

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



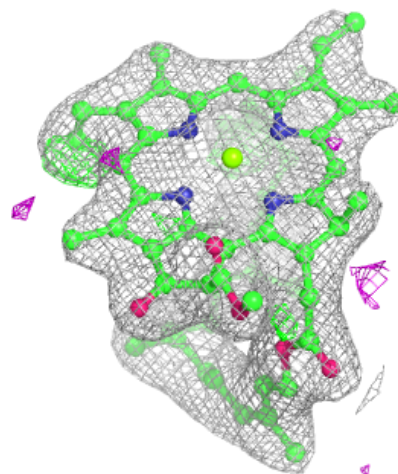
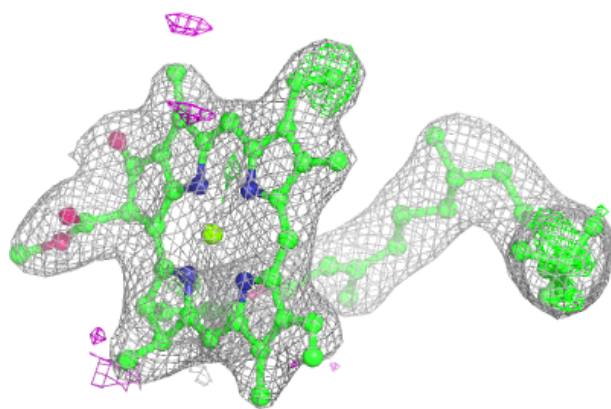
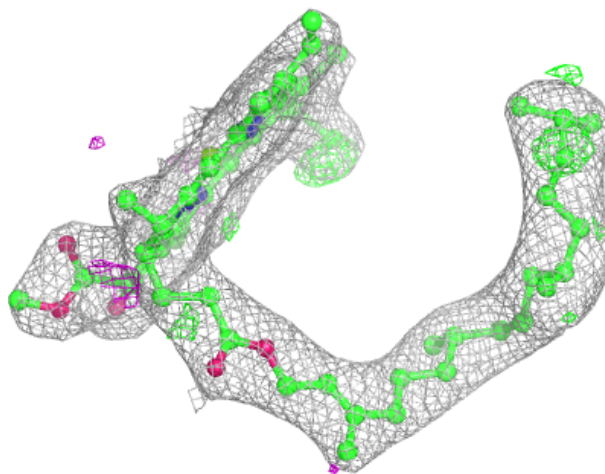
Electron density around CLA C 511:

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



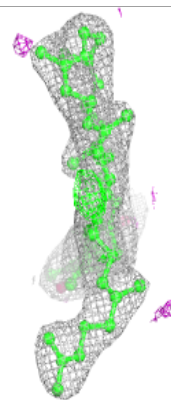
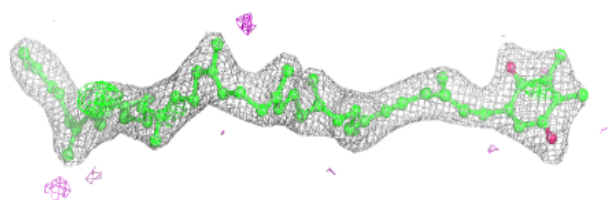
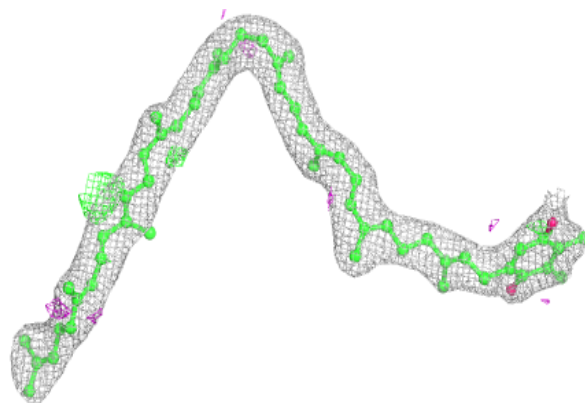
Electron density around CLA b 611:

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

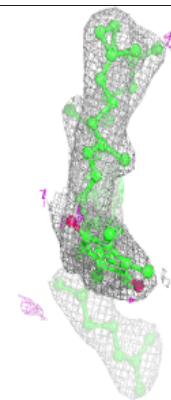
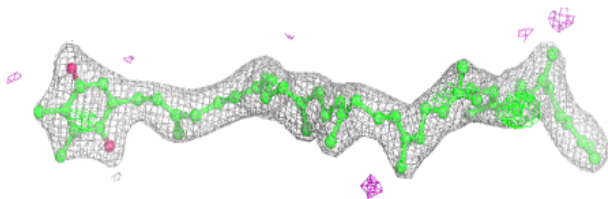
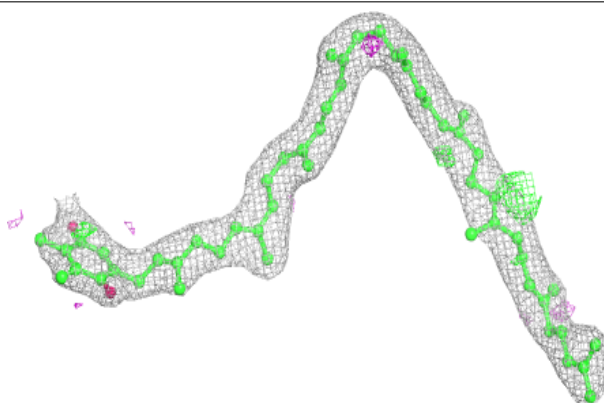


Electron density around PL9 d 406 (A):

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

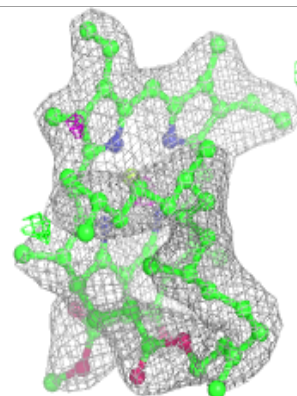
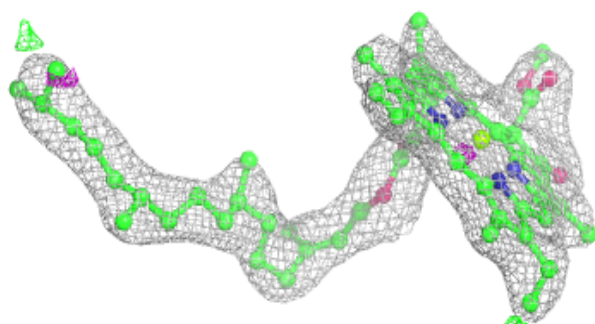
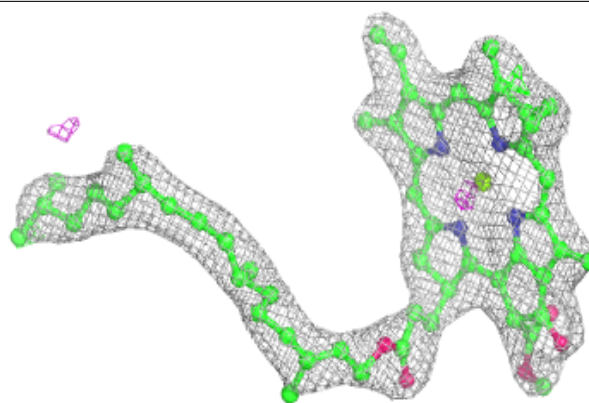
**Electron density around PL9 d 406 (B):**

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

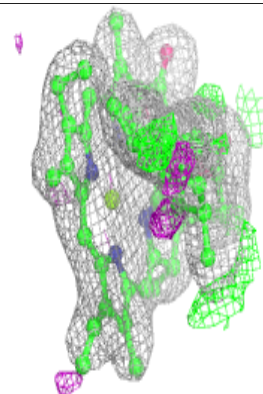
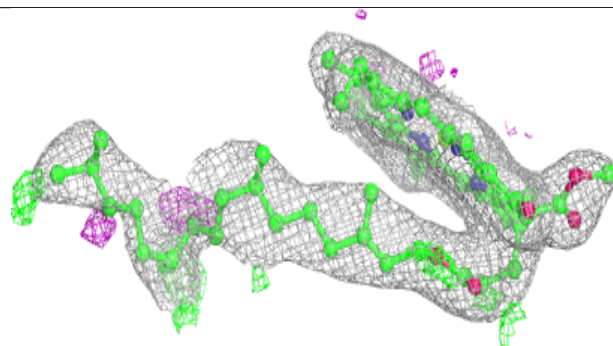
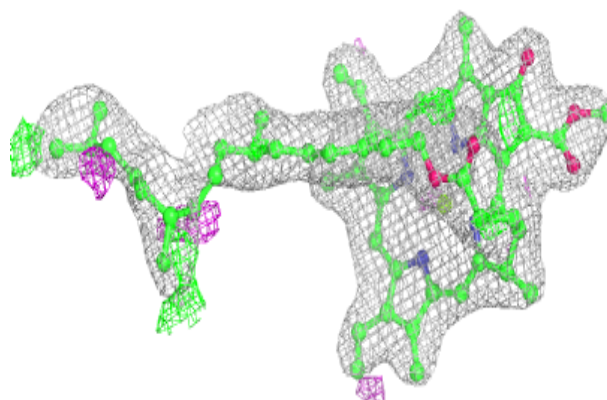


Electron density around CLA C 512:

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

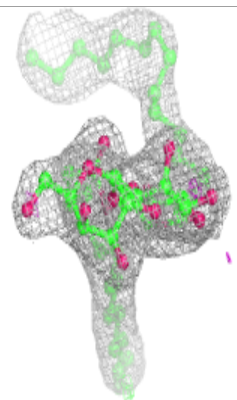
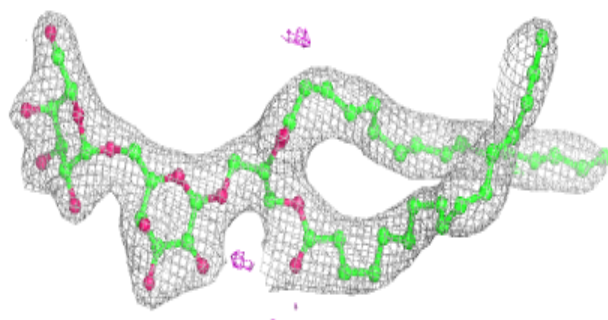
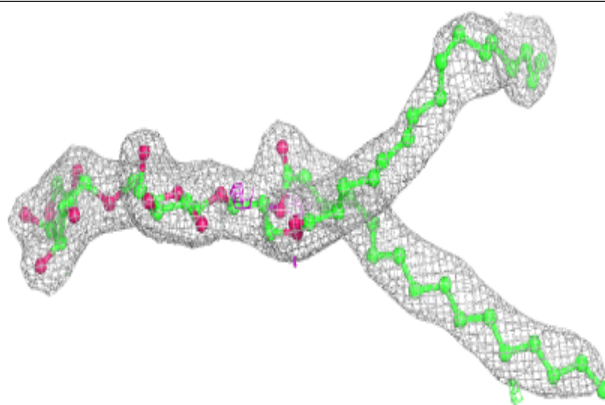
**Electron density around CLA b 614:**

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

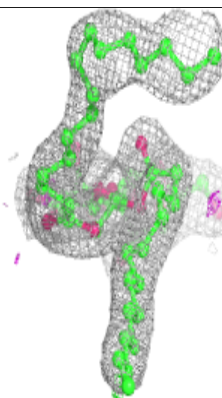
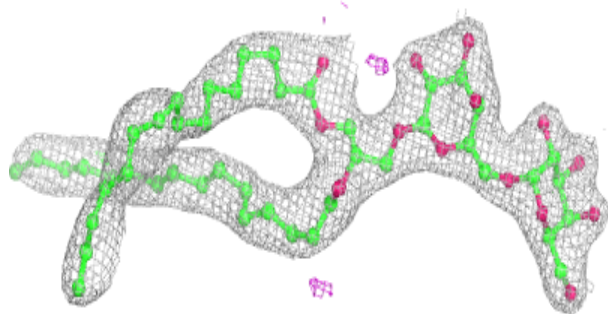
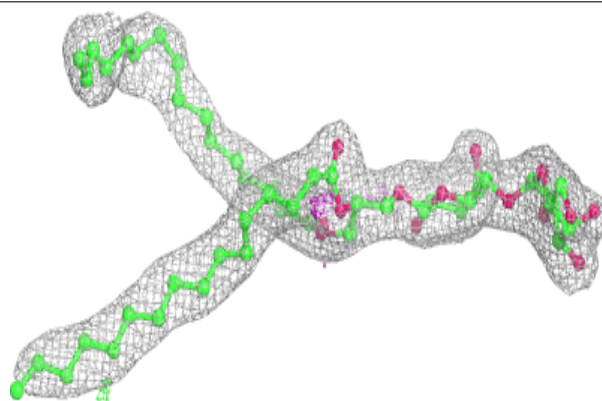


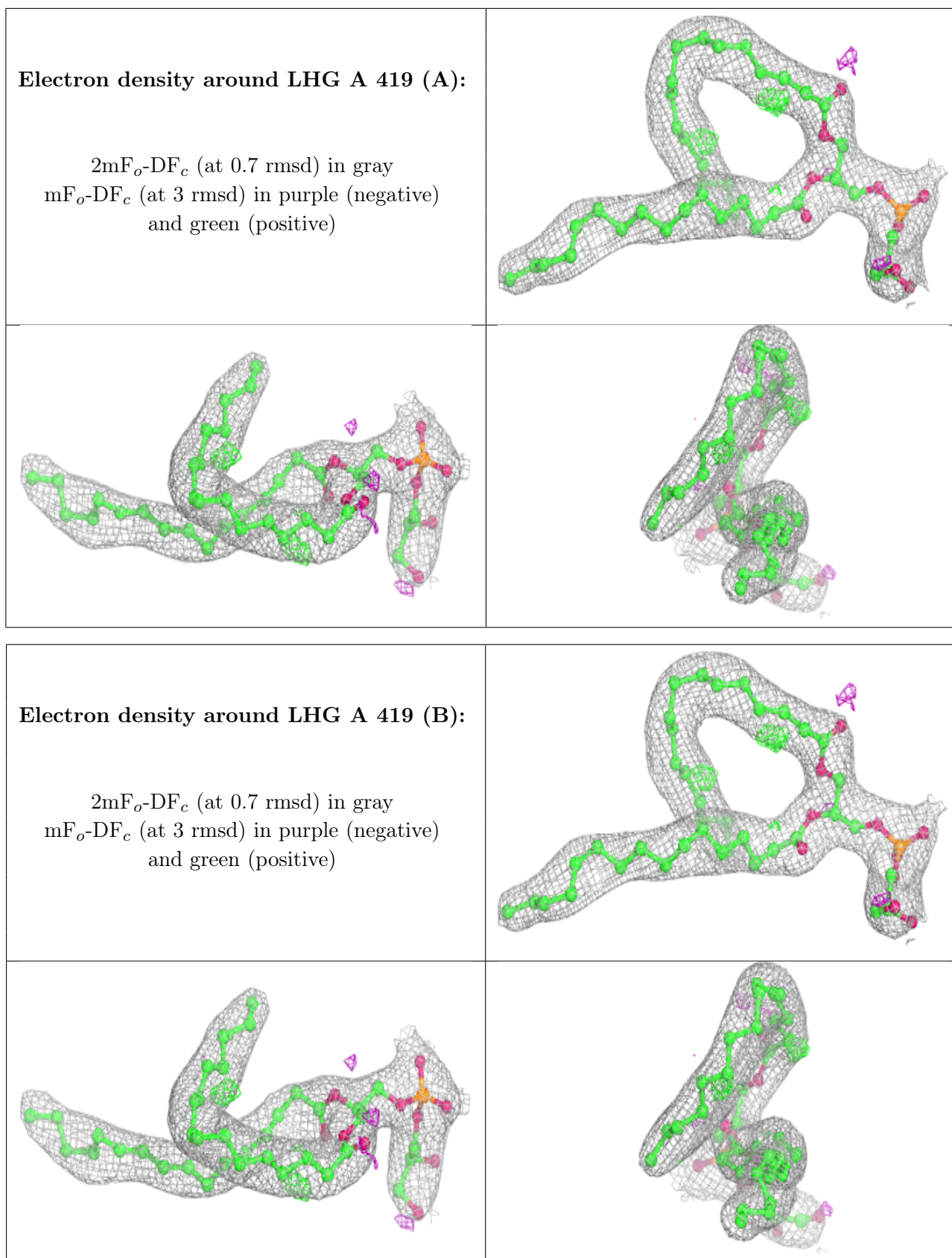
Electron density around DGD C 517 (A):

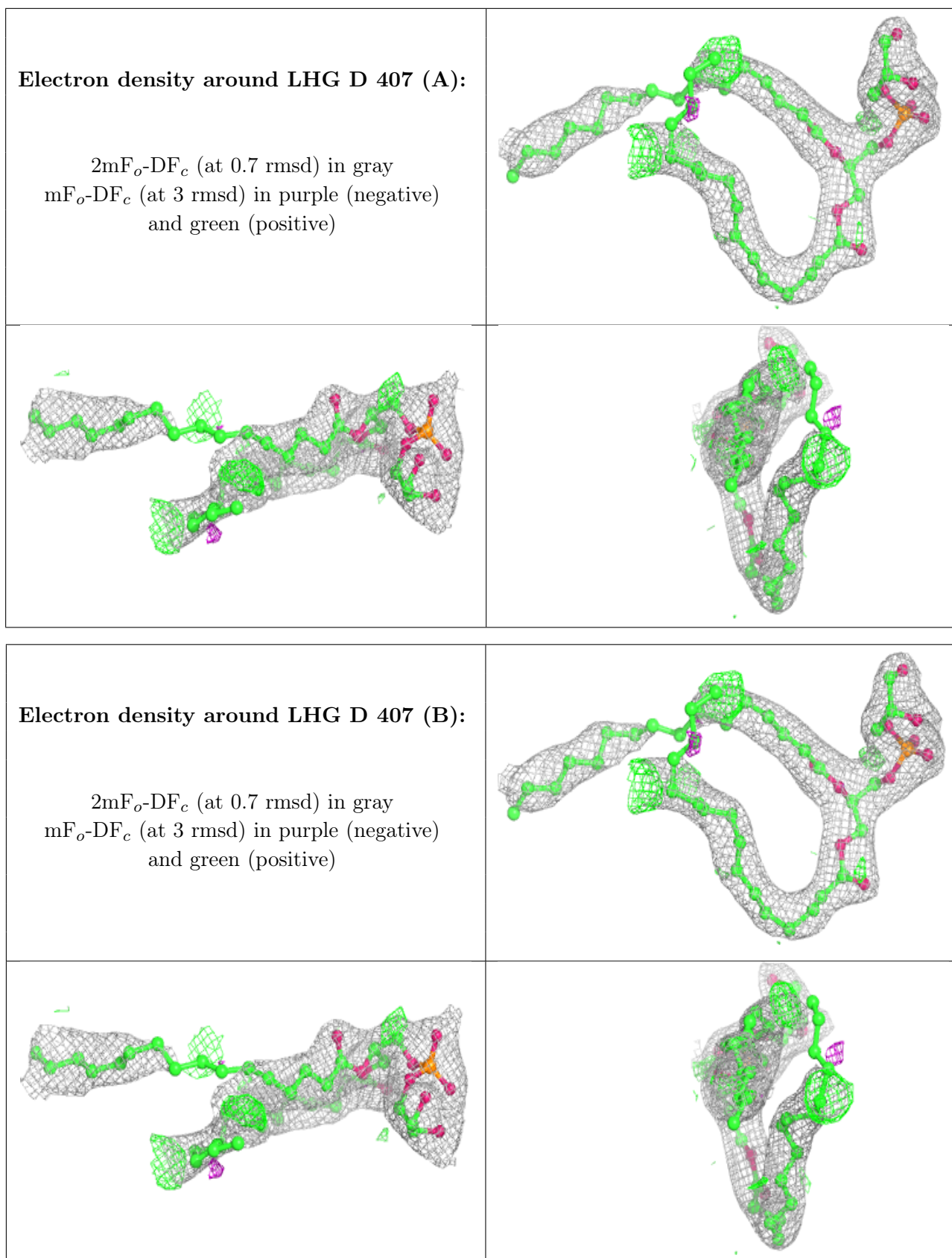
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**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)

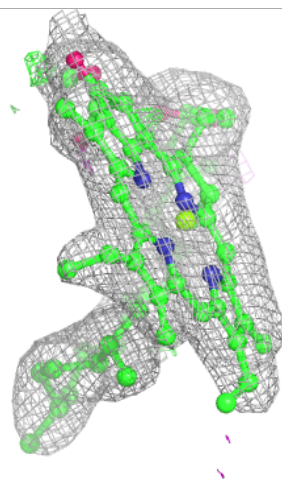
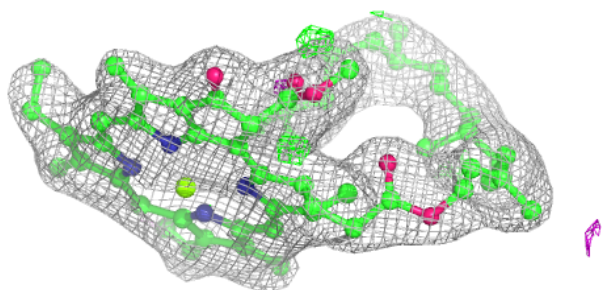
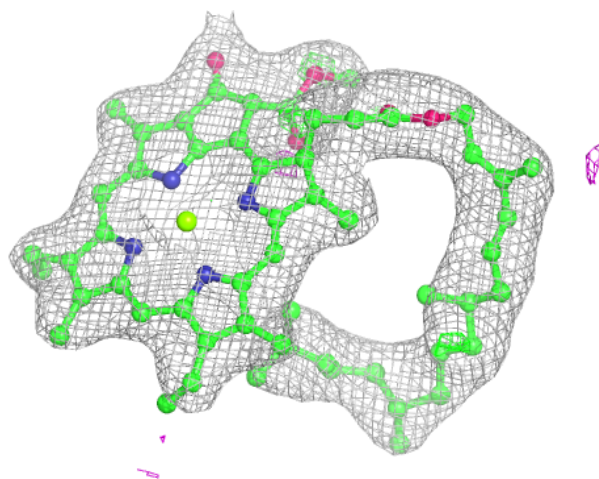


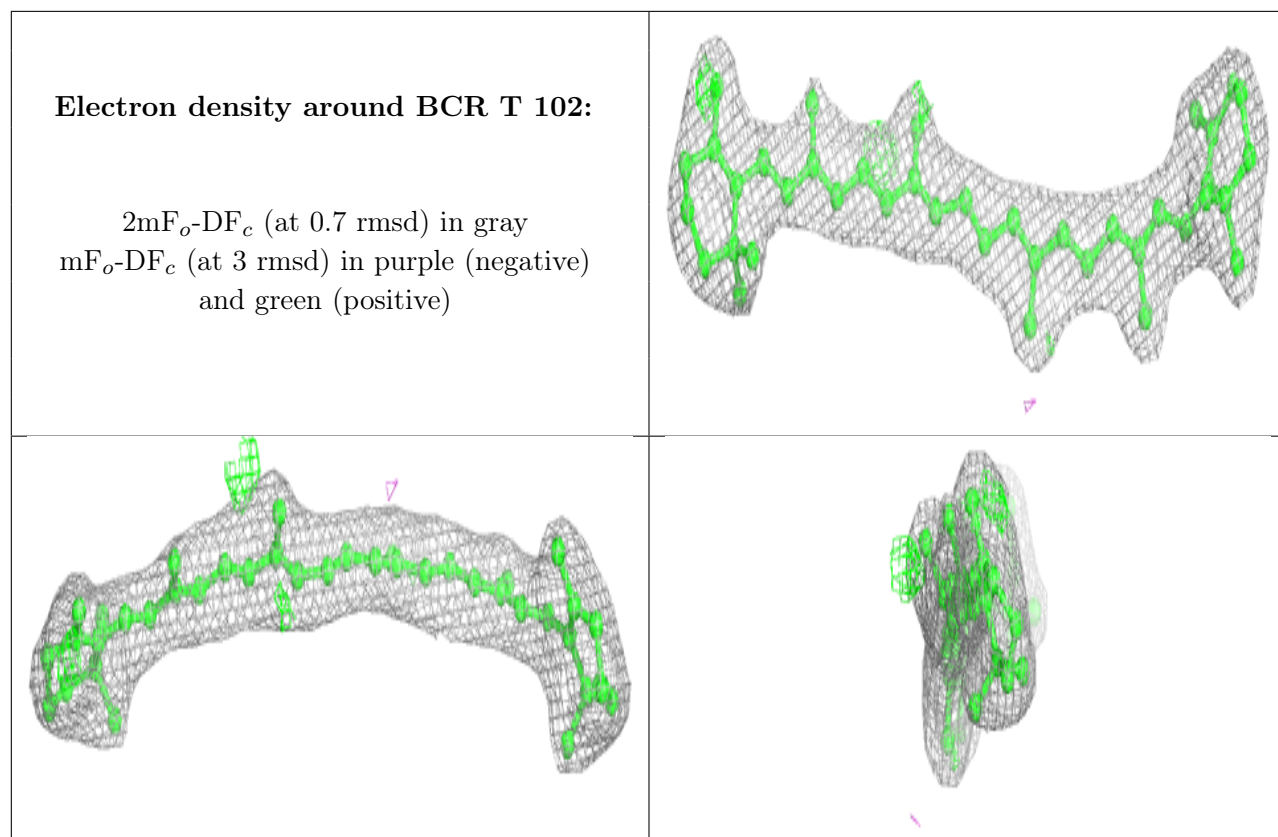




Electron density around CLA b 615:

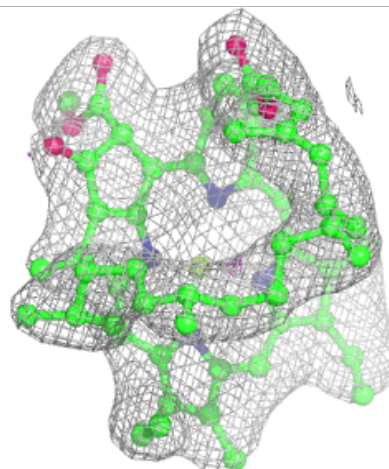
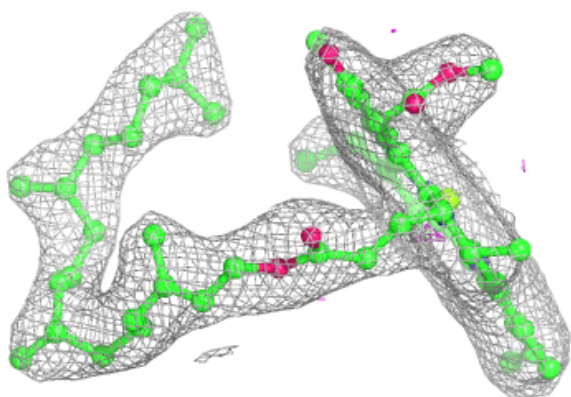
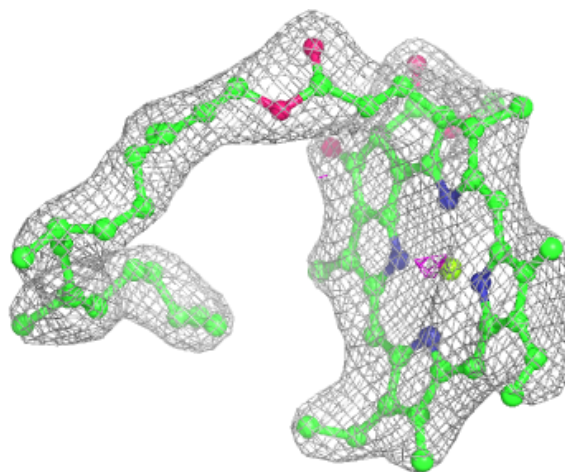
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





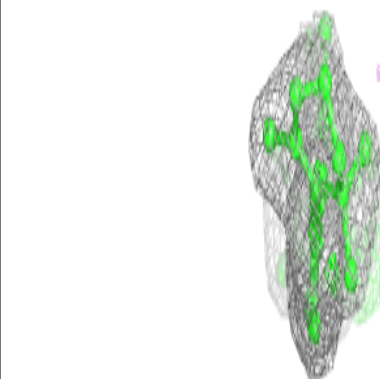
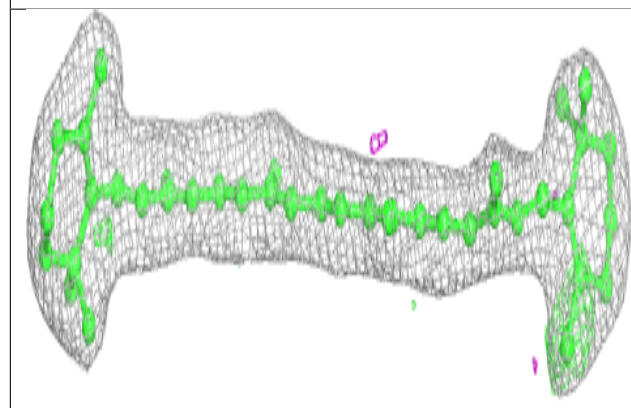
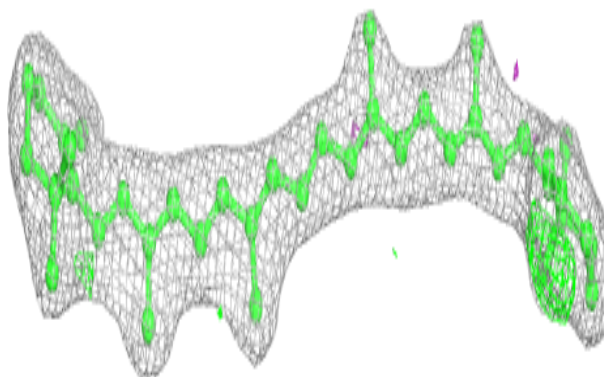
Electron density around CLA C 504:

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

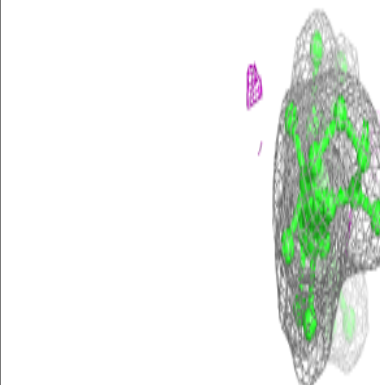
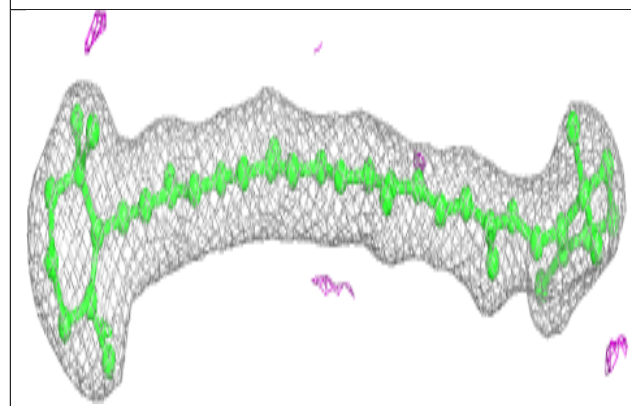
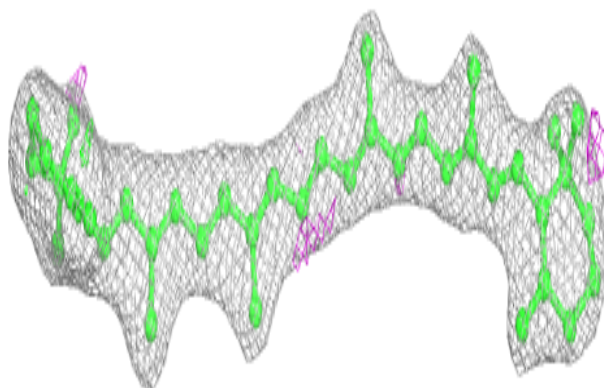


Electron density around BCR a 408:

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

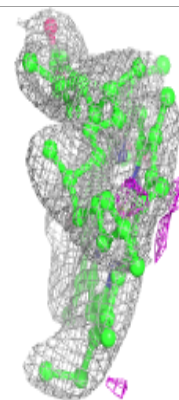
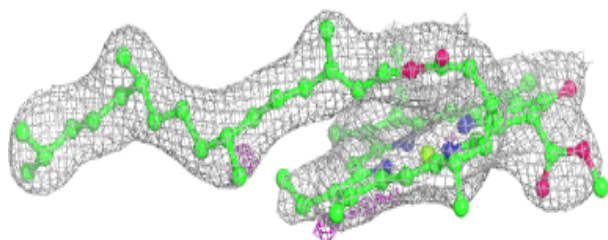
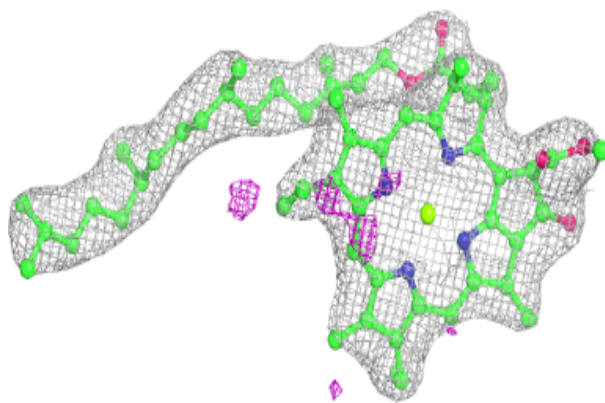
**Electron density around BCR b 617:**

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

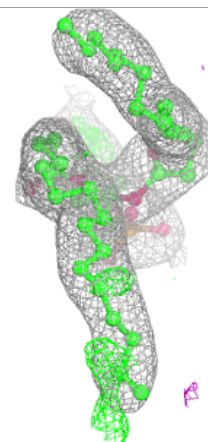
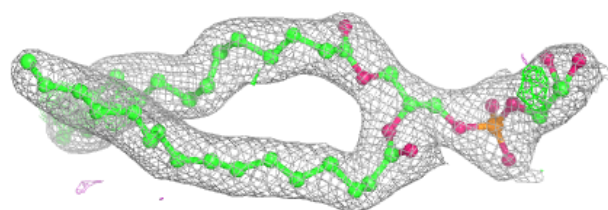
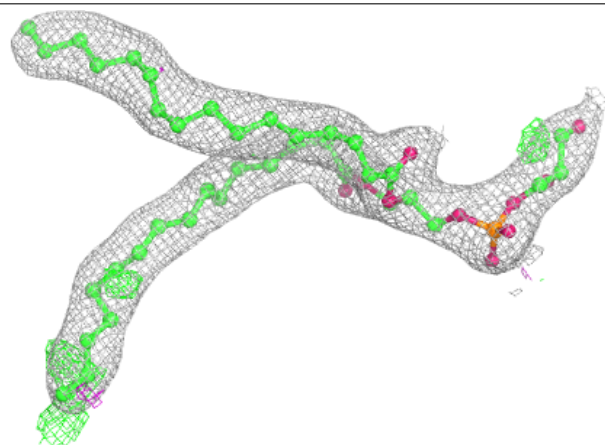


Electron density around CLA c 501:

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

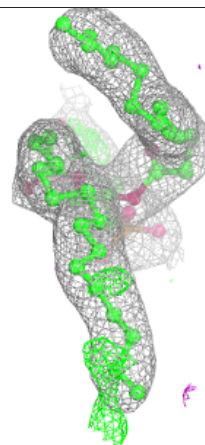
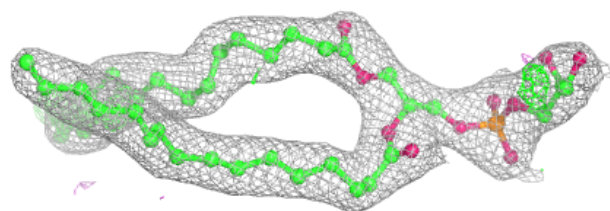
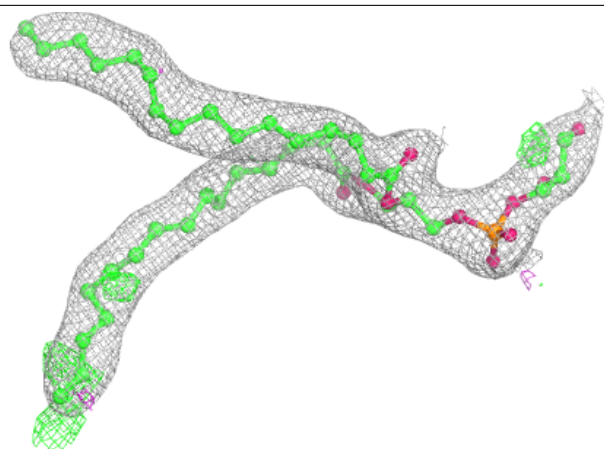
**Electron density around LHG d 407 (A):**

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

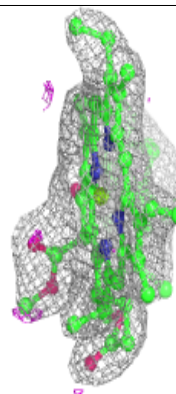
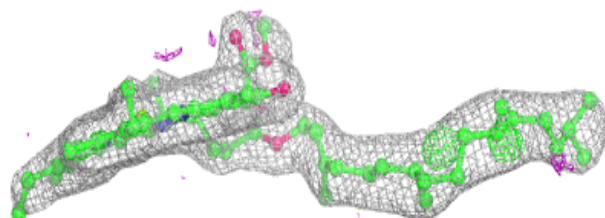
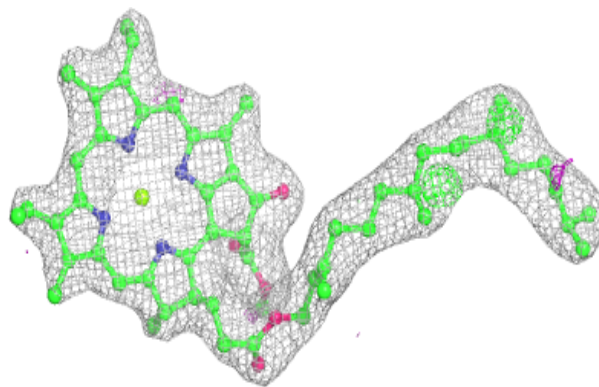


Electron density around LHG d 407 (B):

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

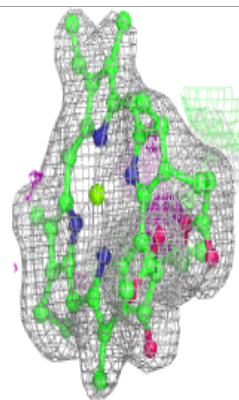
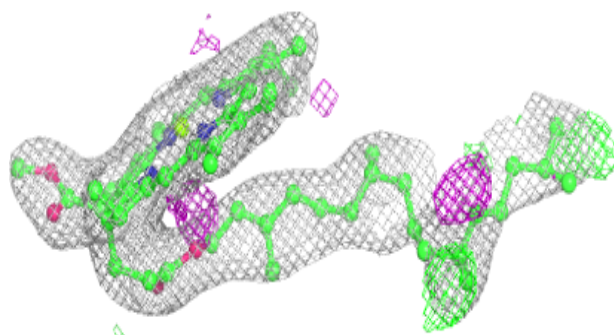
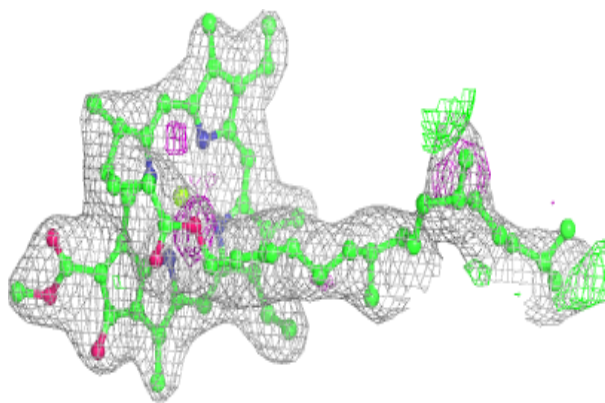
**Electron density around CLA B 602:**

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

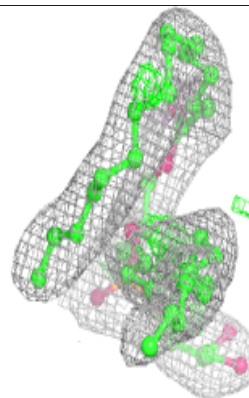
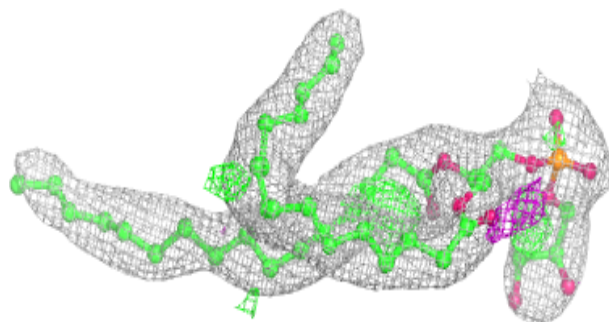
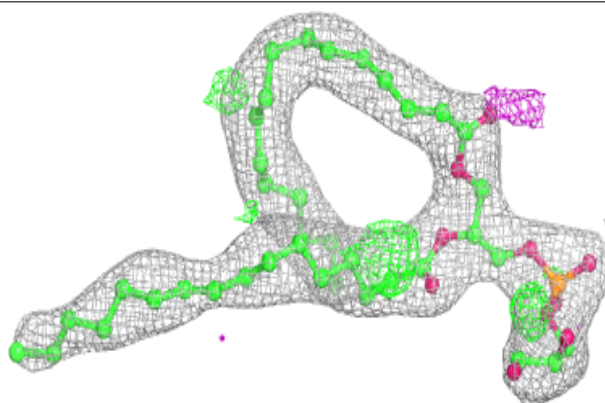


Electron density around CLA B 614:

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

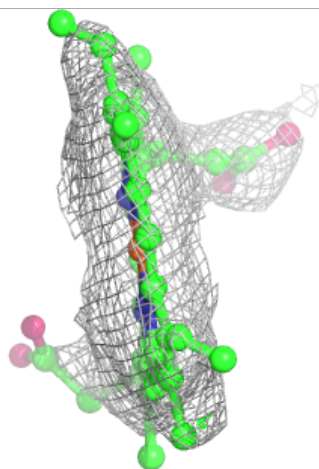
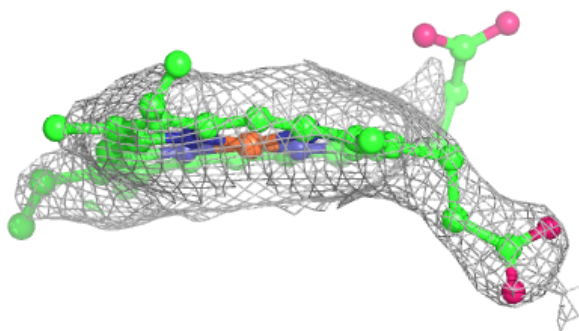
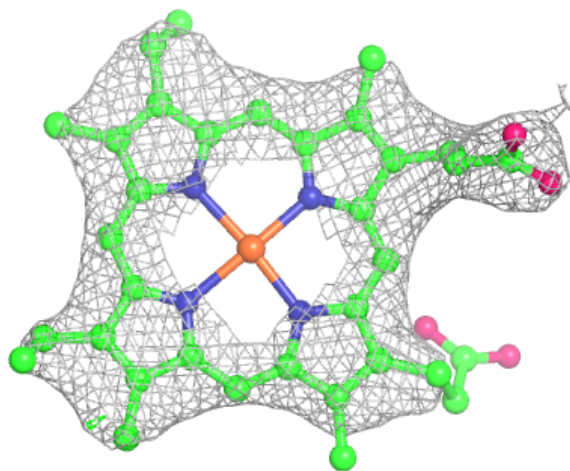
**Electron density around LHG d 414 (A):**

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



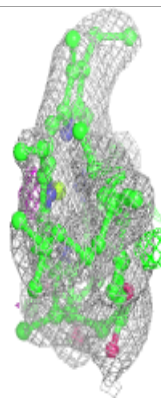
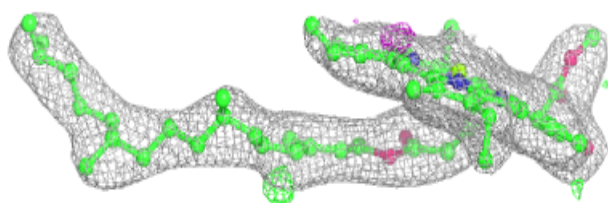
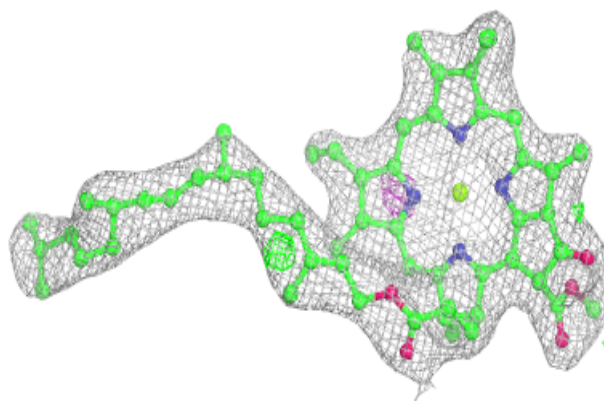
Electron density around HEM f 101:

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

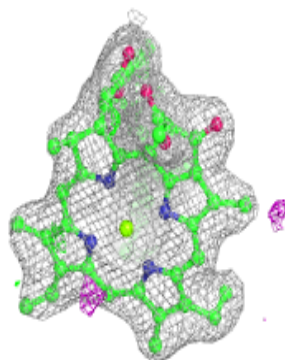
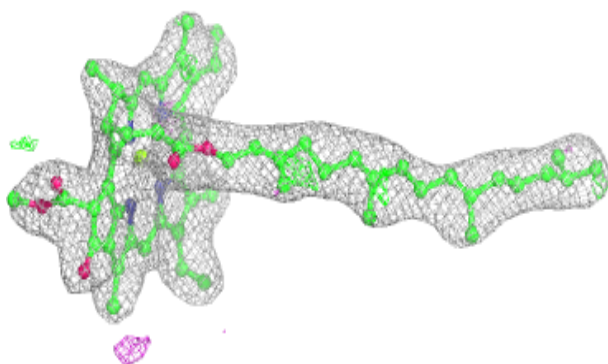
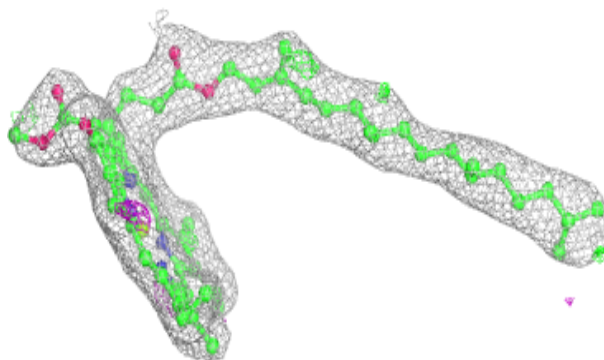


Electron density around CLA b 603:

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

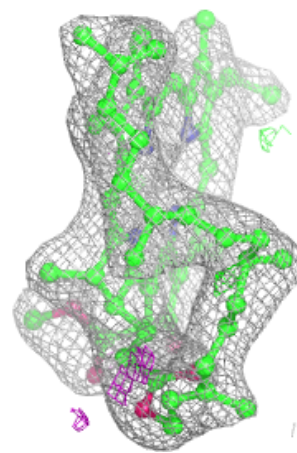
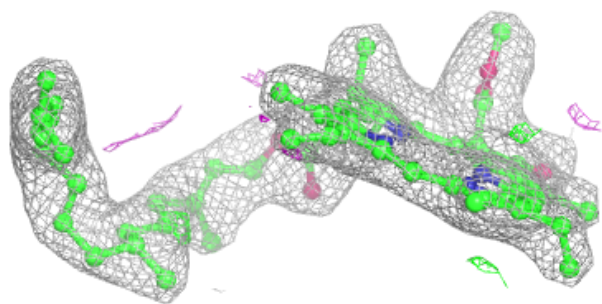
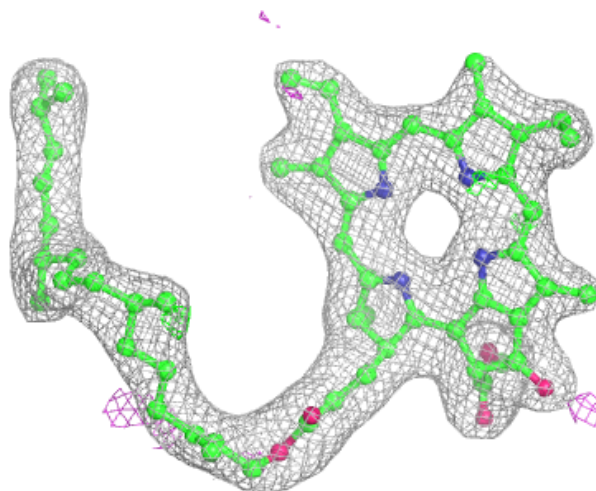
**Electron density around CLA B 607:**

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



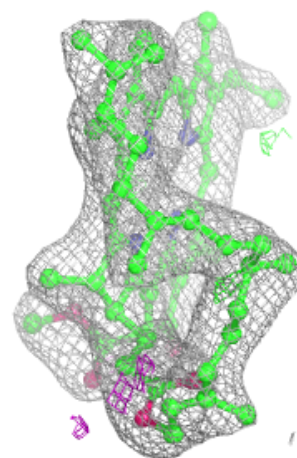
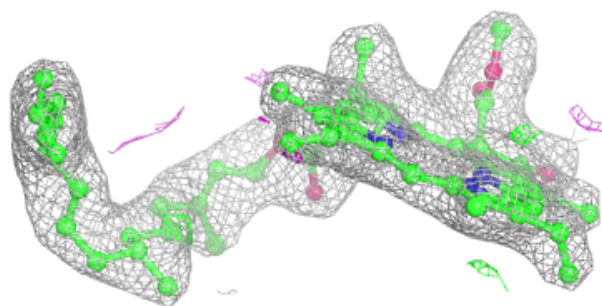
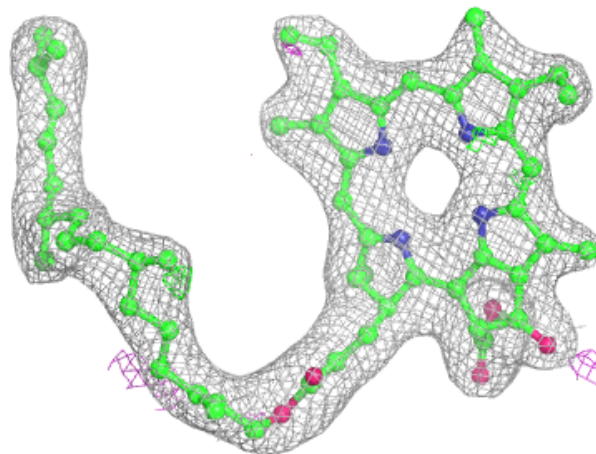
Electron density around PHO A 416 (A):

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



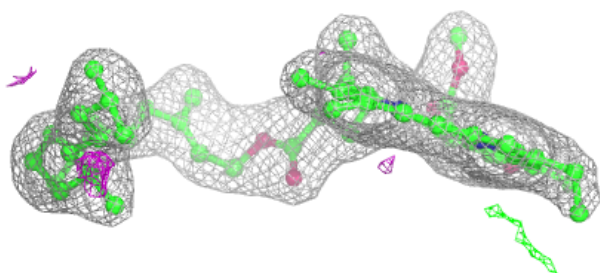
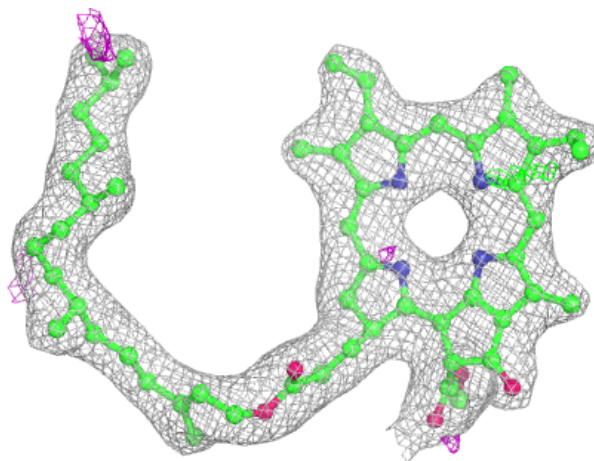
Electron density around PHO A 416 (B):

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



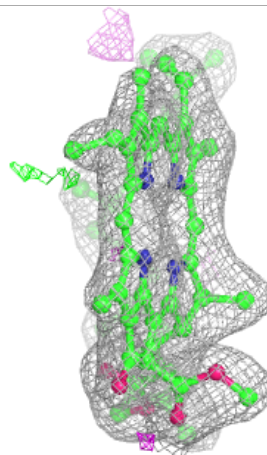
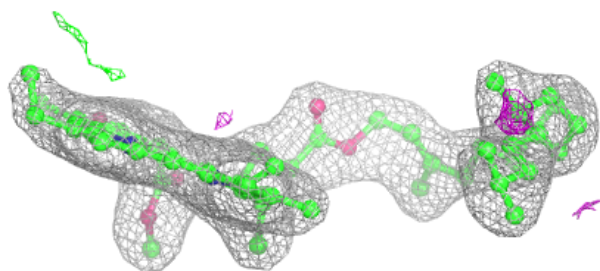
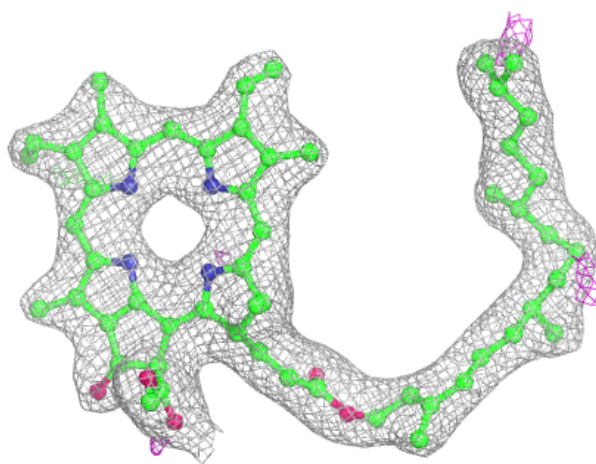
Electron density around PHO a 406 (A):

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



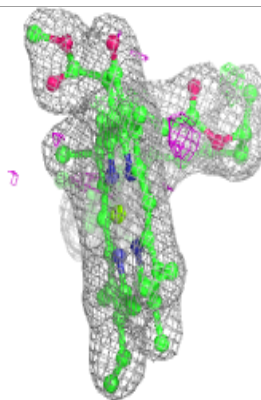
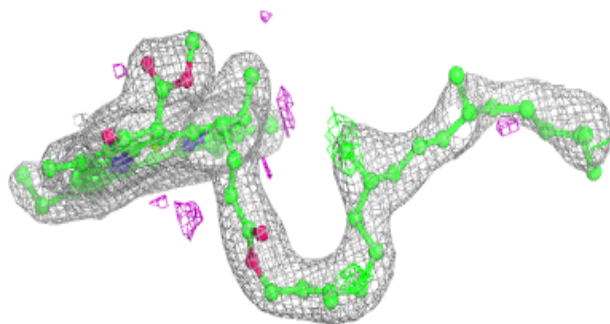
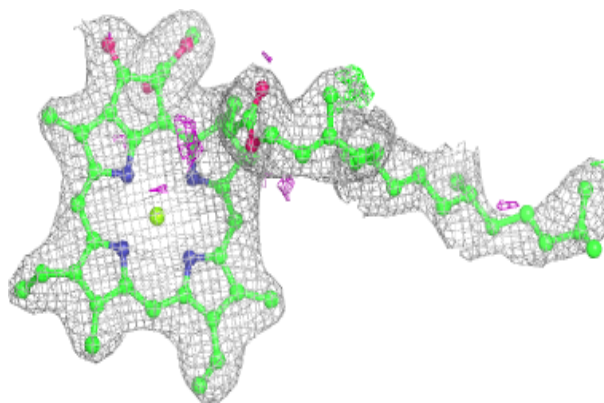
Electron density around PHO a 406 (B):

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



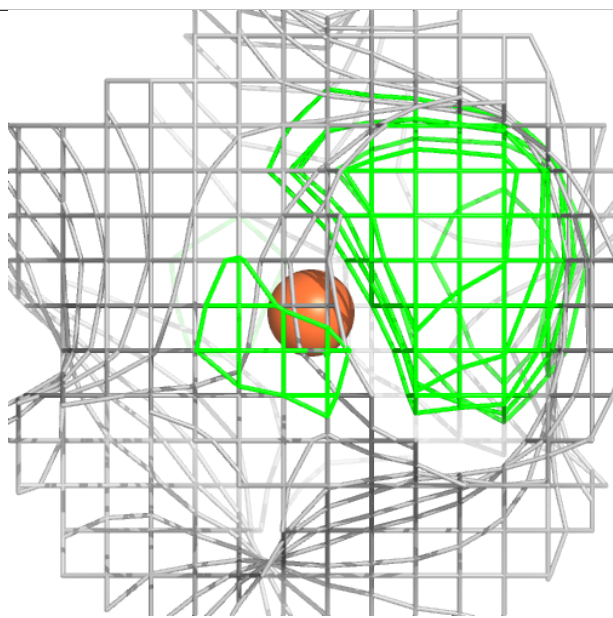
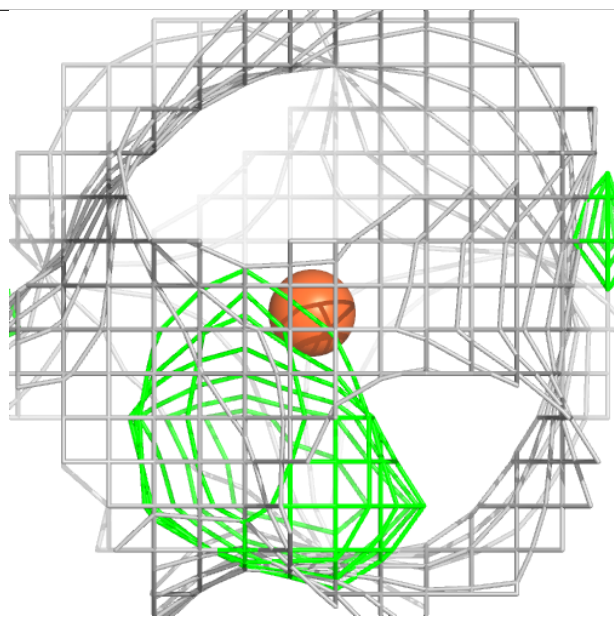
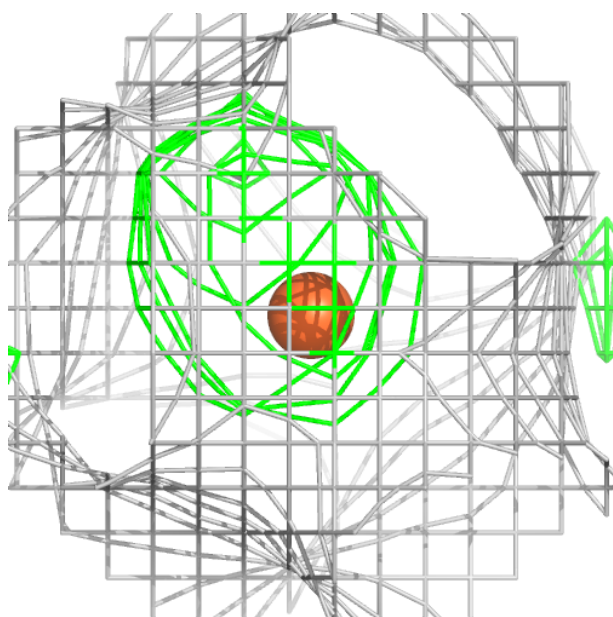
Electron density around CLA A 406 (B):

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



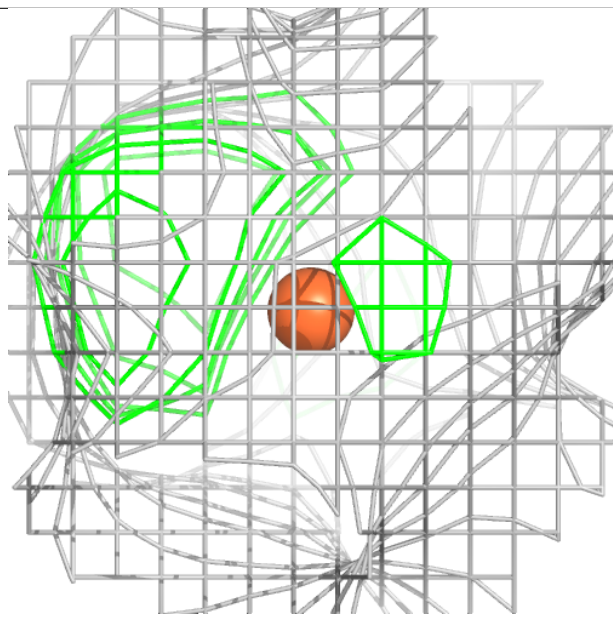
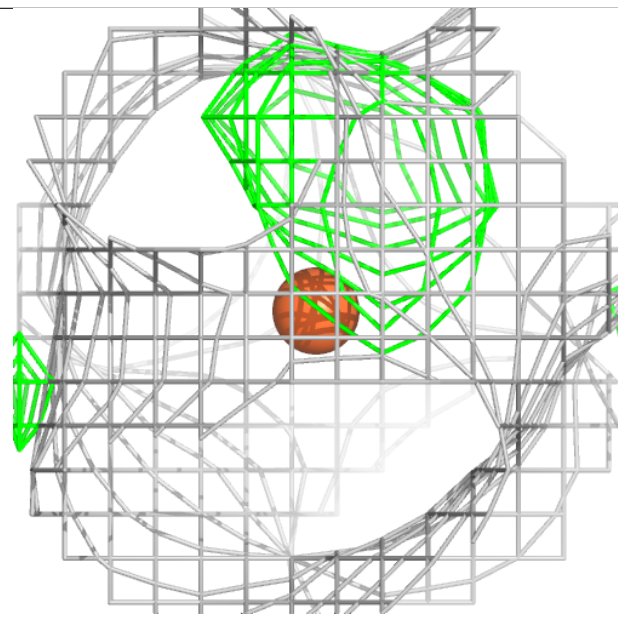
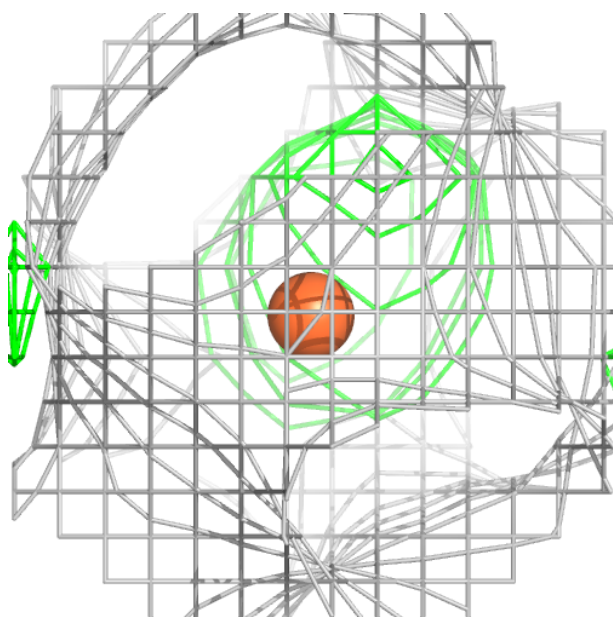
Electron density around FE2 a 401 (A):

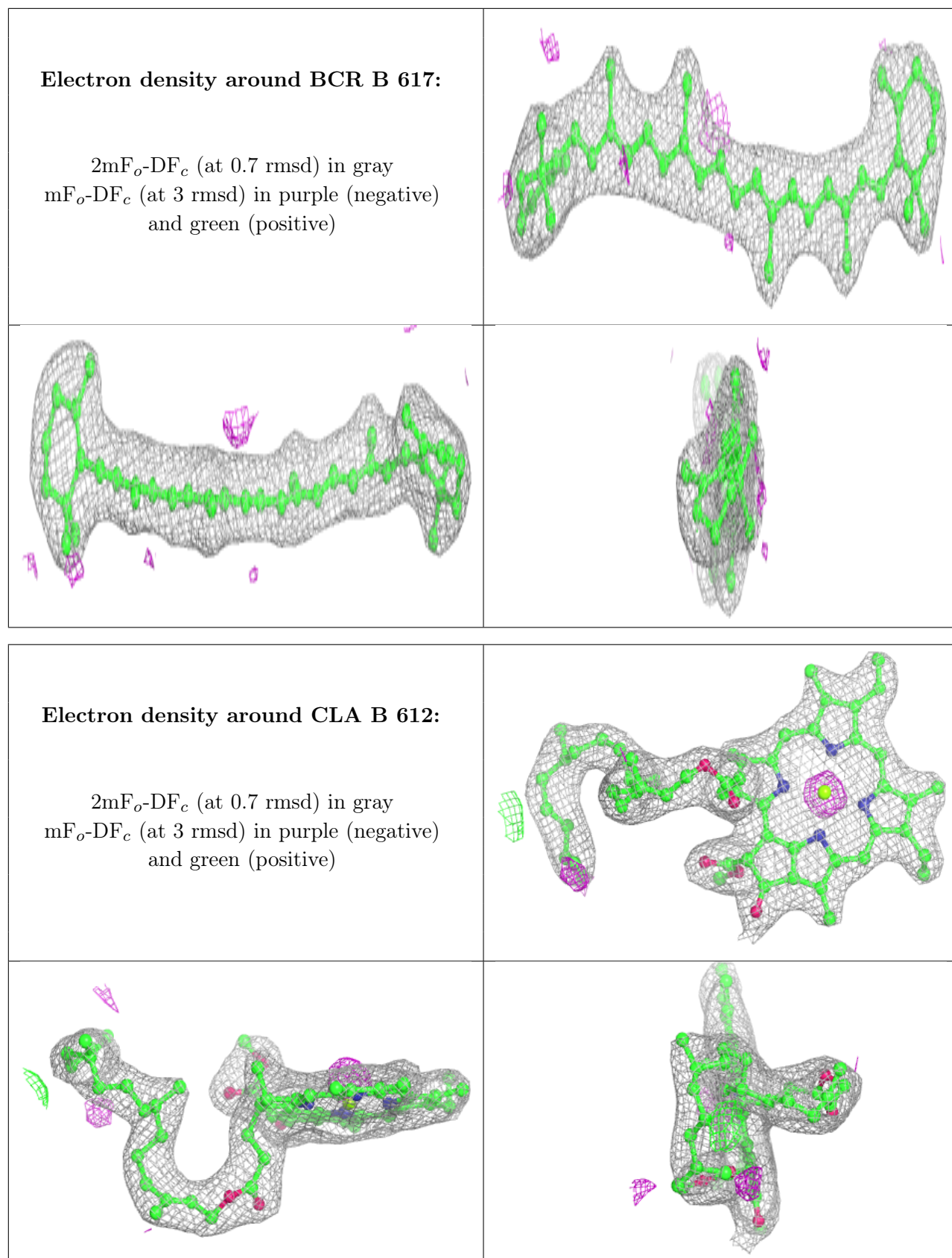
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FE2 a 401 (B):

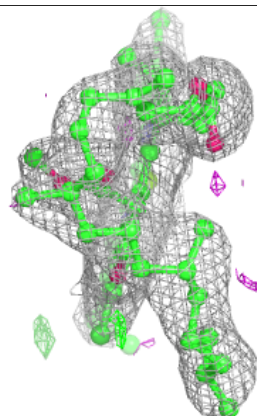
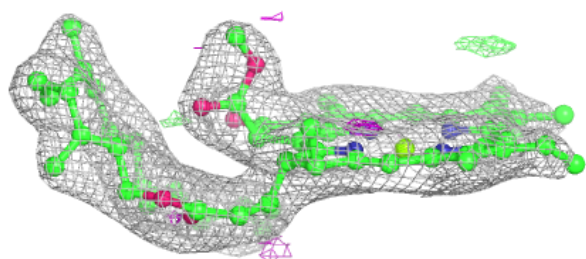
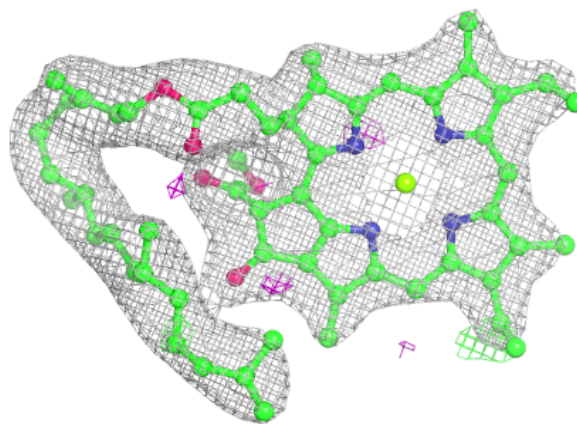
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





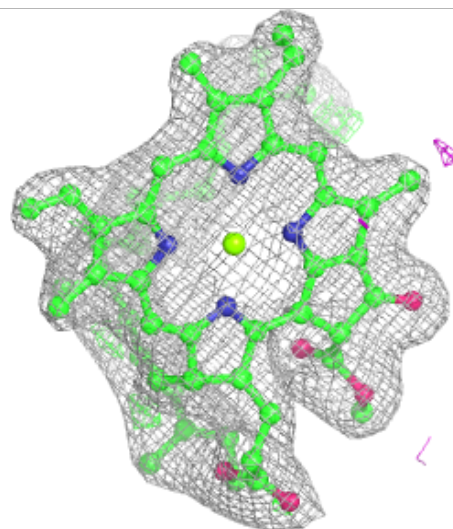
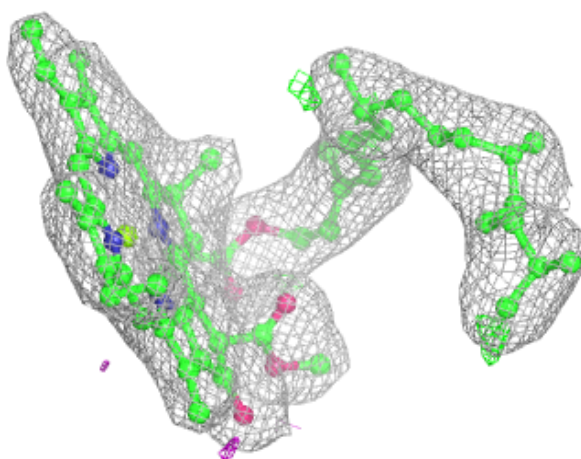
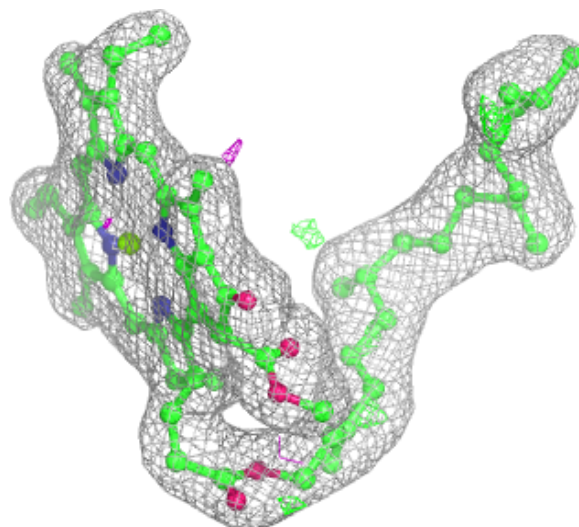
Electron density around CLA b 610:

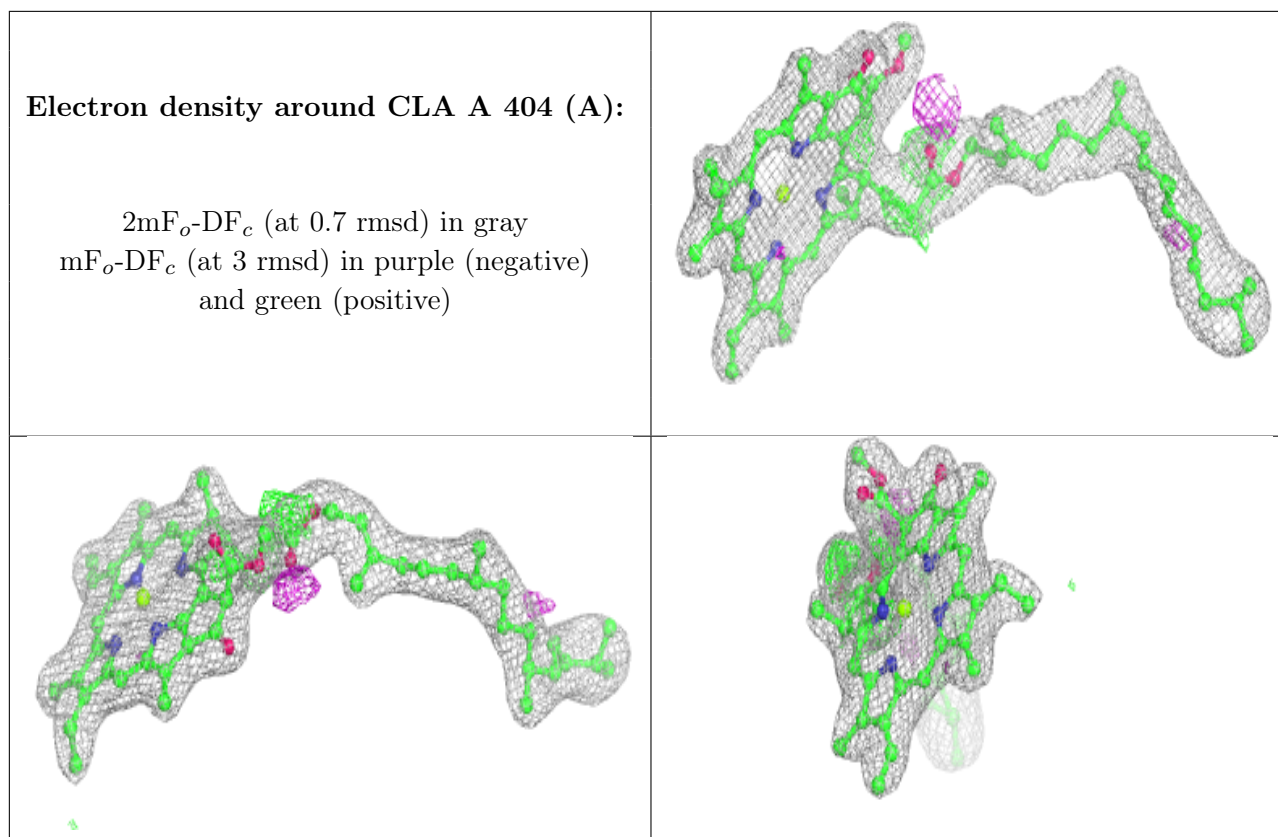
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

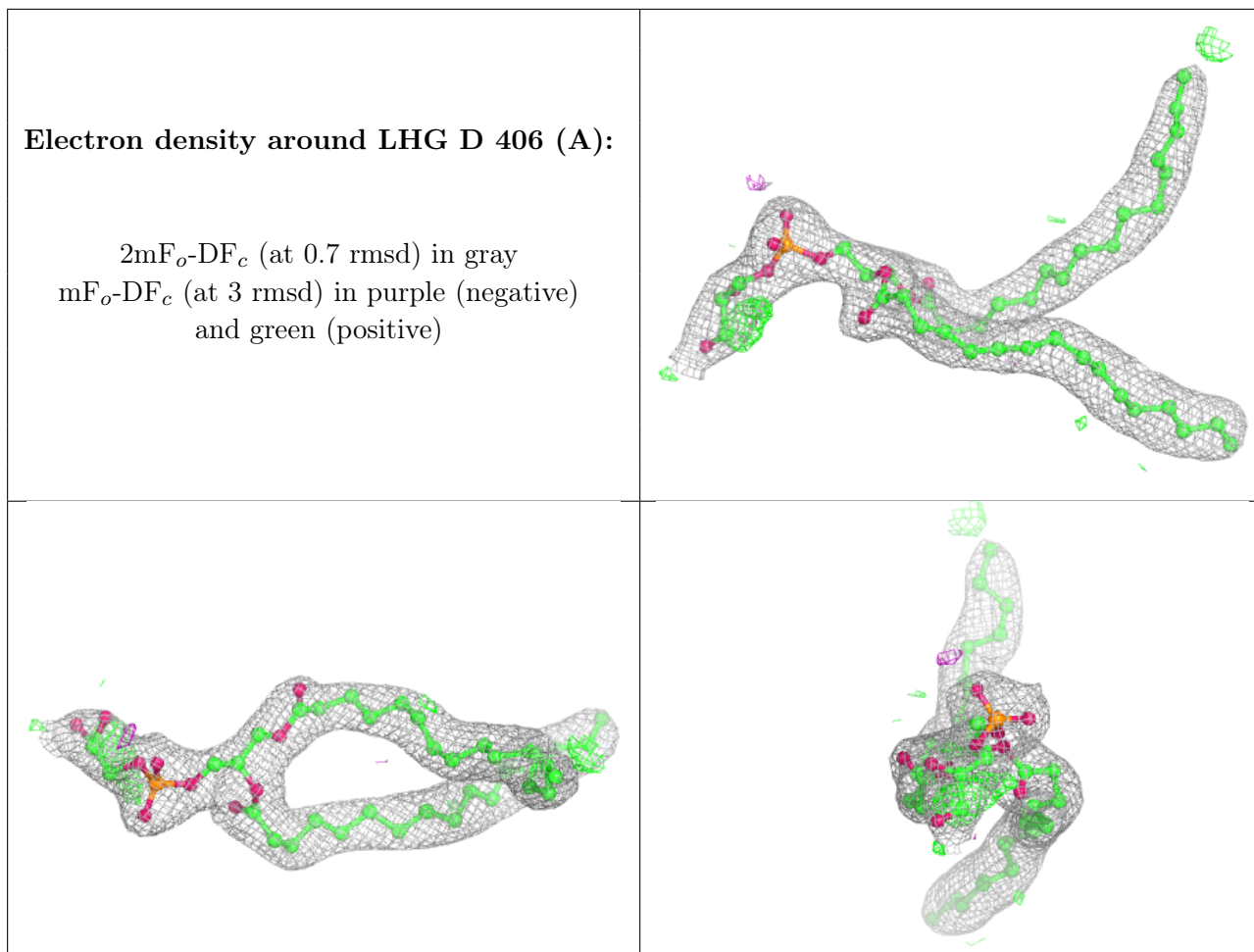


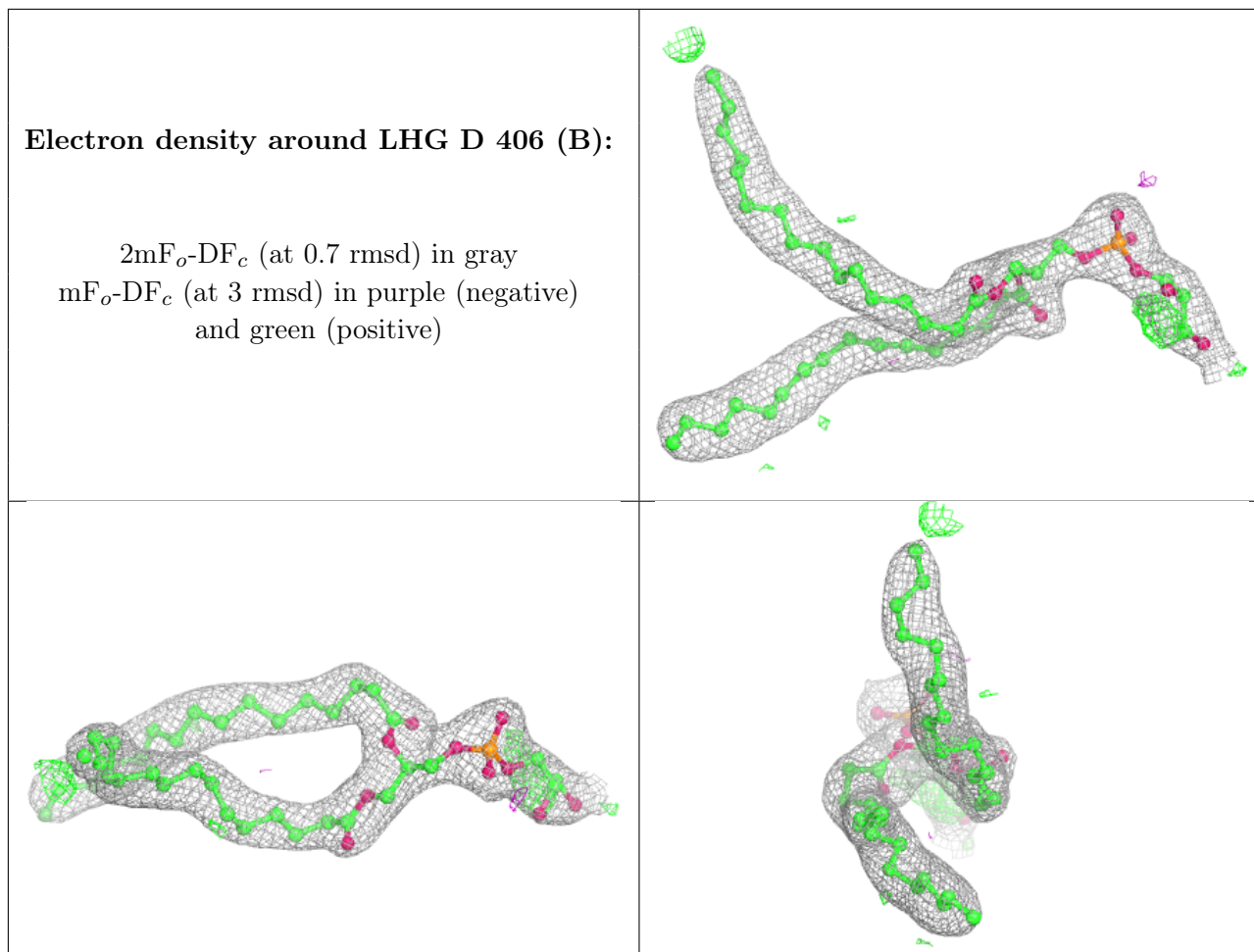
Electron density around CLA B 613:

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



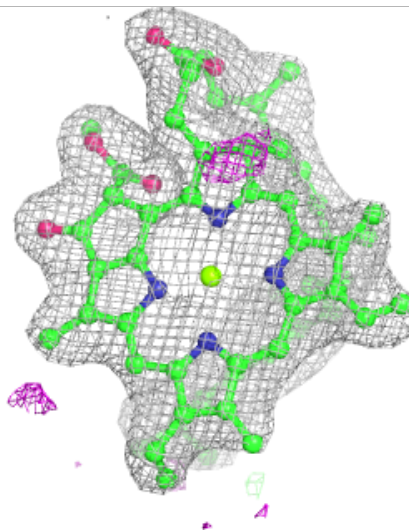
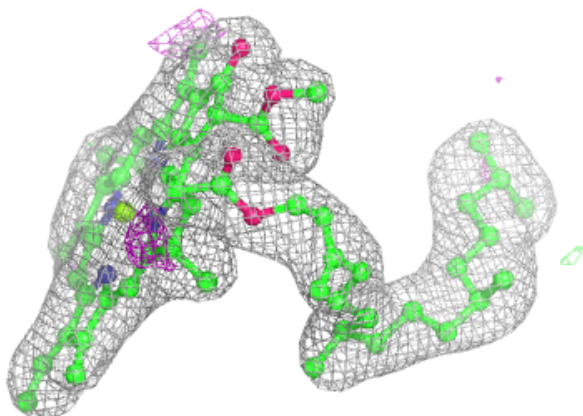
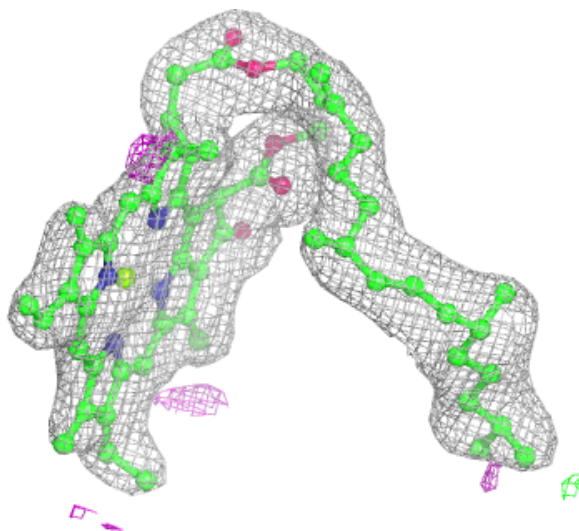






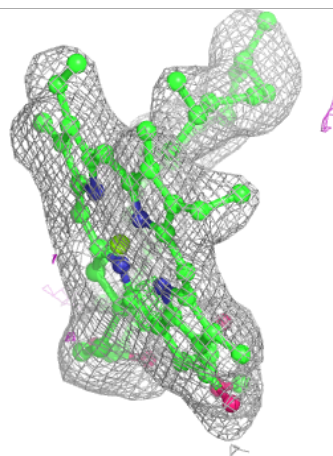
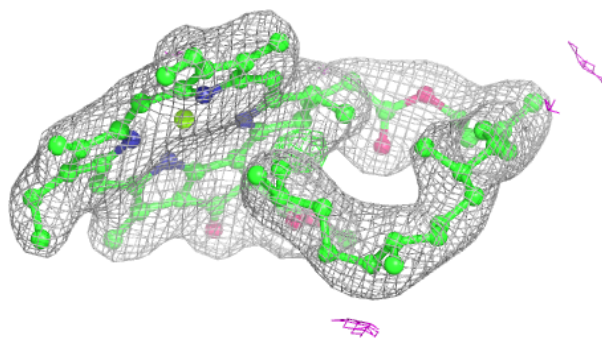
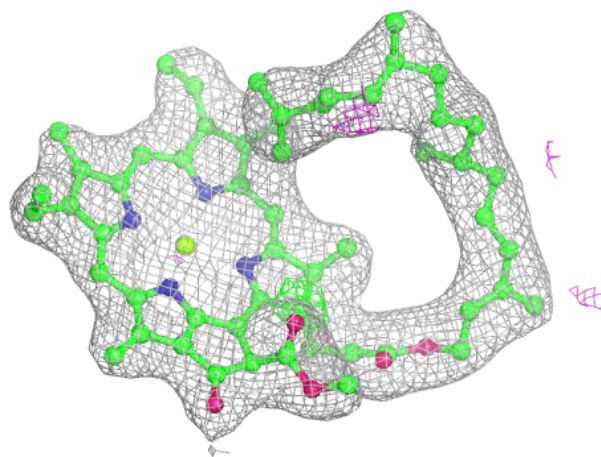
Electron density around CLA b 613:

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



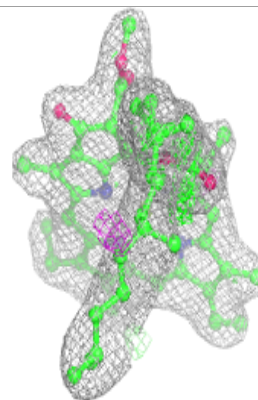
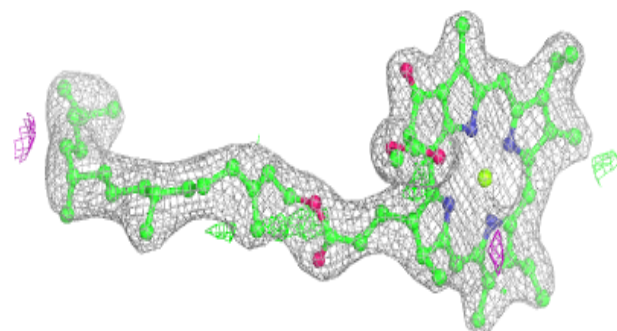
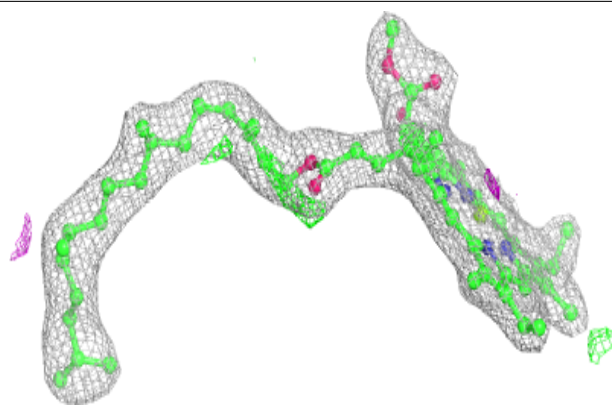
Electron density around CLA B 615:

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

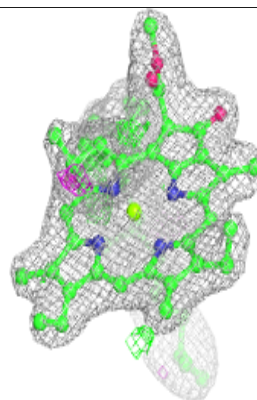
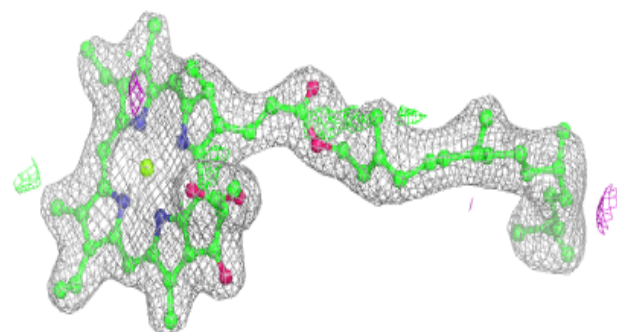
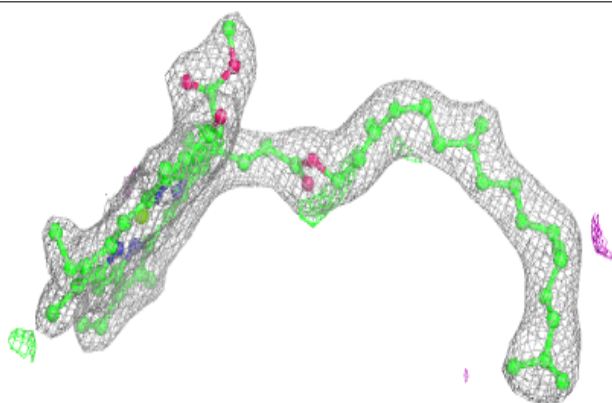


Electron density around CLA D 402 (A):

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

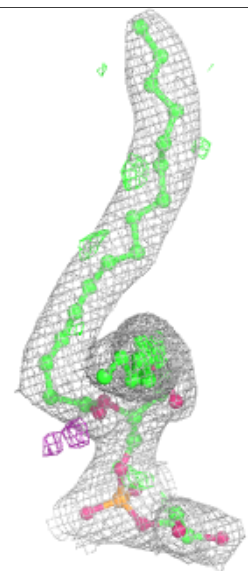
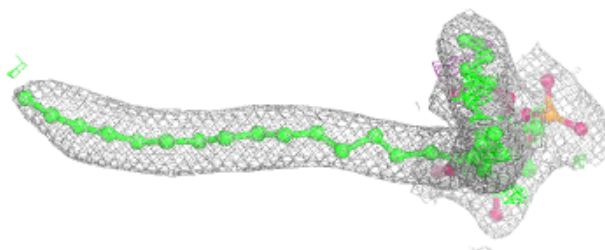
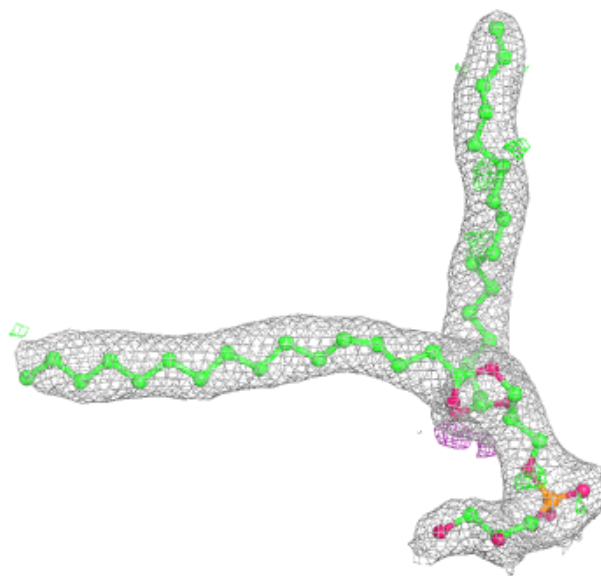
**Electron density around CLA D 402 (B):**

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



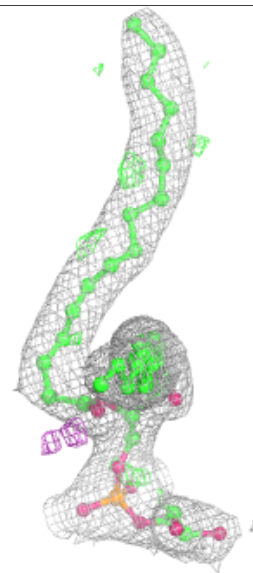
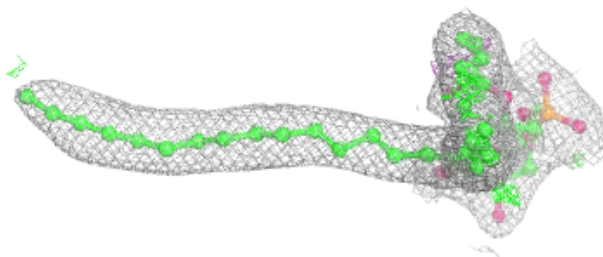
Electron density around LHG L 101 (A):

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



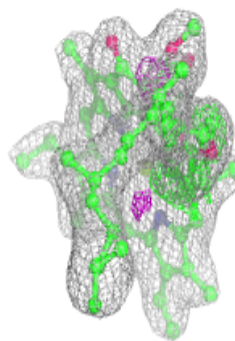
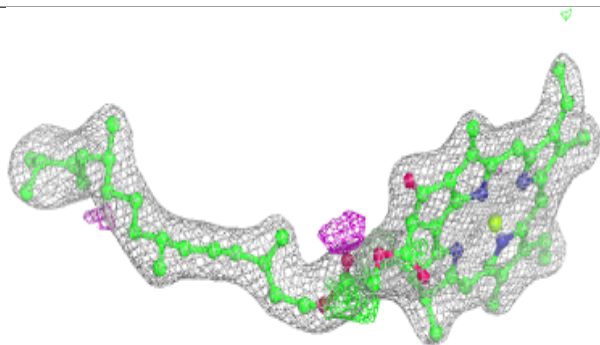
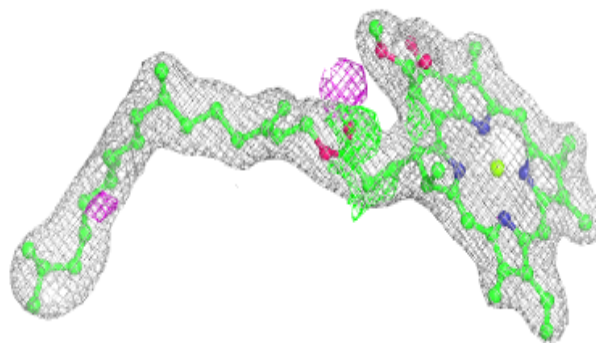
Electron density around LHG L 101 (B):

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

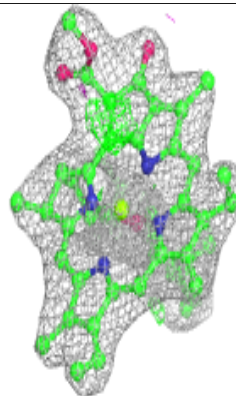
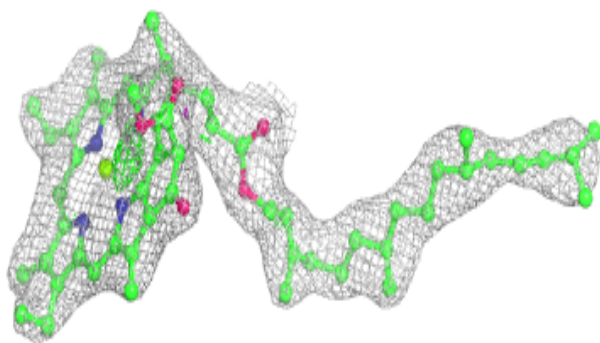
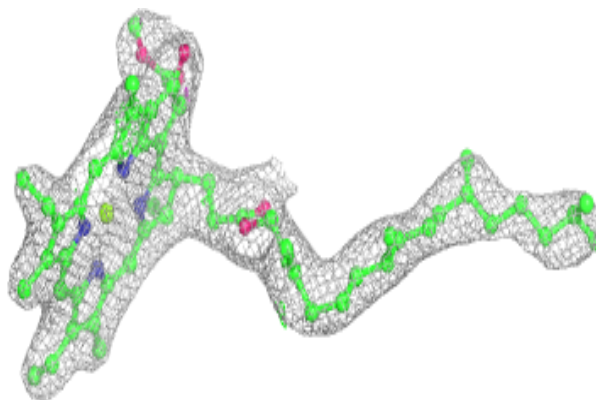


Electron density around CLA A 404 (B):

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

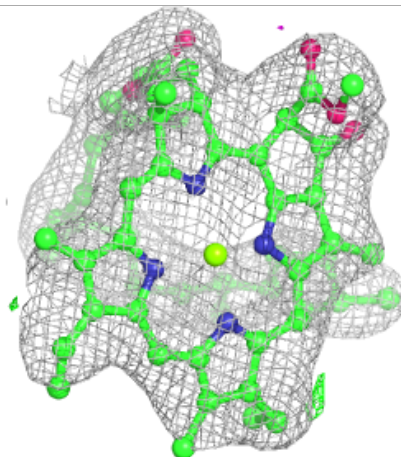
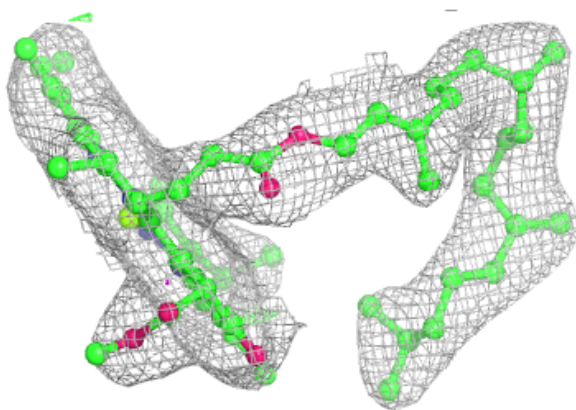
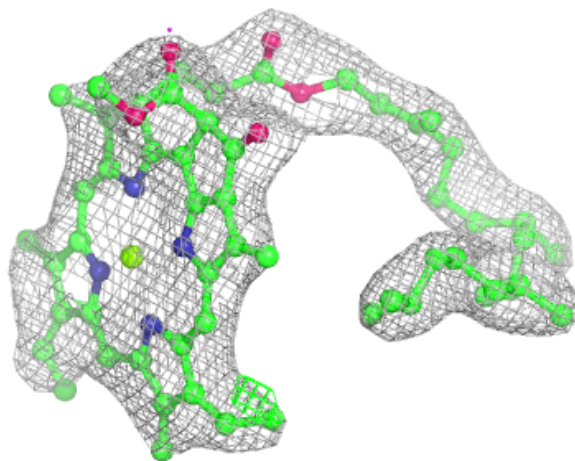
**Electron density around CLA c 502:**

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



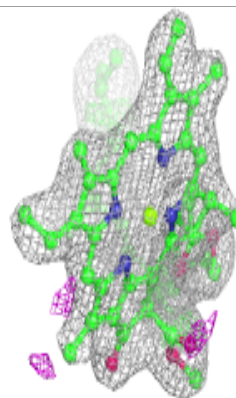
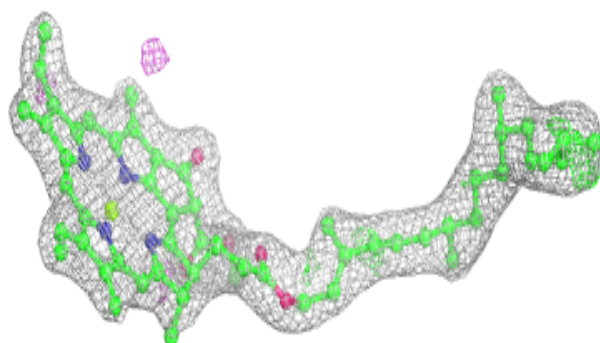
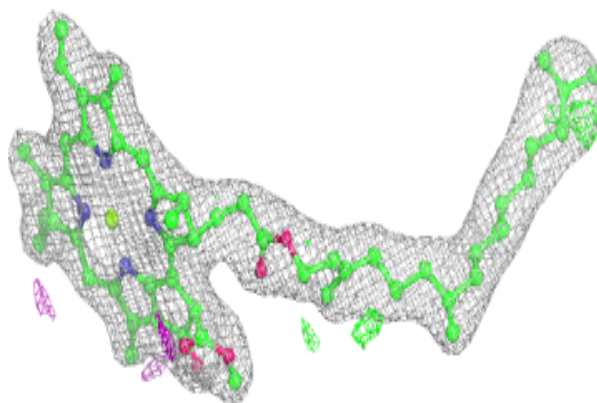
Electron density around CLA c 503:

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

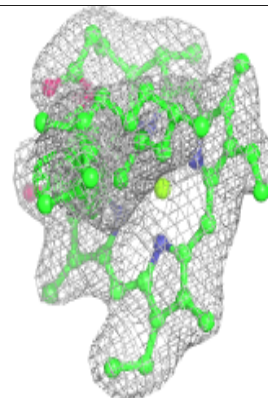
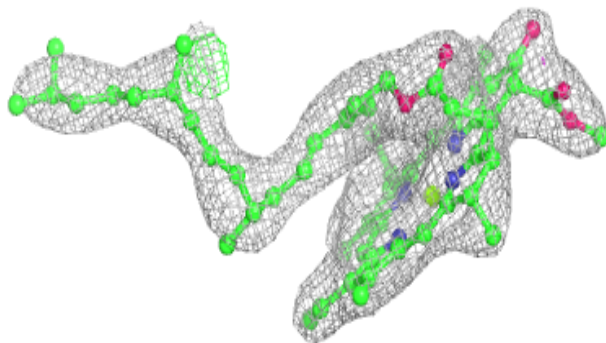
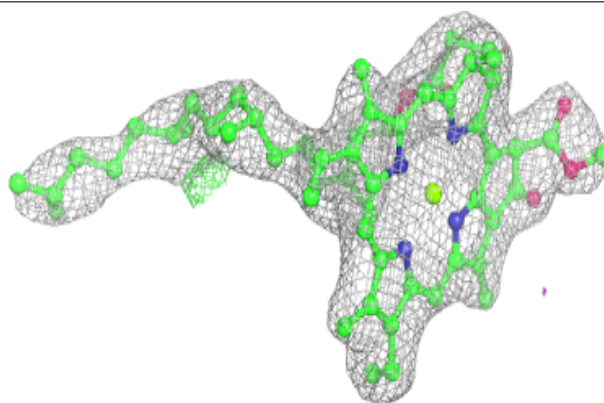


Electron density around CLA a 404 (A):

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

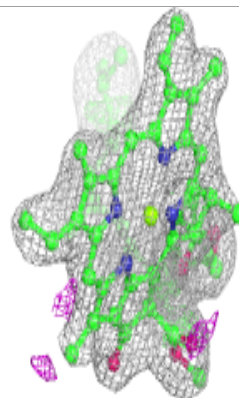
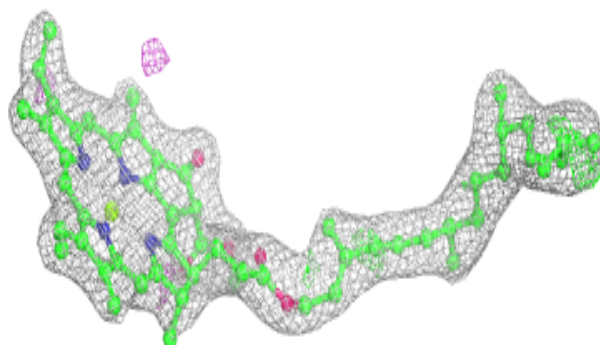
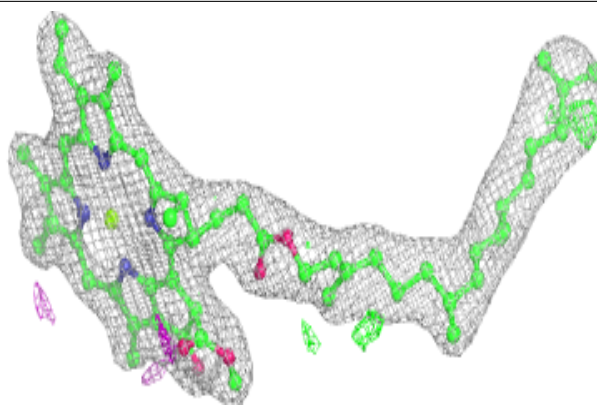
**Electron density around CLA c 505:**

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

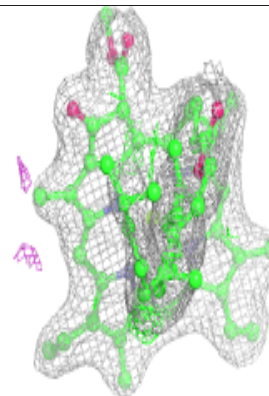
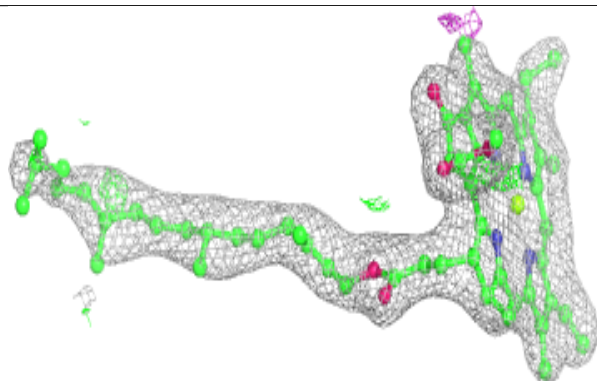
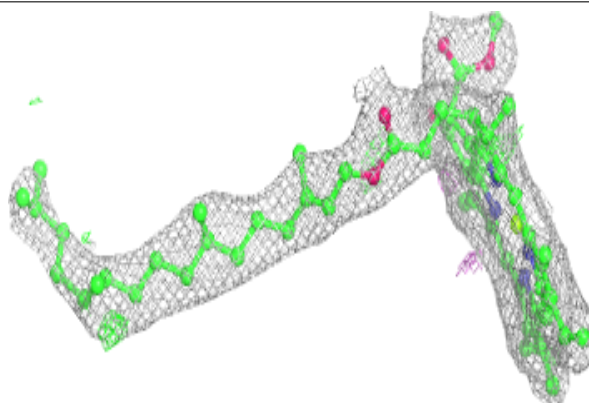


Electron density around CLA a 404 (B):

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

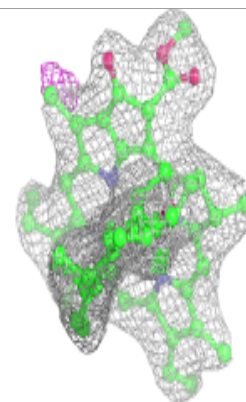
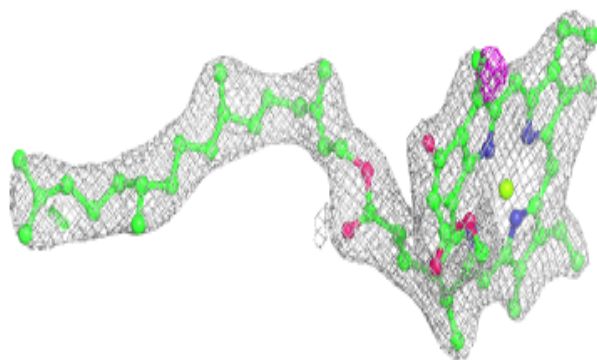
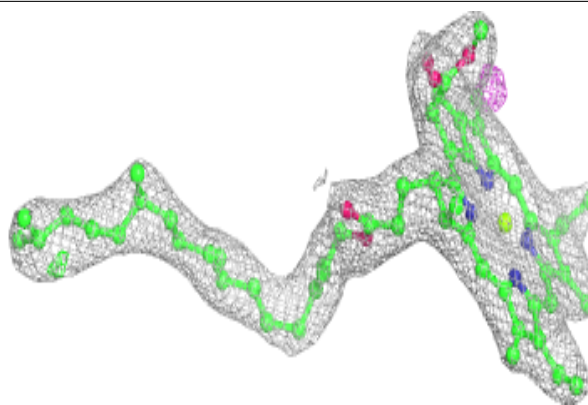
**Electron density around CLA B 604:**

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

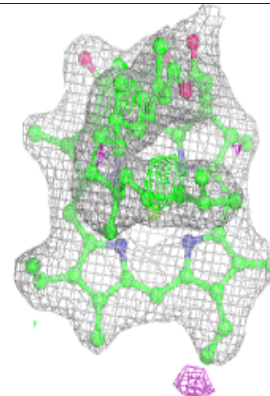
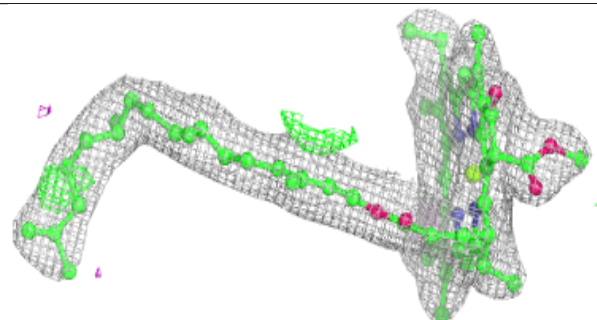
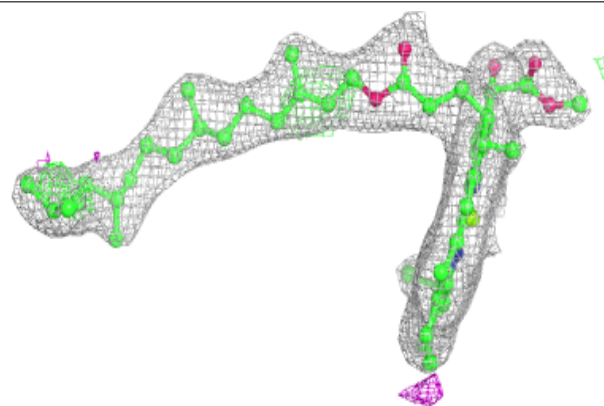


Electron density around CLA C 503:

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

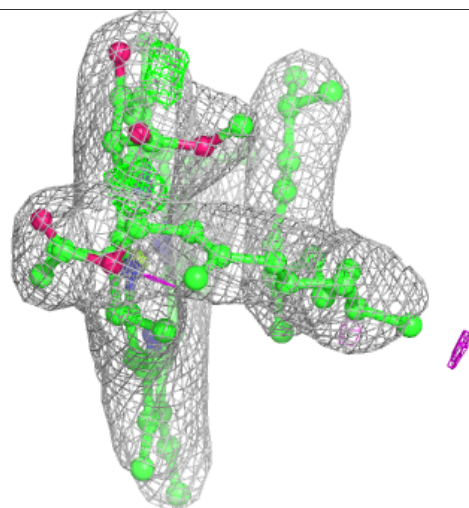
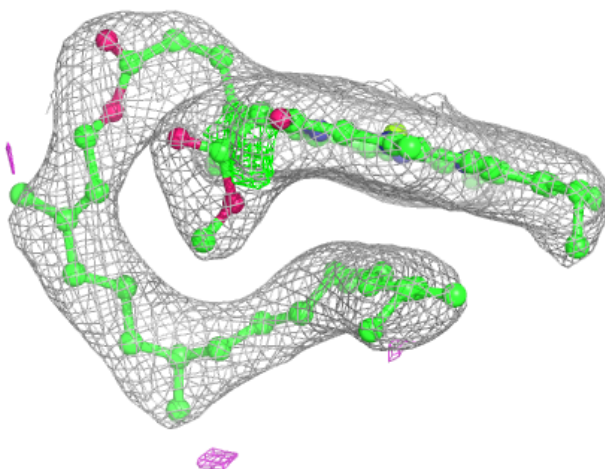
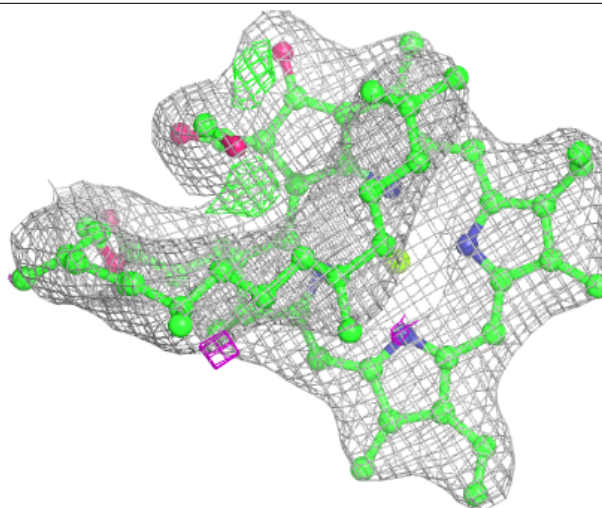
**Electron density around CLA B 605:**

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



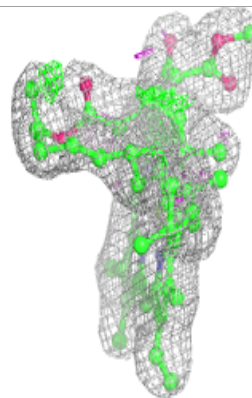
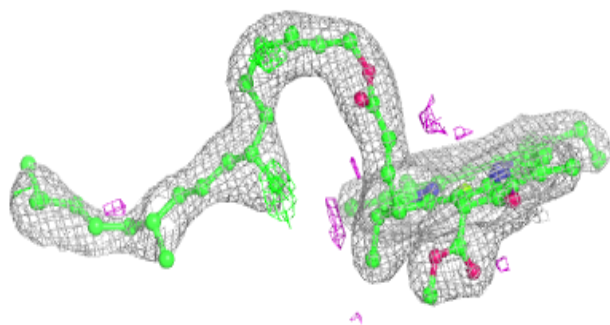
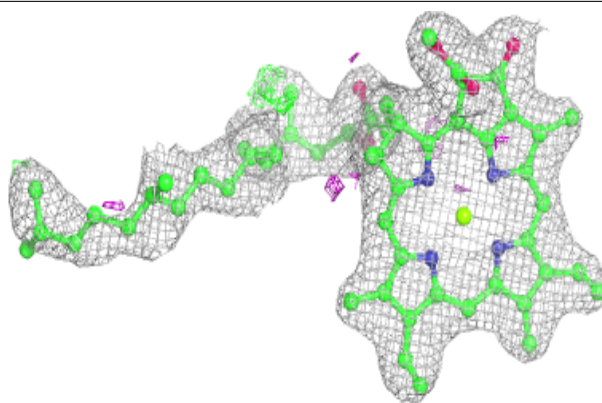
Electron density around CLA c 510:

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

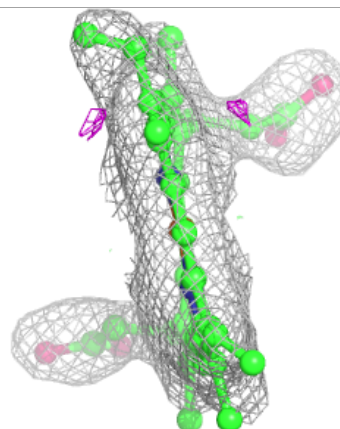
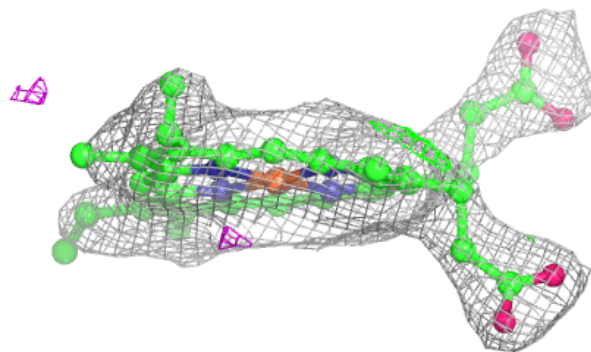
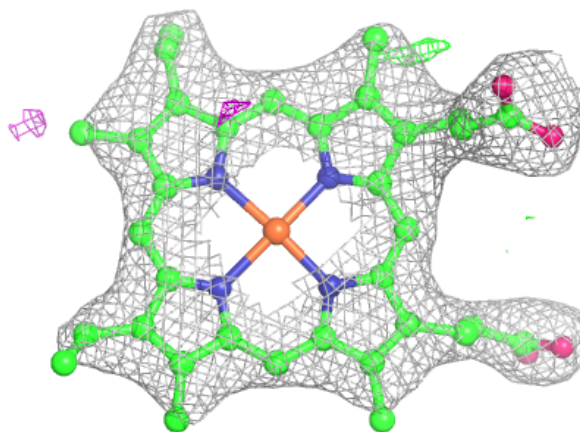


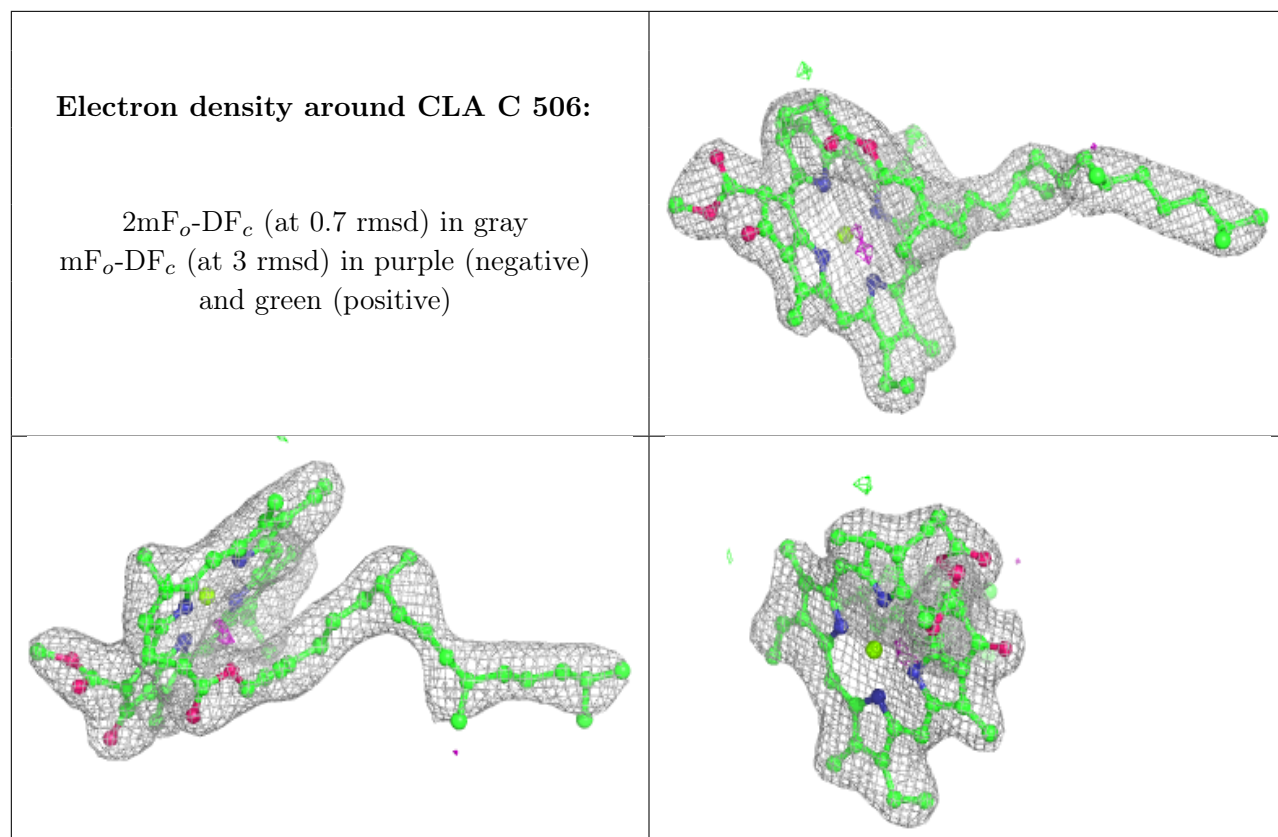
Electron density around CLA A 406 (A):

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

**Electron density around HEM E 102:**

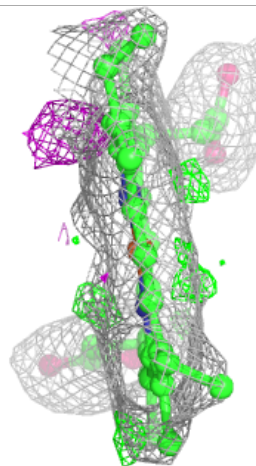
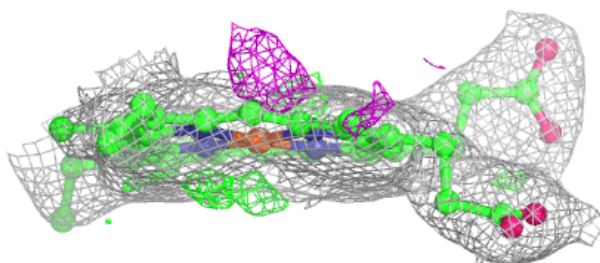
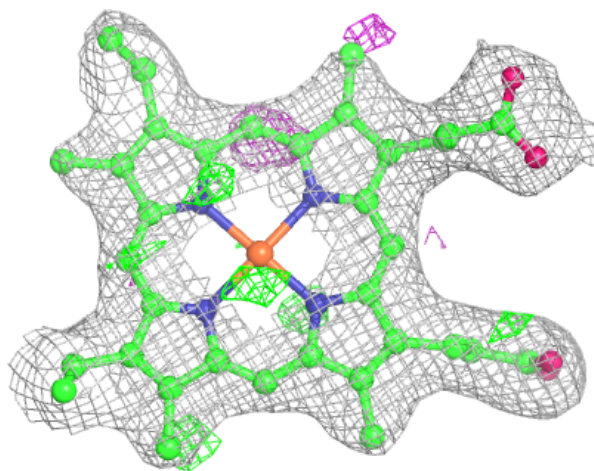
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





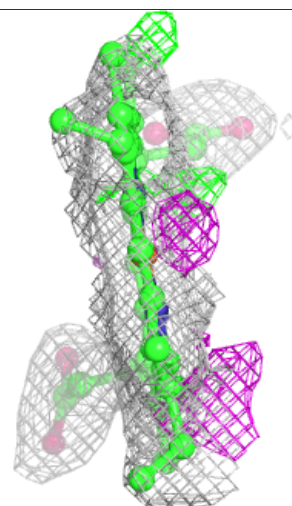
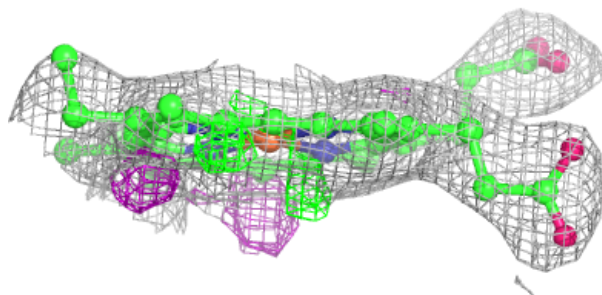
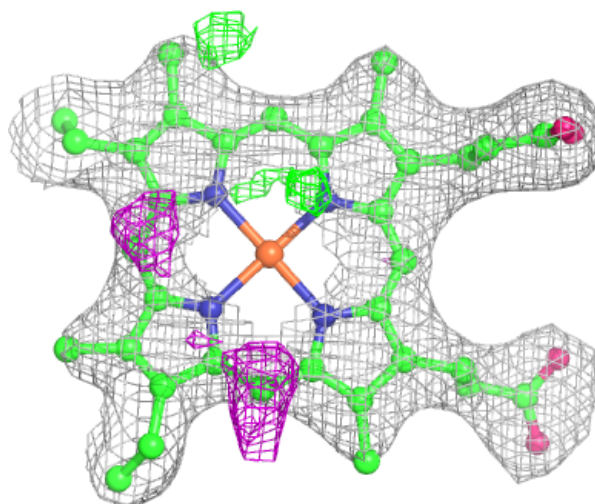
Electron density around HEC V 201:

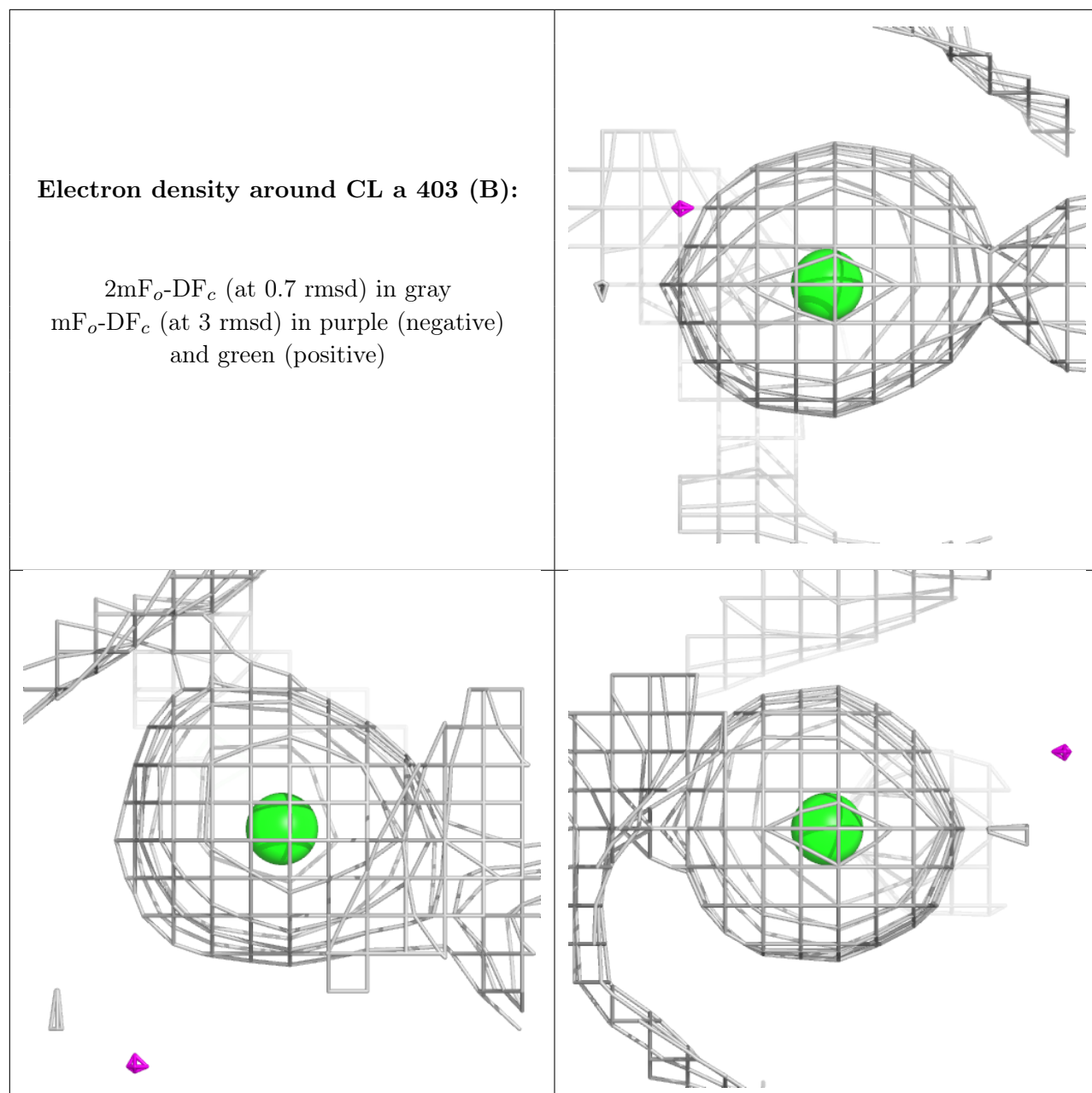
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC v 201:

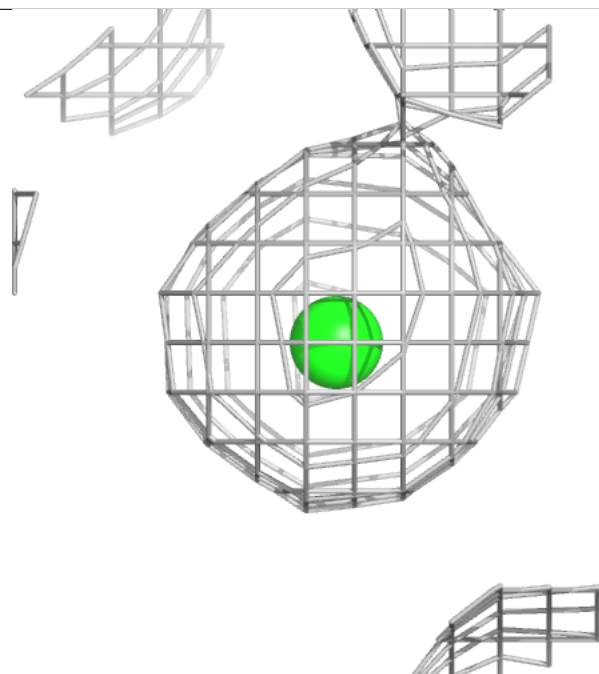
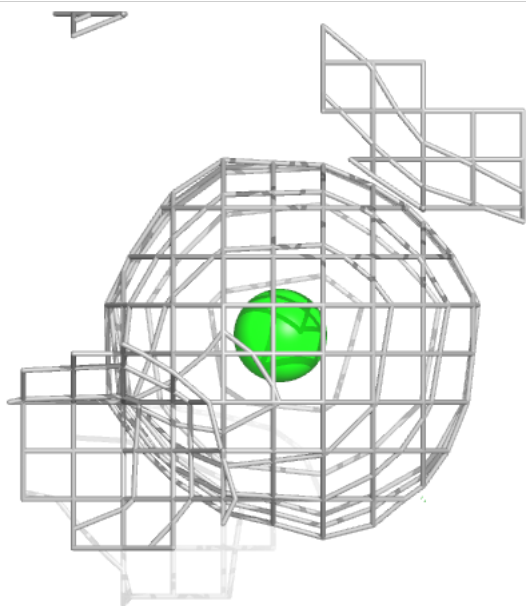
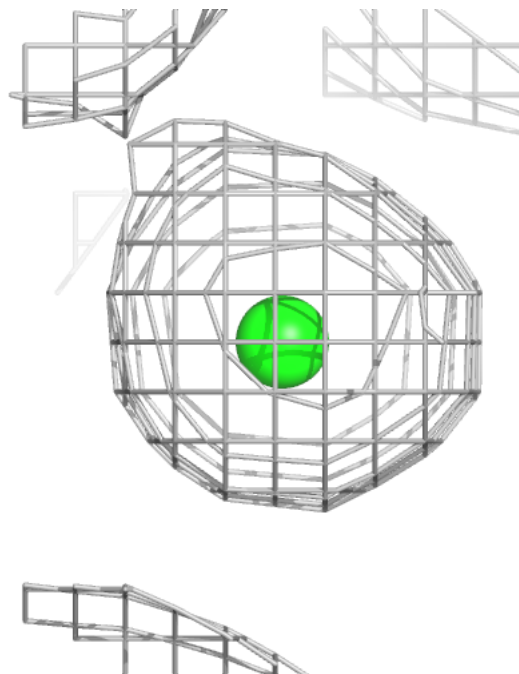
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





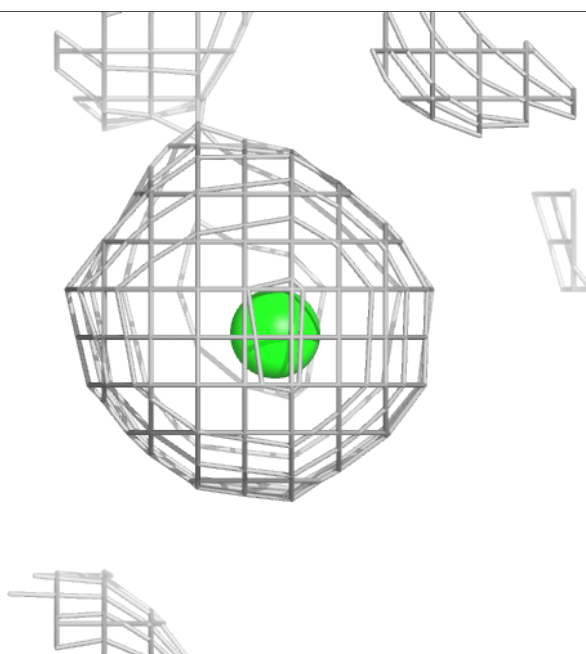
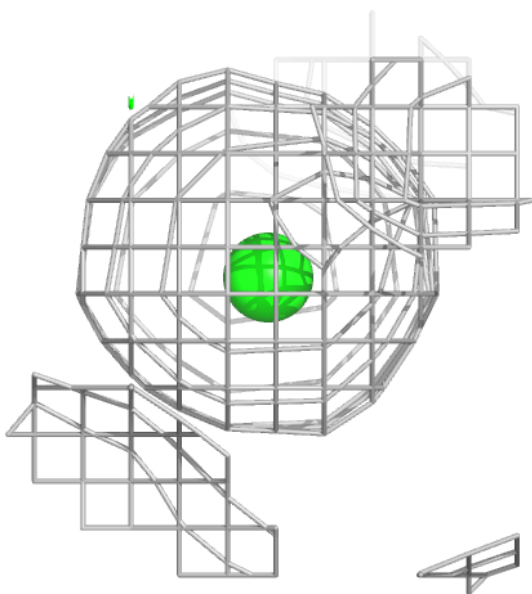
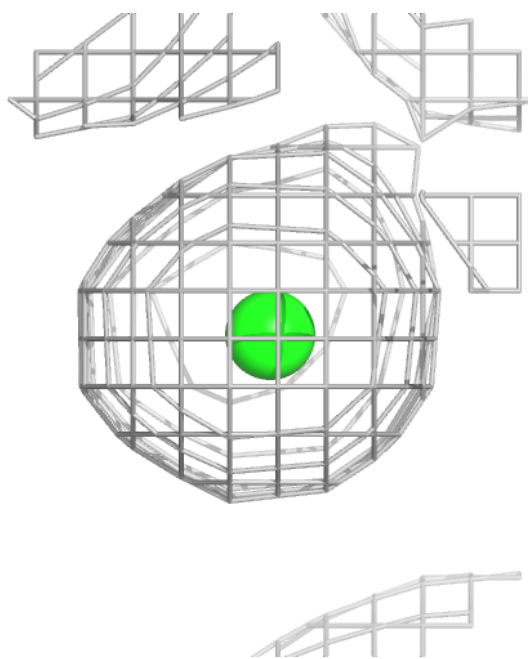
Electron density around CL a 402 (A):

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



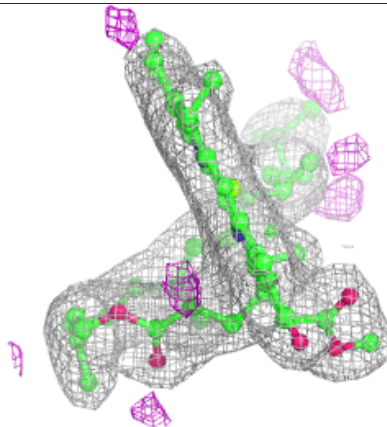
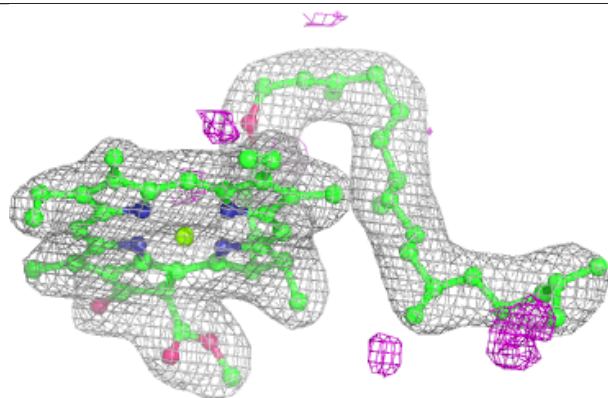
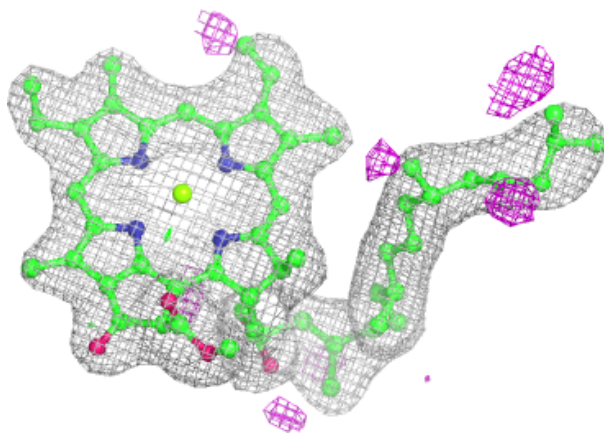
Electron density around CL a 402 (B):

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



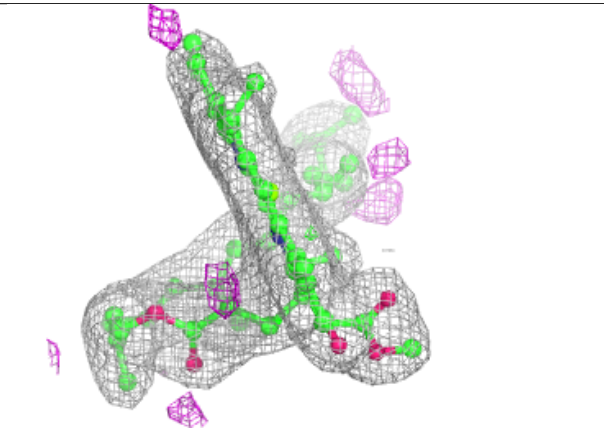
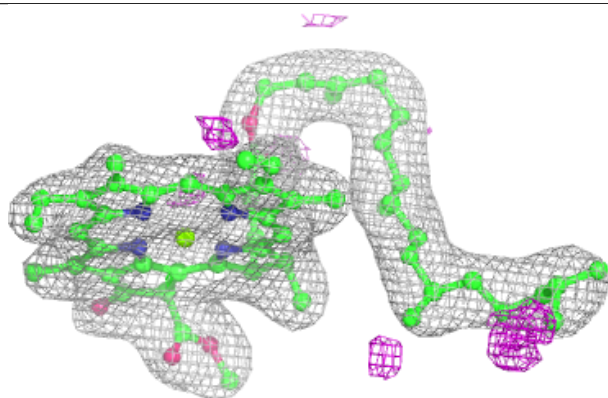
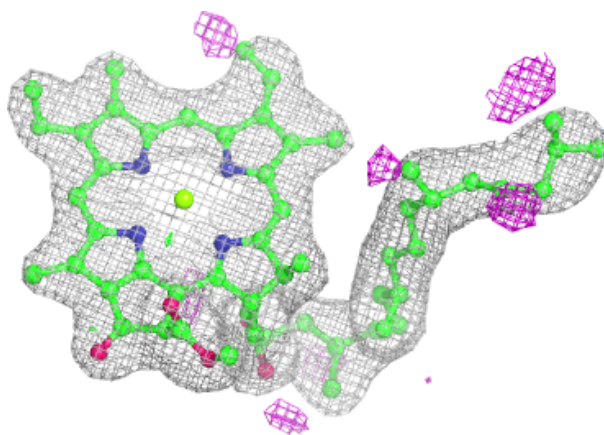
Electron density around CLA d 402 (A):

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

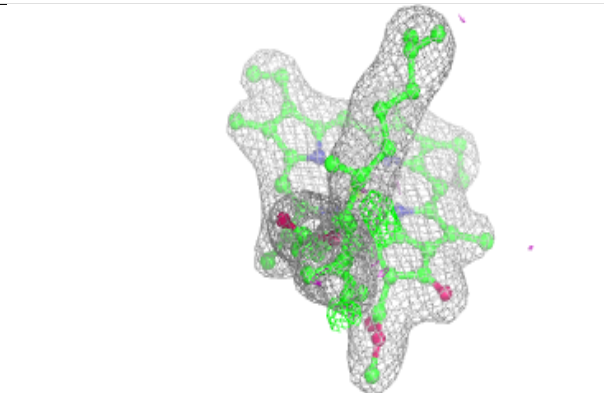
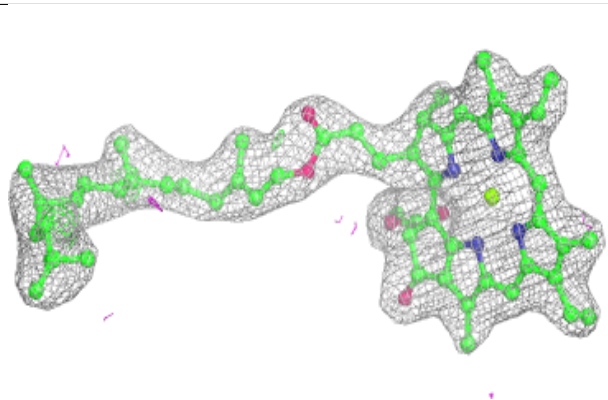
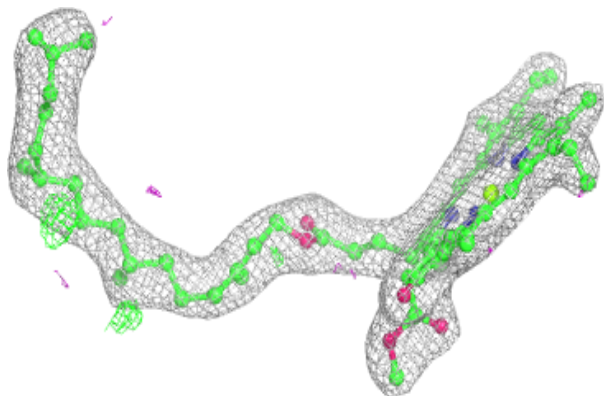


Electron density around CLA d 402 (B):

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

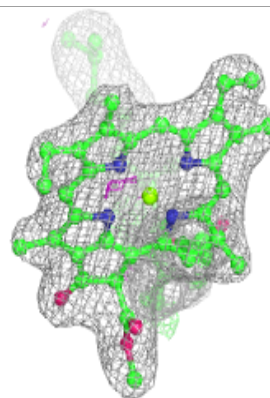
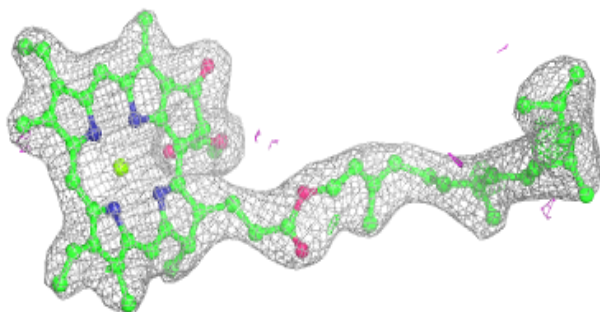
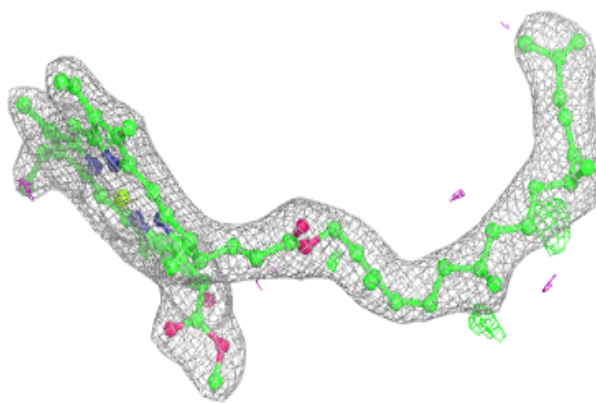
**Electron density around CLA d 403 (A):**

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

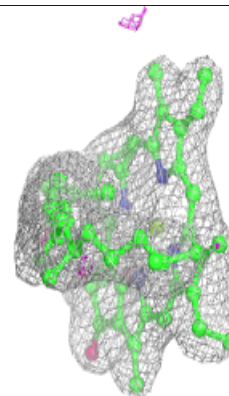
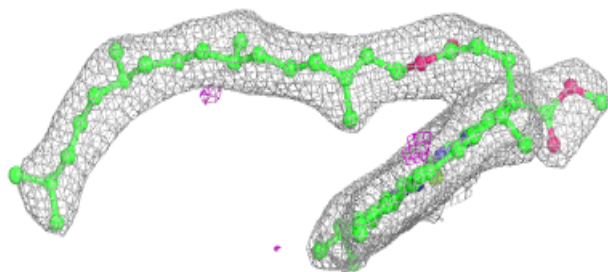
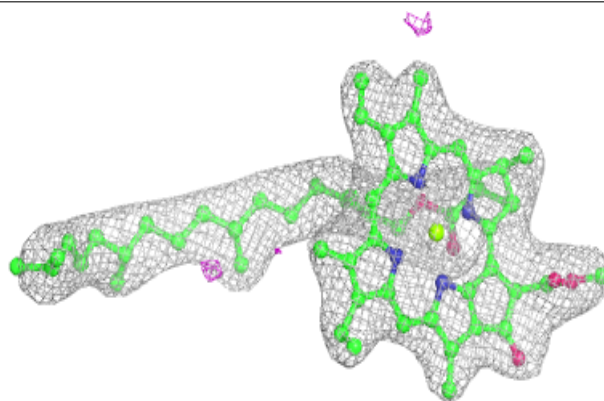


Electron density around CLA d 403 (B):

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

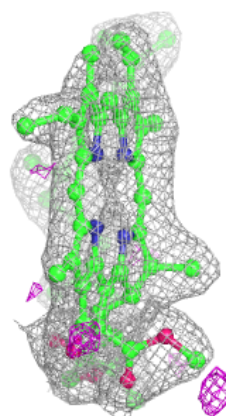
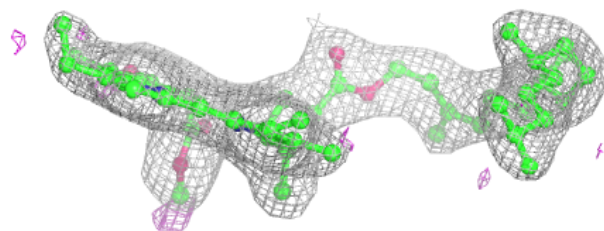
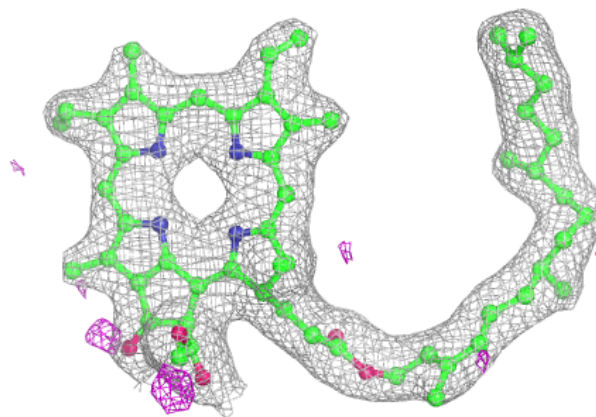
**Electron density around CLA B 608:**

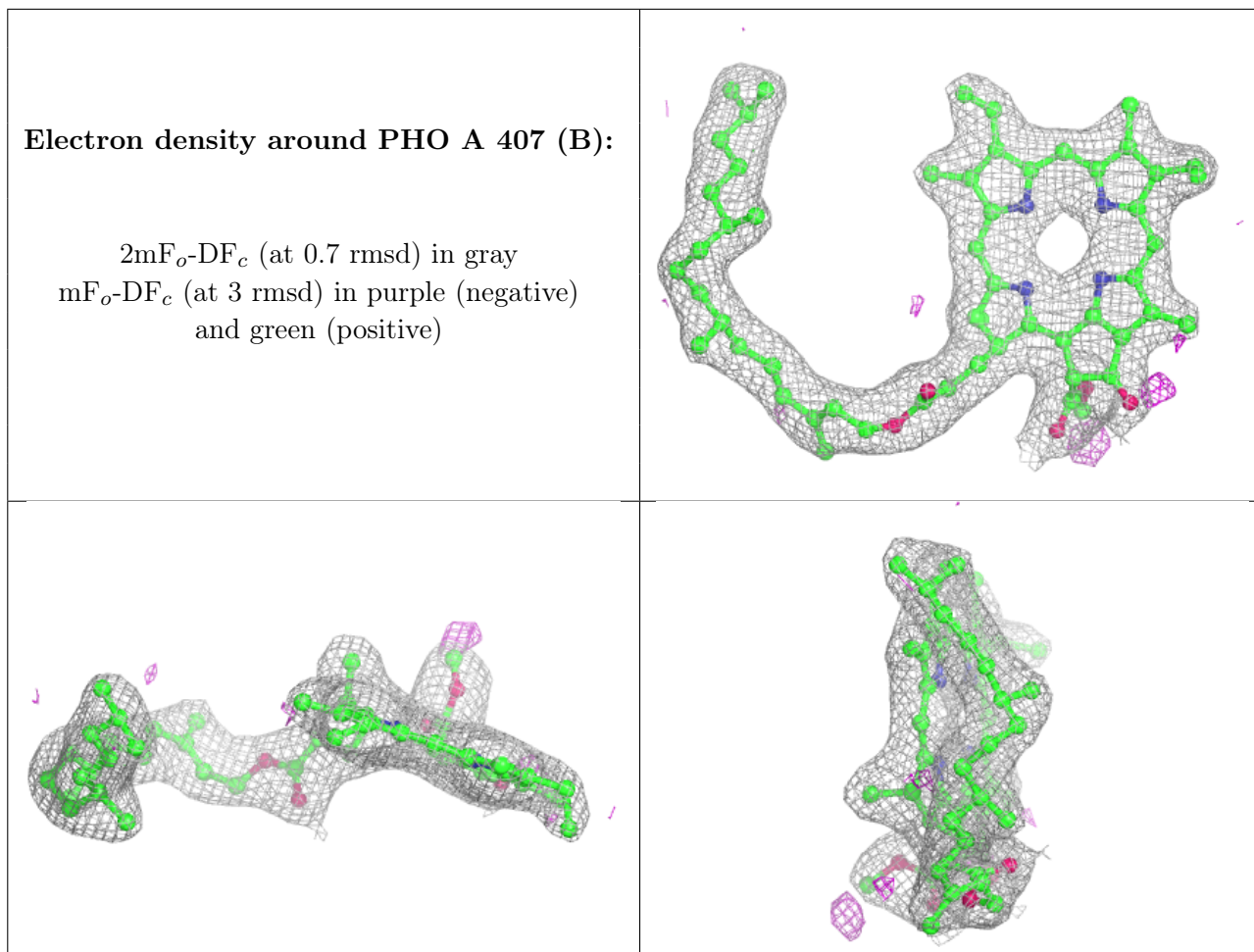
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PHO A 407 (A):

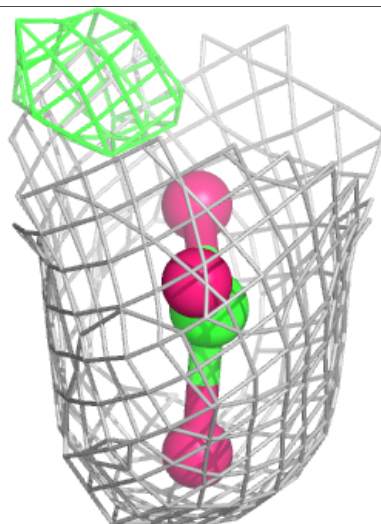
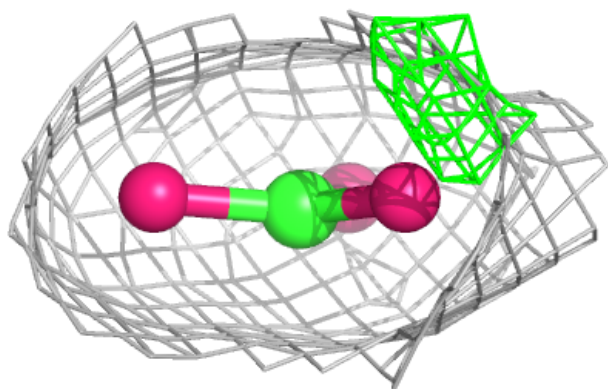
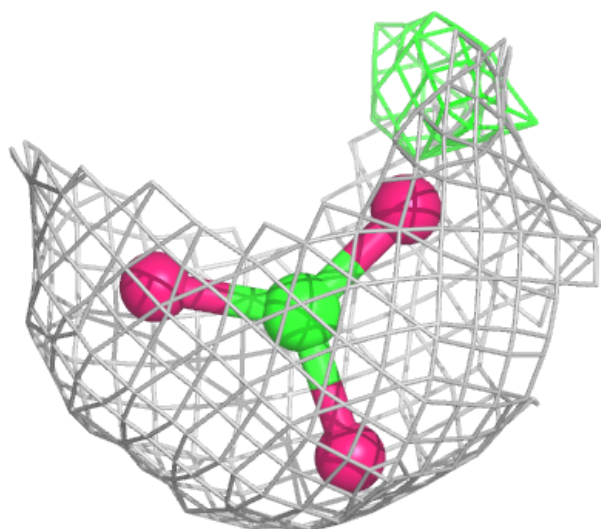
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





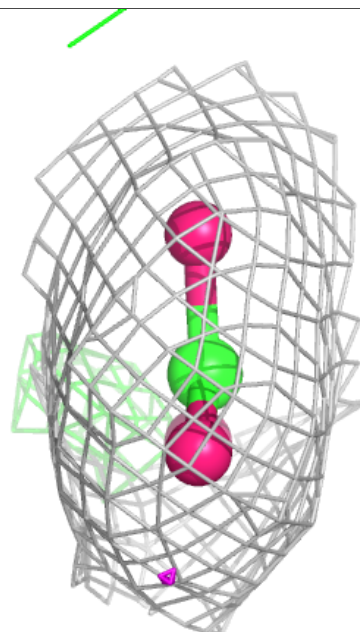
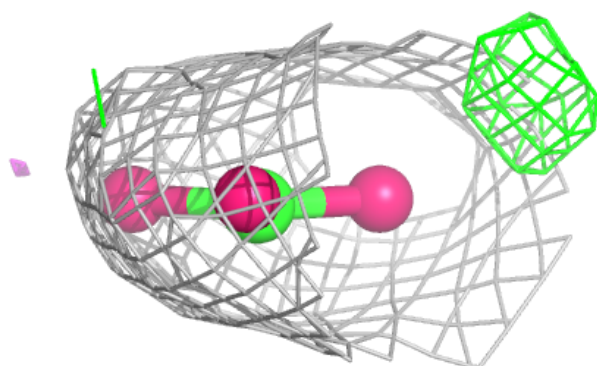
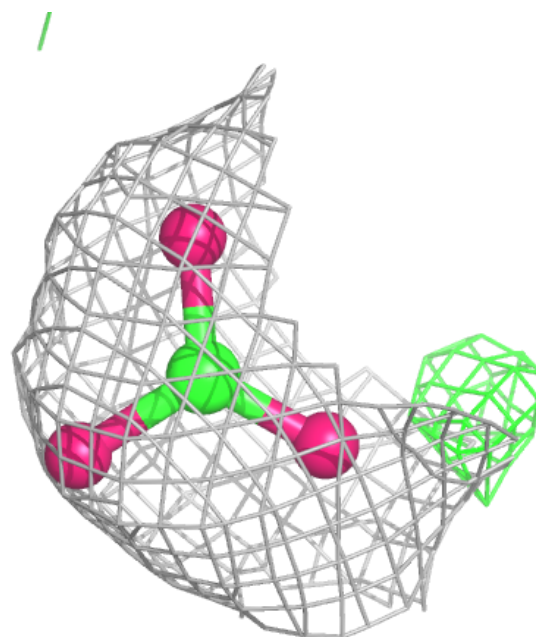
Electron density around BCT D 401 (A):

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



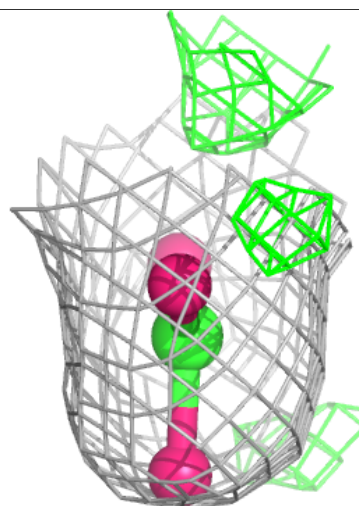
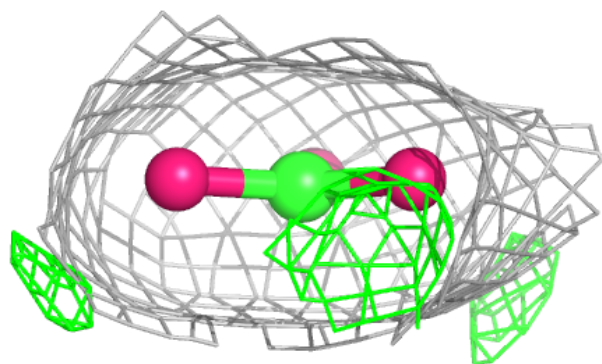
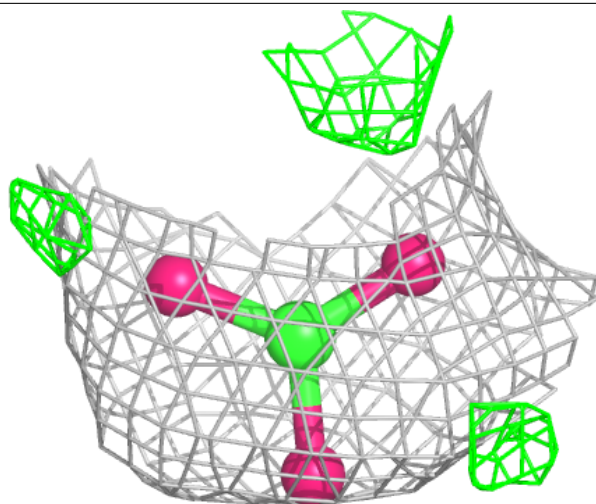
Electron density around BCT D 401 (B):

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



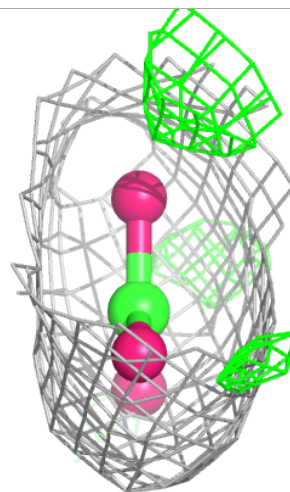
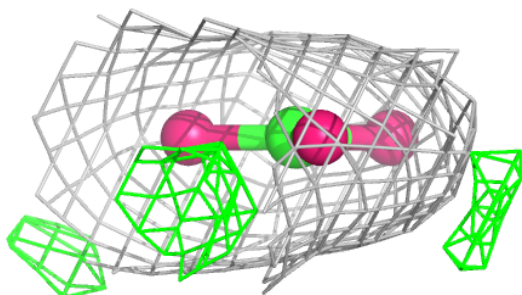
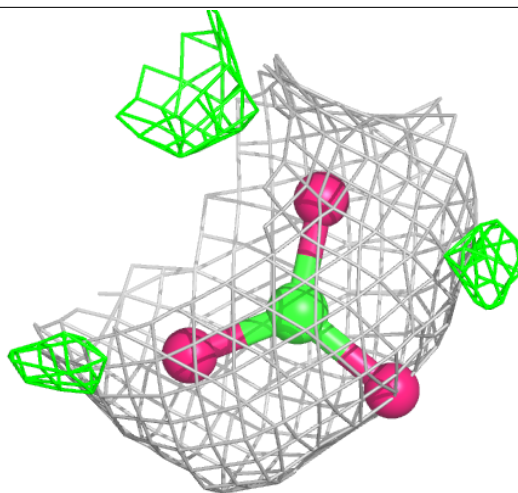
Electron density around BCT d 401 (A):

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



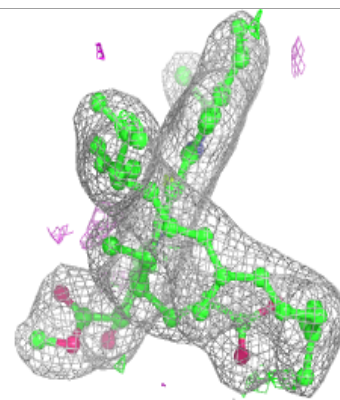
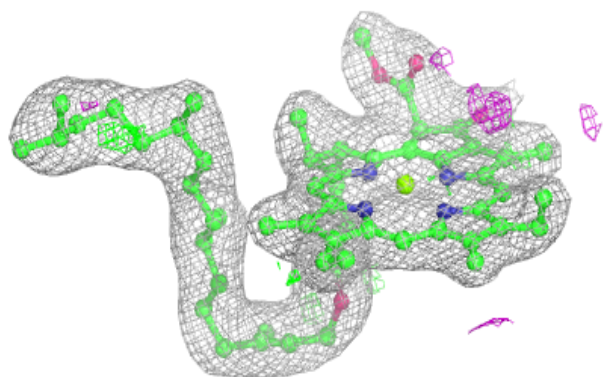
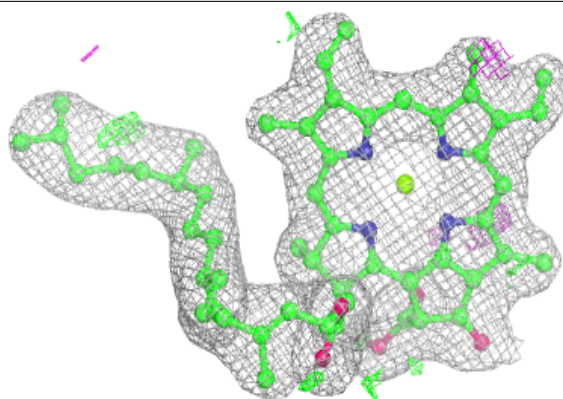
Electron density around BCT d 401 (B):

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

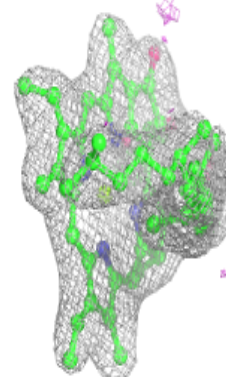
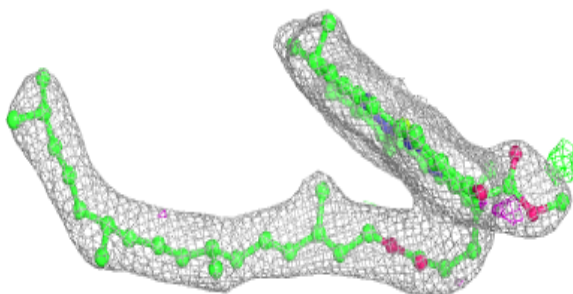
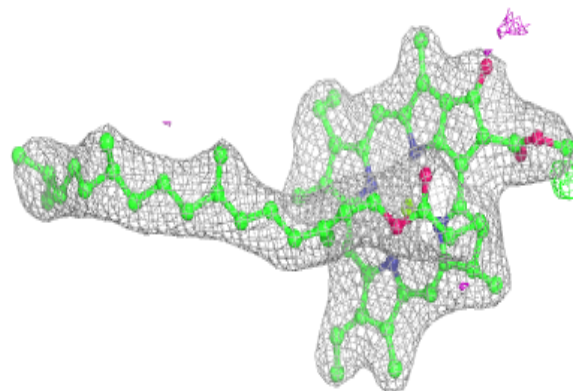


Electron density around CLA A 405 (A):

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

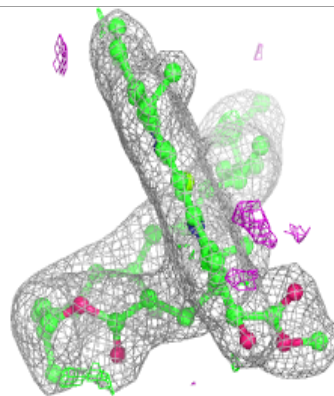
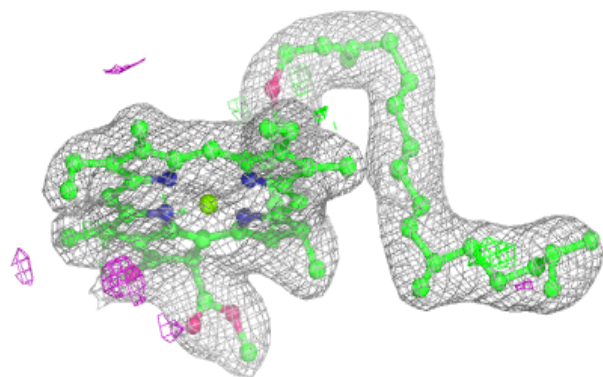
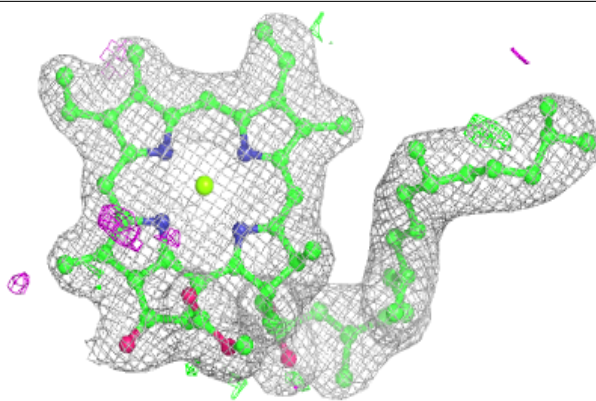
**Electron density around CLA b 608:**

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



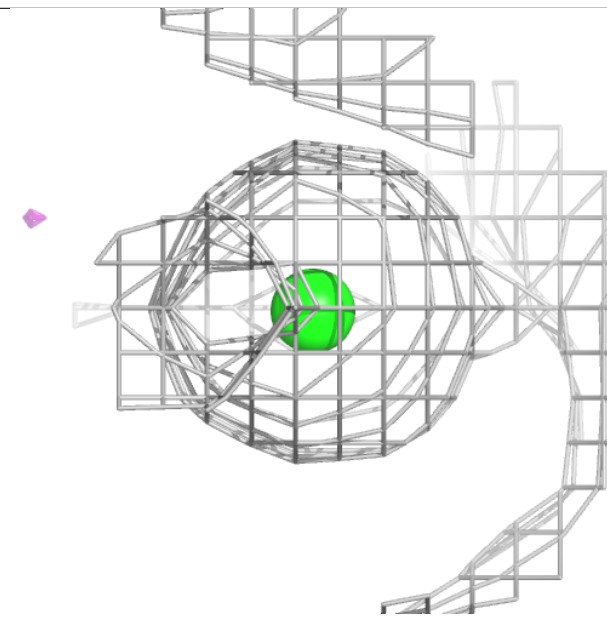
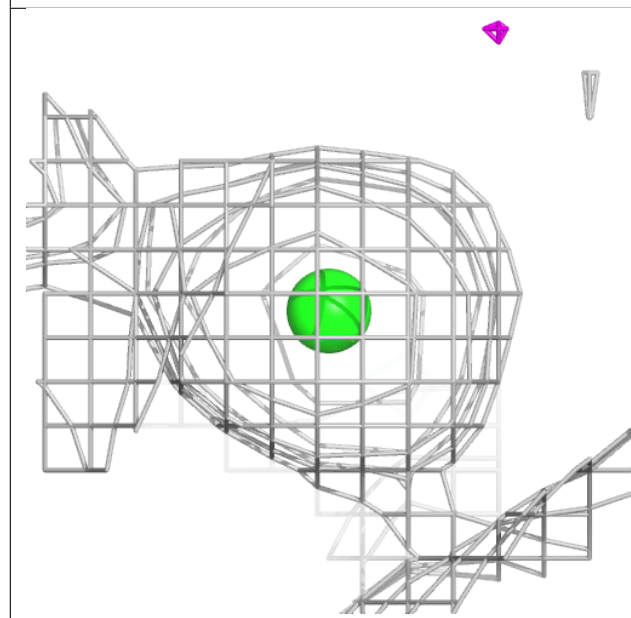
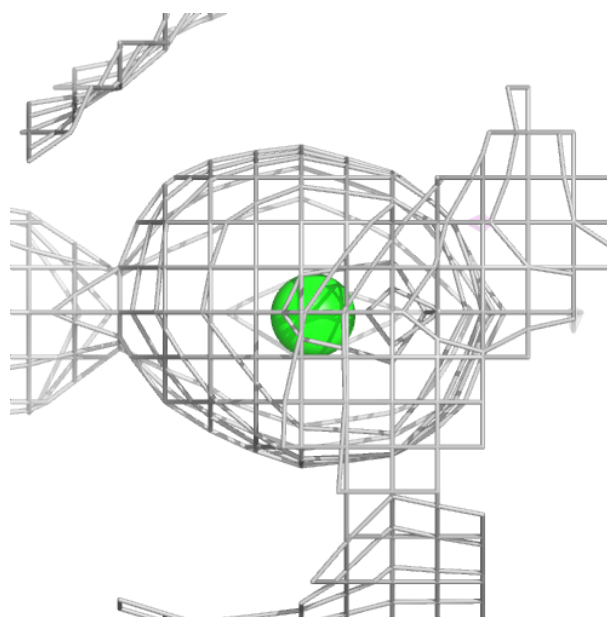
Electron density around CLA A 405 (B):

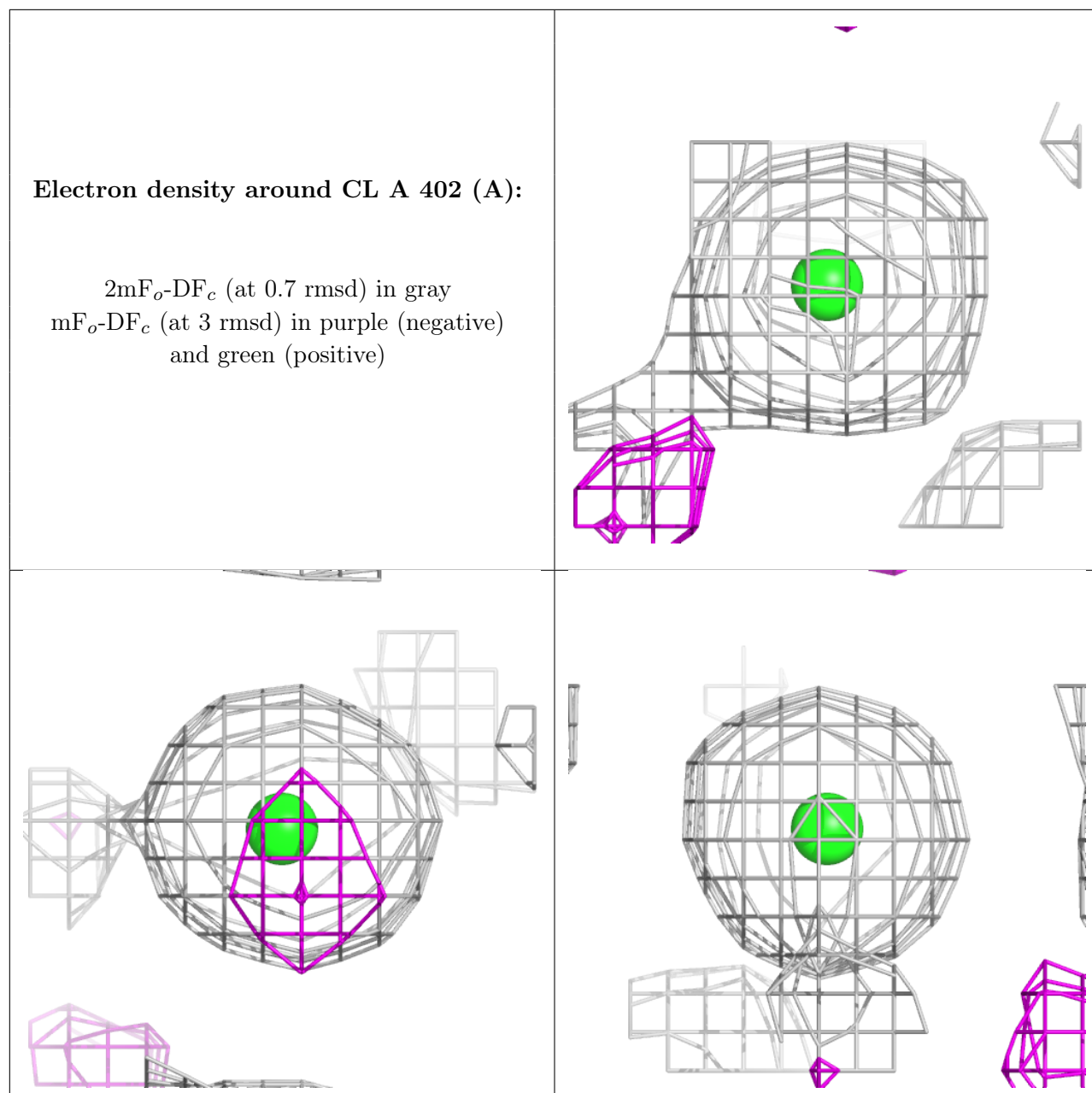
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

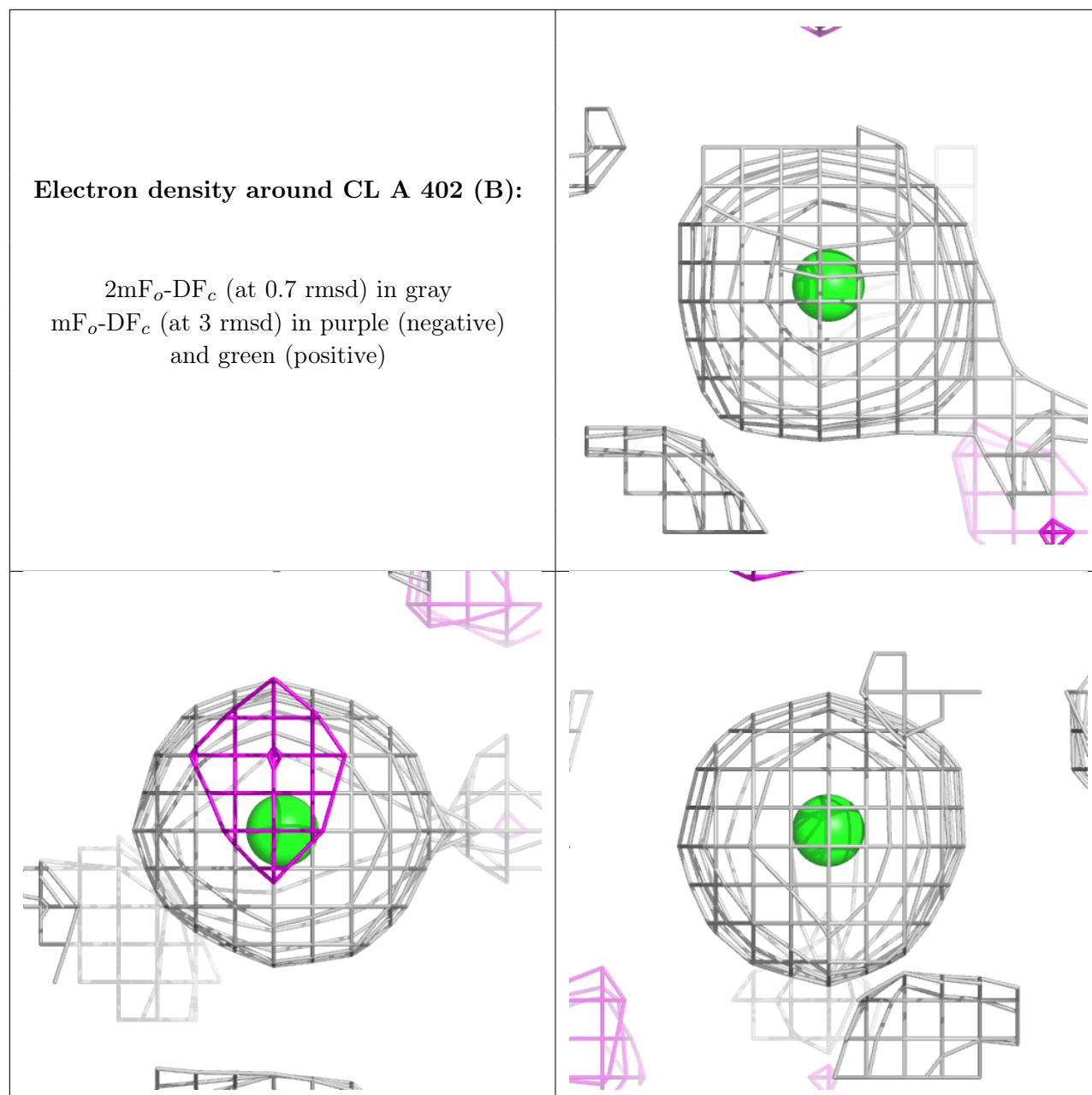


Electron density around CL a 403 (A):

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

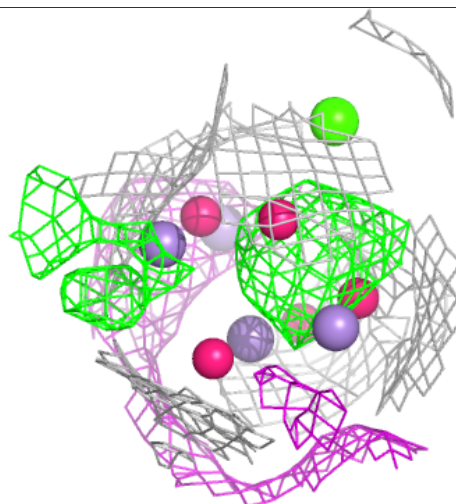
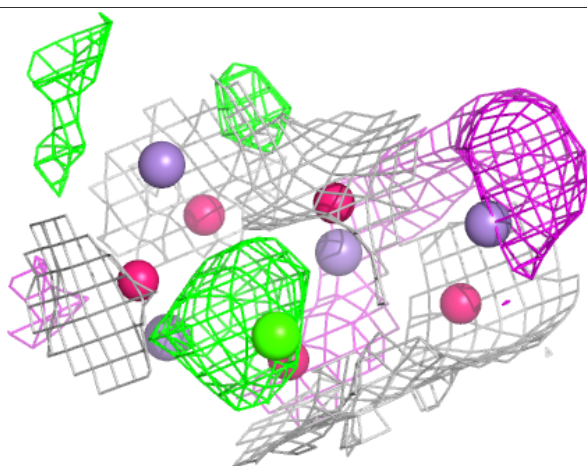
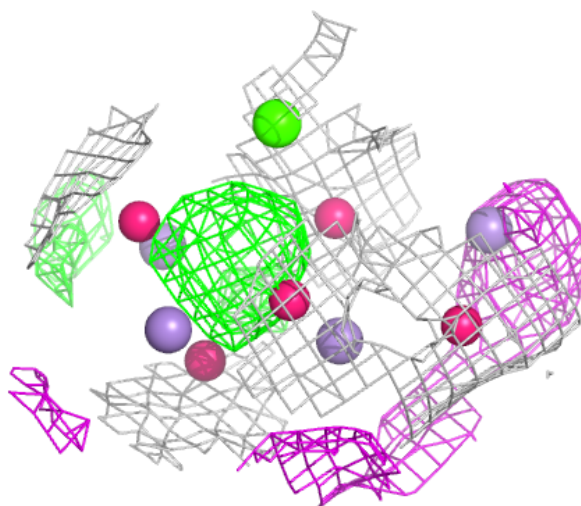






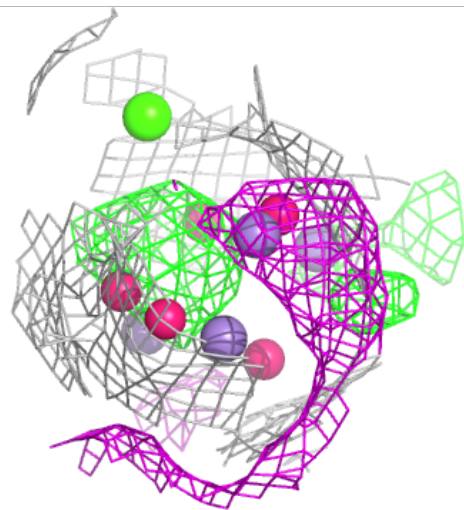
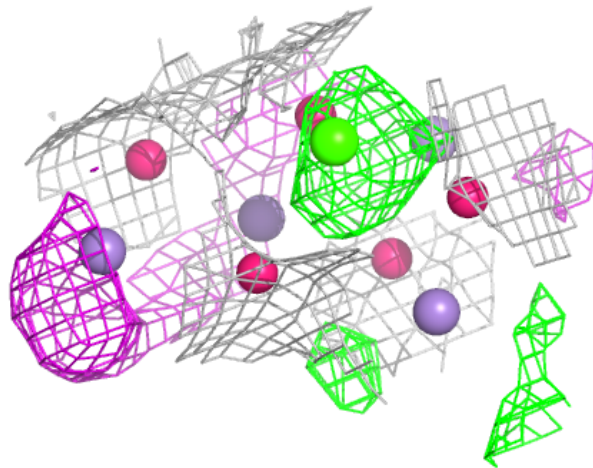
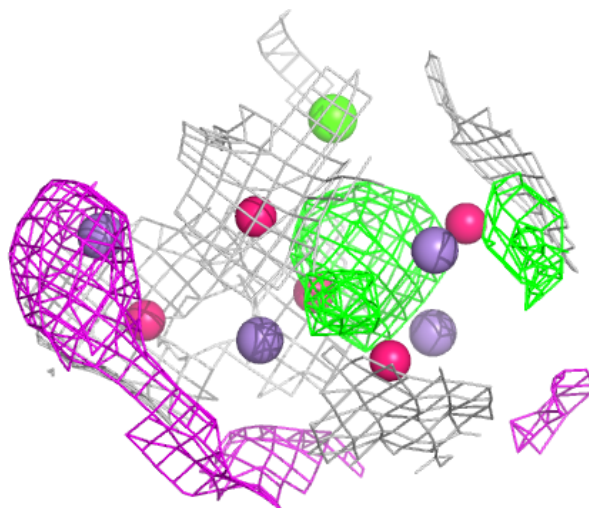
Electron density around OEX A 413 (A):

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



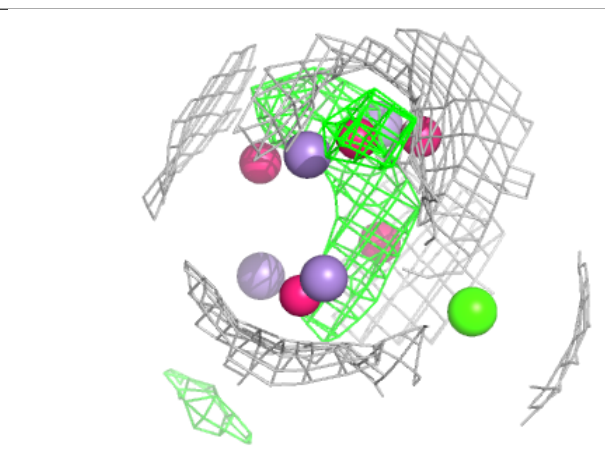
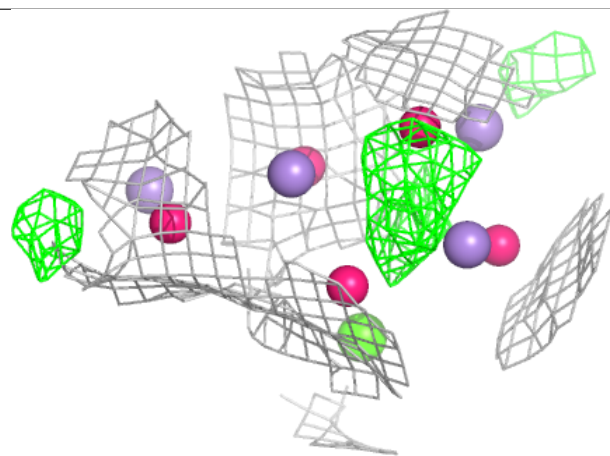
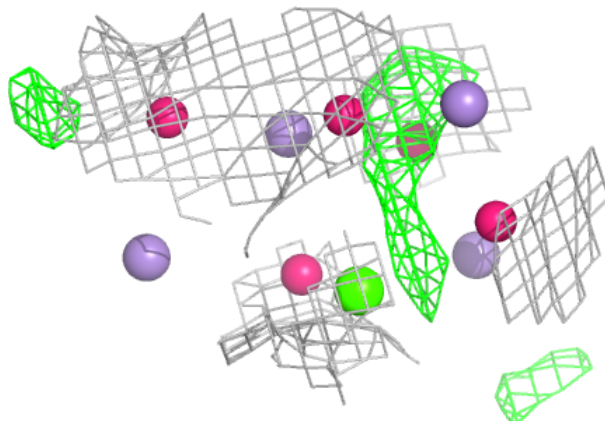
Electron density around OEX A 413 (B):

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



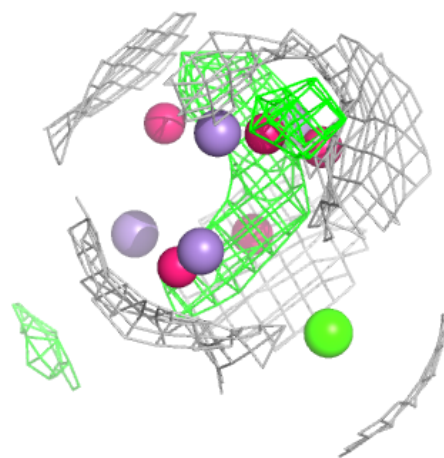
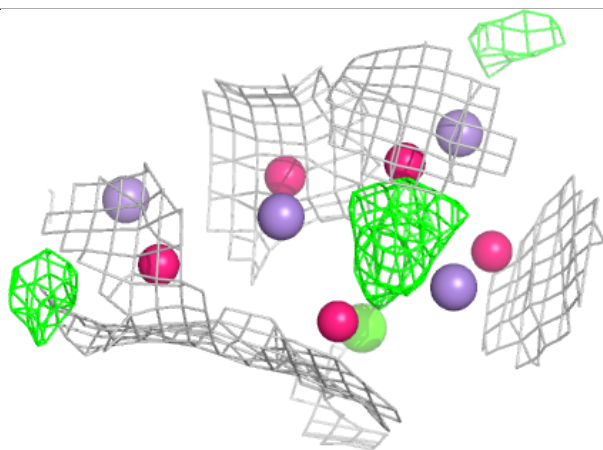
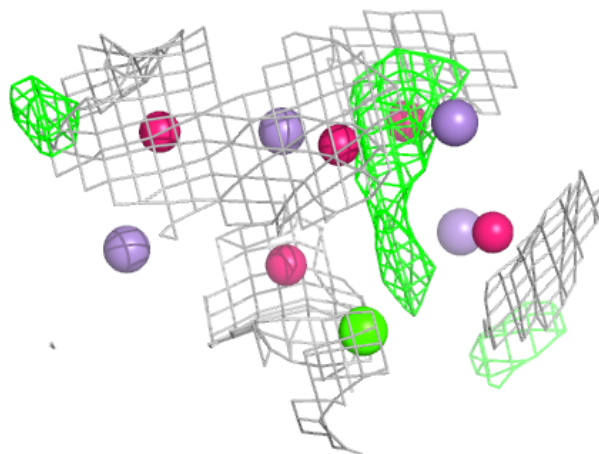
Electron density around OEX a 411 (A):

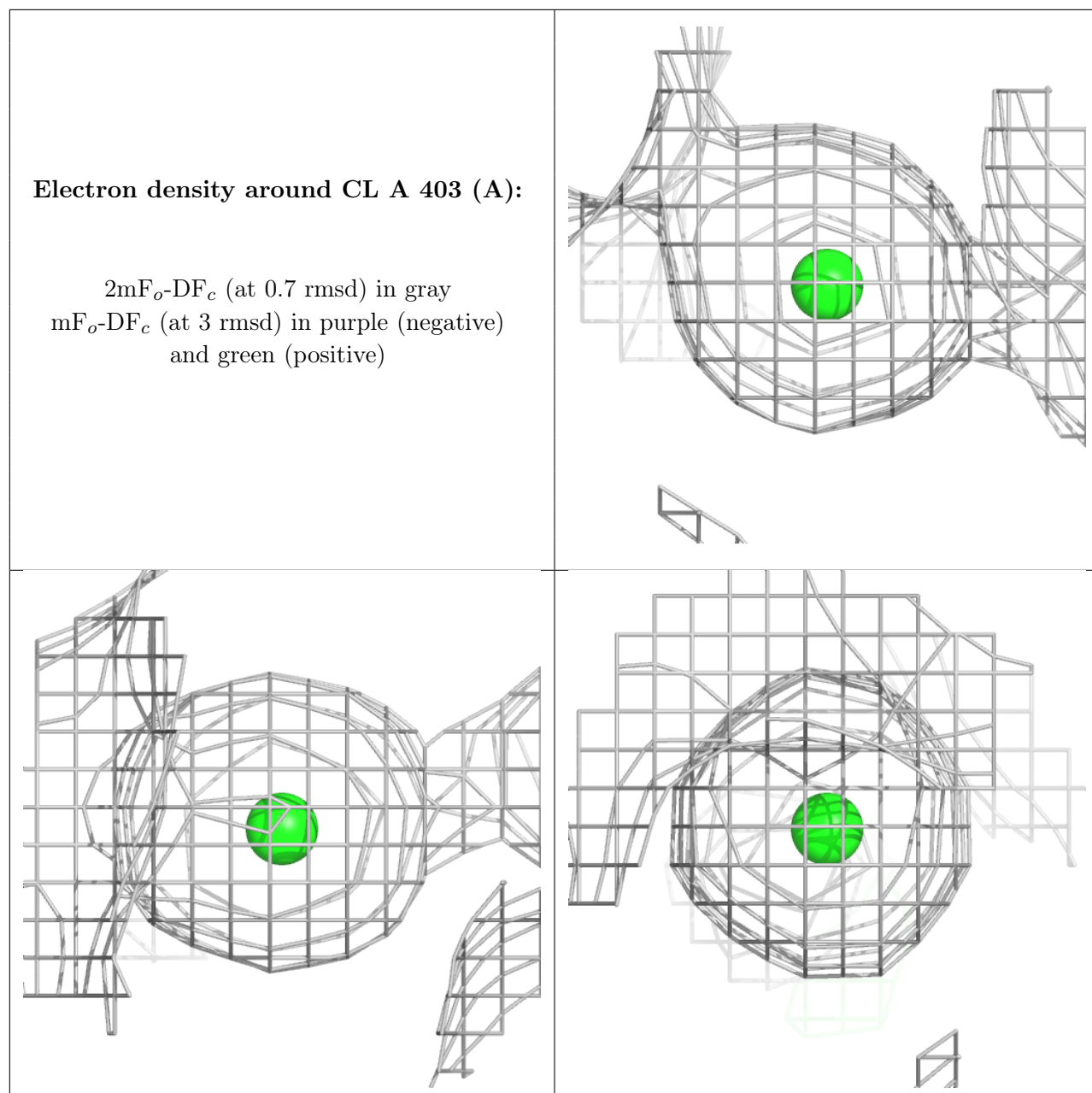
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

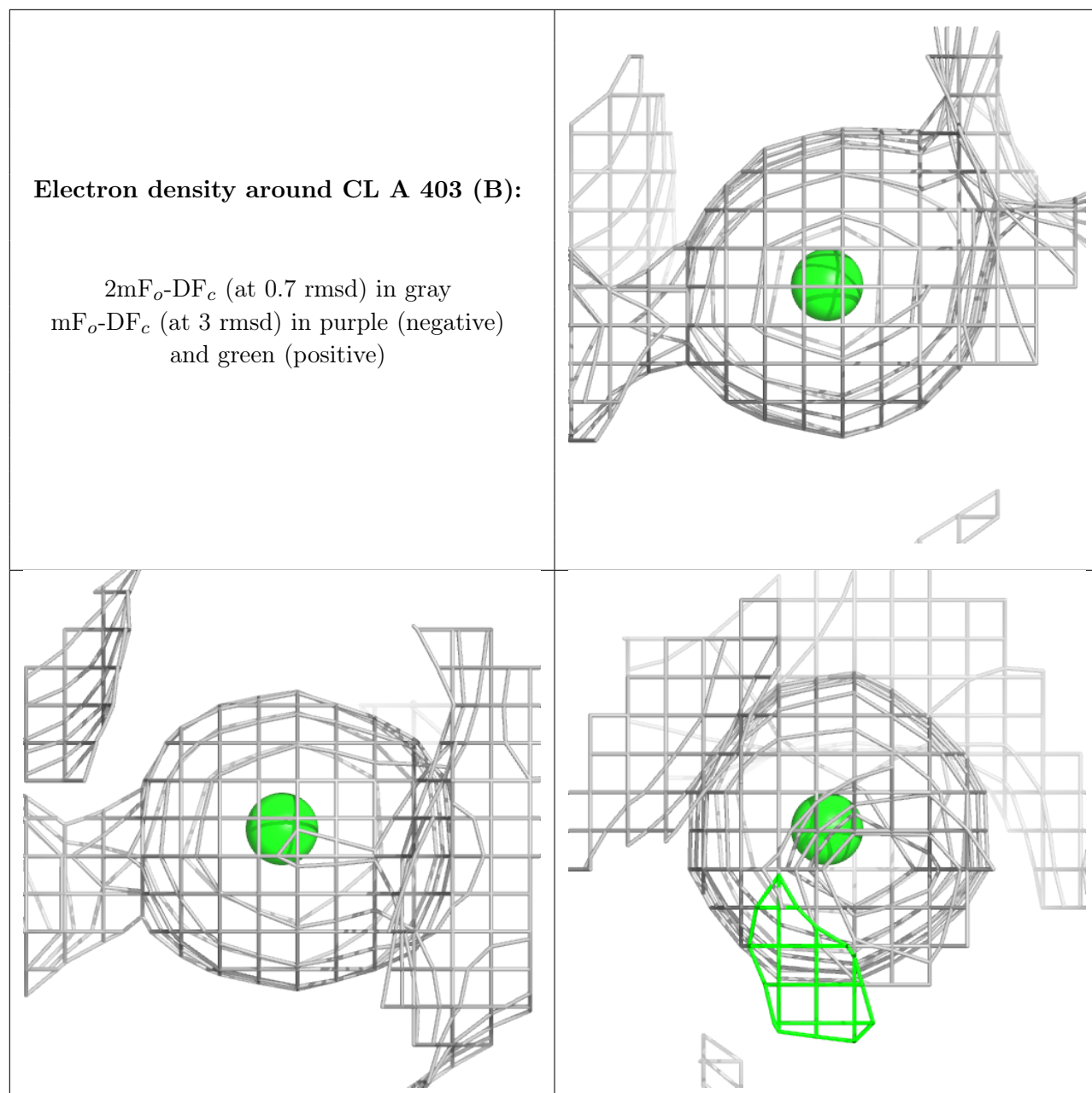


Electron density around OEX a 411 (B):

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

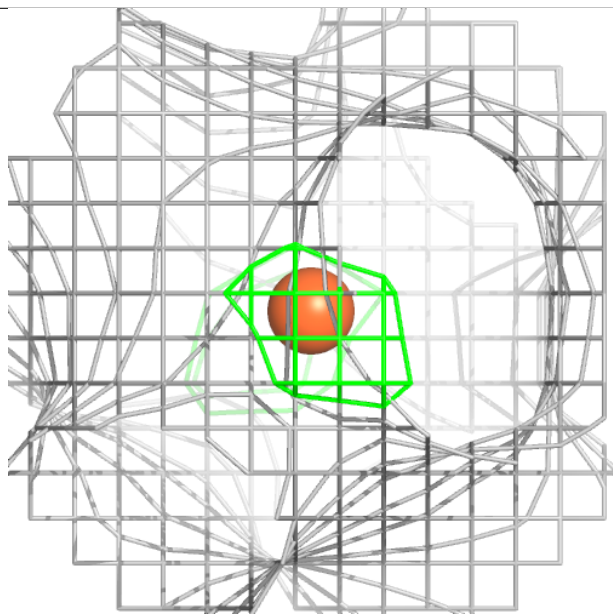
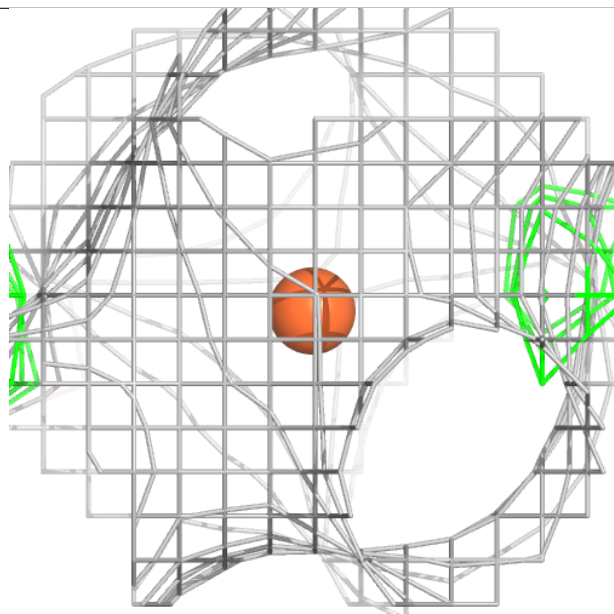
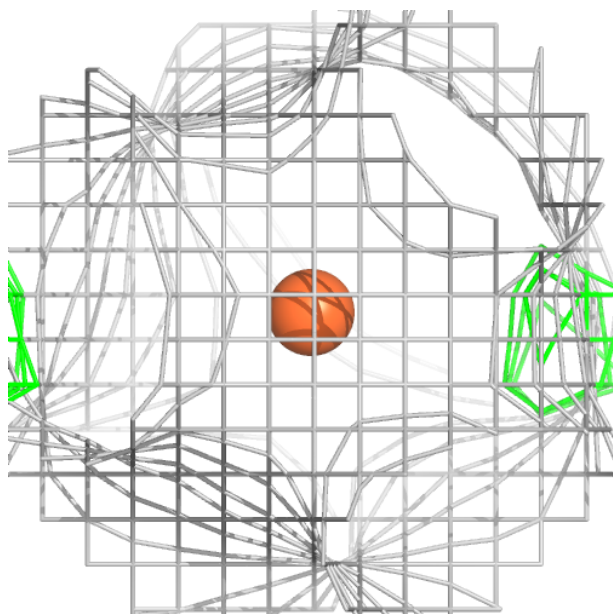


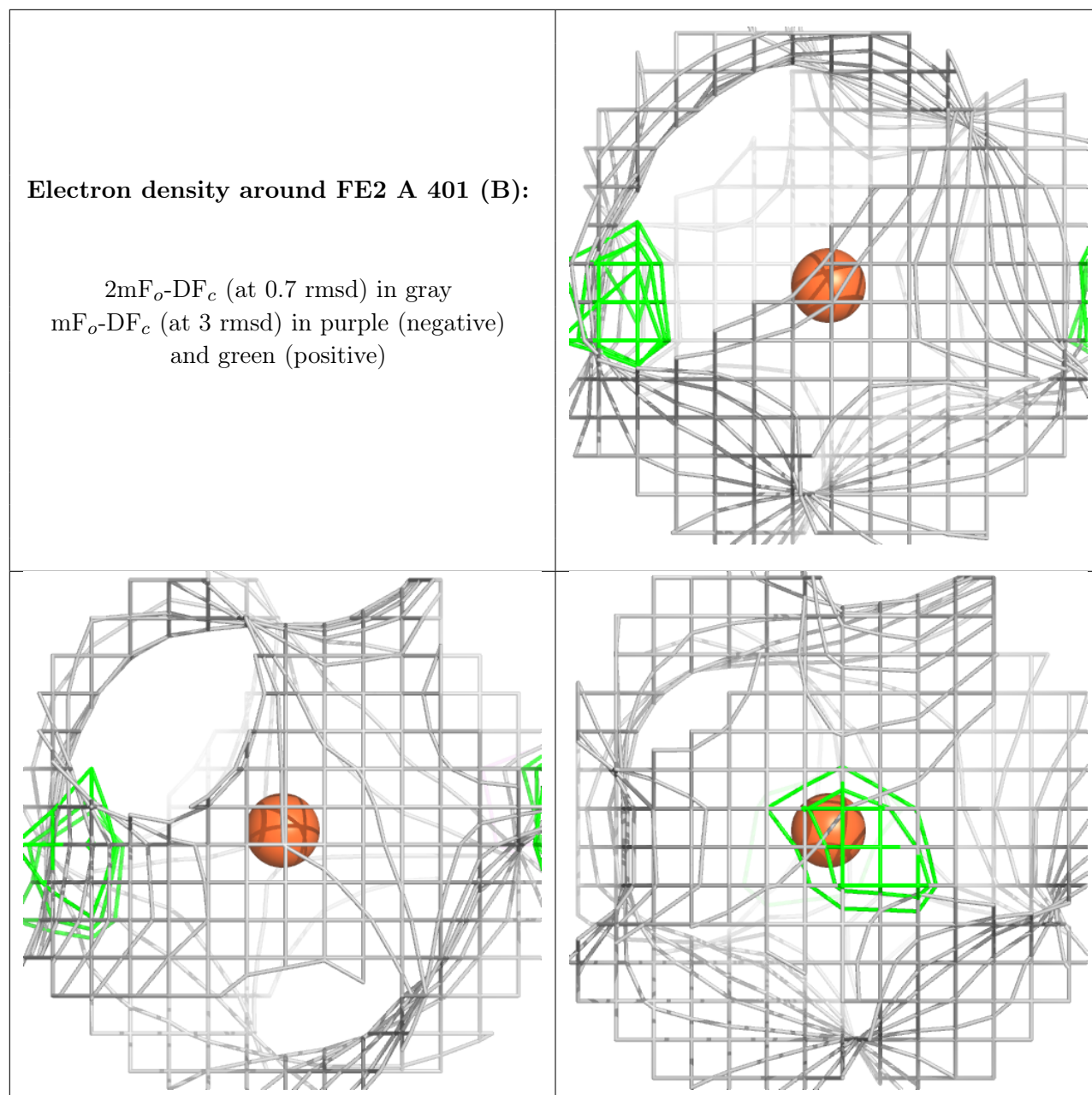




Electron density around FE2 A 401 (A):

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





6.5 Other polymers [i](#)

There are no such residues in this entry.