



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 11, 2023 – 03:34 PM EDT

PDB ID : 7RF3  
Title : RT XFEL structure of the one-flash state of Photosystem II (1F, S2-rich) at 2.26 Angstrom resolution  
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Deposited on : 2021-07-13  
Resolution : 2.26 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](mailto: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>.

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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 : 2.35.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158

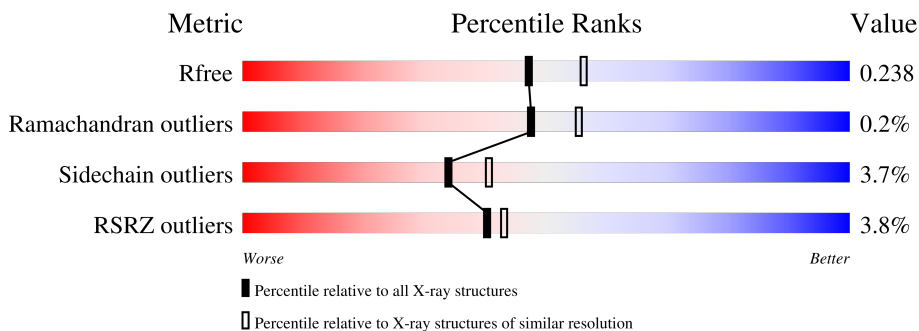
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.26 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	1377 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	 96%
1	a	344	 94%
2	B	510	 97%
2	b	510	 97%

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CCP4 : 7.0.044 (Gargrove)  
 Ideal geometry (proteins) : Engh & Huber (2001)  
 Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
 Validation Pipeline (wwPDB-VP) : 2.35.1

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Mol	Chain	Length	Quality of chain
3	C	461	94%
3	c	461	95%
4	D	352	96%
4	d	352	93%
5	E	84	95%
5	e	84	93%
6	F	45	73%
6	f	45	73%
7	H	66	95%
7	h	66	89%
8	I	38	89%
8	i	38	92%
9	J	40	90%
9	j	40	85%
10	K	46	74%
10	k	46	74%
11	L	37	100%
11	l	37	86%
12	M	36	83%
12	m	36	81%
13	O	272	85%
13	o	272	85%
14	R	41	61%
14	r	41	59%
15	T	32	88%

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Mol	Chain	Length	Quality of chain
15	t	32	
16	U	134	
16	u	134	
17	V	163	
17	v	163	
18	X	41	
18	x	41	
19	Y	46	
19	y	46	
20	Z	62	
20	z	62	

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
22	CLA	A	402	X	-	-	-
22	CLA	A	403	X	-	-	-
22	CLA	A	405	X	-	-	-
22	CLA	B	601	X	-	-	-
22	CLA	B	602	X	-	-	-
22	CLA	B	603	X	-	-	-
22	CLA	B	604	X	-	-	-
22	CLA	B	605	X	-	-	-
22	CLA	B	606	X	-	-	-
22	CLA	B	607	X	-	-	-
22	CLA	B	610	X	-	-	-
22	CLA	B	611	X	-	-	-
22	CLA	B	612	X	-	-	-
22	CLA	B	613	X	-	-	-
22	CLA	B	614	X	-	-	-
22	CLA	B	615	X	-	-	-
22	CLA	B	616	X	-	-	-
22	CLA	C	501	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	CLA	C	502	X	-	-	-
22	CLA	C	503	X	-	-	-
22	CLA	C	504	X	-	-	-
22	CLA	C	505	X	-	-	-
22	CLA	C	506	X	-	-	-
22	CLA	C	507	X	-	-	-
22	CLA	C	509	X	-	-	-
22	CLA	C	510	X	-	-	-
22	CLA	C	511	X	-	-	-
22	CLA	C	512	X	-	-	-
22	CLA	D	403	X	-	-	-
22	CLA	D	404	X	-	-	-
22	CLA	a	402	X	-	-	-
22	CLA	a	403	X	-	-	-
22	CLA	a	405	X	-	-	-
22	CLA	a	411	X	-	-	-
22	CLA	b	601	X	-	-	-
22	CLA	b	602	X	-	-	-
22	CLA	b	603	X	-	-	-
22	CLA	b	604	X	-	-	-
22	CLA	b	605	X	-	-	-
22	CLA	b	606	X	-	-	-
22	CLA	b	607	X	-	-	-
22	CLA	b	609	X	-	-	-
22	CLA	b	610	X	-	-	-
22	CLA	b	611	X	-	-	-
22	CLA	b	612	X	-	-	-
22	CLA	b	613	X	-	-	-
22	CLA	b	614	X	-	-	-
22	CLA	b	615	X	-	-	-
22	CLA	b	616	X	-	-	-
22	CLA	c	501	X	-	-	-
22	CLA	c	502	X	-	-	-
22	CLA	c	503	X	-	-	-
22	CLA	c	504	X	-	-	-
22	CLA	c	505	X	-	-	-
22	CLA	c	506	X	-	-	-
22	CLA	c	507	X	-	-	-
22	CLA	c	508	X	-	-	-
22	CLA	c	509	X	-	-	-
22	CLA	c	510	X	-	-	-
22	CLA	c	511	X	-	-	-

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<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
22	CLA	c	512	X	-	-	-
22	CLA	c	513	X	-	-	-
22	CLA	d	402	X	-	-	-

## 2 Entry composition [i](#)

There are 36 unique types of molecules in this entry. The entry contains 103278 atoms, of which 51563 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 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	334	5141	1717	2519	431	459	15	0	0	0
1	a	334	5129	1714	2510	431	459	15	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
2	B	505	7878	2631	3873	666	695	13	0	5	0
2	b	505	7814	2610	3836	665	690	13	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
3	C	442	6781	2249	3355	571	593	13	0	2	0
3	c	451	6926	2290	3426	587	610	13	0	2	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
4	D	341	5338	1800	2621	444	461	12	0	0	0
4	d	341	5350	1804	2627	444	463	12	0	1	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	82	Total	C	H	N	O	0	1	0
			1317	436	651	107	123			
5	e	82	Total	C	H	N	O	0	0	0
			1312	434	648	108	122			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
6	F	34	Total	C	H	N	O	S	0	0	0
			557	187	282	45	42	1			
6	f	34	Total	C	H	N	O	S	0	0	0
			557	187	282	45	42	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
7	H	65	Total	C	H	N	O	S	0	0	0
			1042	341	532	82	85	2			
7	h	63	Total	C	H	N	O	S	0	0	0
			1016	333	518	80	83	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
8	I	36	Total	C	H	N	O	S	0	0	0
			607	200	311	46	49	1			
8	i	36	Total	C	H	N	O	S	0	0	0
			607	200	311	46	49	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	1	FME	-	initiating methionine	UNP Q8DJZ6
i	1	FME	-	initiating methionine	UNP Q8DJZ6

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
9	J	36	Total	C	H	N	O	S	0	0	0
			525	174	268	40	42	1			
9	j	36	Total	C	H	N	O	S	0	0	0
			525	174	268	40	42	1			



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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
10	K	37	598	204	305	43	46	0	0	0
10	k	37	598	204	305	43	46	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
11	L	37	620	202	316	48	53	1	0	0	0
11	l	36	600	197	304	47	52		0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
12	M	33	525	171	269	37	47	1	0	0	0
12	m	32	518	168	267	36	46	1	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	1	FME	-	initiating methionine	UNP Q8DHA7
m	1	FME	-	initiating methionine	UNP Q8DHA7

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
13	O	244	3700	1168	1830	313	385	4	0	1	0
13	o	244	3720	1170	1846	317	383	4	0	0	0

- Molecule 14 is a protein called Photosystem II protein Y.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
14	R	28	459	151	238	38	32	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	r	28	Total	C	H	N	O	0	0	0
			459	151	238	38	32			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
15	T	30	Total	C	H	N	O	S	0	0	0
			519	181	261	36	39	2			
15	t	30	Total	C	H	N	O	S	0	0	0
			512	180	256	36	38	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	1	FME	-	initiating methionine	UNP Q8DIQ0
t	1	FME	-	initiating methionine	UNP Q8DIQ0

- Molecule 16 is a protein called Photosystem II 12 kDa extrinsic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	U	97	Total	C	H	N	O	0	0	0
			1547	491	773	129	154			
16	u	97	Total	C	H	N	O	0	0	0
			1547	491	773	129	154			

- Molecule 17 is a protein called Cytochrome c-550.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
17	V	137	Total	C	H	N	O	S	0	0	0
			2135	675	1071	177	208	4			
17	v	137	Total	C	H	N	O	S	0	0	0
			2135	675	1071	177	208	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	X	38	Total	C	H	N	O	0	0	0
			593	188	312	45	48			
18	x	39	Total	C	H	N	O	0	0	0
			602	191	316	46	49			

- Molecule 19 is a protein called Photosystem II reaction center protein Ycf12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
19	Y	27	Total 413	C 128	H 217	N 35	O 30	S 3	0	0	0
19	y	30	Total 459	C 144	H 241	N 35	O 36	S 3	0	0	0

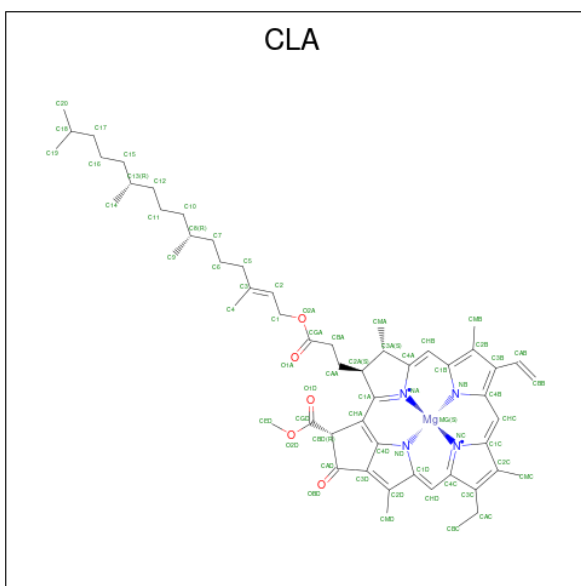
- Molecule 20 is a protein called Photosystem II reaction center protein Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
20	Z	62	Total 995	C 328	H 516	N 72	O 77	S 2	0	0	0
20	z	62	Total 986	C 326	H 509	N 72	O 77	S 2	0	0	0

- Molecule 21 is FE (II) ION (three-letter code: FE2) (formula: Fe).

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

- Molecule 22 is CHLOROPHYLL A (three-letter code: CLA) (formula: C<sub>55</sub>H<sub>72</sub>MgN<sub>4</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
22	A	1	Total 137	C 55	H 72	Mg 1	N 4	O 5	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
22	A	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	A	1	Total	C	H	Mg	N	O	0	0
			102	44	48	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	B	1	Total	C	H	Mg	N	O	0	0
			119	50	59	1	4	5		
22	C	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	C	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	C	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
22	C	1	Total	C	H	Mg	N	O	0	0
			117	49	58	1	4	5		
22	C	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	C	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	C	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	C	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	C	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	C	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	C	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	D	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	D	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	D	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	a	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	a	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	a	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	a	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		

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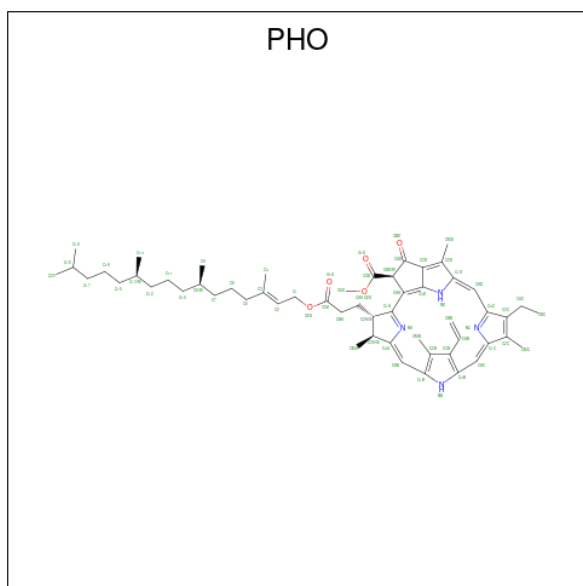
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	b	1	Total	C	H	Mg	N	O	0	0
			119	50	59	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			119	50	59	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			132	54	68	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		

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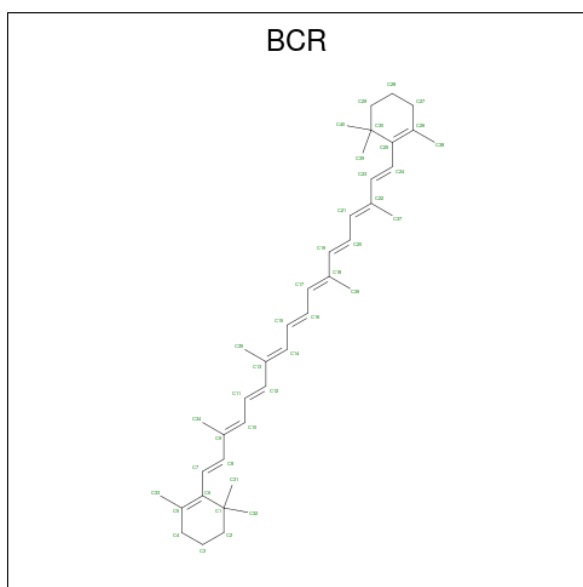
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
22	c	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	c	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	d	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		
22	d	1	Total	C	H	Mg	N	O	0	0
			137	55	72	1	4	5		

- Molecule 23 is PHEOPHYTIN A (three-letter code: PHO) (formula:  $C_{55}H_{74}N_4O_5$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
23	A	1	Total	C	H	N	O	0	0
			138	55	74	4	5		
23	D	1	Total	C	H	N	O	0	0
			138	55	74	4	5		
23	a	1	Total	C	H	N	O	0	0
			138	55	74	4	5		
23	d	1	Total	C	H	N	O	0	0
			138	55	74	4	5		

- Molecule 24 is BETA-CAROTENE (three-letter code: BCR) (formula:  $C_{40}H_{56}$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
24	A	1	Total	C	H	0	0
			96	40	56		
24	B	1	Total	C	H	0	0
			96	40	56		
24	B	1	Total	C	H	0	0
			96	40	56		
24	B	1	Total	C	H	0	0
			96	40	56		
24	C	1	Total	C	H	0	0
			96	40	56		
24	D	1	Total	C	H	0	0
			96	40	56		
24	H	1	Total	C	H	0	0
			96	40	56		
24	K	1	Total	C	H	0	0
			96	40	56		
24	K	1	Total	C	H	0	0
			96	40	56		
24	T	1	Total	C	H	0	0
			96	40	56		
24	Z	1	Total	C	H	0	0
			96	40	56		
24	a	1	Total	C	H	0	0
			96	40	56		
24	b	1	Total	C	H	0	0
			96	40	56		
24	b	1	Total	C	H	0	0
			96	40	56		

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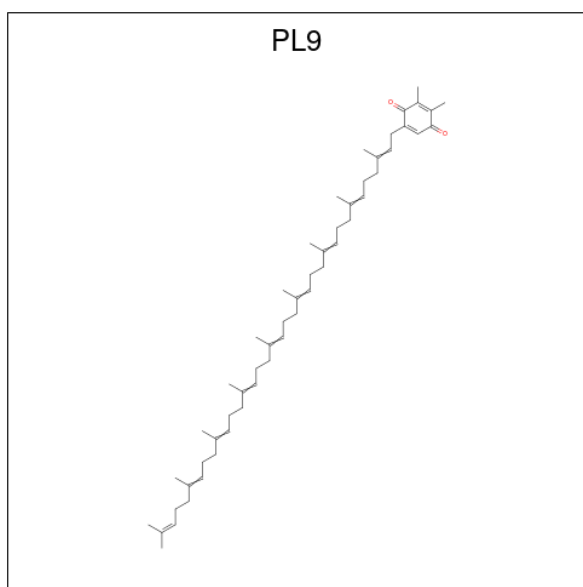
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
24	b	1	Total	C	H	0	0
			96	40	56		
24	c	1	Total	C	H	0	0
			96	40	56		
24	d	1	Total	C	H	0	0
			96	40	56		
24	k	1	Total	C	H	0	0
			96	40	56		
24	k	1	Total	C	H	0	0
			96	40	56		
24	k	1	Total	C	H	0	0
			96	40	56		
24	t	1	Total	C	H	0	0
			96	40	56		
24	x	1	Total	C	H	0	0
			96	40	56		

- Molecule 25 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

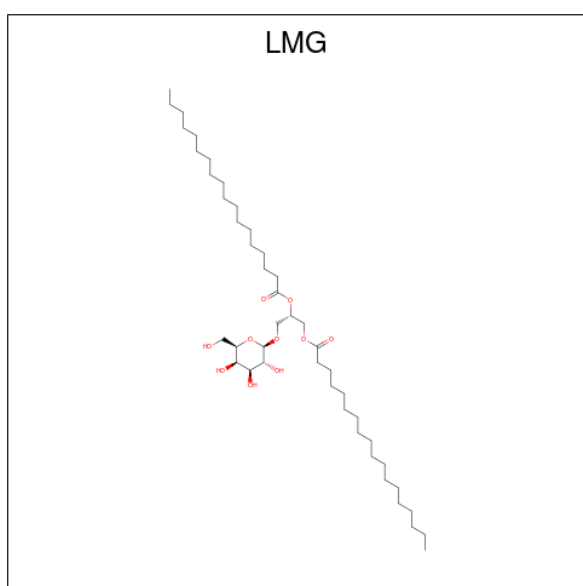
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	A	2	Total	Cl	0	0
			2	2		
25	a	2	Total	Cl	0	0
			2	2		

- Molecule 26 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: C<sub>53</sub>H<sub>80</sub>O<sub>2</sub>).



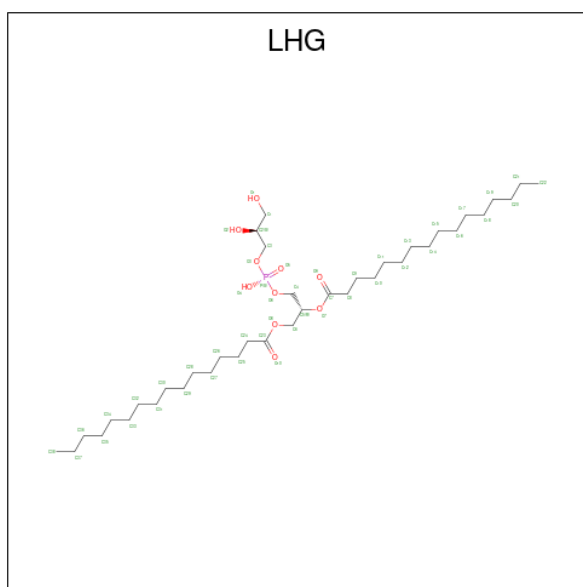
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
26	A	1	135	53	80	2	0	0
26	D	1	135	53	80	2	0	0
26	a	1	135	53	80	2	0	0
26	d	1	135	53	80	2	0	0

- Molecule 27 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (three-letter code: LMG) (formula:  $C_{45}H_{86}O_{10}$ ).



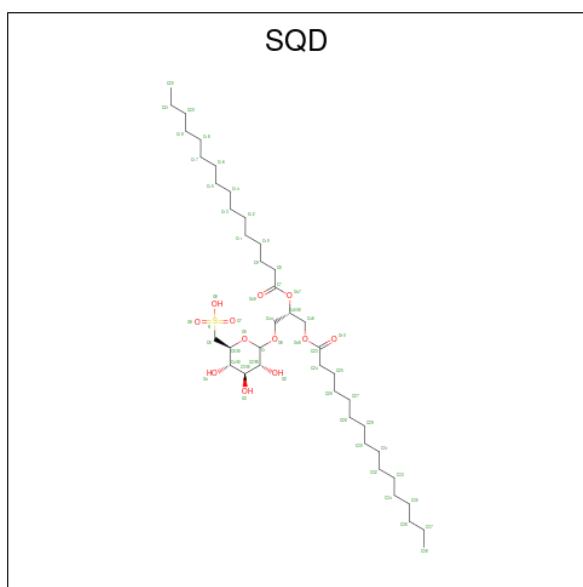
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
27	A	1	Total	C	H	O	0	0
			114	38	66	10		
27	C	1	Total	C	H	O	0	0
			114	38	66	10		
27	D	1	Total	C	H	O	0	0
			123	41	72	10		
27	D	1	Total	C	H	O	0	0
			78	27	45	6		
27	D	1	Total	C	H	O	0	0
			68	24	40	4		
27	M	1	Total	C	H	O	0	0
			123	41	72	10		
27	a	1	Total	C	H	O	0	0
			117	39	68	10		
27	b	1	Total	C	H	O	0	0
			141	45	86	10		
27	c	1	Total	C	H	O	0	0
			81	27	44	10		
27	c	1	Total	C	H	O	0	0
			117	38	69	10		
27	d	1	Total	C	H	O	0	0
			57	21	34	2		
27	d	1	Total	C	H	O	0	0
			102	34	58	10		
27	m	1	Total	C	H	O	0	0
			123	41	72	10		

- Molecule 28 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (three-letter code: LHG) (formula: C<sub>38</sub>H<sub>75</sub>O<sub>10</sub>P).



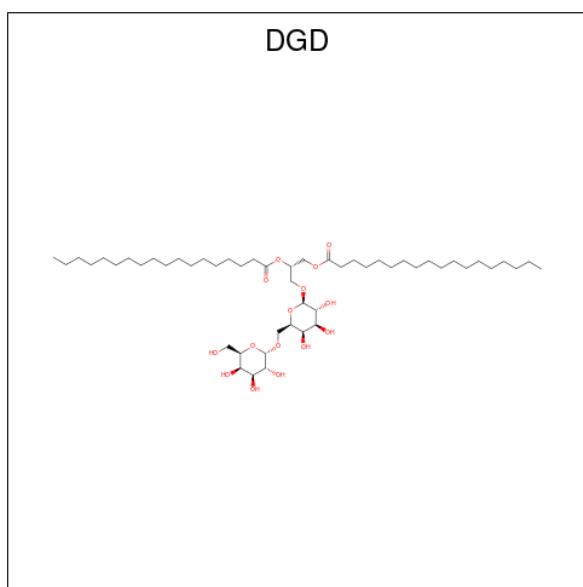
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	O	P		
28	A	1	114	36	67	10	1	0	0
28	B	1	123	38	74	10	1	0	0
28	D	1	123	38	74	10	1	0	0
28	E	1	123	38	74	10	1	0	0
28	L	1	123	38	74	10	1	0	0
28	b	1	123	38	74	10	1	0	0
28	d	1	123	38	74	10	1	0	0
28	d	1	90	28	51	10	1	0	0
28	e	1	99	31	57	10	1	0	0
28	l	1	123	38	74	10	1	0	0

- Molecule 29 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (three-letter code: SQD) (formula:  $C_{41}H_{78}O_{12}S$ ).



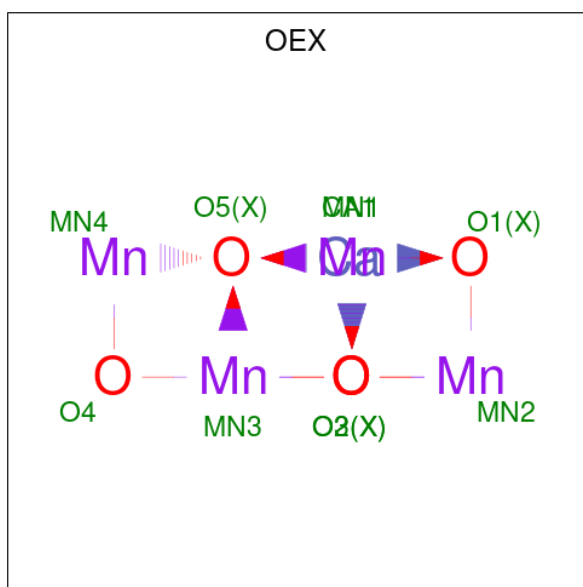
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	O	S		
29	A	1	122	39	70	12	1	0	0
29	A	1	104	35	65	4		0	0
29	B	1	132	41	78	12	1	0	0
29	F	1	81	25	45	10	1	0	0
29	L	1	114	36	65	12	1	0	0
29	a	1	131	41	77	12	1	0	0
29	a	1	92	31	56	5		0	0
29	f	1	89	28	48	12	1	0	0

- Molecule 30 is DIGALACTOSYL DIACYL GLYCEROL (DGDG) (three-letter code: DGD) (formula:  $C_{51}H_{96}O_{15}$ ).



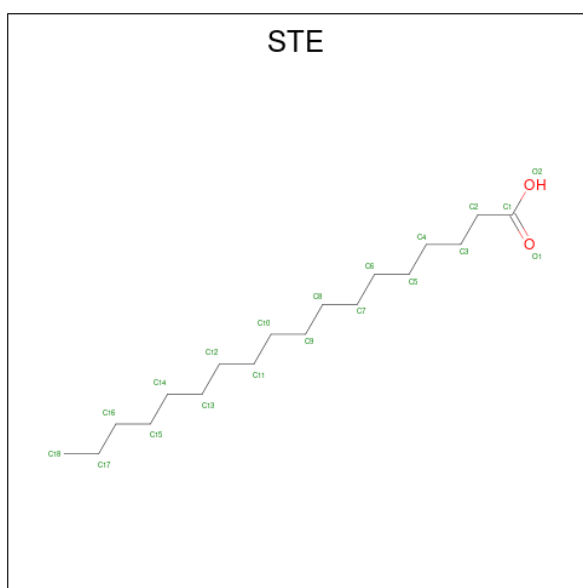
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
30	A	1	Total 162	C 51	H 96	O 15	0	0
30	B	1	Total 119	C 39	H 75	O 5	0	0
30	C	1	Total 144	C 47	H 82	O 15	0	0
30	C	1	Total 143	C 47	H 81	O 15	0	0
30	C	1	Total 144	C 47	H 82	O 15	0	0
30	H	1	Total 144	C 47	H 82	O 15	0	0
30	c	1	Total 144	C 47	H 82	O 15	0	0
30	c	1	Total 144	C 47	H 82	O 15	0	0
30	c	1	Total 144	C 47	H 82	O 15	0	0
30	h	1	Total 144	C 47	H 82	O 15	0	0

- Molecule 31 is CA-MN4-O5 CLUSTER (three-letter code: OEX) (formula:  $\text{CaMn}_4\text{O}_5$ ).



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

- Molecule 32 is STEARIC ACID (three-letter code: STE) (formula:  $C_{18}H_{36}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	H			O
32	B	1	43	15	26	2	0	0
32	B	1	28	10	16	2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
32	B	1	Total C H O 46 16 28 2	0	0
32	B	1	Total C H 47 16 31	0	0
32	B	1	Total C H O 28 10 16 2	0	0
32	C	1	Total C H O 28 10 16 2	0	0
32	C	1	Total C H 47 16 31	0	0
32	C	1	Total C H O 28 10 16 2	0	0
32	D	1	Total C H O 55 18 35 2	0	0
32	E	1	Total C H O 28 10 16 2	0	0
32	H	1	Total C H 53 18 35	0	0
32	I	1	Total C H 41 15 26	0	0
32	J	1	Total C H O 28 10 16 2	0	0
32	M	1	Total C H O 37 13 22 2	0	0
32	M	1	Total C H 26 10 16	0	0
32	M	1	Total C H 44 15 29	0	0
32	a	1	Total C H O 28 10 16 2	0	0
32	b	1	Total C H 47 16 31	0	0
32	b	1	Total C H O 55 18 35 2	0	0
32	b	1	Total C H O 40 14 24 2	0	0
32	b	1	Total C H O 55 18 35 2	0	0
32	b	1	Total C H 26 10 16	0	0
32	c	1	Total C H O 55 18 35 2	0	0

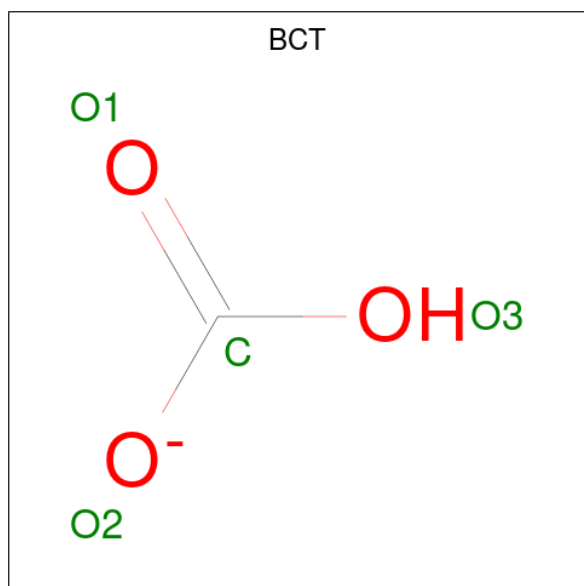
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
32	d	1	Total	C	H	O	0	0
			43	15	26	2		
32	j	1	Total	C	H	O	0	0
			28	10	16	2		
32	k	1	Total	C	H	O	0	0
			28	10	16	2		
32	l	1	Total	C	H		0	0
			53	18	35			
32	m	1	Total	C	H	O	0	0
			28	10	16	2		
32	t	1	Total	C	H	O	0	0
			34	12	20	2		
32	t	1	Total	C	H		0	0
			26	10	16			
32	x	1	Total	C	H	O	0	0
			55	18	35	2		

- Molecule 33 is BICARBONATE ION (three-letter code: BCT) (formula:  $\text{CHO}_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
33	D	1	Total	C	H	O	0	0
			5	1	1	3		
33	a	1	Total	C	H	O	0	0
			5	1	1	3		

- Molecule 34 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $\text{C}_{34}\text{H}_{32}\text{FeN}_4\text{O}_4$ ).



- Molecule 36 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	A	124	Total O 124 124	0	0
36	B	170	Total O 170 170	0	0
36	C	137	Total O 137 137	0	0
36	D	106	Total O 106 106	0	0
36	E	26	Total O 26 26	0	0
36	F	8	Total O 8 8	0	0
36	H	20	Total O 20 20	0	0
36	I	9	Total O 9 9	0	0
36	J	9	Total O 9 9	0	0
36	K	7	Total O 7 7	0	0
36	L	11	Total O 11 11	0	0
36	M	10	Total O 10 10	0	0
36	O	82	Total O 82 82	0	0
36	R	1	Total O 1 1	0	0
36	T	9	Total O 9 9	0	0
36	U	32	Total O 32 32	0	0
36	V	46	Total O 46 46	0	0
36	X	11	Total O 11 11	0	0
36	Y	3	Total O 3 3	0	0
36	Z	4	Total O 4 4	0	0
36	a	111	Total O 111 111	0	0

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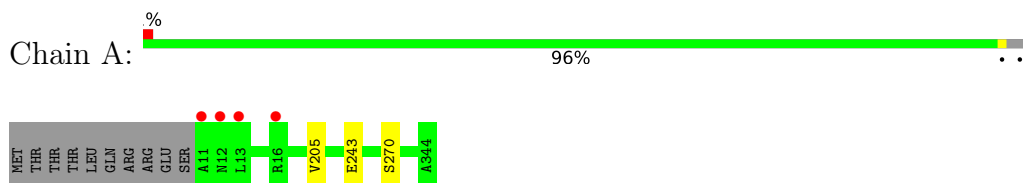
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	b	140	Total 140	O 140	0	0
36	c	115	Total 115	O 115	0	0
36	d	102	Total 102	O 102	0	0
36	e	19	Total 19	O 19	0	0
36	f	10	Total 10	O 10	0	0
36	h	22	Total 22	O 22	0	0
36	i	10	Total 10	O 10	0	0
36	j	10	Total 10	O 10	0	0
36	k	7	Total 7	O 7	0	0
36	l	7	Total 7	O 7	0	0
36	m	7	Total 7	O 7	0	0
36	o	79	Total 79	O 79	0	0
36	r	12	Total 12	O 12	0	0
36	t	10	Total 10	O 10	0	0
36	u	40	Total 40	O 40	0	0
36	v	39	Total 39	O 39	0	0
36	x	5	Total 5	O 5	0	0
36	y	5	Total 5	O 5	0	0
36	z	6	Total 6	O 6	0	0

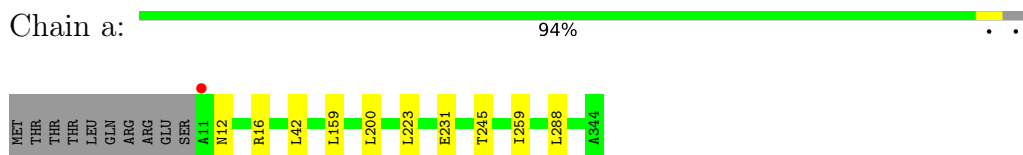
### 3 Residue-property plots [i](#)

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.

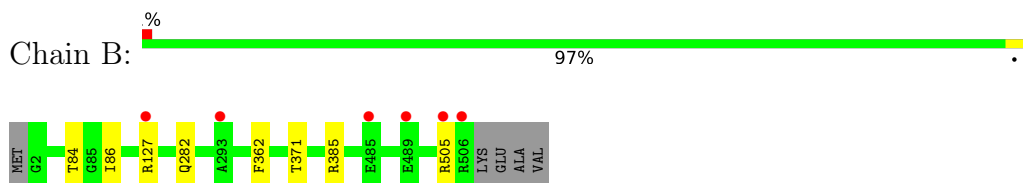
- Molecule 1: Photosystem II protein D1 1



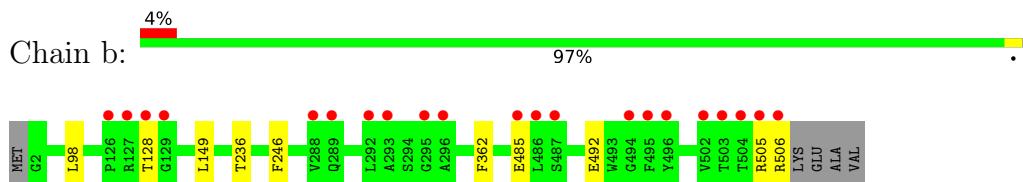
- Molecule 1: Photosystem II protein D1 1



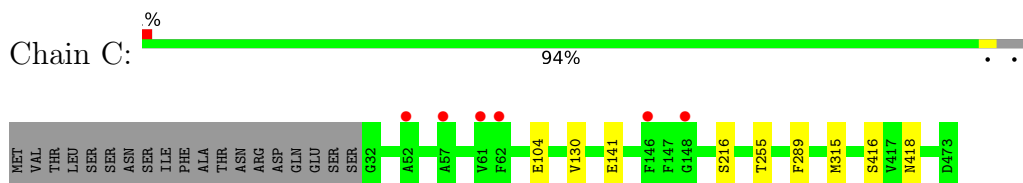
- Molecule 2: Photosystem II CP47 reaction center protein



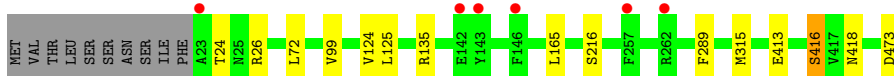
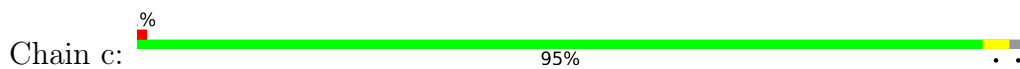
- Molecule 2: Photosystem II CP47 reaction center protein



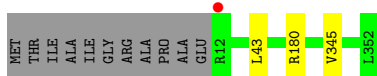
- Molecule 3: Photosystem II CP43 reaction center protein



- Molecule 3: Photosystem II CP43 reaction center protein



- Molecule 4: Photosystem II D2 protein



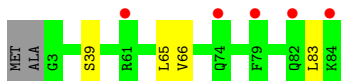
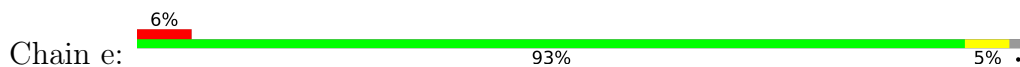
- Molecule 4: Photosystem II D2 protein



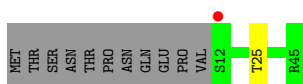
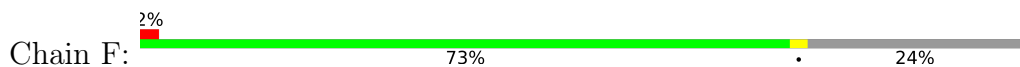
- Molecule 5: Cytochrome b559 subunit alpha



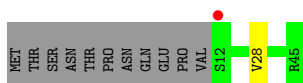
- Molecule 5: Cytochrome b559 subunit alpha



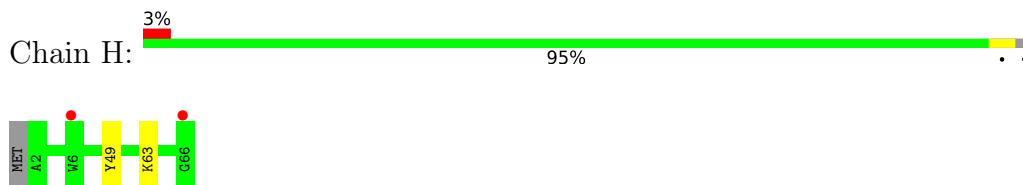
- Molecule 6: Cytochrome b559 subunit beta



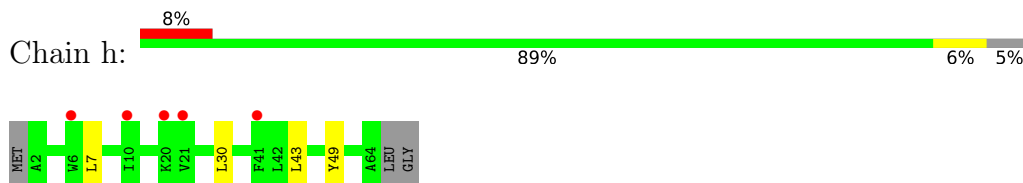
- Molecule 6: Cytochrome b559 subunit beta



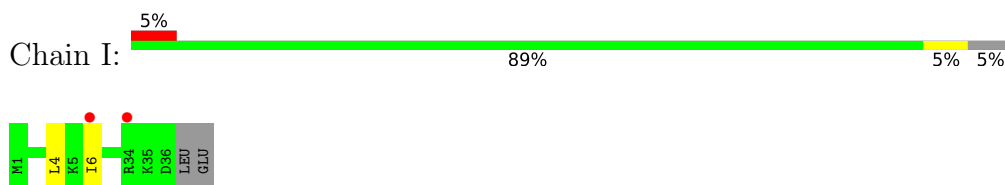
- Molecule 7: Photosystem II reaction center protein H



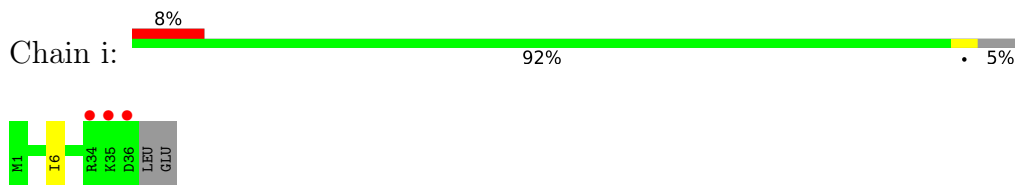
- Molecule 7: Photosystem II reaction center protein H



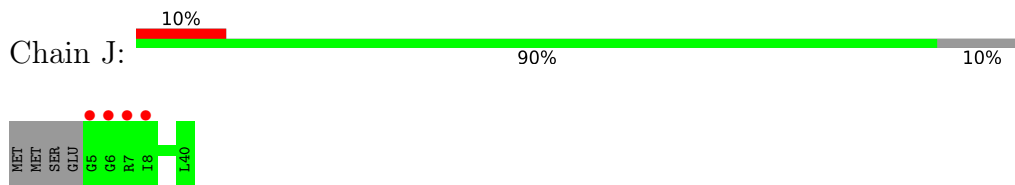
- Molecule 8: Photosystem II reaction center protein I



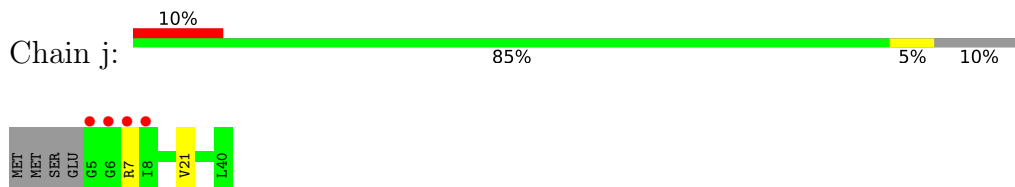
- Molecule 8: Photosystem II reaction center protein I



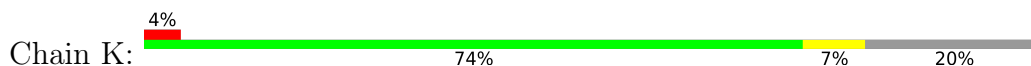
- Molecule 9: Photosystem II reaction center protein J

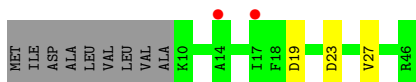


- Molecule 9: Photosystem II reaction center protein J

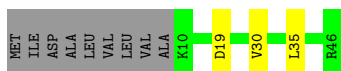


- Molecule 10: Photosystem II reaction center protein K





- Molecule 10: Photosystem II reaction center protein K

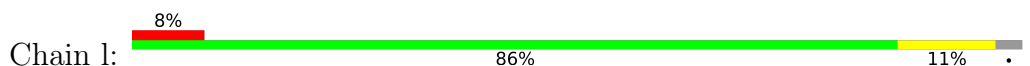


- Molecule 11: Photosystem II reaction center protein L

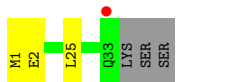
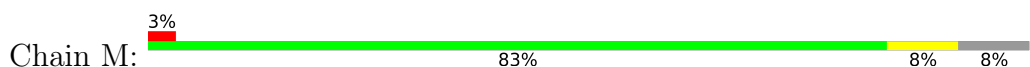


There are no outlier residues recorded for this chain.

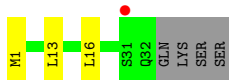
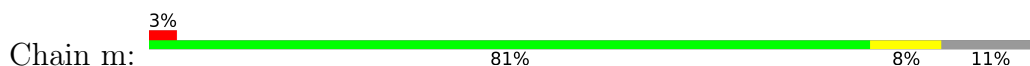
- Molecule 11: Photosystem II reaction center protein L



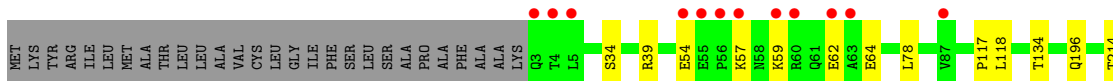
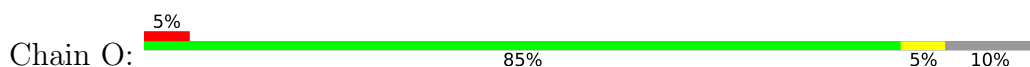
- Molecule 12: Photosystem II reaction center protein M



- Molecule 12: Photosystem II reaction center protein M

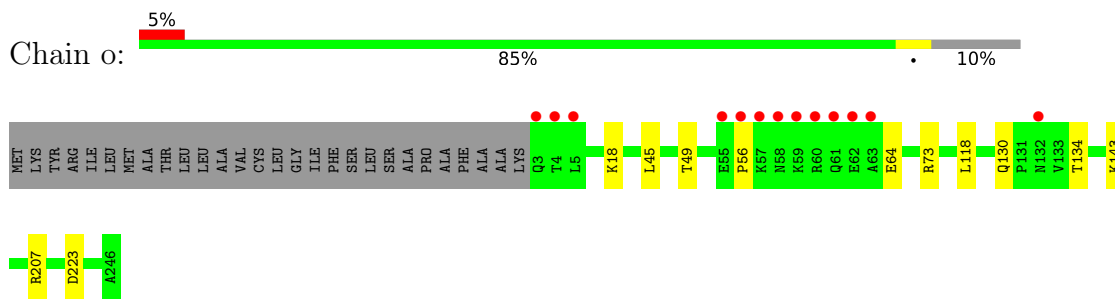


- Molecule 13: Photosystem II manganese-stabilizing polypeptide

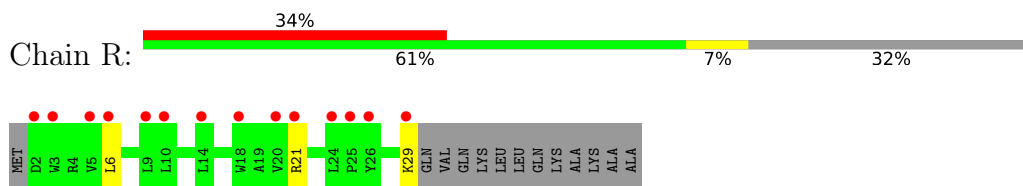


- Molecule 13: Photosystem II manganese-stabilizing polypeptide

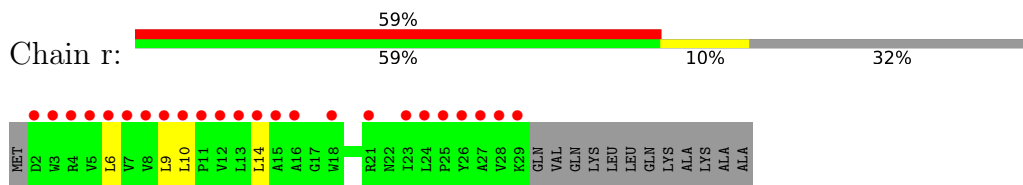




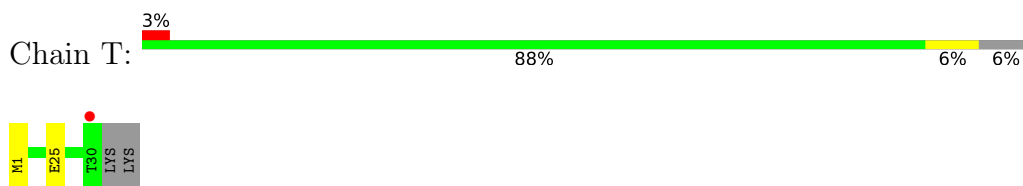
• Molecule 14: Photosystem II protein Y



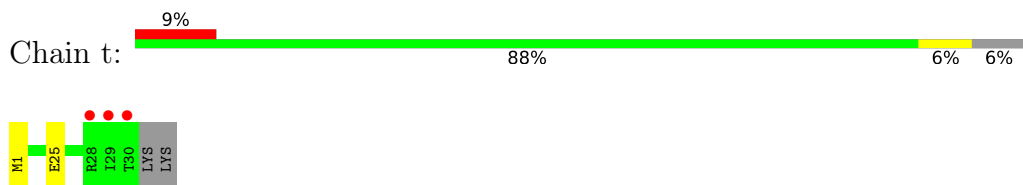
• Molecule 14: Photosystem II protein Y



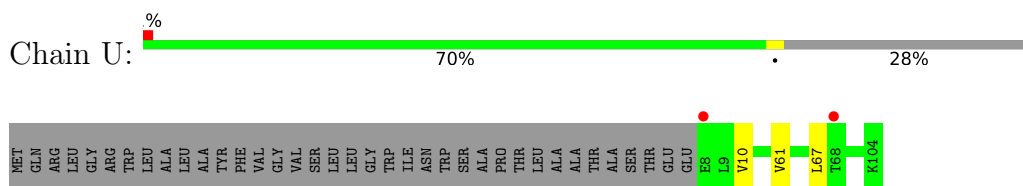
• Molecule 15: Photosystem II reaction center protein T



• Molecule 15: Photosystem II reaction center protein T

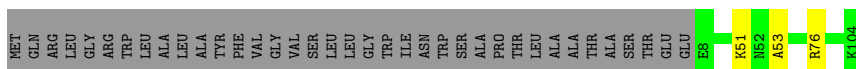


• Molecule 16: Photosystem II 12 kDa extrinsic protein

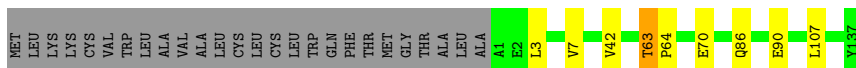
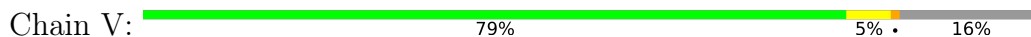


• Molecule 16: Photosystem II 12 kDa extrinsic protein

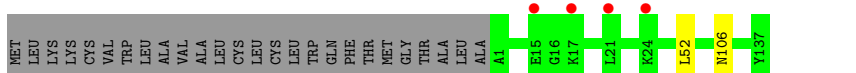
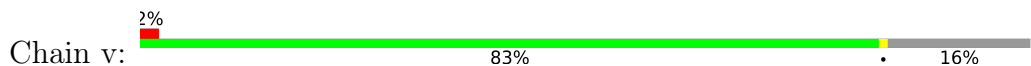




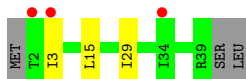
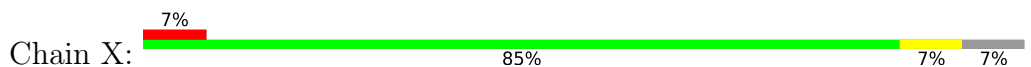
- Molecule 17: Cytochrome c-550



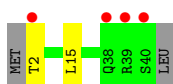
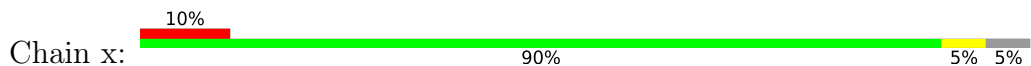
- Molecule 17: Cytochrome c-550



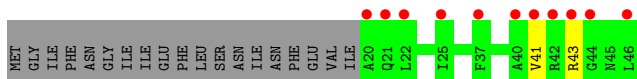
- Molecule 18: Photosystem II reaction center X protein



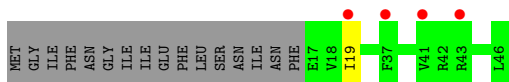
- Molecule 18: Photosystem II reaction center X protein



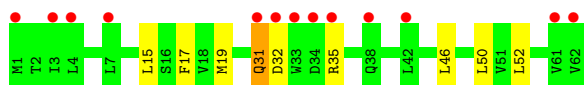
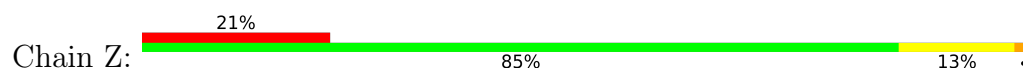
- Molecule 19: Photosystem II reaction center protein Ycf12



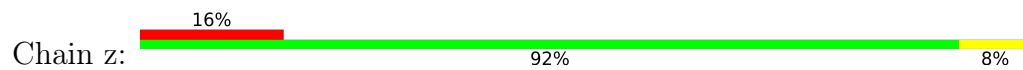
- Molecule 19: Photosystem II reaction center protein Ycf12



- Molecule 20: Photosystem II reaction center protein Z



- Molecule 20: Photosystem II reaction center protein Z



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	116.96Å 221.64Å 307.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.54 – 2.26 33.54 – 2.26	Depositor EDS
% Data completeness (in resolution range)	99.8 (33.54-2.26) 86.8 (33.54-2.26)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.83 (at 2.27Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, $R_{free}$	0.178 , 0.238 0.178 , 0.238	Depositor DCC
$R_{free}$ test set	3302 reflections (0.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.1	Xtrriage
Anisotropy	0.248	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 56.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	103278	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: SQD, PHO, DGD, LMG, LHG, OEX, BCR, HEC, FME, FE2, STE, CLA, BCT, PL9, HEM, CL

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	0.64	0/2707	0.67	0/3692
1	a	0.63	0/2704	0.67	0/3688
2	B	0.64	0/4161	0.68	0/5669
2	b	0.61	0/4118	0.67	0/5611
3	C	0.60	0/3547	0.66	0/4830
3	c	0.56	0/3619	0.65	1/4926 (0.0%)
4	D	0.63	0/2812	0.67	0/3832
4	d	0.61	0/2821	0.69	1/3844 (0.0%)
5	E	0.52	0/688	0.62	0/940
5	e	0.53	0/683	0.65	0/932
6	F	0.51	0/284	0.60	0/387
6	f	0.59	0/284	0.62	0/387
7	H	0.64	0/523	0.70	0/713
7	h	0.59	0/511	0.69	0/697
8	I	0.62	0/293	0.66	0/396
8	i	0.62	0/293	0.66	0/396
9	J	0.53	0/263	0.63	0/356
9	j	0.49	0/263	0.62	0/356
10	K	0.50	0/303	0.69	1/416 (0.2%)
10	k	0.48	0/303	0.59	0/416
11	L	0.67	0/311	0.65	0/422
11	l	0.66	0/303	0.70	0/412
12	M	0.65	0/249	0.64	0/341
12	m	0.70	0/244	0.69	0/334
13	O	0.58	0/1904	0.74	1/2585 (0.0%)
13	o	0.61	0/1905	0.73	1/2583 (0.0%)
14	R	0.46	0/227	0.60	0/313
14	r	0.41	0/227	0.58	0/313
15	T	0.68	0/257	0.63	0/349
15	t	0.65	0/255	0.62	0/346
16	U	0.58	0/785	0.68	0/1064
16	u	0.58	0/785	0.71	0/1064

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
17	V	0.56	0/1085	0.68	1/1473 (0.1%)
17	v	0.59	0/1085	0.65	0/1473
18	X	0.48	0/284	0.62	0/384
18	x	0.46	0/289	0.58	0/391
19	Y	0.47	0/197	0.61	0/264
19	y	0.38	0/219	0.51	0/294
20	Z	0.47	0/490	0.55	0/669
20	z	0.42	0/488	0.53	0/666
All	All	0.60	0/42769	0.67	6/58224 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
17	V	0	1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	V	63	THR	C-N-CD	-6.35	106.63	120.60
4	d	297	ASP	CB-CG-OD1	6.25	123.92	118.30
13	O	223	ASP	CB-CG-OD1	6.22	123.90	118.30
3	c	473	ASP	CB-CG-OD1	5.70	123.43	118.30
10	K	23	ASP	CB-CG-OD1	5.56	123.31	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	V	63	THR	Peptide

## 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

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	332/344 (96%)	327 (98%)	5 (2%)	0	100	100
1	a	332/344 (96%)	326 (98%)	5 (2%)	1 (0%)	41	46
2	B	508/510 (100%)	500 (98%)	8 (2%)	0	100	100
2	b	503/510 (99%)	493 (98%)	10 (2%)	0	100	100
3	C	442/461 (96%)	431 (98%)	10 (2%)	1 (0%)	47	55
3	c	451/461 (98%)	437 (97%)	13 (3%)	1 (0%)	47	55
4	D	339/352 (96%)	331 (98%)	8 (2%)	0	100	100
4	d	340/352 (97%)	328 (96%)	12 (4%)	0	100	100
5	E	81/84 (96%)	79 (98%)	2 (2%)	0	100	100
5	e	80/84 (95%)	80 (100%)	0	0	100	100
6	F	32/45 (71%)	32 (100%)	0	0	100	100
6	f	32/45 (71%)	32 (100%)	0	0	100	100
7	H	63/66 (96%)	61 (97%)	2 (3%)	0	100	100
7	h	61/66 (92%)	57 (93%)	4 (7%)	0	100	100
8	I	34/38 (90%)	33 (97%)	1 (3%)	0	100	100
8	i	34/38 (90%)	32 (94%)	2 (6%)	0	100	100
9	J	34/40 (85%)	32 (94%)	2 (6%)	0	100	100
9	j	34/40 (85%)	32 (94%)	2 (6%)	0	100	100
10	K	35/46 (76%)	34 (97%)	1 (3%)	0	100	100
10	k	35/46 (76%)	35 (100%)	0	0	100	100
11	L	35/37 (95%)	35 (100%)	0	0	100	100
11	l	34/37 (92%)	34 (100%)	0	0	100	100
12	M	31/36 (86%)	31 (100%)	0	0	100	100
12	m	30/36 (83%)	27 (90%)	3 (10%)	0	100	100
13	O	243/272 (89%)	232 (96%)	8 (3%)	3 (1%)	13	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	o	242/272 (89%)	229 (95%)	11 (4%)	2 (1%)	19	17
14	R	26/41 (63%)	26 (100%)	0	0	100	100
14	r	26/41 (63%)	26 (100%)	0	0	100	100
15	T	28/32 (88%)	27 (96%)	1 (4%)	0	100	100
15	t	28/32 (88%)	28 (100%)	0	0	100	100
16	U	95/134 (71%)	92 (97%)	3 (3%)	0	100	100
16	u	95/134 (71%)	90 (95%)	4 (4%)	1 (1%)	14	10
17	V	135/163 (83%)	129 (96%)	5 (4%)	1 (1%)	22	21
17	v	135/163 (83%)	132 (98%)	3 (2%)	0	100	100
18	X	36/41 (88%)	34 (94%)	2 (6%)	0	100	100
18	x	37/41 (90%)	37 (100%)	0	0	100	100
19	Y	25/46 (54%)	24 (96%)	0	1 (4%)	3	1
19	y	28/46 (61%)	26 (93%)	2 (7%)	0	100	100
20	Z	60/62 (97%)	56 (93%)	3 (5%)	1 (2%)	9	4
20	z	60/62 (97%)	60 (100%)	0	0	100	100
All	All	5231/5700 (92%)	5087 (97%)	132 (2%)	12 (0%)	47	55

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	O	59	LYS
13	O	62	GLU
17	V	64	PRO
3	c	416	SER
16	u	53	ALA

### 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	270/280 (96%)	267 (99%)	3 (1%)	73	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	269/280 (96%)	260 (97%)	9 (3%)	38	46
2	B	408/407 (100%)	400 (98%)	8 (2%)	55	64
2	b	402/407 (99%)	392 (98%)	10 (2%)	47	56
3	C	346/362 (96%)	338 (98%)	8 (2%)	50	59
3	c	354/362 (98%)	339 (96%)	15 (4%)	30	34
4	D	276/283 (98%)	273 (99%)	3 (1%)	73	82
4	d	277/283 (98%)	264 (95%)	13 (5%)	26	29
5	E	72/73 (99%)	69 (96%)	3 (4%)	30	34
5	e	71/73 (97%)	67 (94%)	4 (6%)	21	21
6	F	28/39 (72%)	27 (96%)	1 (4%)	35	42
6	f	28/39 (72%)	27 (96%)	1 (4%)	35	42
7	H	54/55 (98%)	52 (96%)	2 (4%)	34	40
7	h	53/55 (96%)	49 (92%)	4 (8%)	13	12
8	I	32/34 (94%)	30 (94%)	2 (6%)	18	17
8	i	32/34 (94%)	31 (97%)	1 (3%)	40	49
9	J	24/28 (86%)	24 (100%)	0	100	100
9	j	24/28 (86%)	22 (92%)	2 (8%)	11	9
10	K	30/37 (81%)	28 (93%)	2 (7%)	16	15
10	k	30/37 (81%)	27 (90%)	3 (10%)	7	5
11	L	35/35 (100%)	35 (100%)	0	100	100
11	l	34/35 (97%)	30 (88%)	4 (12%)	5	3
12	M	28/32 (88%)	26 (93%)	2 (7%)	14	13
12	m	28/32 (88%)	26 (93%)	2 (7%)	14	13
13	O	206/228 (90%)	196 (95%)	10 (5%)	25	27
13	o	207/228 (91%)	198 (96%)	9 (4%)	29	33
14	R	22/33 (67%)	19 (86%)	3 (14%)	3	2
14	r	22/33 (67%)	18 (82%)	4 (18%)	1	0
15	T	26/28 (93%)	25 (96%)	1 (4%)	33	39
15	t	25/28 (89%)	24 (96%)	1 (4%)	31	37
16	U	84/112 (75%)	81 (96%)	3 (4%)	35	42
16	u	84/112 (75%)	83 (99%)	1 (1%)	71	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	V	117/138 (85%)	111 (95%)	6 (5%)	24	25
17	v	117/138 (85%)	115 (98%)	2 (2%)	60	71
18	X	31/34 (91%)	28 (90%)	3 (10%)	8	6
18	x	31/34 (91%)	29 (94%)	2 (6%)	17	16
19	Y	19/37 (51%)	18 (95%)	1 (5%)	22	23
19	y	22/37 (60%)	21 (96%)	1 (4%)	27	31
20	Z	52/52 (100%)	43 (83%)	9 (17%)	2	0
20	z	51/52 (98%)	46 (90%)	5 (10%)	8	6
All	All	4321/4654 (93%)	4158 (96%)	163 (4%)	34	39

5 of 163 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	d	321	LEU
13	o	130	GLN
5	e	66	VAL
10	k	30	VAL
14	r	14	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
7	h	59	ASN
16	u	78	ASN
20	z	31	GLN
13	o	61	GLN
16	U	81	HIS

### 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	0.86	0	7,9,11	0.99	0
15	FME	t	1	15	8,9,10	1.17	1 (12%)	7,9,11	0.87	0
12	FME	m	1	12	8,9,10	1.10	1 (12%)	7,9,11	0.50	0
8	FME	I	1	8	8,9,10	1.04	0	7,9,11	0.66	0
12	FME	M	1	12	8,9,10	1.00	0	7,9,11	1.17	1 (14%)
15	FME	T	1	15	8,9,10	0.82	0	7,9,11	1.33	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	FME	i	1	8	-	4/7/9/11	-
15	FME	t	1	15	-	2/7/9/11	-
12	FME	m	1	12	-	0/7/9/11	-
8	FME	I	1	8	-	0/7/9/11	-
12	FME	M	1	12	-	0/7/9/11	-
15	FME	T	1	15	-	1/7/9/11	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	t	1	FME	CA-N	-2.41	1.42	1.46
12	m	1	FME	CA-N	-2.37	1.43	1.46

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	M	1	FME	CA-N-CN	-2.37	119.18	122.82
15	T	1	FME	C-CA-N	2.04	113.42	109.73

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	i	1	FME	N-CA-CB-CG
8	i	1	FME	C-CA-CB-CG
15	t	1	FME	O-C-CA-CB
15	T	1	FME	CB-CG-SD-CE
8	i	1	FME	CA-CB-CG-SD

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 186 ligands modelled in this entry, 6 are monoatomic - leaving 180 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$
32	STE	E	102	-	11,11,19	0.84	0	11,11,19	0.96	1 (9%)
32	STE	B	620	-	16,16,19	0.84	1 (6%)	16,16,19	0.88	1 (6%)
22	CLA	B	613	-	65,73,73	1.61	10 (15%)	76,113,113	1.49	9 (11%)
32	STE	B	626	-	15,15,19	0.45	0	14,14,19	0.72	0
30	DGD	A	414	-	67,67,67	1.23	8 (11%)	81,81,81	1.33	9 (11%)
33	BCT	a	409	21	2,3,3	1.35	0	2,3,3	3.73	2 (100%)
27	LMG	A	410	-	48,48,55	0.94	3 (6%)	56,56,63	1.28	7 (12%)
22	CLA	B	614	-	65,73,73	1.82	10 (15%)	76,113,113	1.51	12 (15%)
22	CLA	B	602	-	65,73,73	1.63	8 (12%)	76,113,113	1.47	11 (14%)
22	CLA	B	606	-	65,73,73	1.62	9 (13%)	76,113,113	1.65	9 (11%)
22	CLA	B	608	-	65,73,73	1.76	13 (20%)	76,113,113	1.38	13 (17%)
22	CLA	C	506	-	65,73,73	1.51	8 (12%)	76,113,113	1.28	8 (10%)
23	PHO	d	401	-	51,69,69	1.05	4 (7%)	47,99,99	1.41	7 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
22	CLA	B	604	-	65,73,73	1.40	9 (13%)	76,113,113	1.82	17 (22%)
28	LHG	D	409	-	48,48,48	0.77	3 (6%)	51,54,54	1.31	7 (13%)
22	CLA	D	404	36	65,73,73	1.32	8 (12%)	76,113,113	1.42	8 (10%)
23	PHO	a	404	-	51,69,69	1.13	6 (11%)	47,99,99	1.26	5 (10%)
30	DGD	C	517	-	63,63,67	1.14	6 (9%)	77,77,81	1.34	11 (14%)
30	DGD	h	101	-	63,63,67	1.22	9 (14%)	77,77,81	1.47	15 (19%)
22	CLA	c	504	36	60,68,73	1.59	7 (11%)	70,107,113	1.46	8 (11%)
30	DGD	c	515	-	63,63,67	1.12	8 (12%)	77,77,81	1.37	9 (11%)
22	CLA	A	402	-	65,73,73	1.44	7 (10%)	76,113,113	1.43	10 (13%)
32	STE	D	412	-	19,19,19	0.64	0	19,19,19	1.21	1 (5%)
24	BCR	B	619	-	41,41,41	1.27	3 (7%)	56,56,56	1.43	9 (16%)
24	BCR	K	101	-	41,41,41	1.09	2 (4%)	56,56,56	1.25	6 (10%)
22	CLA	C	504	36	59,67,73	1.52	8 (13%)	68,105,113	1.39	10 (14%)
22	CLA	A	403	36	65,73,73	1.55	10 (15%)	76,113,113	1.32	10 (13%)
22	CLA	B	601	36	65,73,73	1.83	10 (15%)	76,113,113	1.28	4 (5%)
22	CLA	C	505	-	65,73,73	1.59	8 (12%)	76,113,113	1.47	7 (9%)
34	HEM	F	101	5,6	41,50,50	1.53	5 (12%)	45,82,82	1.37	7 (15%)
22	CLA	c	505	-	65,73,73	1.43	7 (10%)	76,113,113	1.32	6 (7%)
27	LMG	D	408	-	51,51,55	1.00	4 (7%)	59,59,63	1.27	6 (10%)
22	CLA	C	513	-	65,73,73	1.52	12 (18%)	76,113,113	1.42	10 (13%)
35	HEC	v	201	17	32,50,50	2.28	4 (12%)	24,82,82	1.56	4 (16%)
24	BCR	Z	101	-	41,41,41	1.11	3 (7%)	56,56,56	1.46	11 (19%)
32	STE	I	101	-	14,14,19	0.51	0	13,13,19	0.58	0
22	CLA	c	513	-	65,73,73	1.56	11 (16%)	76,113,113	1.35	8 (10%)
32	STE	M	104	-	14,14,19	0.39	0	13,13,19	0.83	0
22	CLA	d	403	-	65,73,73	1.57	11 (16%)	76,113,113	1.31	9 (11%)
27	LMG	a	414	-	49,49,55	0.91	1 (2%)	57,57,63	1.34	5 (8%)
24	BCR	D	406	-	41,41,41	1.19	2 (4%)	56,56,56	1.13	4 (7%)
22	CLA	B	609	-	65,73,73	1.43	10 (15%)	76,113,113	1.41	9 (11%)
30	DGD	C	515	-	63,63,67	1.26	8 (12%)	77,77,81	1.42	9 (11%)
22	CLA	c	502	-	65,73,73	1.45	8 (12%)	76,113,113	1.41	10 (13%)
32	STE	C	519	-	11,11,19	0.79	0	11,11,19	1.41	2 (18%)
28	LHG	e	102	-	41,41,48	0.93	3 (7%)	44,47,54	1.29	4 (9%)
22	CLA	b	613	-	65,73,73	1.40	10 (15%)	76,113,113	1.61	13 (17%)
32	STE	c	519	-	19,19,19	0.60	0	19,19,19	1.21	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
27	LMG	d	408	-	21,21,55	0.67	1 (4%)	20,20,63	1.04	0
22	CLA	b	611	-	65,73,73	1.55	7 (10%)	76,113,113	1.53	11 (14%)
23	PHO	D	401	-	51,69,69	1.15	6 (11%)	47,99,99	1.30	7 (14%)
24	BCR	b	618	-	41,41,41	1.31	4 (9%)	56,56,56	1.33	8 (14%)
32	STE	M	102	-	14,14,19	0.74	0	14,14,19	1.16	2 (14%)
30	DGD	C	516	-	63,63,67	1.25	7 (11%)	77,77,81	1.49	11 (14%)
29	SQD	f	101	-	40,41,54	1.13	5 (12%)	49,52,65	1.88	8 (16%)
22	CLA	d	402	-	65,73,73	1.48	7 (10%)	76,113,113	1.46	8 (10%)
32	STE	k	104	-	11,11,19	0.94	1 (9%)	11,11,19	1.15	1 (9%)
30	DGD	c	516	-	63,63,67	1.09	5 (7%)	77,77,81	1.40	11 (14%)
22	CLA	C	501	-	65,73,73	1.64	11 (16%)	76,113,113	1.34	10 (13%)
22	CLA	c	511	3	65,73,73	1.83	10 (15%)	76,113,113	1.36	4 (5%)
22	CLA	b	605	-	65,73,73	1.40	9 (13%)	76,113,113	1.59	11 (14%)
22	CLA	D	403	-	65,73,73	1.44	10 (15%)	76,113,113	1.55	9 (11%)
22	CLA	b	609	-	65,73,73	1.84	10 (15%)	76,113,113	1.64	9 (11%)
27	LMG	C	518	-	48,48,55	1.05	6 (12%)	56,56,63	1.37	5 (8%)
32	STE	d	410	-	16,16,19	0.63	0	16,16,19	1.04	0
22	CLA	b	608	-	65,73,73	1.45	8 (12%)	76,113,113	1.21	7 (9%)
32	STE	b	624	-	15,15,19	0.92	1 (6%)	15,15,19	0.73	0
22	CLA	b	606	-	65,73,73	1.72	9 (13%)	76,113,113	1.62	9 (11%)
27	LMG	m	101	-	51,51,55	1.09	4 (7%)	59,59,63	1.46	8 (13%)
27	LMG	c	520	-	48,48,55	1.10	5 (10%)	56,56,63	1.24	6 (10%)
29	SQD	B	622	-	53,54,54	0.98	3 (5%)	62,65,65	1.91	13 (20%)
22	CLA	b	601	36	65,73,73	1.69	7 (10%)	76,113,113	1.56	9 (11%)
28	LHG	B	621	-	48,48,48	0.99	2 (4%)	51,54,54	1.33	7 (13%)
28	LHG	d	406	-	48,48,48	0.70	1 (2%)	51,54,54	1.24	5 (9%)
30	DGD	B	623	-	43,43,67	1.21	6 (13%)	45,45,81	1.26	5 (11%)
32	STE	l	102	-	17,17,19	0.41	0	16,16,19	0.79	0
22	CLA	C	507	36	65,73,73	1.43	7 (10%)	76,113,113	1.39	9 (11%)
22	CLA	a	405	-	65,73,73	1.56	11 (16%)	76,113,113	1.36	10 (13%)
22	CLA	C	508	-	65,73,73	1.72	8 (12%)	76,113,113	1.36	11 (14%)
24	BCR	b	619	-	41,41,41	1.19	2 (4%)	56,56,56	1.40	9 (16%)
26	PL9	a	410	-	55,55,55	0.83	2 (3%)	68,69,69	1.76	13 (19%)
32	STE	C	520	-	15,15,19	0.53	0	14,14,19	0.60	0
22	CLA	b	612	-	65,73,73	1.39	5 (7%)	76,113,113	1.46	8 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
32	STE	H	103	-	17,17,19	0.51	0	16,16,19	0.55	0
32	STE	t	103	-	9,9,19	0.39	0	8,8,19	0.63	0
28	LHG	b	623	-	48,48,48	0.99	4 (8%)	51,54,54	1.24	7 (13%)
24	BCR	k	101	-	41,41,41	1.07	2 (4%)	56,56,56	1.30	5 (8%)
32	STE	m	102	-	11,11,19	0.64	0	11,11,19	1.27	1 (9%)
22	CLA	b	616	-	60,68,73	1.46	10 (16%)	70,107,113	1.65	8 (11%)
24	BCR	k	103	-	41,41,41	1.01	2 (4%)	56,56,56	1.18	7 (12%)
27	LMG	D	411	-	26,26,55	0.94	2 (7%)	26,26,63	1.35	3 (11%)
30	DGD	c	517	-	63,63,67	1.14	8 (12%)	77,77,81	1.50	14 (18%)
22	CLA	B	607	36	65,73,73	1.44	10 (15%)	76,113,113	1.60	10 (13%)
24	BCR	A	406	-	41,41,41	1.08	2 (4%)	56,56,56	1.39	11 (19%)
28	LHG	E	101	-	48,48,48	0.94	4 (8%)	51,54,54	1.24	8 (15%)
24	BCR	d	404	-	41,41,41	1.13	2 (4%)	56,56,56	1.17	5 (8%)
32	STE	a	415	-	11,11,19	0.93	1 (9%)	11,11,19	0.98	1 (9%)
26	PL9	A	409	-	55,55,55	1.18	2 (3%)	68,69,69	1.71	15 (22%)
32	STE	C	521	-	11,11,19	0.60	0	11,11,19	1.40	3 (27%)
32	STE	B	624	-	11,11,19	0.84	0	11,11,19	0.98	0
22	CLA	B	605	-	65,73,73	1.49	9 (13%)	76,113,113	1.47	9 (11%)
22	CLA	c	506	-	65,73,73	1.55	11 (16%)	76,113,113	1.33	9 (11%)
32	STE	b	620	-	15,15,19	0.52	0	14,14,19	0.70	0
32	STE	x	102	-	19,19,19	0.65	0	19,19,19	1.13	1 (5%)
27	LMG	M	101	-	51,51,55	0.96	3 (5%)	59,59,63	1.36	6 (10%)
22	CLA	c	510	-	65,73,73	1.66	11 (16%)	76,113,113	1.52	10 (13%)
24	BCR	C	514	-	41,41,41	1.21	4 (9%)	56,56,56	1.26	4 (7%)
24	BCR	B	617	-	41,41,41	1.24	4 (9%)	56,56,56	1.29	8 (14%)
23	PHO	A	404	-	51,69,69	1.21	6 (11%)	47,99,99	1.37	9 (19%)
22	CLA	C	512	-	65,73,73	1.45	5 (7%)	76,113,113	1.58	11 (14%)
32	STE	t	102	-	13,13,19	0.66	0	13,13,19	1.15	1 (7%)
22	CLA	c	512	-	65,73,73	1.56	9 (13%)	76,113,113	1.56	15 (19%)
22	CLA	B	611	-	65,73,73	1.43	7 (10%)	76,113,113	1.51	10 (13%)
24	BCR	B	618	-	41,41,41	1.10	3 (7%)	56,56,56	1.12	1 (1%)
22	CLA	C	510	-	65,73,73	1.60	9 (13%)	76,113,113	1.45	8 (10%)
22	CLA	B	612	-	65,73,73	1.33	6 (9%)	76,113,113	1.52	11 (14%)
26	PL9	D	407	-	55,55,55	1.61	8 (14%)	68,69,69	1.73	16 (23%)
32	STE	b	621	-	19,19,19	0.67	0	19,19,19	0.90	0
24	BCR	a	406	-	41,41,41	1.09	4 (9%)	56,56,56	1.16	3 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
22	CLA	a	402	-	65,73,73	1.57	10 (15%)	76,113,113	1.38	9 (11%)
22	CLA	c	503	-	65,73,73	1.62	10 (15%)	76,113,113	1.49	9 (11%)
22	CLA	B	615	-	65,73,73	1.57	8 (12%)	76,113,113	1.42	9 (11%)
24	BCR	K	102	-	41,41,41	1.15	3 (7%)	56,56,56	1.29	6 (10%)
24	BCR	c	514	-	41,41,41	1.13	4 (9%)	56,56,56	1.32	6 (10%)
29	SQD	L	101	-	48,49,54	0.97	2 (4%)	57,60,65	2.26	16 (28%)
32	STE	b	626	-	9,9,19	0.41	0	8,8,19	0.67	0
27	LMG	d	409	-	44,44,55	1.04	4 (9%)	52,52,63	1.35	6 (11%)
29	SQD	A	412	-	51,52,54	1.06	5 (9%)	60,63,65	1.99	10 (16%)
22	CLA	B	616	-	60,68,73	1.59	12 (20%)	70,107,113	1.81	9 (12%)
26	PL9	d	405	-	55,55,55	1.42	7 (12%)	68,69,69	1.77	15 (22%)
24	BCR	x	101	-	41,41,41	1.09	2 (4%)	56,56,56	1.28	7 (12%)
22	CLA	b	614	-	65,73,73	1.71	9 (13%)	76,113,113	1.40	9 (11%)
22	CLA	b	602	-	65,73,73	1.63	10 (15%)	76,113,113	1.63	13 (17%)
22	CLA	c	508	-	64,72,73	1.51	10 (15%)	74,111,113	1.61	9 (12%)
22	CLA	B	610	36	65,73,73	1.69	8 (12%)	76,113,113	1.33	9 (11%)
33	BCT	D	402	21	2,3,3	1.28	0	2,3,3	2.79	1 (50%)
24	BCR	H	101	-	41,41,41	1.10	2 (4%)	56,56,56	1.36	7 (12%)
24	BCR	t	101	-	41,41,41	1.22	3 (7%)	56,56,56	1.30	7 (12%)
22	CLA	b	604	-	65,73,73	1.44	8 (12%)	76,113,113	1.65	12 (15%)
29	SQD	A	413	-	38,38,54	1.05	3 (7%)	40,40,65	1.58	6 (15%)
30	DGD	H	102	-	63,63,67	1.42	14 (22%)	77,77,81	1.38	11 (14%)
22	CLA	A	405	-	54,62,73	1.80	11 (20%)	62,99,113	1.68	10 (16%)
29	SQD	a	413	-	35,35,54	1.09	2 (5%)	37,37,65	1.33	4 (10%)
32	STE	b	625	-	19,19,19	0.78	0	19,19,19	0.88	1 (5%)
22	CLA	C	503	-	65,73,73	1.67	8 (12%)	76,113,113	1.81	10 (13%)
22	CLA	a	403	36	65,73,73	1.64	7 (10%)	76,113,113	1.62	13 (17%)
22	CLA	a	411	36	65,73,73	1.61	10 (15%)	76,113,113	1.60	13 (17%)
24	BCR	b	617	-	41,41,41	1.19	3 (7%)	56,56,56	1.35	8 (14%)
27	LMG	c	518	-	37,37,55	0.98	1 (2%)	45,45,63	1.33	6 (13%)
22	CLA	c	507	36	65,73,73	1.56	13 (20%)	76,113,113	1.35	7 (9%)
28	LHG	L	102	-	48,48,48	0.89	2 (4%)	51,54,54	1.16	4 (7%)
22	CLA	c	509	-	65,73,73	1.57	7 (10%)	76,113,113	1.46	7 (9%)
32	STE	B	627	-	11,11,19	0.76	0	11,11,19	1.10	1 (9%)
32	STE	J	101	-	11,11,19	0.57	0	11,11,19	1.48	2 (18%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
22	CLA	b	603	-	65,73,73	1.53	11 (16%)	76,113,113	1.64	12 (15%)
22	CLA	C	502	-	65,73,73	1.50	12 (18%)	76,113,113	1.37	9 (11%)
35	HEC	V	201	17	32,50,50	1.89	3 (9%)	24,82,82	2.17	6 (25%)
22	CLA	D	405	-	65,73,73	1.60	8 (12%)	76,113,113	1.58	11 (14%)
22	CLA	C	511	3	65,73,73	1.53	7 (10%)	76,113,113	1.45	9 (11%)
28	LHG	A	411	-	46,46,48	0.99	3 (6%)	49,52,54	1.22	3 (6%)
24	BCR	T	101	-	41,41,41	1.21	5 (12%)	56,56,56	1.31	6 (10%)
22	CLA	c	501	-	65,73,73	1.42	10 (15%)	76,113,113	1.59	11 (14%)
28	LHG	l	101	-	48,48,48	0.68	0	51,54,54	1.26	6 (11%)
22	CLA	b	607	36	65,73,73	1.52	9 (13%)	76,113,113	1.38	7 (9%)
22	CLA	b	610	36	65,73,73	1.49	13 (20%)	76,113,113	1.38	12 (15%)
22	CLA	C	509	-	65,73,73	1.32	8 (12%)	76,113,113	1.60	9 (11%)
27	LMG	D	410	-	31,31,55	0.86	1 (3%)	33,33,63	1.18	1 (3%)
28	LHG	d	407	-	38,38,48	0.83	2 (5%)	41,44,54	1.19	2 (4%)
27	LMG	b	622	-	55,55,55	1.13	6 (10%)	63,63,63	1.45	8 (12%)
22	CLA	b	615	-	65,73,73	1.80	12 (18%)	76,113,113	1.32	8 (10%)
29	SQD	a	412	-	53,54,54	0.99	4 (7%)	62,65,65	1.88	13 (20%)
29	SQD	F	102	-	35,36,54	0.95	3 (8%)	42,45,65	2.10	13 (30%)
31	OEX	a	416	36,3,1	0,15,15	-	-	-	-	-
32	STE	M	103	-	9,9,19	0.38	0	8,8,19	0.74	0
31	OEX	A	415	36,3,1	0,15,15	-	-	-	-	-
32	STE	j	101	-	11,11,19	0.96	0	11,11,19	0.88	0
34	HEM	e	101	5,6	41,50,50	1.46	4 (9%)	45,82,82	1.65	9 (20%)
22	CLA	B	603	-	65,73,73	1.56	8 (12%)	76,113,113	1.54	16 (21%)
24	BCR	k	102	-	41,41,41	1.11	3 (7%)	56,56,56	1.23	4 (7%)
32	STE	B	625	-	17,17,19	0.75	0	17,17,19	0.95	0

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
32	STE	E	102	-	-	7/9/9/17	-
32	STE	B	620	-	-	8/14/14/17	-
22	CLA	B	613	-	1/1/20/20	14/37/115/115	-
32	STE	B	626	-	-	6/13/13/17	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	DGD	A	414	-	-	27/55/95/95	0/2/2/2
27	LMG	A	410	-	-	24/43/63/70	0/1/1/1
22	CLA	B	614	-	1/1/20/20	16/37/115/115	-
22	CLA	B	602	-	1/1/20/20	12/37/115/115	-
22	CLA	B	606	-	1/1/20/20	10/37/115/115	-
22	CLA	B	608	-	-	1/37/115/115	-
22	CLA	C	506	-	1/1/20/20	13/37/115/115	-
23	PHO	d	401	-	-	6/37/103/103	0/5/6/6
22	CLA	B	604	-	1/1/20/20	12/37/115/115	-
28	LHG	D	409	-	-	19/53/53/53	-
22	CLA	D	404	36	1/1/20/20	7/37/115/115	-
23	PHO	a	404	-	-	7/37/103/103	0/5/6/6
30	DGD	C	517	-	-	12/51/91/95	0/2/2/2
30	DGD	h	101	-	-	16/51/91/95	0/2/2/2
22	CLA	c	504	36	1/1/19/20	12/31/109/115	-
30	DGD	c	515	-	-	24/51/91/95	0/2/2/2
22	CLA	A	402	-	1/1/20/20	2/37/115/115	-
32	STE	D	412	-	-	10/17/17/17	-
24	BCR	B	619	-	-	6/29/63/63	0/2/2/2
24	BCR	K	101	-	-	11/29/63/63	0/2/2/2
22	CLA	C	504	36	1/1/18/20	9/30/108/115	-
22	CLA	A	403	36	1/1/20/20	6/37/115/115	-
22	CLA	B	601	36	1/1/20/20	17/37/115/115	-
22	CLA	C	505	-	1/1/20/20	10/37/115/115	-
34	HEM	F	101	5,6	-	2/12/54/54	-
22	CLA	c	505	-	1/1/20/20	7/37/115/115	-
27	LMG	D	408	-	-	17/46/66/70	0/1/1/1
22	CLA	C	513	-	-	16/37/115/115	-
35	HEC	v	201	17	-	2/10/54/54	-
24	BCR	Z	101	-	-	10/29/63/63	0/2/2/2
32	STE	I	101	-	-	7/12/12/17	-
22	CLA	c	513	-	1/1/20/20	8/37/115/115	-
32	STE	M	104	-	-	8/12/12/17	-
22	CLA	d	403	-	-	6/37/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	LMG	a	414	-	-	21/44/64/70	0/1/1/1
24	BCR	D	406	-	-	6/29/63/63	0/2/2/2
22	CLA	B	609	-	-	5/37/115/115	-
30	DGD	C	515	-	-	21/51/91/95	0/2/2/2
22	CLA	c	502	-	1/1/20/20	16/37/115/115	-
32	STE	C	519	-	-	6/9/9/17	-
28	LHG	e	102	-	-	25/46/46/53	-
22	CLA	b	613	-	1/1/20/20	9/37/115/115	-
32	STE	c	519	-	-	12/17/17/17	-
27	LMG	d	408	-	-	9/17/17/70	-
22	CLA	b	611	-	1/1/20/20	11/37/115/115	-
23	PHO	D	401	-	-	1/37/103/103	0/5/6/6
24	BCR	b	618	-	-	1/29/63/63	0/2/2/2
32	STE	M	102	-	-	4/12/12/17	-
30	DGD	C	516	-	-	27/51/91/95	0/2/2/2
29	SQD	f	101	-	-	13/36/56/69	0/1/1/1
22	CLA	d	402	-	1/1/20/20	6/37/115/115	-
32	STE	k	104	-	-	2/9/9/17	-
30	DGD	c	516	-	-	22/51/91/95	0/2/2/2
22	CLA	C	501	-	1/1/20/20	4/37/115/115	-
22	CLA	c	511	3	1/1/20/20	12/37/115/115	-
22	CLA	b	605	-	1/1/20/20	12/37/115/115	-
22	CLA	D	403	-	1/1/20/20	7/37/115/115	-
22	CLA	b	609	-	1/1/20/20	7/37/115/115	-
27	LMG	C	518	-	-	20/43/63/70	0/1/1/1
32	STE	d	410	-	-	7/14/14/17	-
22	CLA	b	608	-	-	9/37/115/115	-
32	STE	b	624	-	-	8/13/13/17	-
22	CLA	b	606	-	1/1/20/20	10/37/115/115	-
27	LMG	m	101	-	-	23/46/66/70	0/1/1/1
27	LMG	c	520	-	-	26/43/63/70	0/1/1/1
29	SQD	B	622	-	-	16/49/69/69	0/1/1/1
22	CLA	b	601	36	1/1/20/20	17/37/115/115	-
28	LHG	B	621	-	-	16/53/53/53	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	LHG	d	406	-	-	22/53/53/53	-
30	DGD	B	623	-	-	24/45/45/95	-
32	STE	l	102	-	-	13/15/15/17	-
22	CLA	C	507	36	1/1/20/20	8/37/115/115	-
22	CLA	a	405	-	1/1/20/20	11/37/115/115	-
22	CLA	C	508	-	-	8/37/115/115	-
24	BCR	b	619	-	-	14/29/63/63	0/2/2/2
26	PL9	a	410	-	-	26/53/73/73	0/1/1/1
32	STE	C	520	-	-	4/13/13/17	-
22	CLA	b	612	-	1/1/20/20	14/37/115/115	-
32	STE	H	103	-	-	10/15/15/17	-
32	STE	t	103	-	-	4/7/7/17	-
28	LHG	b	623	-	-	24/53/53/53	-
24	BCR	k	101	-	-	13/29/63/63	0/2/2/2
32	STE	m	102	-	-	4/9/9/17	-
22	CLA	b	616	-	1/1/19/20	6/31/109/115	-
24	BCR	k	103	-	-	9/29/63/63	0/2/2/2
27	LMG	D	411	-	-	15/22/22/70	-
30	DGD	c	517	-	-	19/51/91/95	0/2/2/2
22	CLA	B	607	36	1/1/20/20	12/37/115/115	-
24	BCR	A	406	-	-	4/29/63/63	0/2/2/2
28	LHG	E	101	-	-	25/53/53/53	-
24	BCR	d	404	-	-	5/29/63/63	0/2/2/2
32	STE	a	415	-	-	3/9/9/17	-
26	PL9	A	409	-	-	24/53/73/73	0/1/1/1
32	STE	C	521	-	-	1/9/9/17	-
32	STE	B	624	-	-	7/9/9/17	-
22	CLA	B	605	-	1/1/20/20	11/37/115/115	-
22	CLA	c	506	-	1/1/20/20	13/37/115/115	-
32	STE	b	620	-	-	7/13/13/17	-
32	STE	x	102	-	-	12/17/17/17	-
27	LMG	M	101	-	-	25/46/66/70	0/1/1/1
22	CLA	c	510	-	1/1/20/20	10/37/115/115	-
24	BCR	C	514	-	-	6/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	BCR	B	617	-	-	7/29/63/63	0/2/2/2
23	PHO	A	404	-	-	3/37/103/103	0/5/6/6
22	CLA	C	512	-	1/1/20/20	19/37/115/115	-
32	STE	t	102	-	-	3/11/11/17	-
22	CLA	c	512	-	1/1/20/20	20/37/115/115	-
22	CLA	B	611	-	1/1/20/20	7/37/115/115	-
24	BCR	B	618	-	-	6/29/63/63	0/2/2/2
22	CLA	C	510	-	1/1/20/20	9/37/115/115	-
22	CLA	B	612	-	1/1/20/20	9/37/115/115	-
26	PL9	D	407	-	-	6/53/73/73	0/1/1/1
32	STE	b	621	-	-	9/17/17/17	-
24	BCR	a	406	-	-	5/29/63/63	0/2/2/2
22	CLA	a	402	-	1/1/20/20	3/37/115/115	-
22	CLA	c	503	-	1/1/20/20	10/37/115/115	-
22	CLA	B	615	-	1/1/20/20	7/37/115/115	-
24	BCR	K	102	-	-	6/29/63/63	0/2/2/2
24	BCR	c	514	-	-	4/29/63/63	0/2/2/2
29	SQD	L	101	-	-	25/44/64/69	0/1/1/1
32	STE	b	626	-	-	5/7/7/17	-
27	LMG	d	409	-	-	12/39/59/70	0/1/1/1
29	SQD	A	412	-	-	17/47/67/69	0/1/1/1
22	CLA	B	616	-	1/1/19/20	9/31/109/115	-
26	PL9	d	405	-	-	19/53/73/73	0/1/1/1
24	BCR	x	101	-	-	9/29/63/63	0/2/2/2
22	CLA	b	614	-	1/1/20/20	21/37/115/115	-
22	CLA	b	602	-	1/1/20/20	11/37/115/115	-
22	CLA	c	508	-	1/1/19/20	17/36/114/115	-
22	CLA	B	610	36	1/1/20/20	5/37/115/115	-
24	BCR	H	101	-	-	6/29/63/63	0/2/2/2
24	BCR	t	101	-	-	8/29/63/63	0/2/2/2
22	CLA	b	604	-	1/1/20/20	8/37/115/115	-
29	SQD	A	413	-	-	12/39/39/69	-
30	DGD	H	102	-	-	19/51/91/95	0/2/2/2
22	CLA	A	405	-	1/1/17/20	6/24/102/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
29	SQD	a	413	-	-	17/37/37/69	-
32	STE	b	625	-	-	6/17/17/17	-
22	CLA	C	503	-	1/1/20/20	4/37/115/115	-
22	CLA	a	403	36	1/1/20/20	15/37/115/115	-
22	CLA	a	411	36	1/1/20/20	13/37/115/115	-
24	BCR	b	617	-	-	5/29/63/63	0/2/2/2
27	LMG	c	518	-	-	9/31/51/70	0/1/1/1
22	CLA	c	507	36	1/1/20/20	10/37/115/115	-
28	LHG	L	102	-	-	22/53/53/53	-
22	CLA	c	509	-	1/1/20/20	16/37/115/115	-
32	STE	B	627	-	-	7/9/9/17	-
32	STE	J	101	-	-	5/9/9/17	-
22	CLA	b	603	-	1/1/20/20	14/37/115/115	-
22	CLA	C	502	-	1/1/20/20	7/37/115/115	-
35	HEC	V	201	17	-	2/10/54/54	-
22	CLA	D	405	-	-	11/37/115/115	-
22	CLA	C	511	3	1/1/20/20	15/37/115/115	-
28	LHG	A	411	-	-	22/51/51/53	-
24	BCR	T	101	-	-	10/29/63/63	0/2/2/2
22	CLA	c	501	-	1/1/20/20	3/37/115/115	-
28	LHG	l	101	-	-	18/53/53/53	-
22	CLA	b	607	36	1/1/20/20	13/37/115/115	-
22	CLA	b	610	36	1/1/20/20	8/37/115/115	-
22	CLA	C	509	-	1/1/20/20	8/37/115/115	-
27	LMG	D	410	-	-	17/33/33/70	-
28	LHG	d	407	-	-	15/43/43/53	-
27	LMG	b	622	-	-	24/50/70/70	0/1/1/1
22	CLA	b	615	-	1/1/20/20	9/37/115/115	-
29	SQD	a	412	-	-	21/49/69/69	0/1/1/1
29	SQD	F	102	-	-	11/28/48/69	0/1/1/1
32	STE	M	103	-	-	3/7/7/17	-
32	STE	j	101	-	-	2/9/9/17	-
34	HEM	e	101	5,6	-	2/12/54/54	-
22	CLA	B	603	-	1/1/20/20	13/37/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	BCR	k	102	-	-	13/29/63/63	0/2/2/2
32	STE	B	625	-	-	10/15/15/17	-

The worst 5 of 935 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	B	601	CLA	C4B-NB	8.52	1.42	1.35
26	D	407	PL9	C7-C3	-8.51	1.42	1.51
22	b	609	CLA	C4B-NB	8.40	1.42	1.35
22	c	504	CLA	C4B-NB	8.19	1.42	1.35
22	C	508	CLA	C4B-NB	8.18	1.42	1.35

The worst 5 of 1265 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	C	503	CLA	C4A-NA-C1A	10.28	111.33	106.71
22	B	616	CLA	C4A-NA-C1A	9.55	111.00	106.71
22	B	606	CLA	C4A-NA-C1A	8.85	110.69	106.71
29	a	412	SQD	O6-C1-C2	8.69	121.87	108.30
29	A	412	SQD	O6-C1-C2	8.59	121.72	108.30

5 of 63 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
22	A	402	CLA	ND
22	A	403	CLA	ND
22	A	405	CLA	ND
22	B	601	CLA	ND
22	B	602	CLA	ND

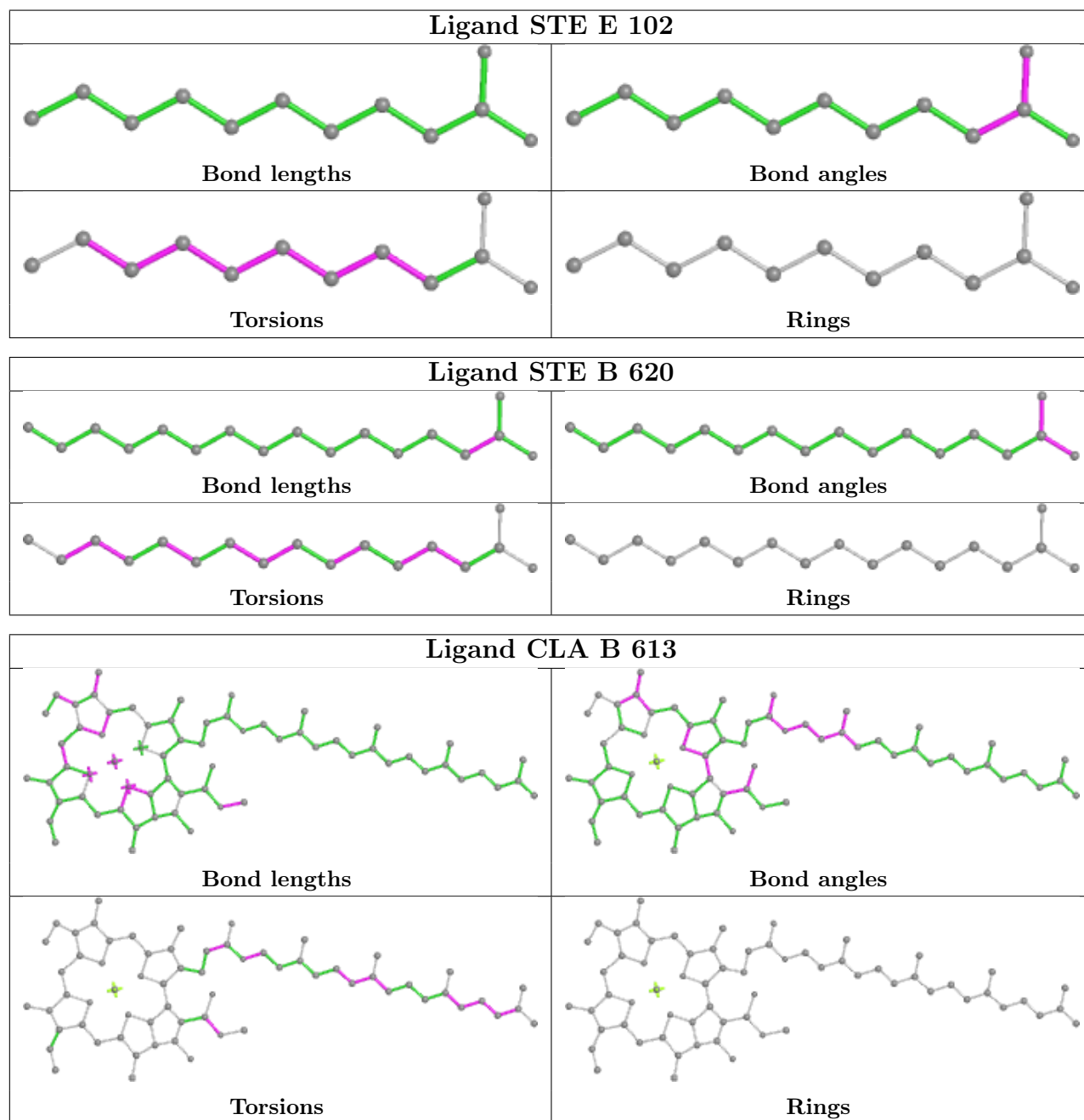
5 of 1973 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	A	405	CLA	C4-C3-C5-C6
22	B	601	CLA	C1A-C2A-CAA-CBA
22	B	601	CLA	CAD-CBD-CGD-O1D
22	B	601	CLA	CAD-CBD-CGD-O2D
22	B	605	CLA	C4-C3-C5-C6

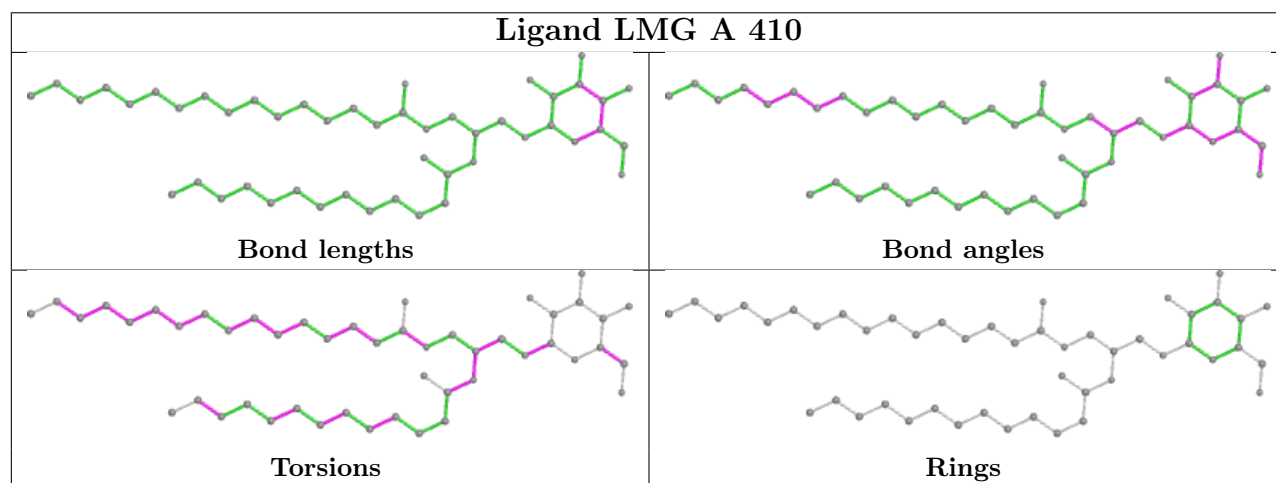
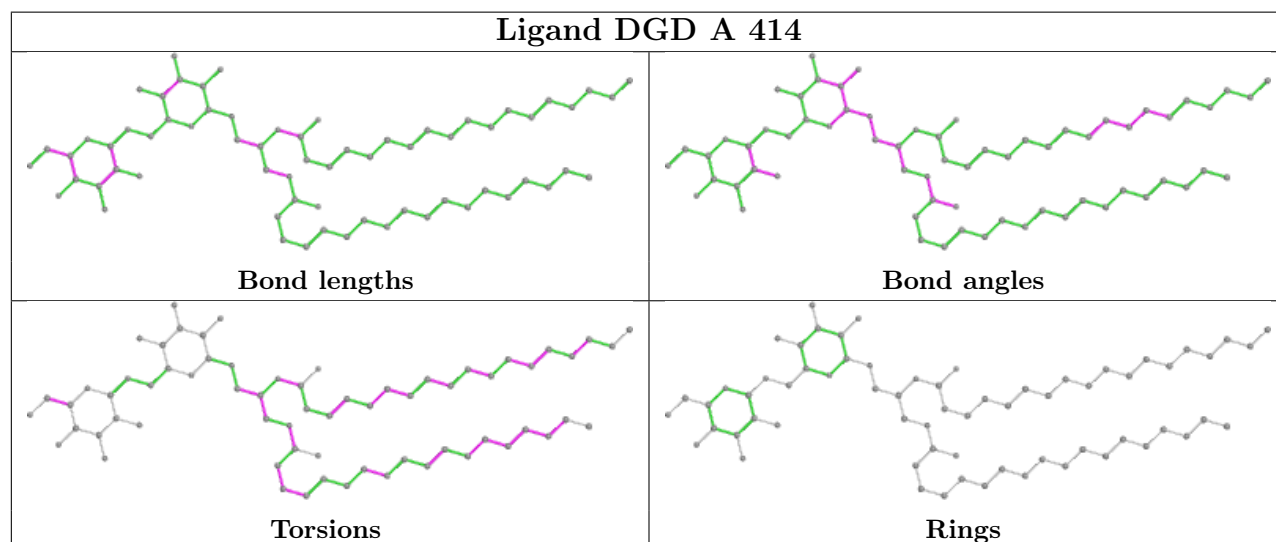
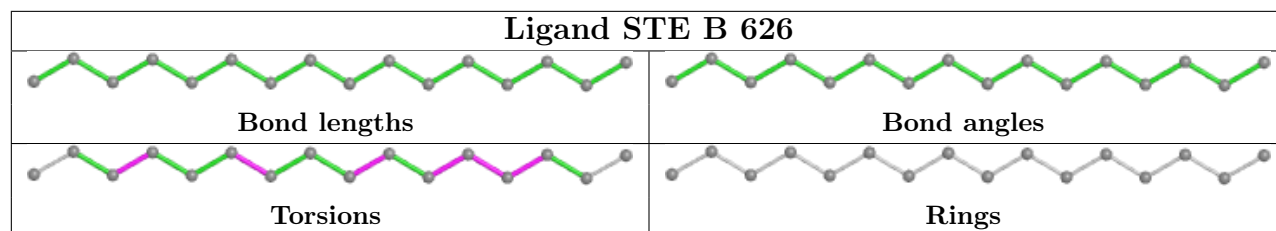
There are no ring outliers.

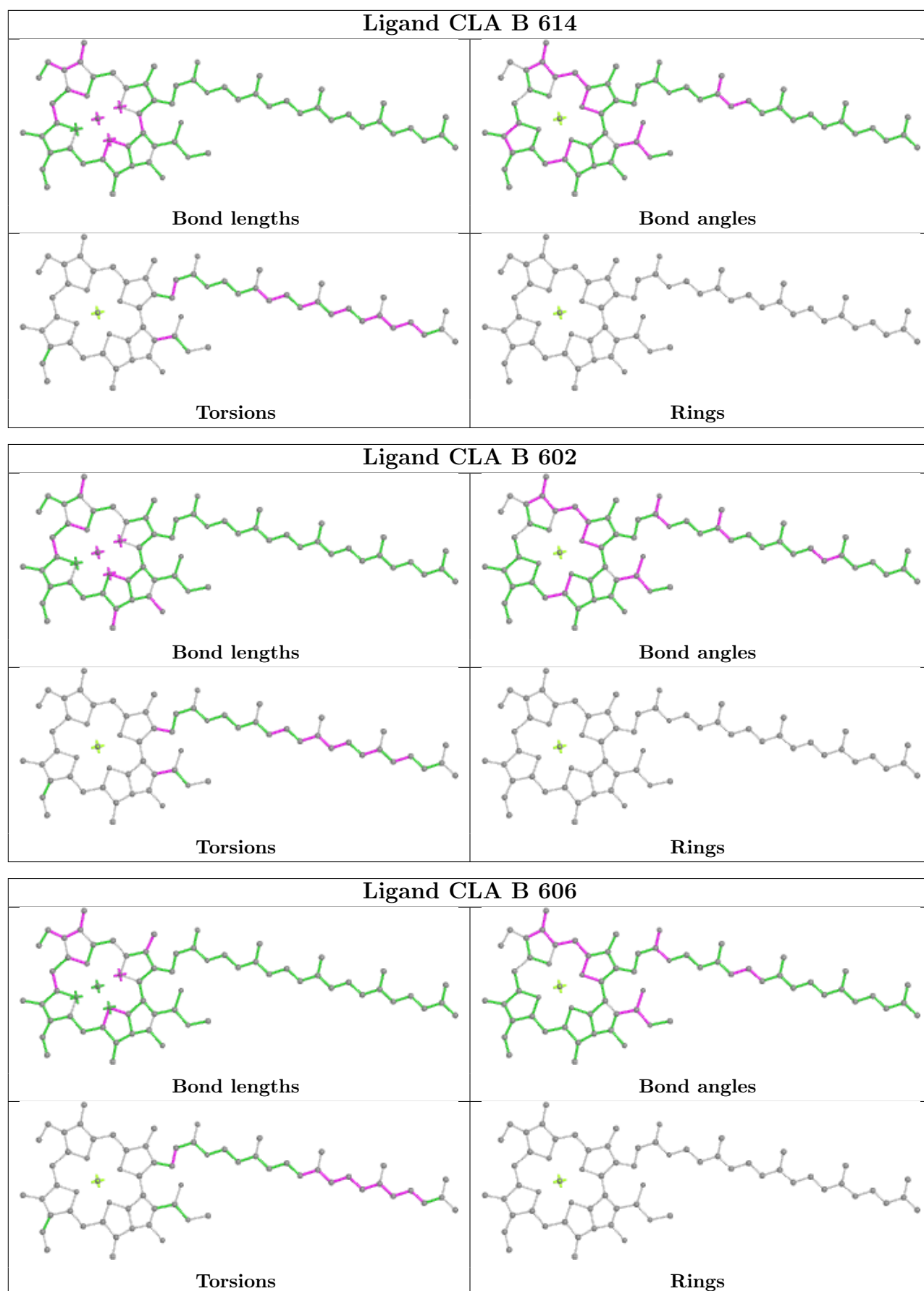
No monomer is involved in short contacts.

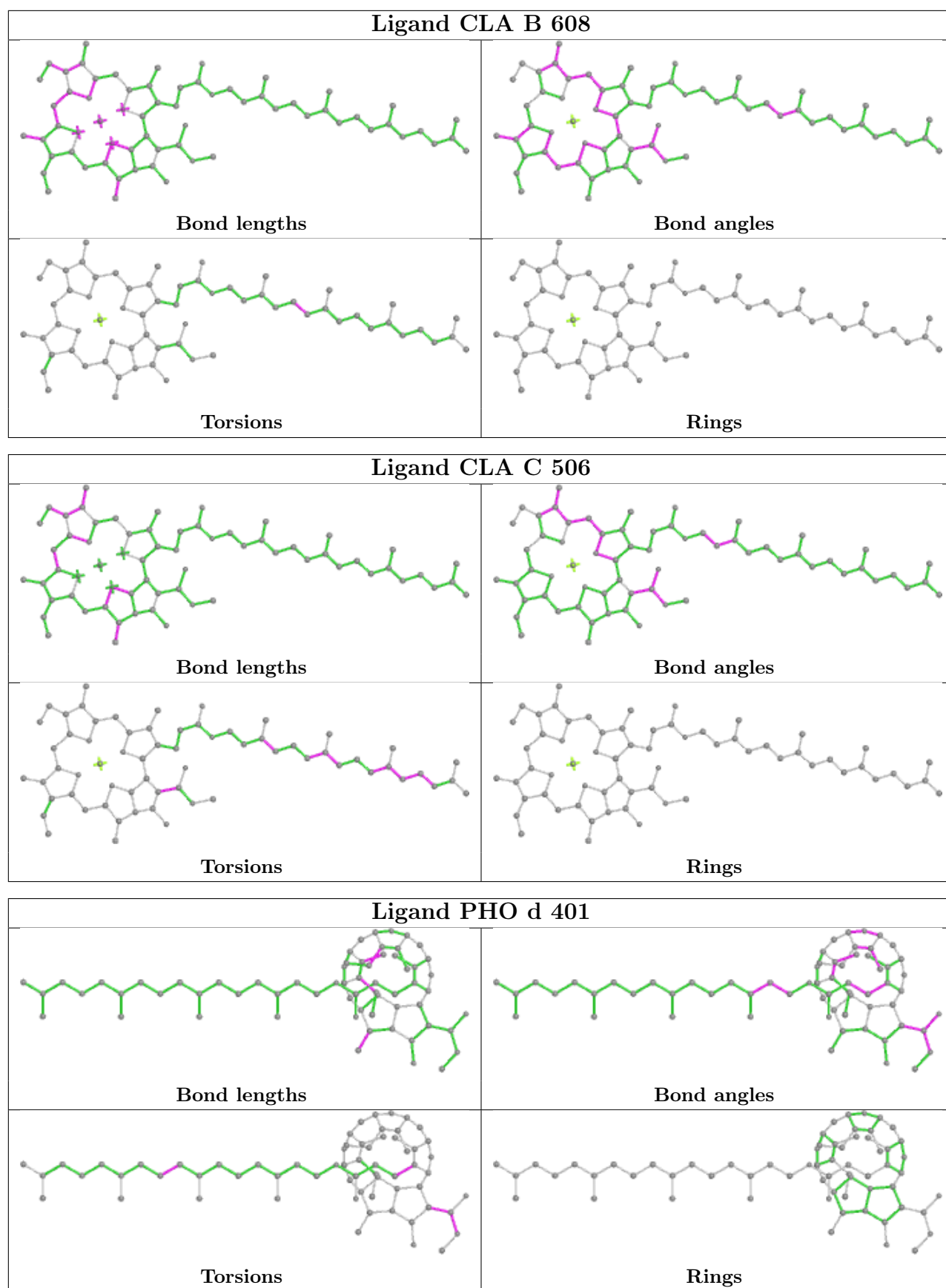
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

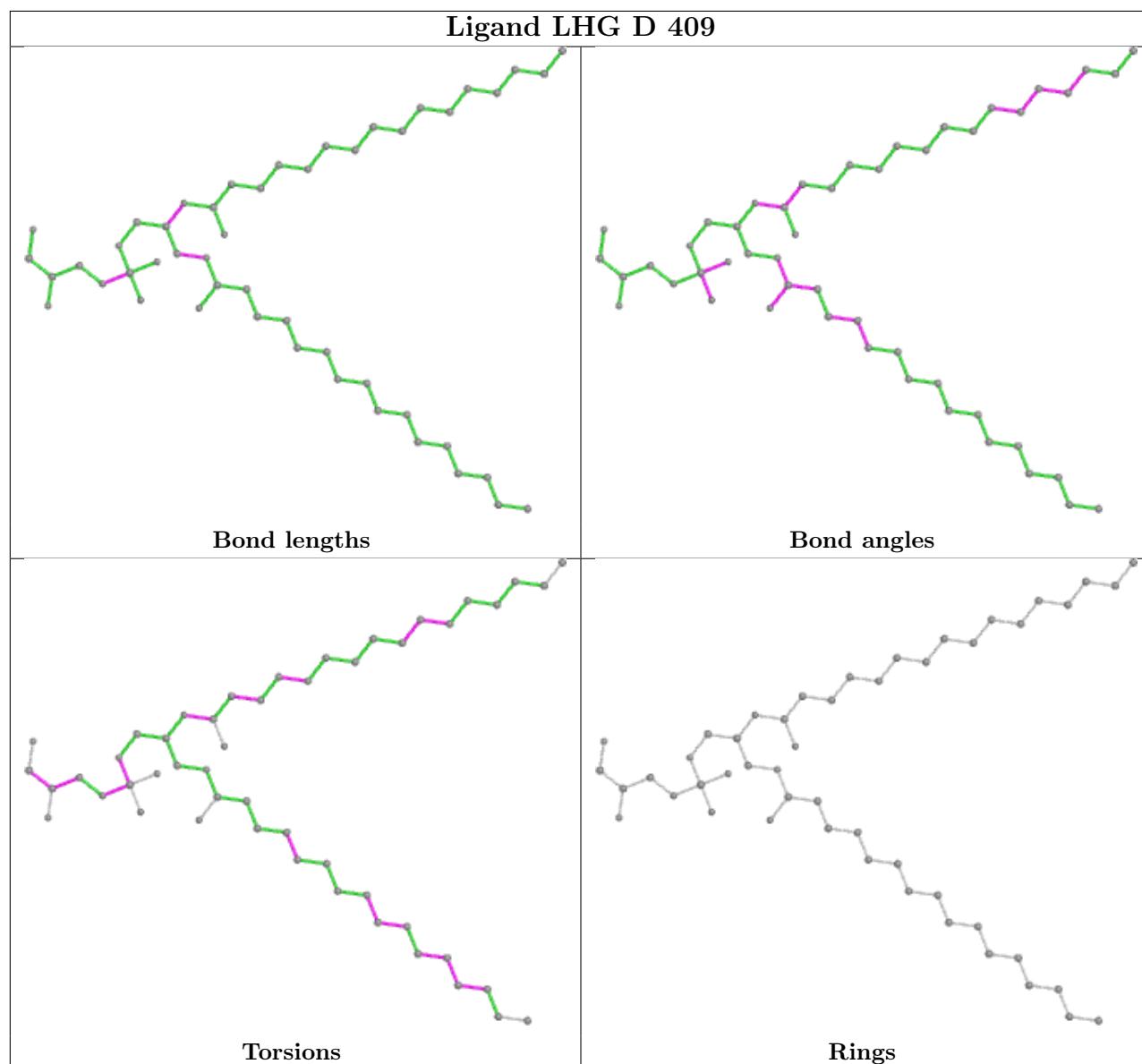
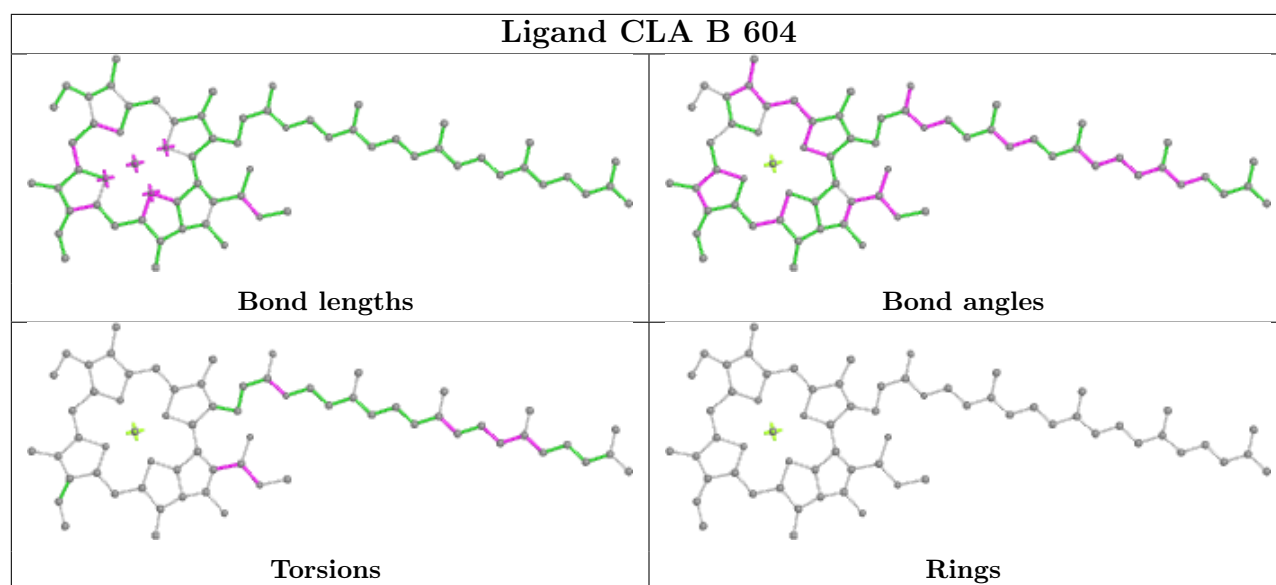


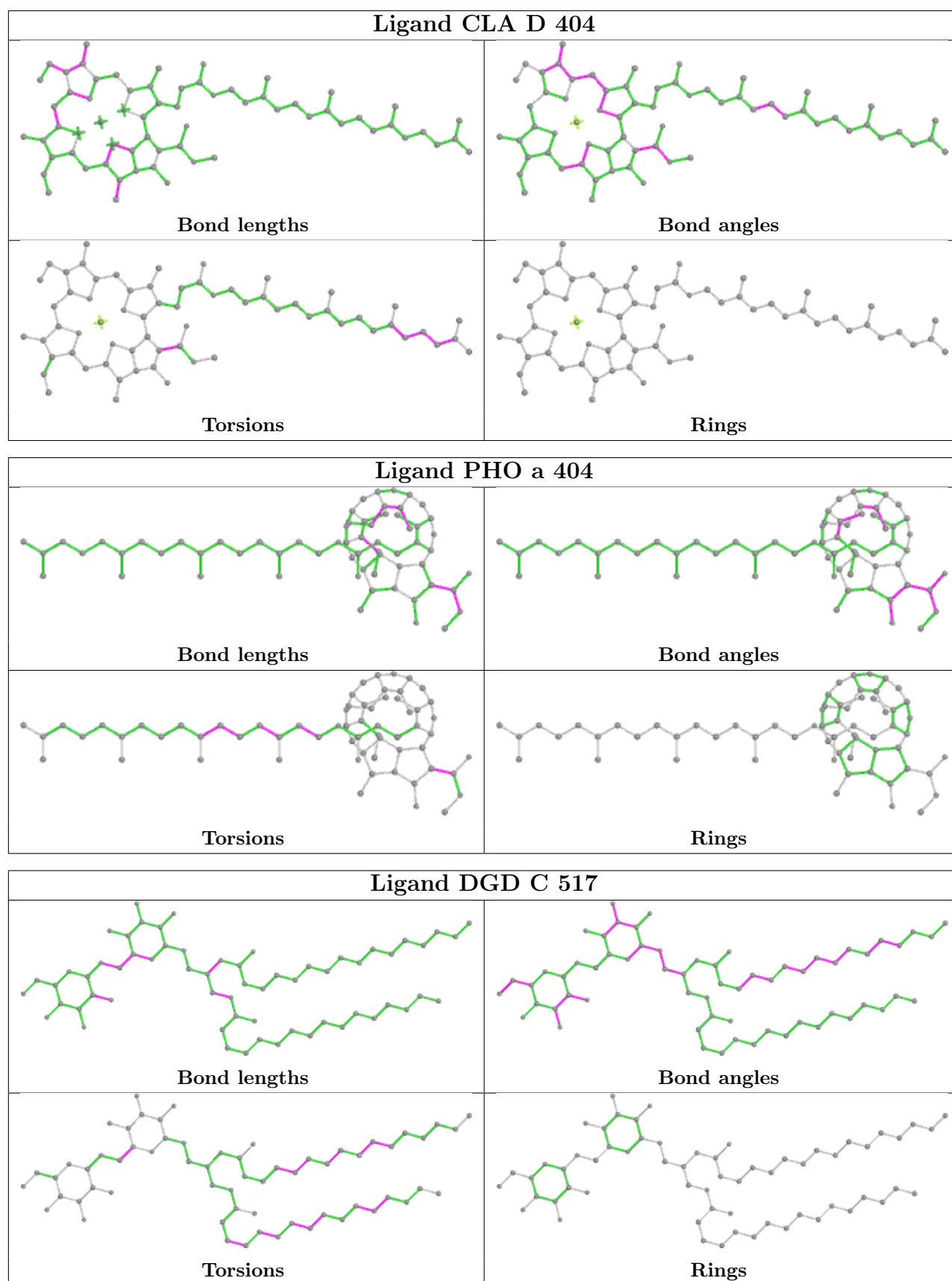


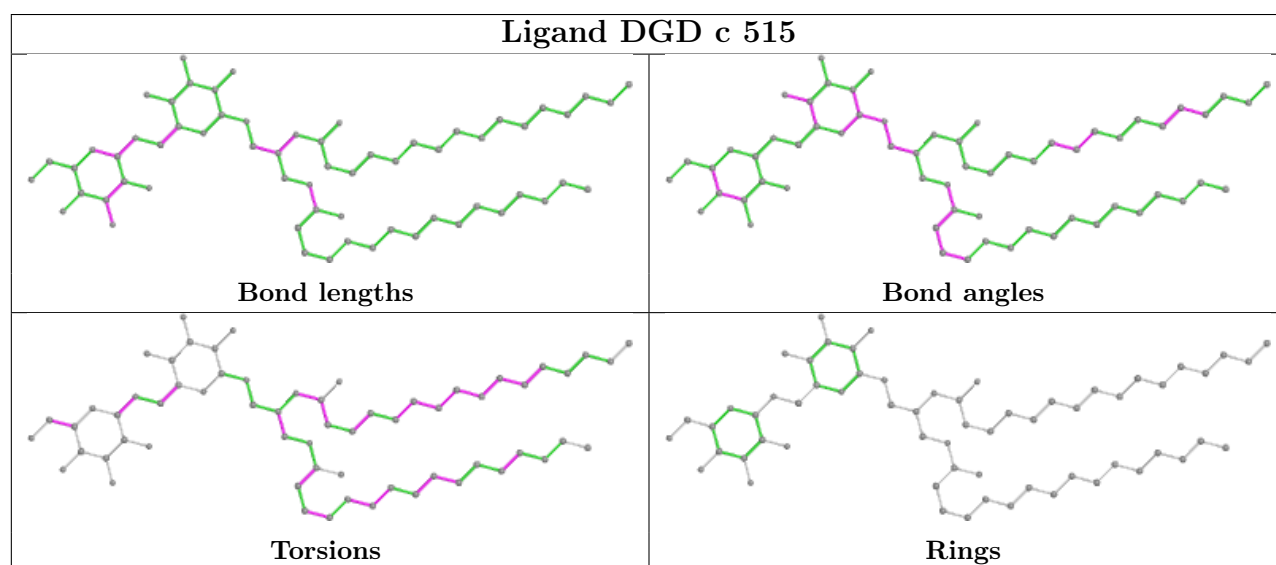
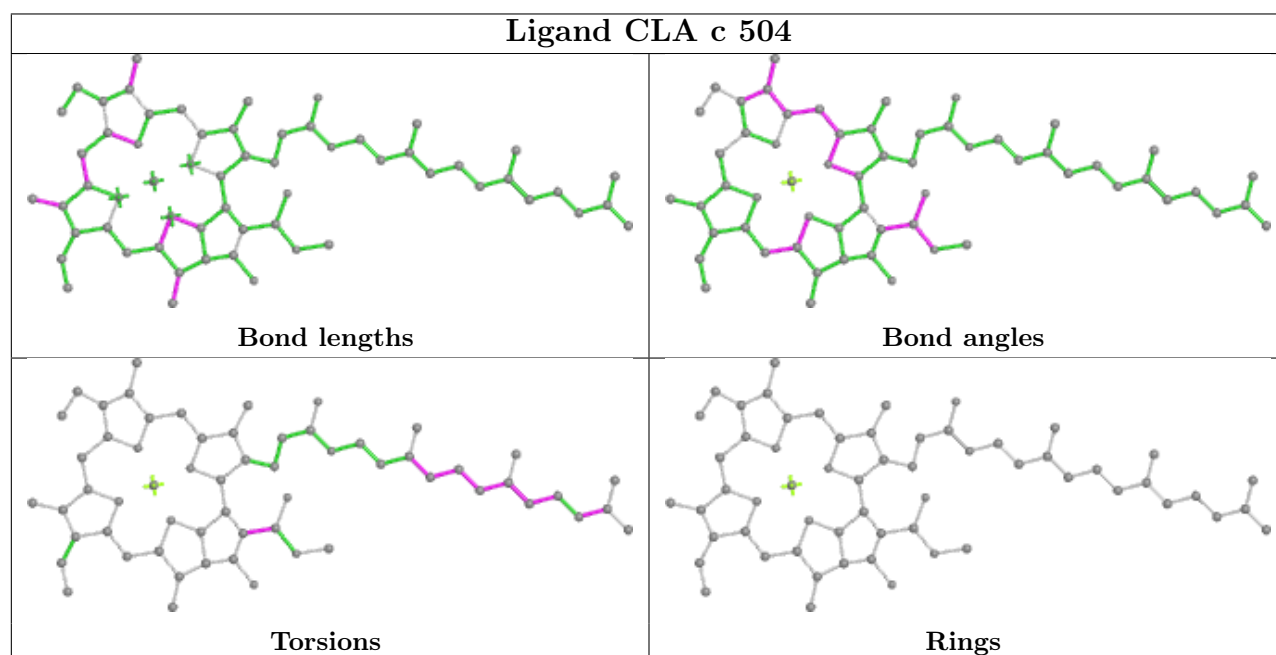
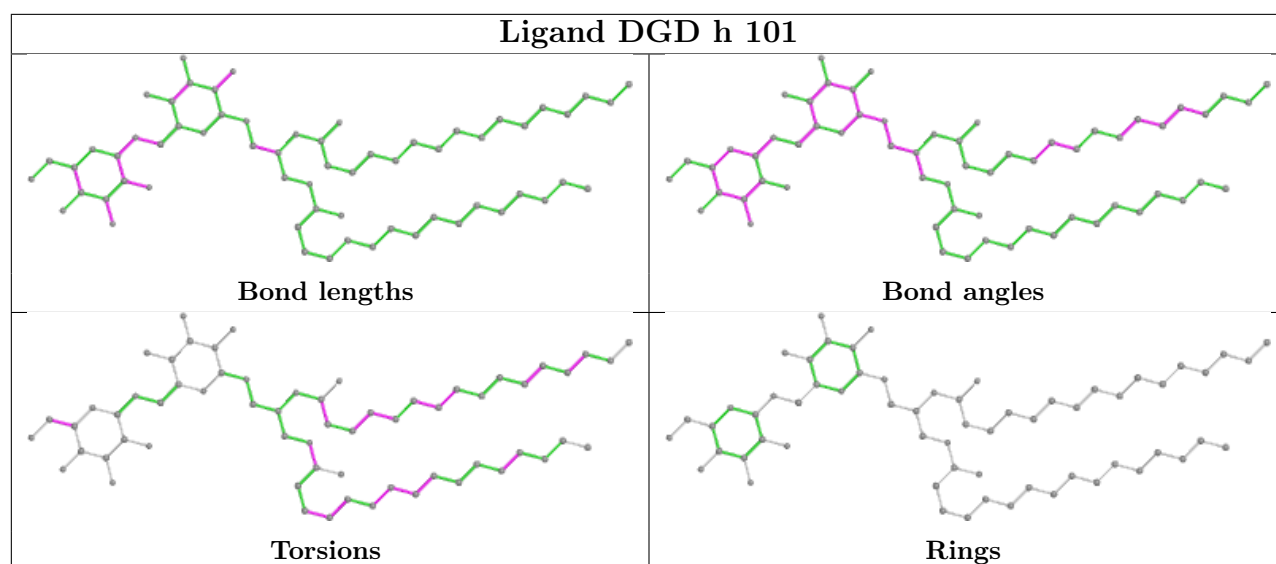


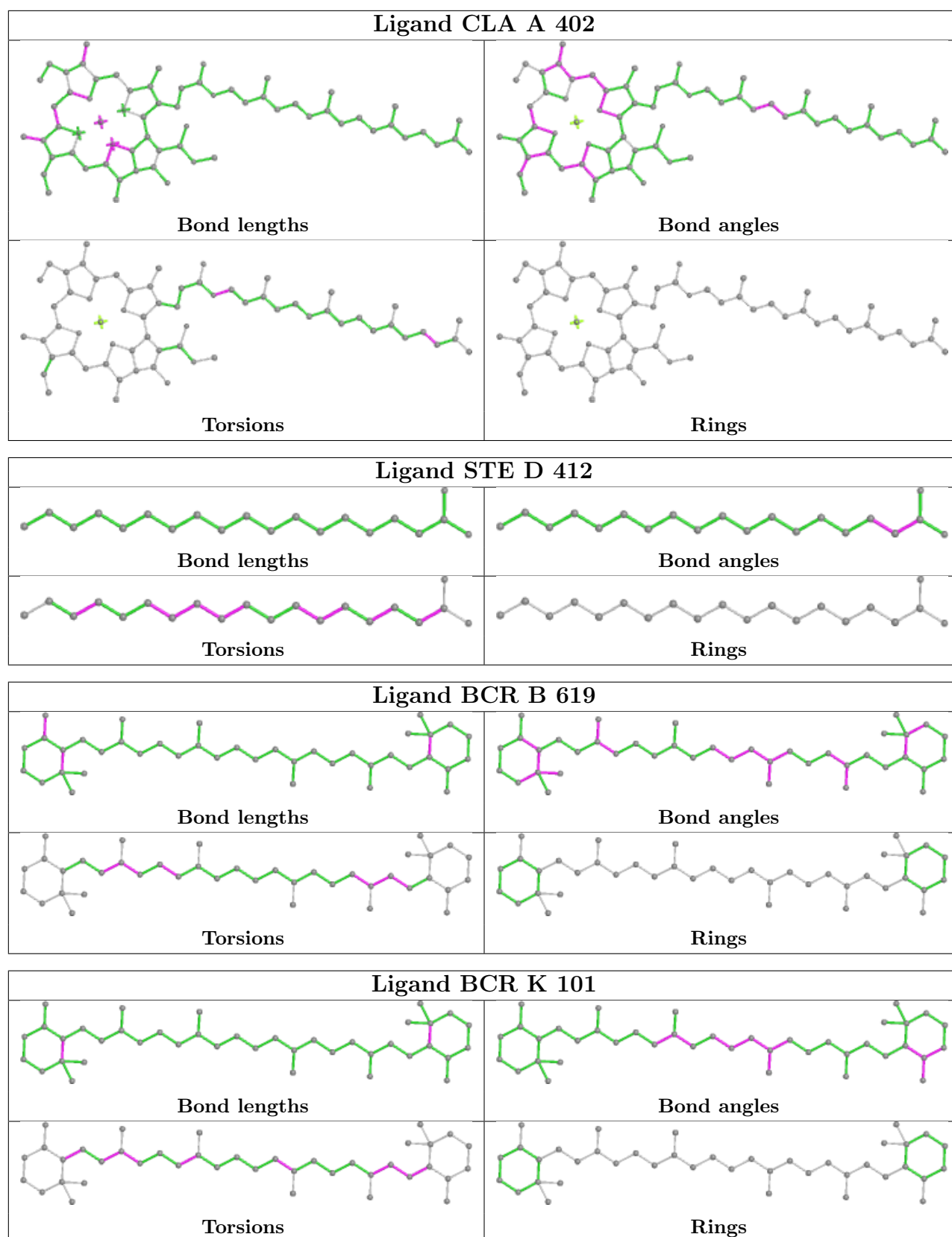


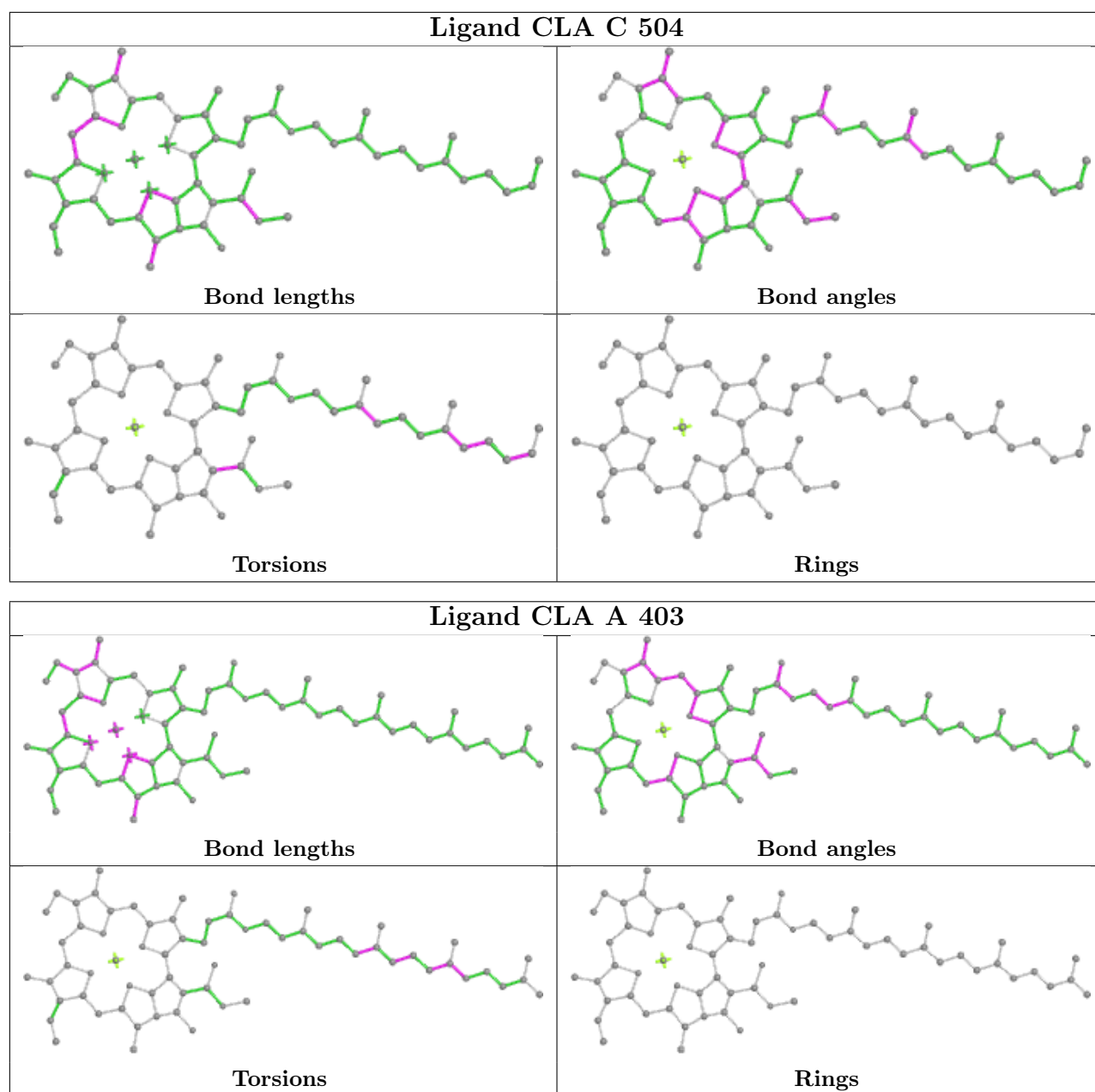




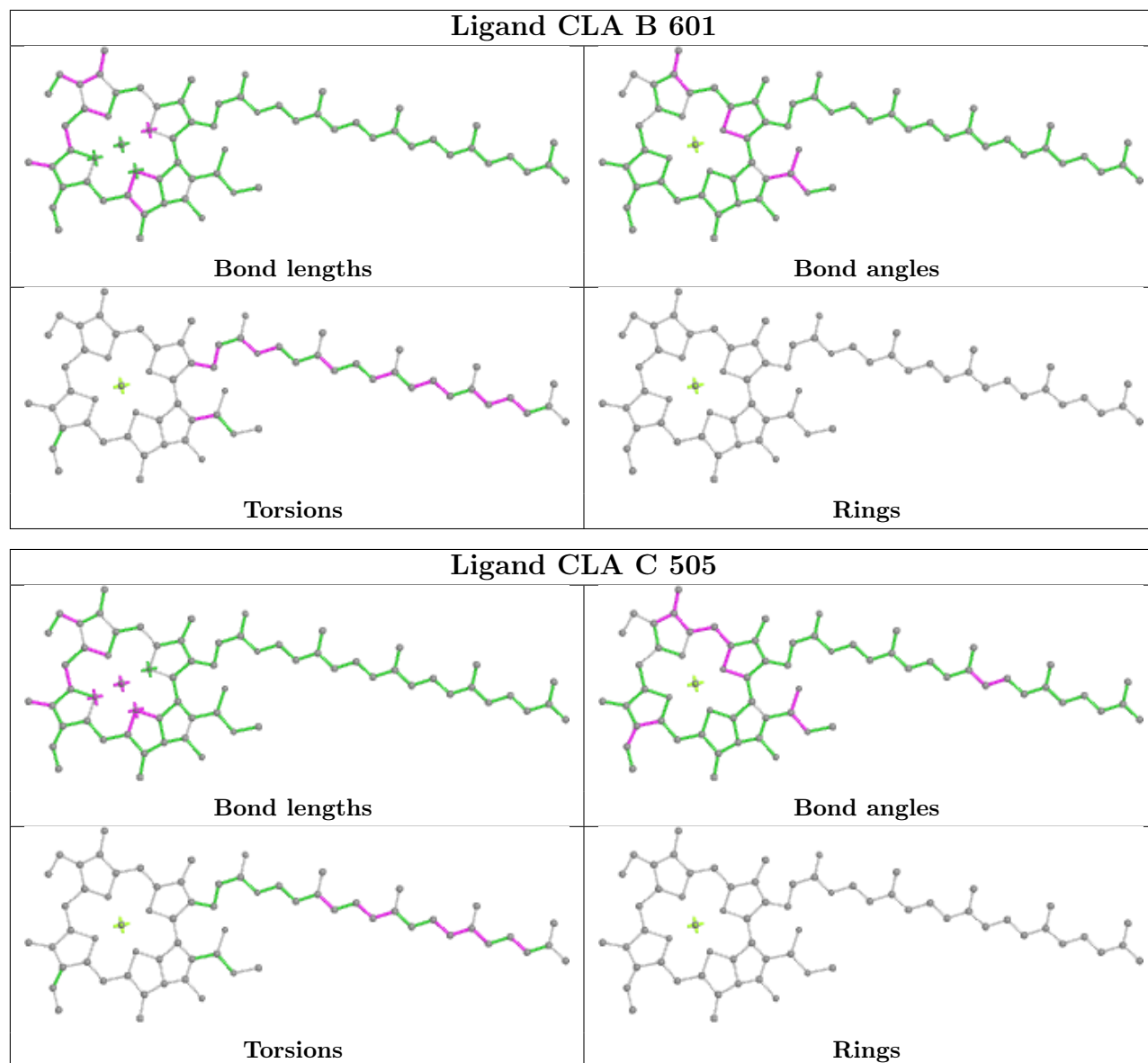


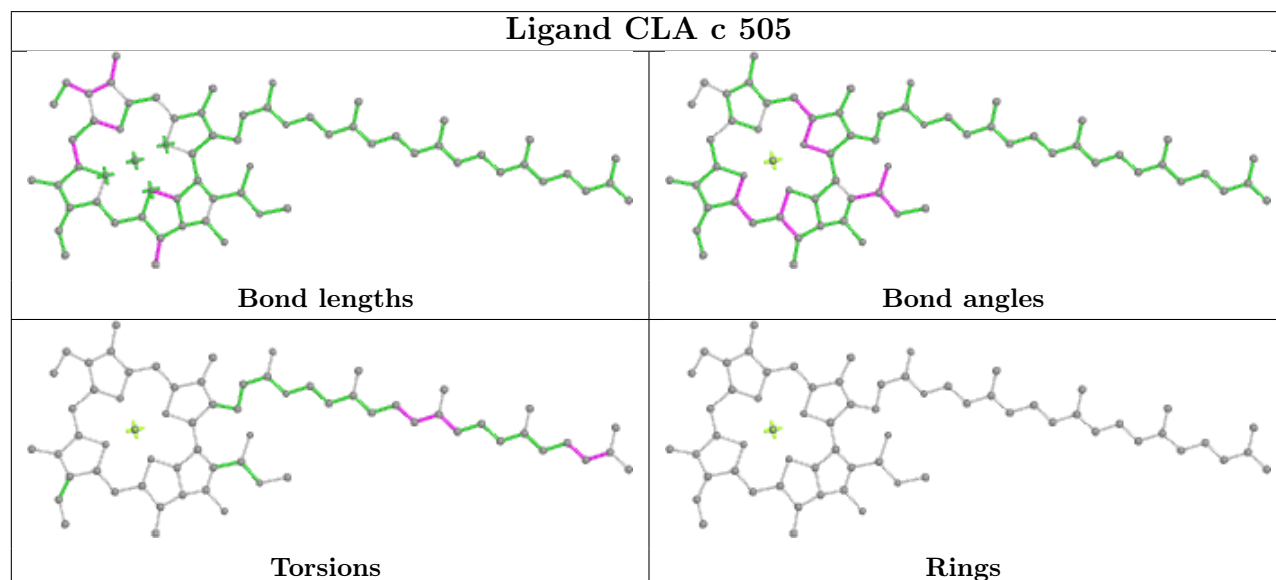
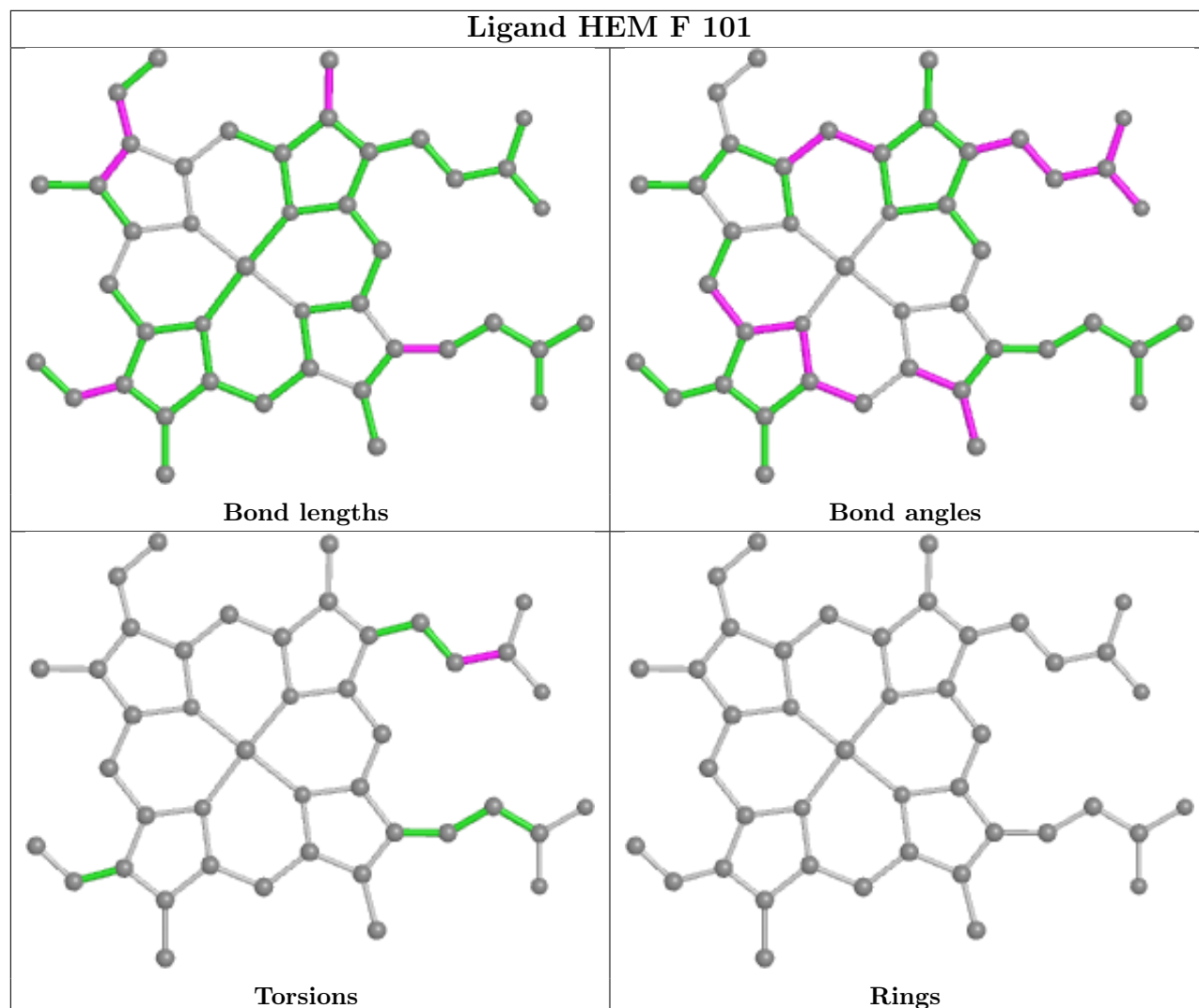


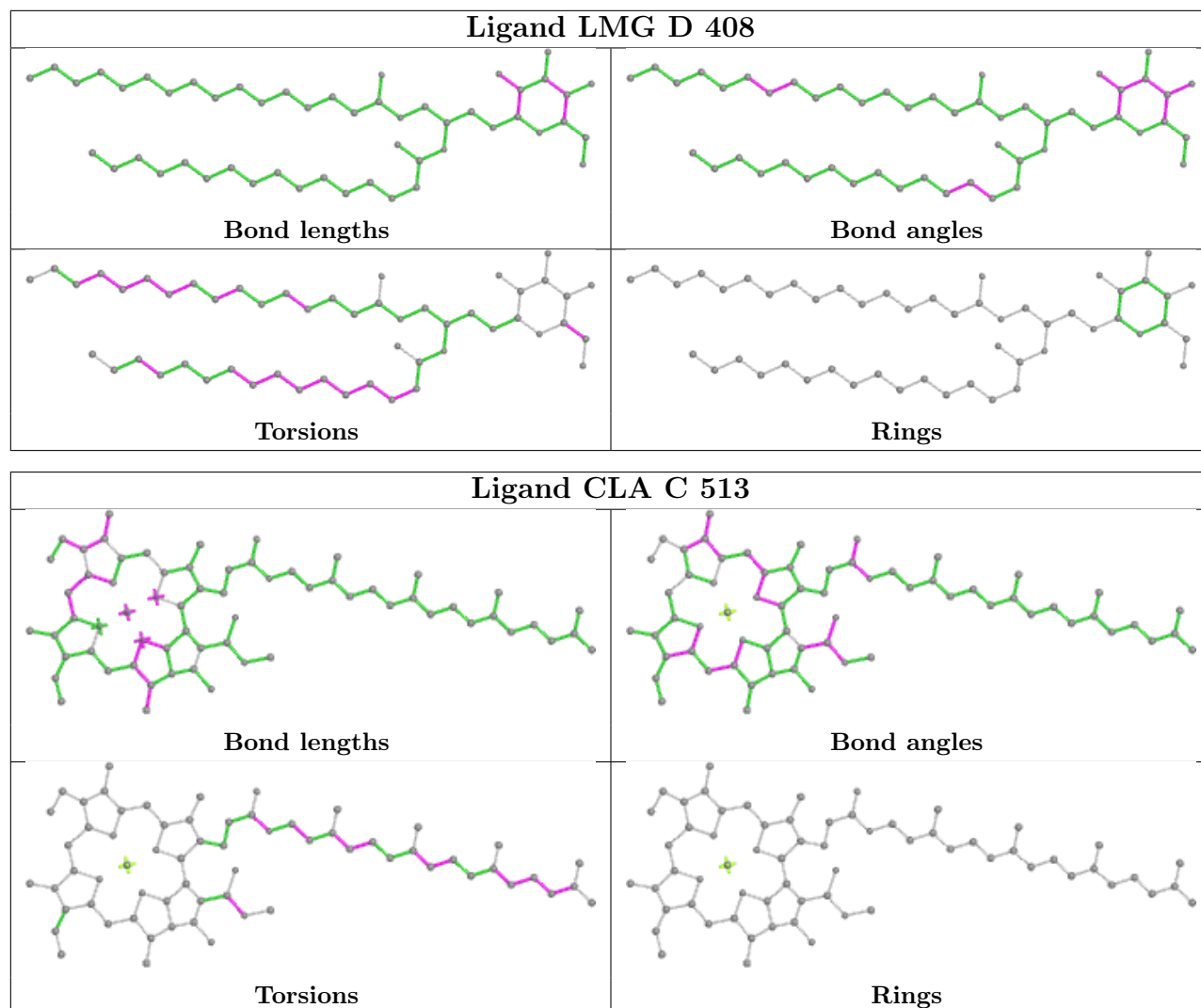


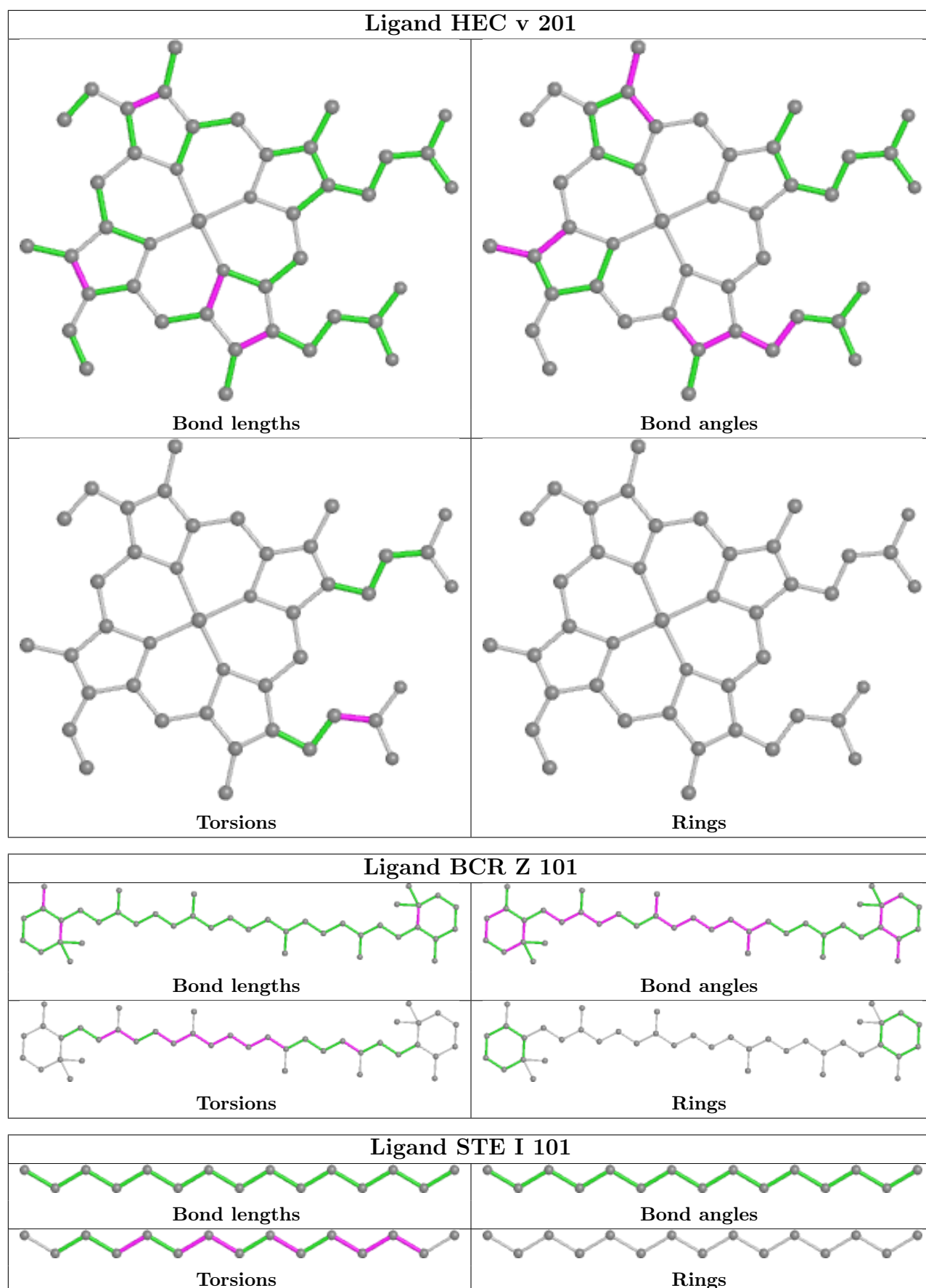


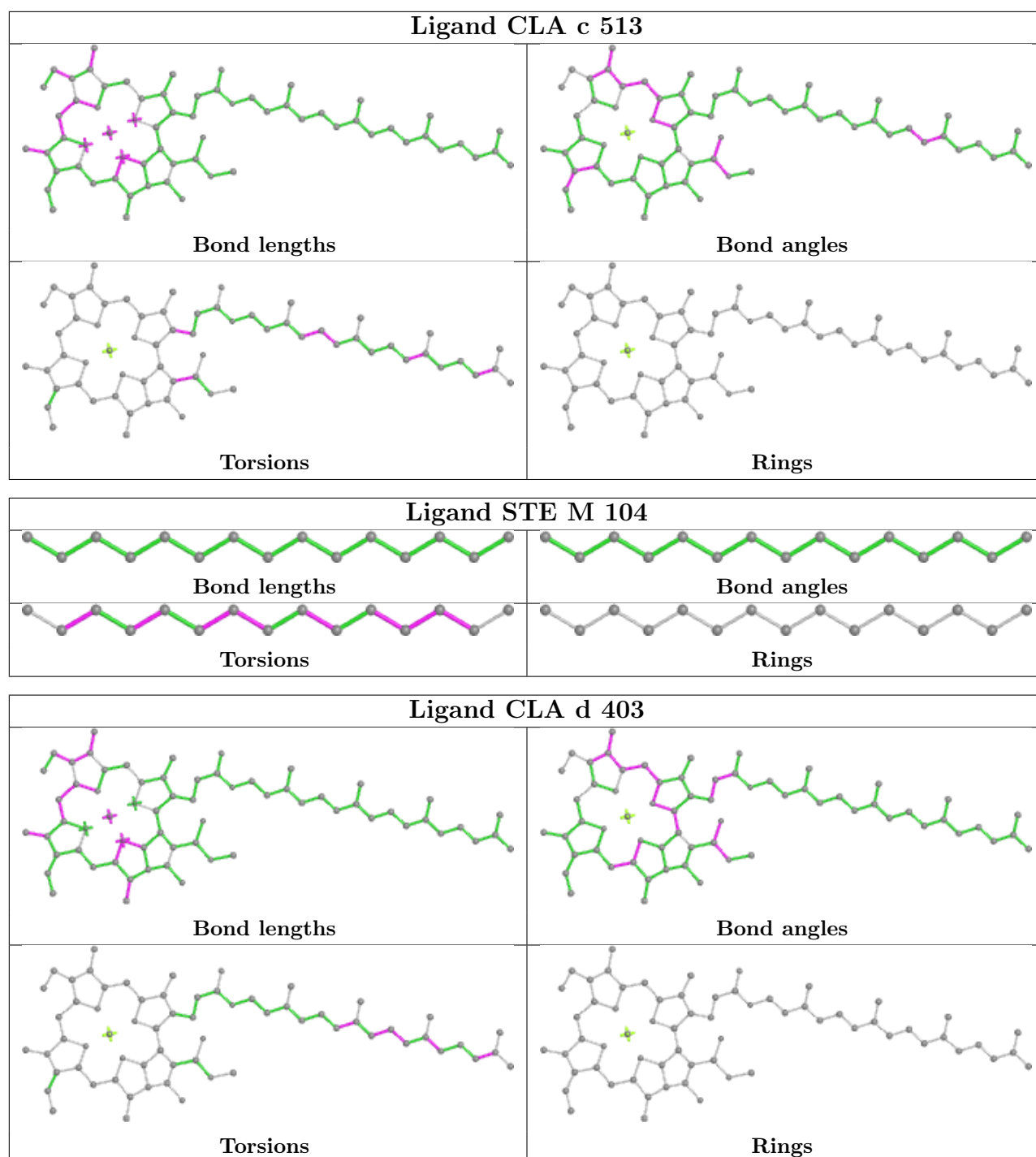


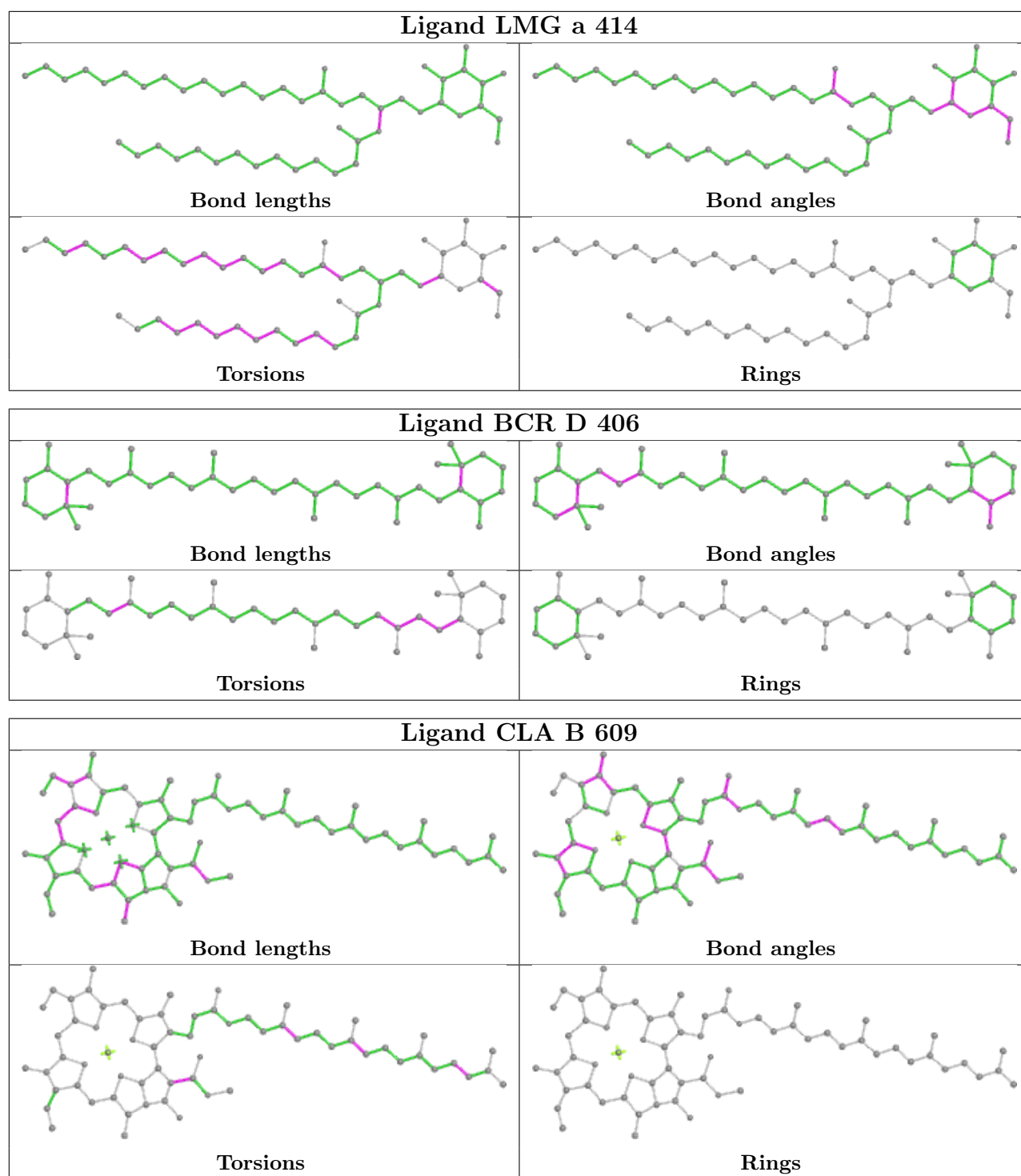


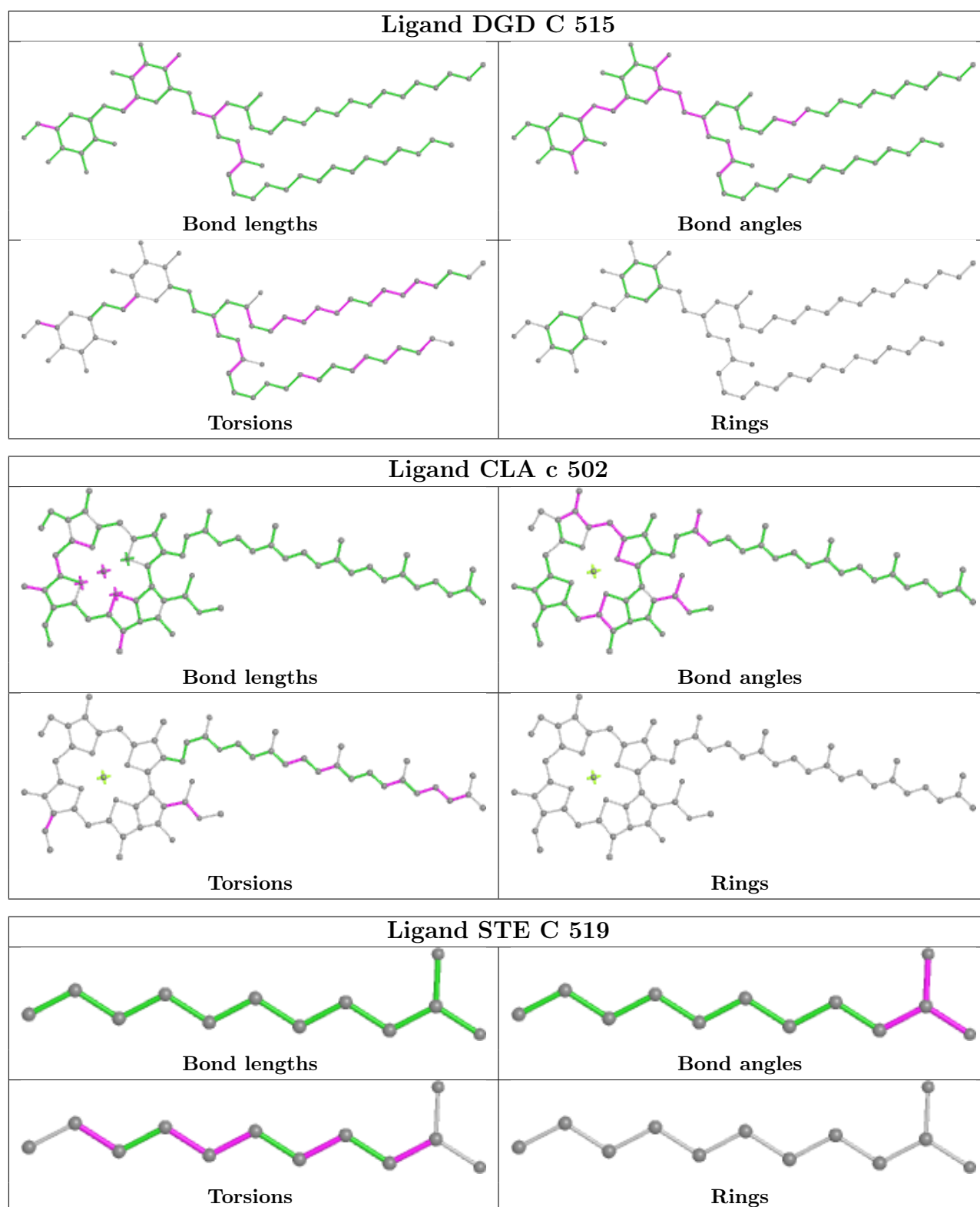


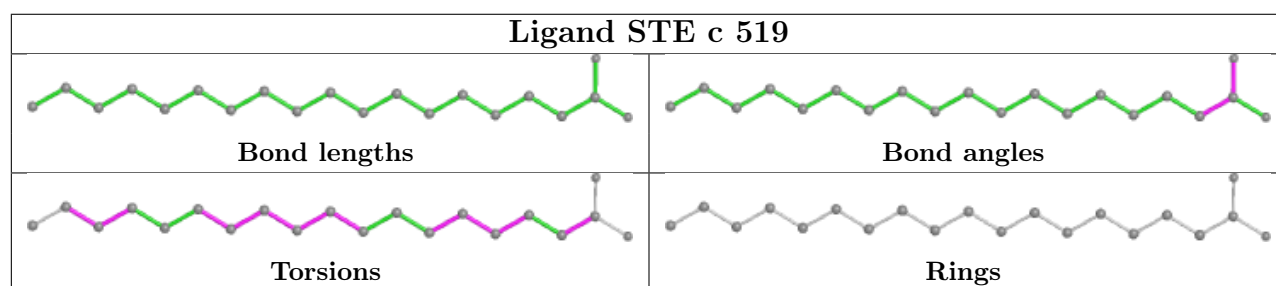
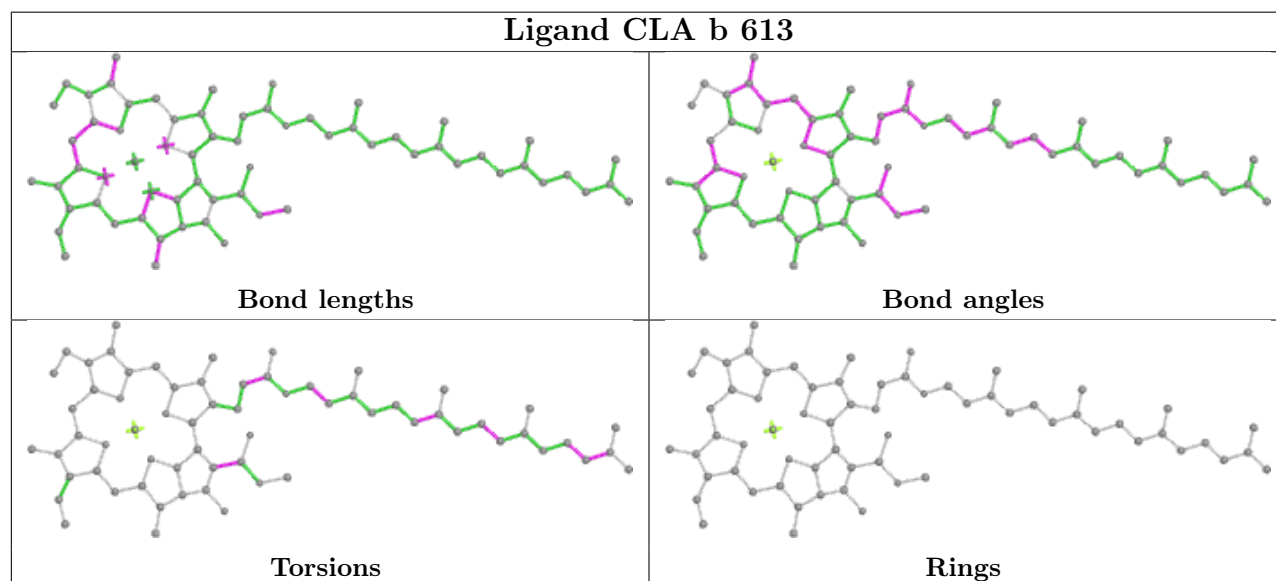
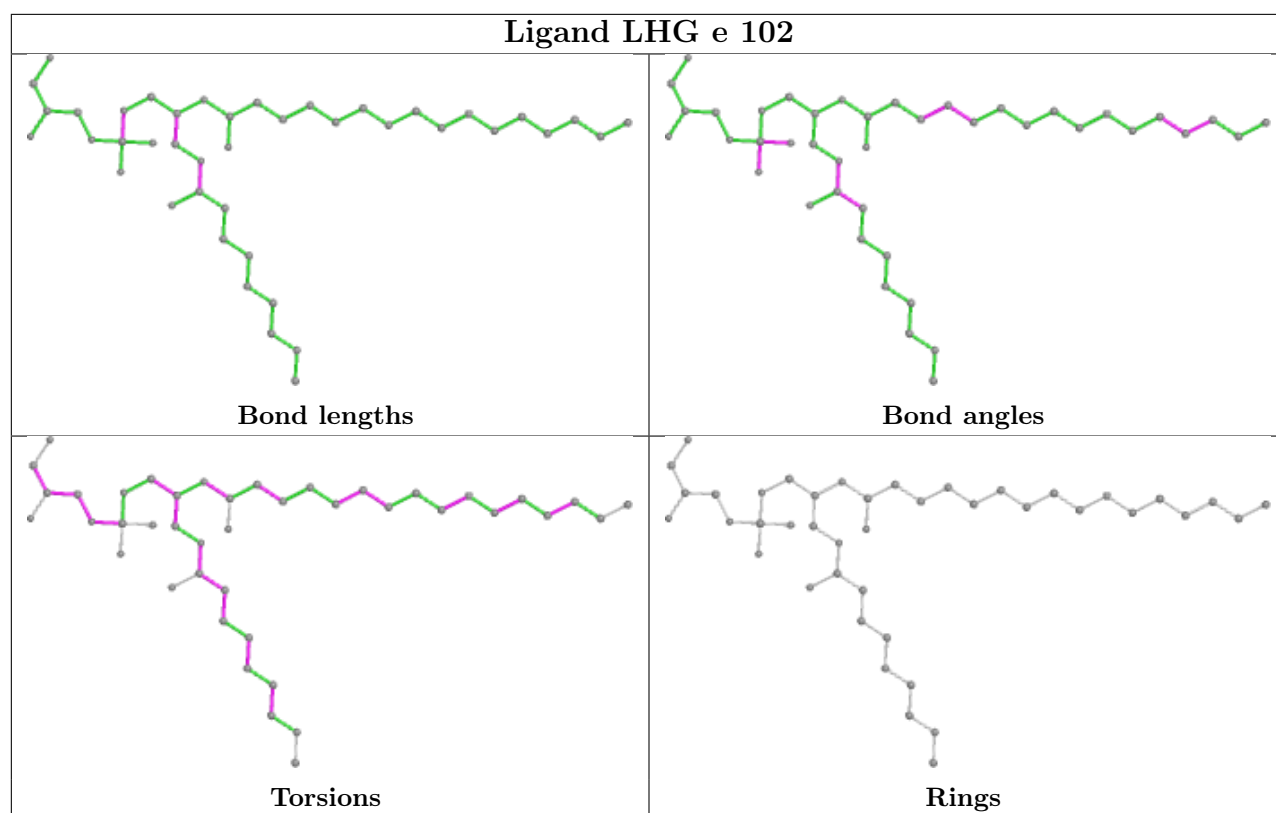




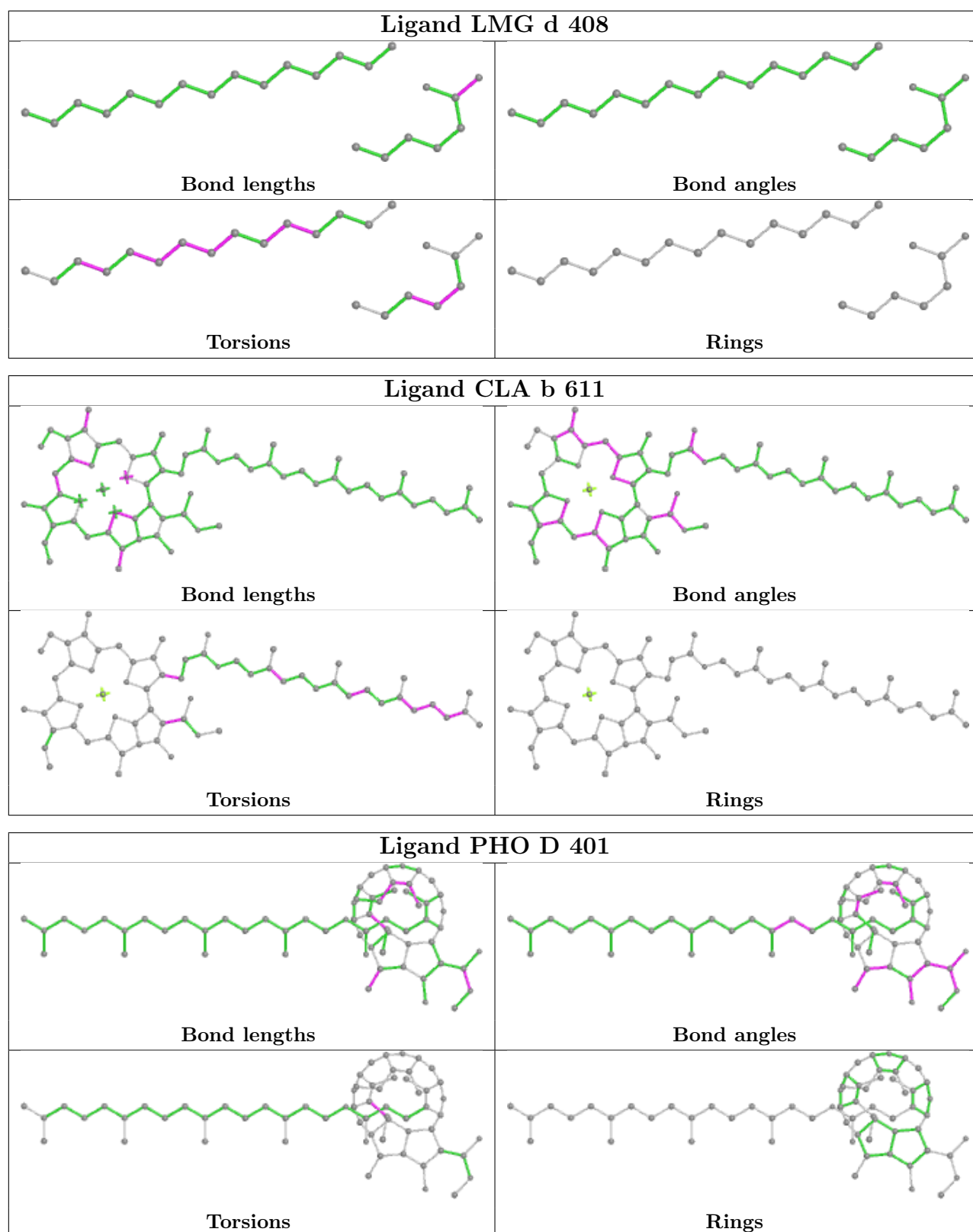


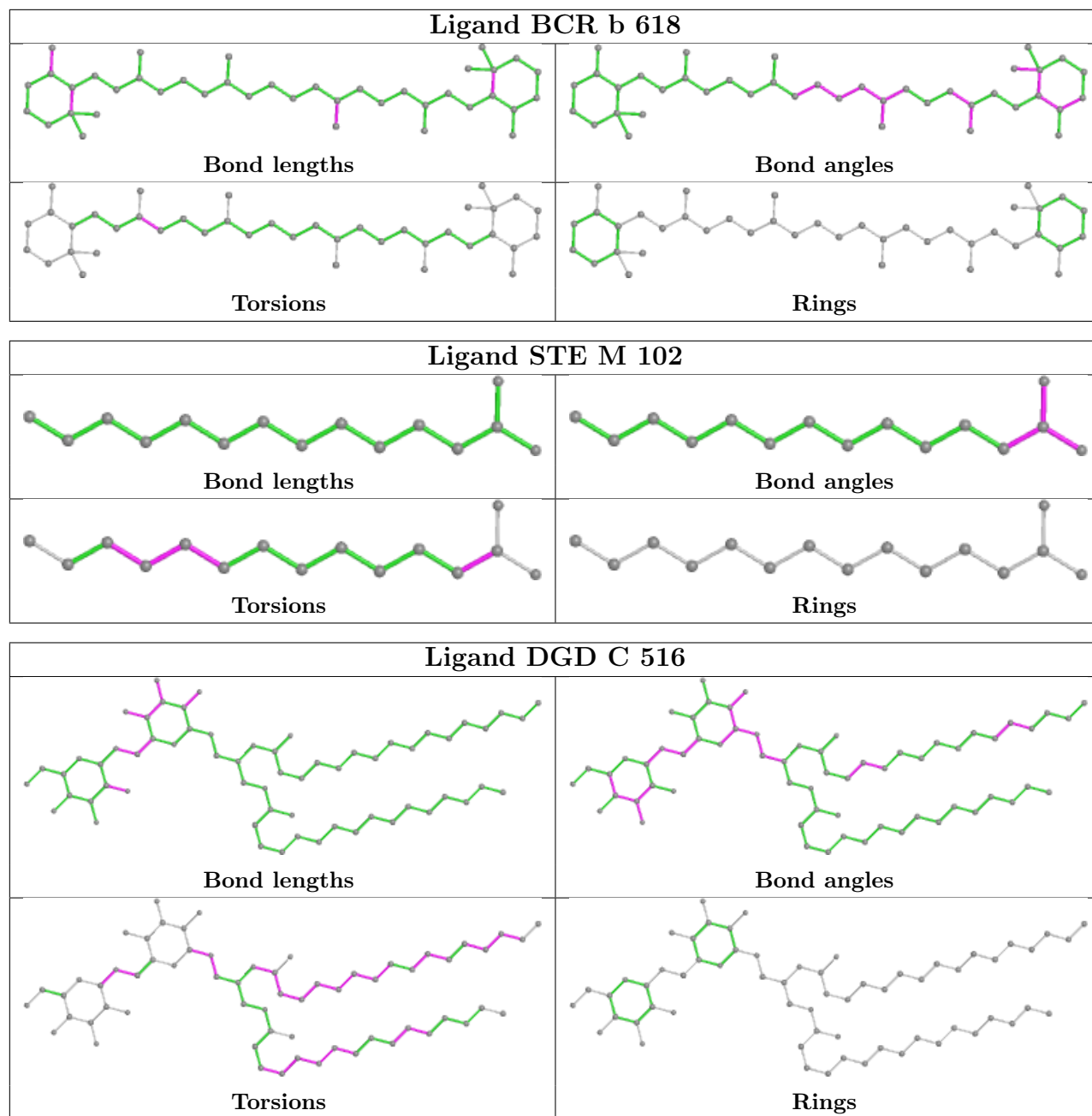


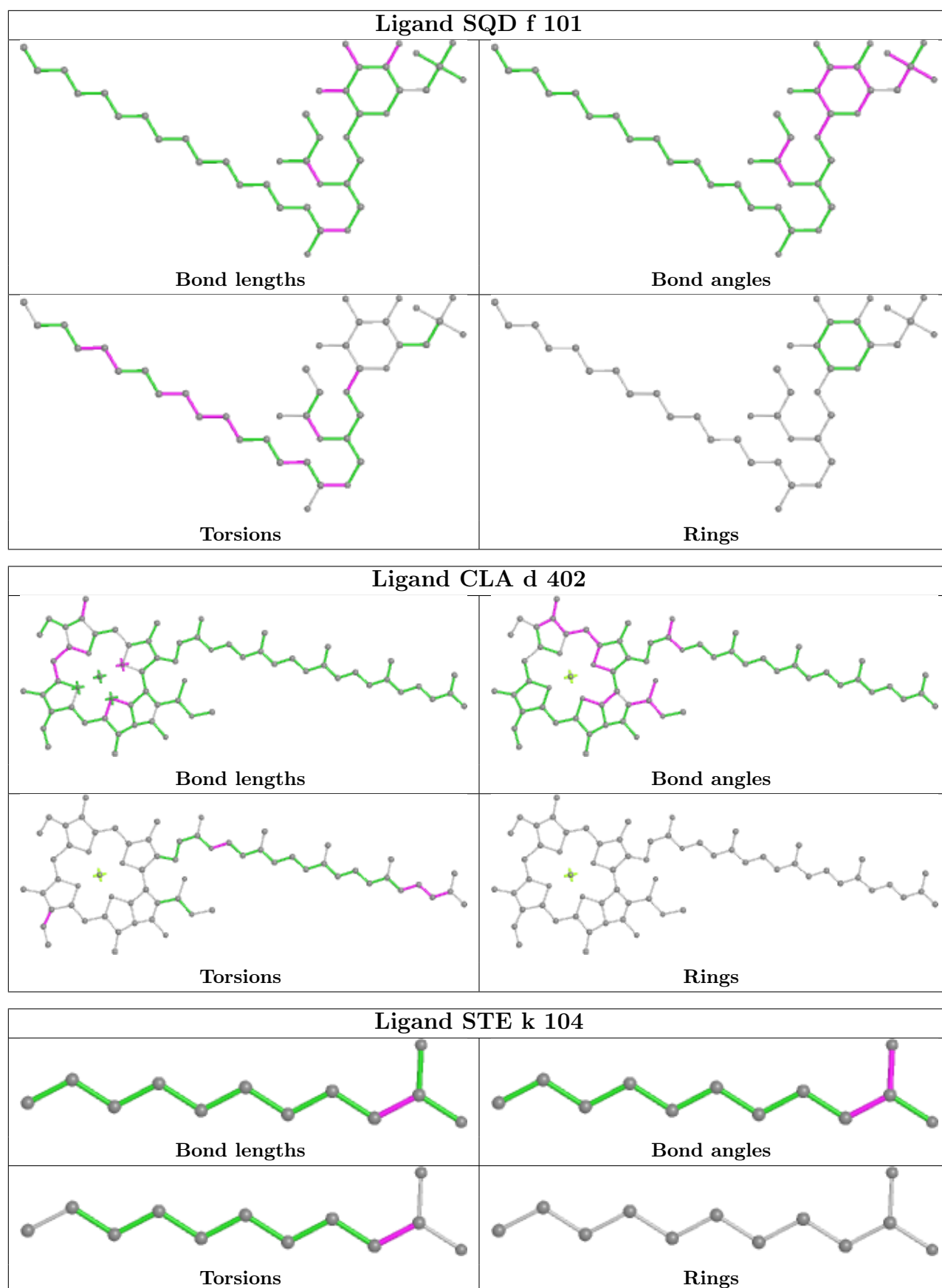


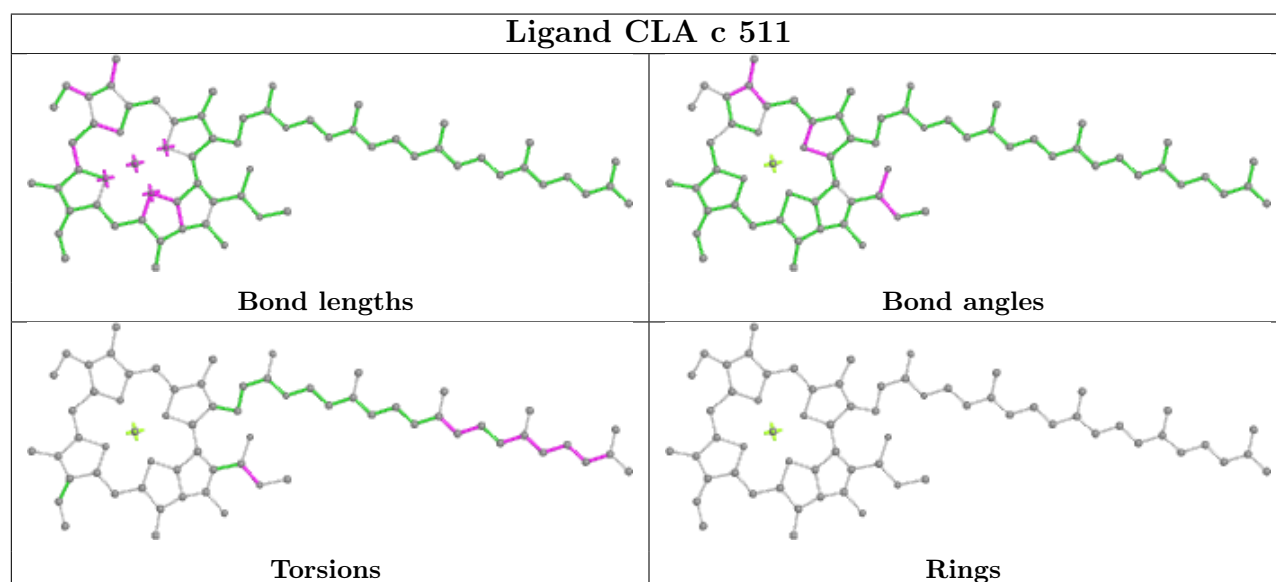
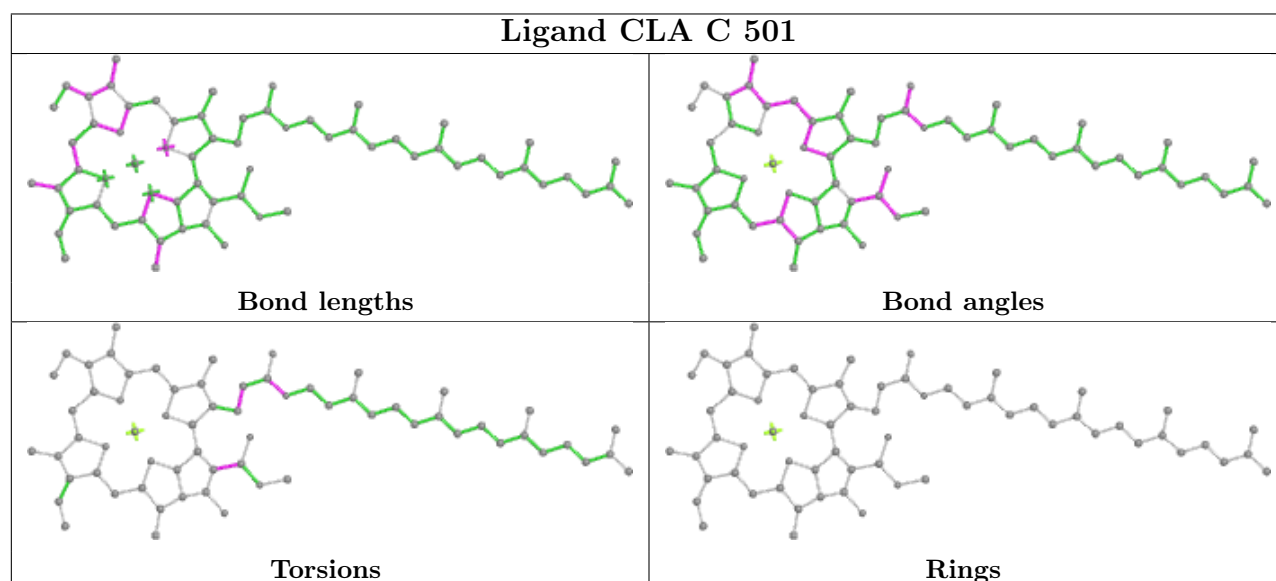
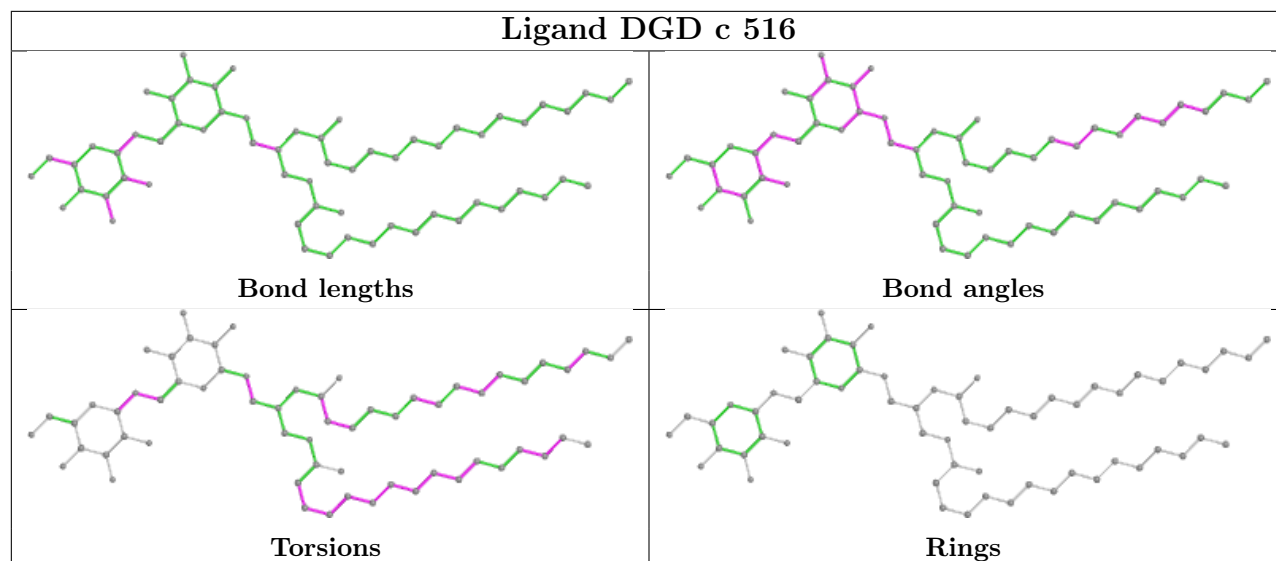


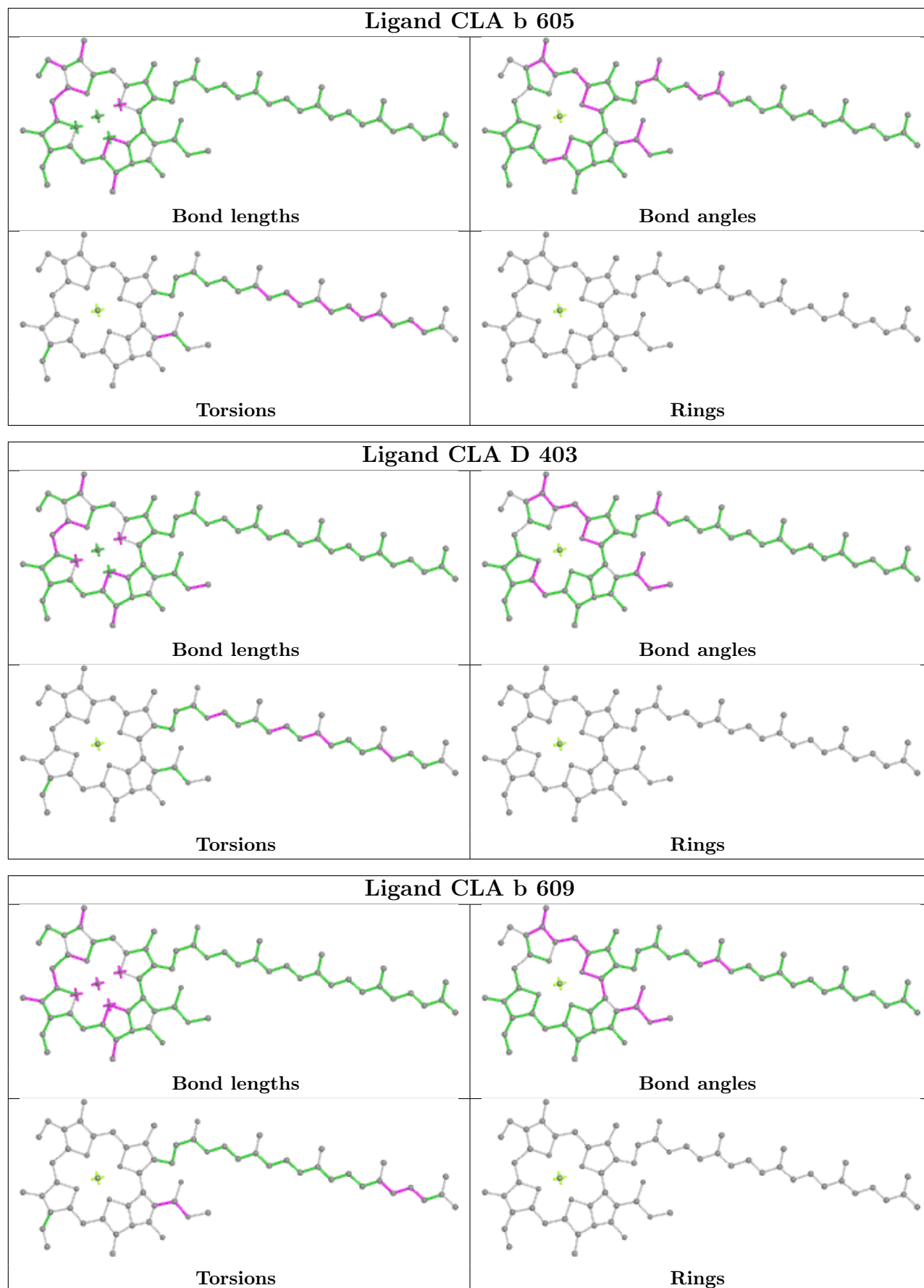


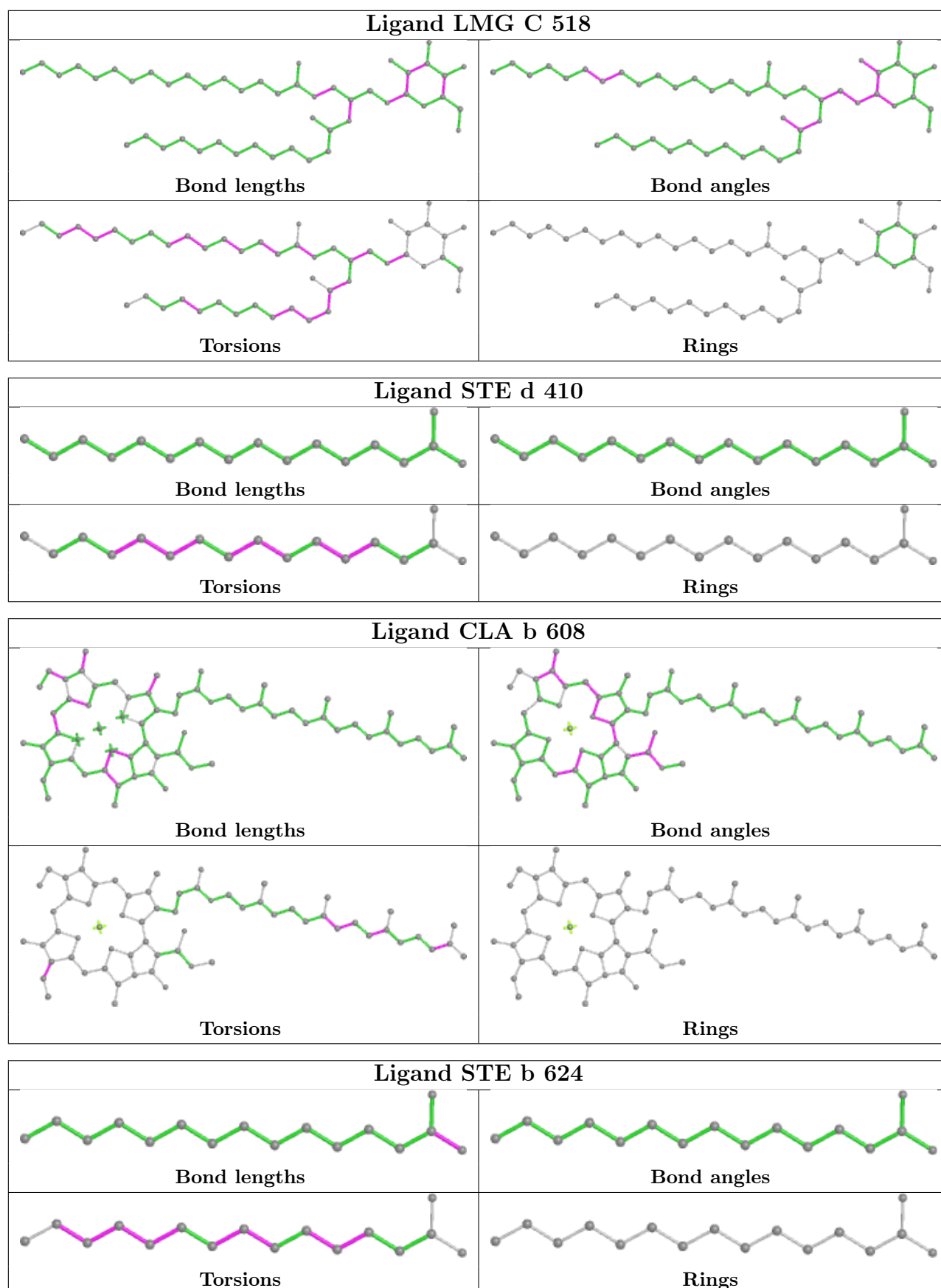


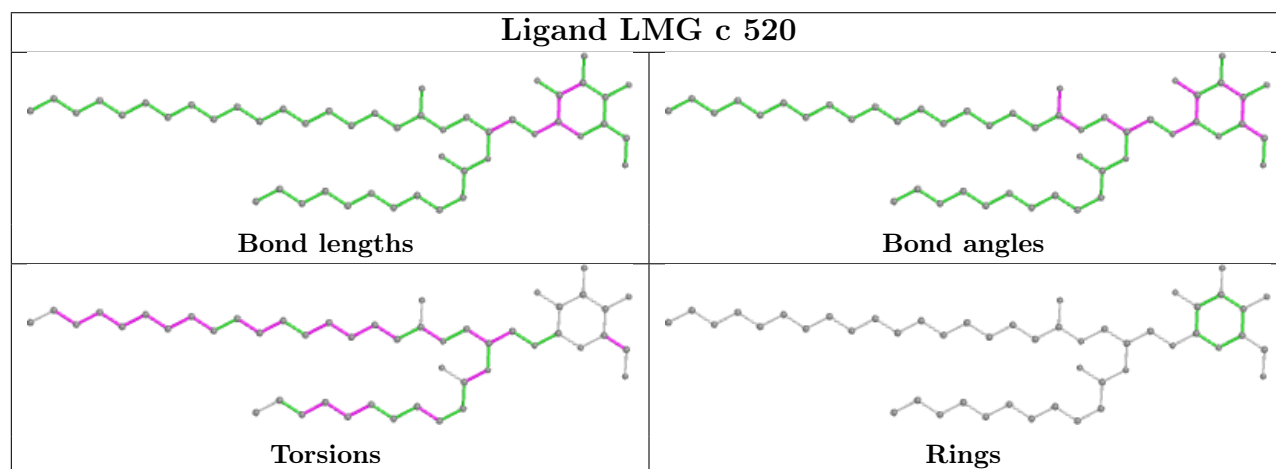
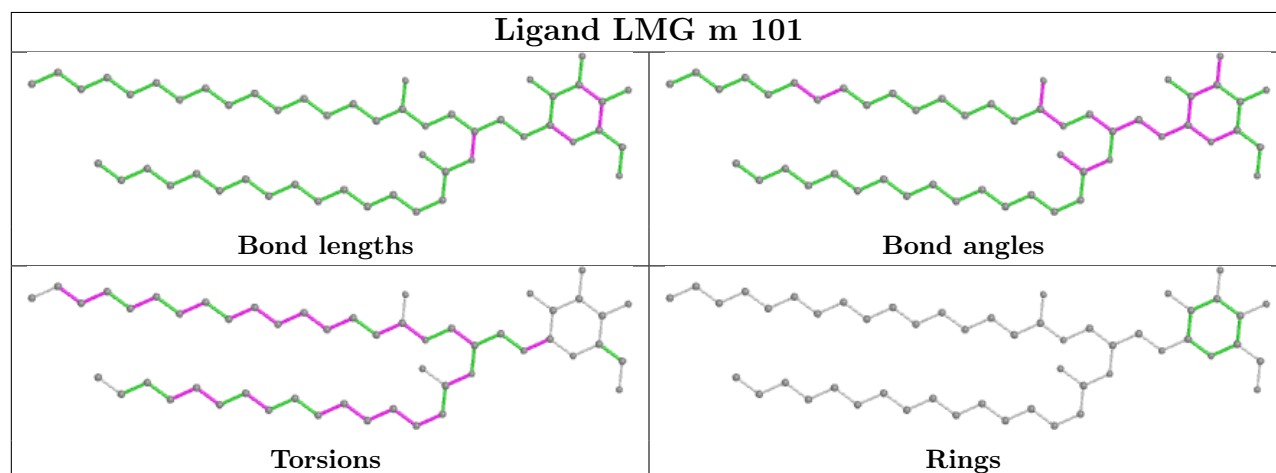
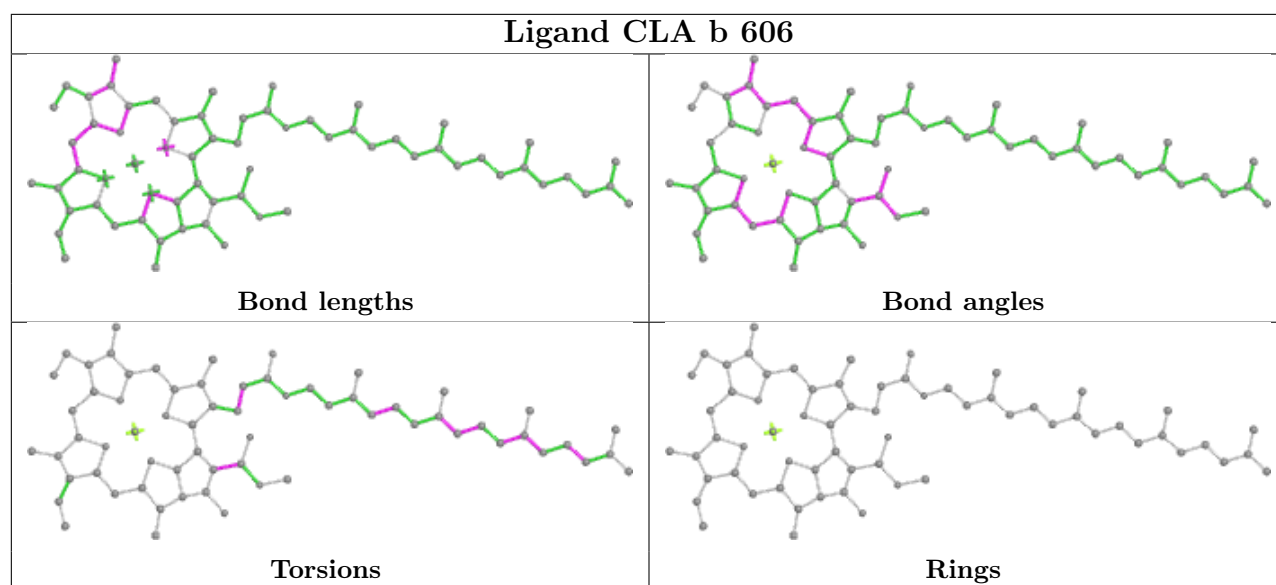


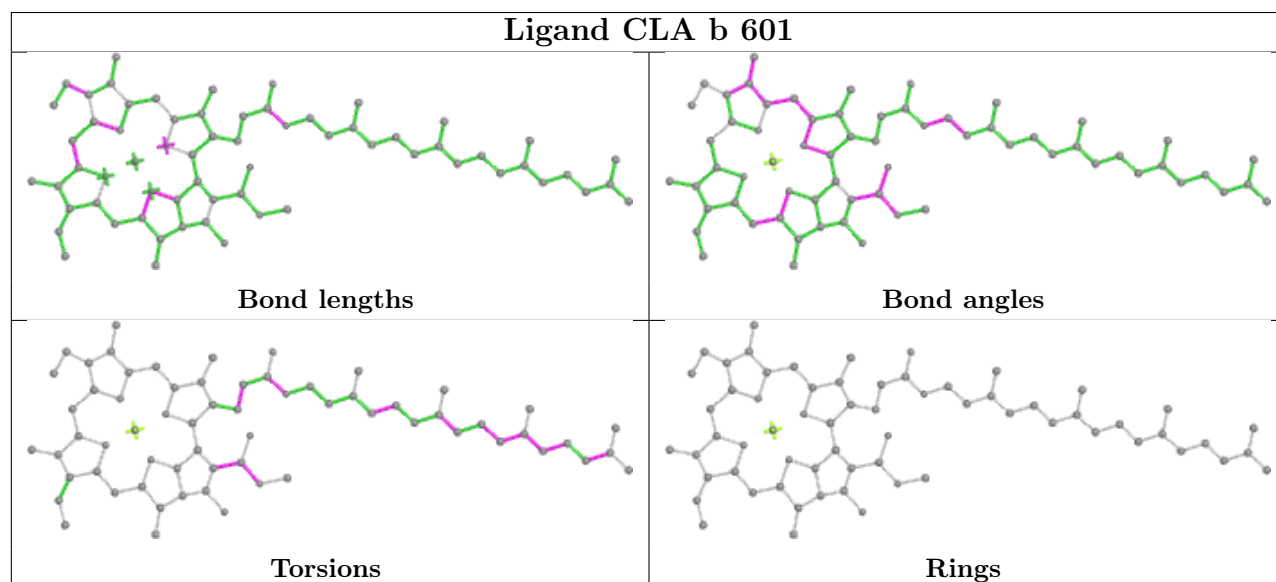
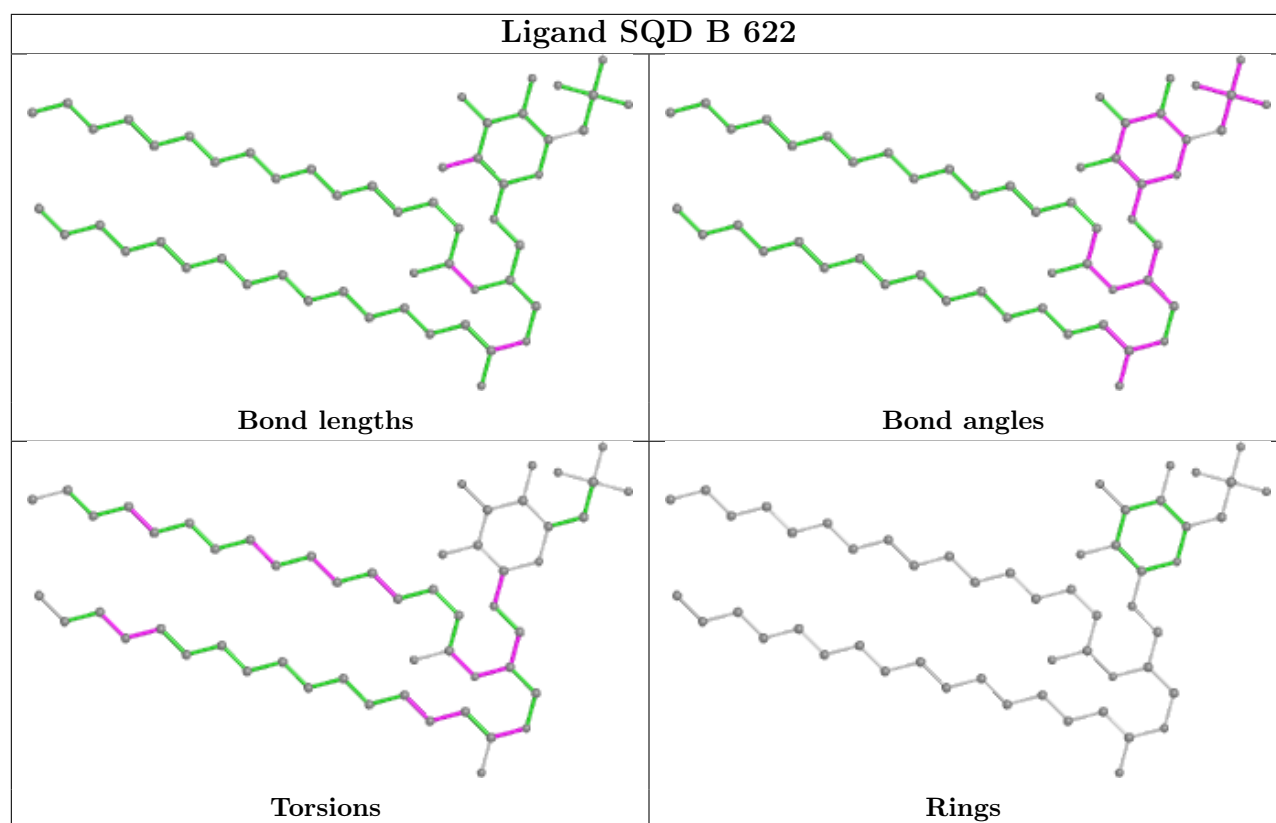




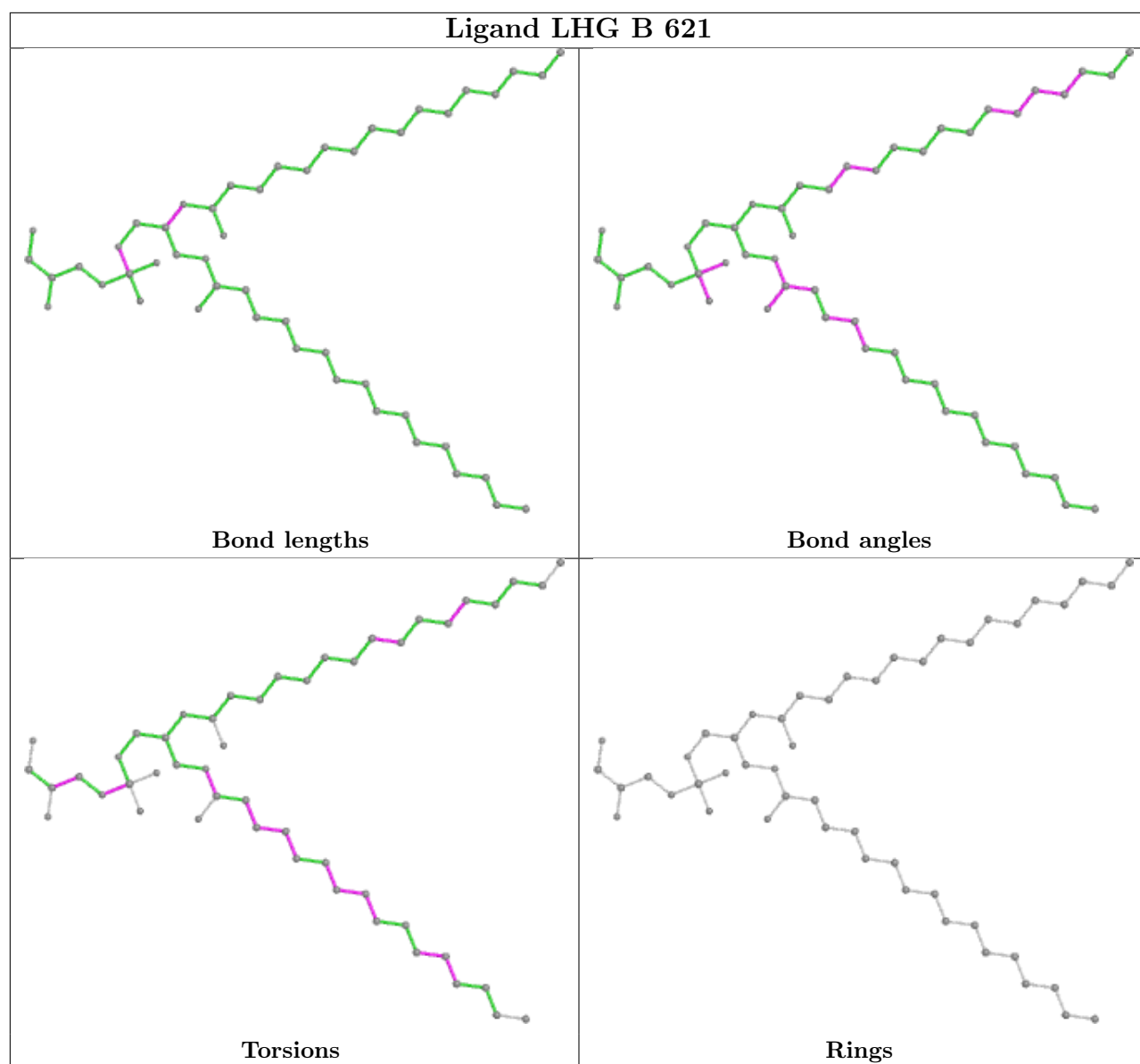


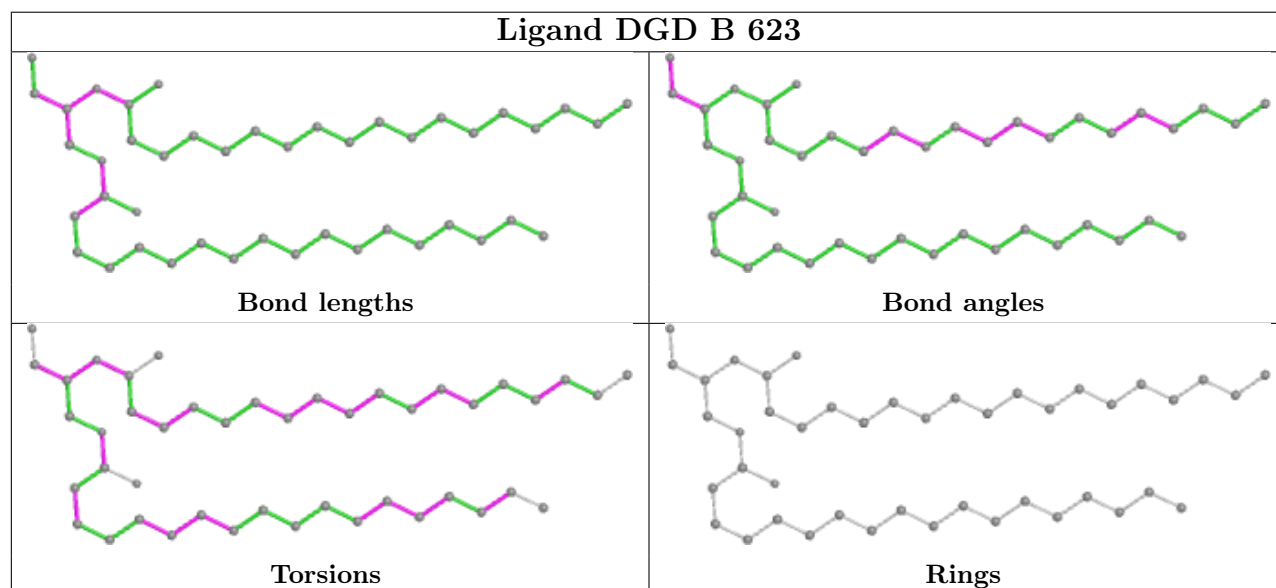
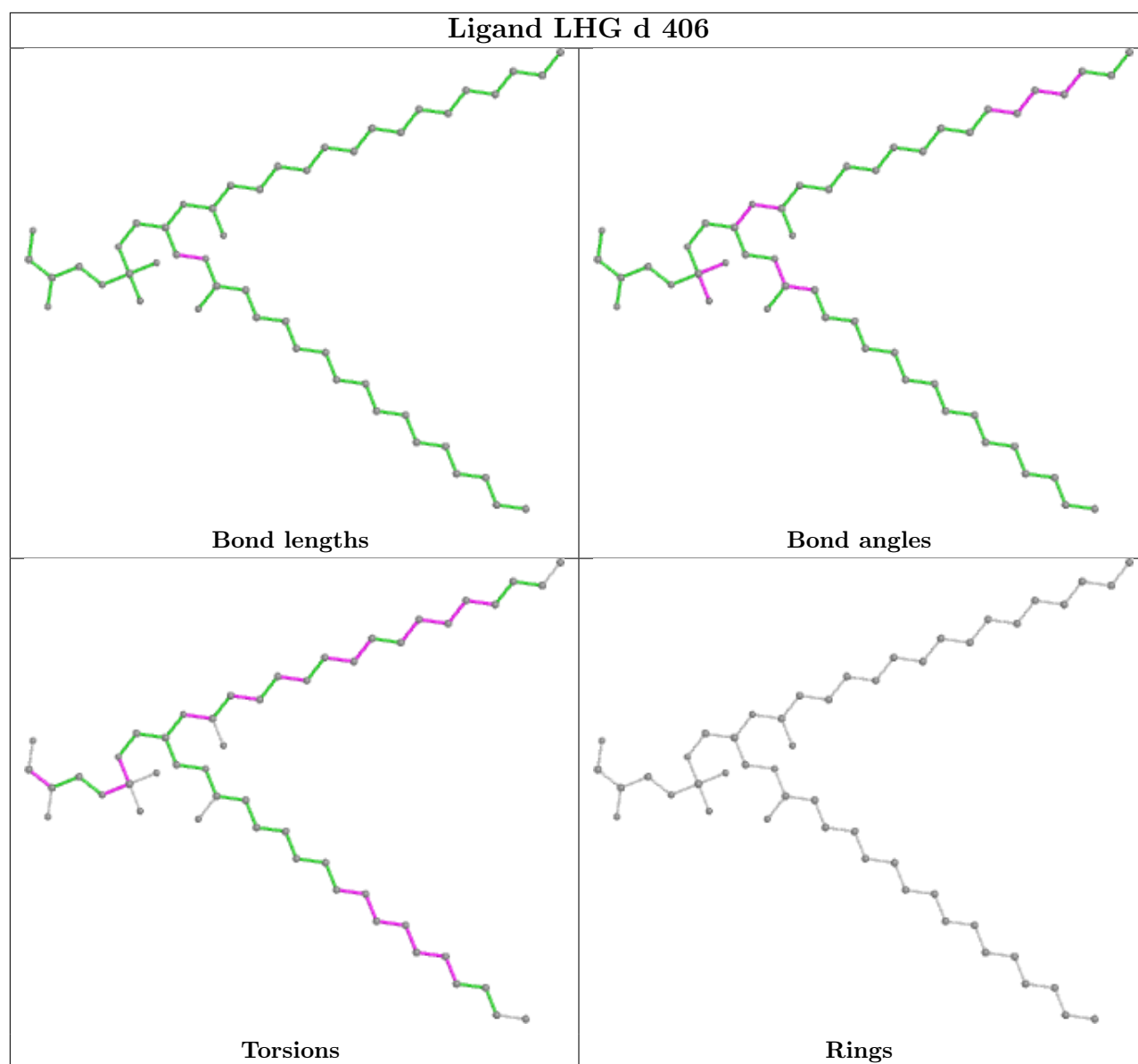


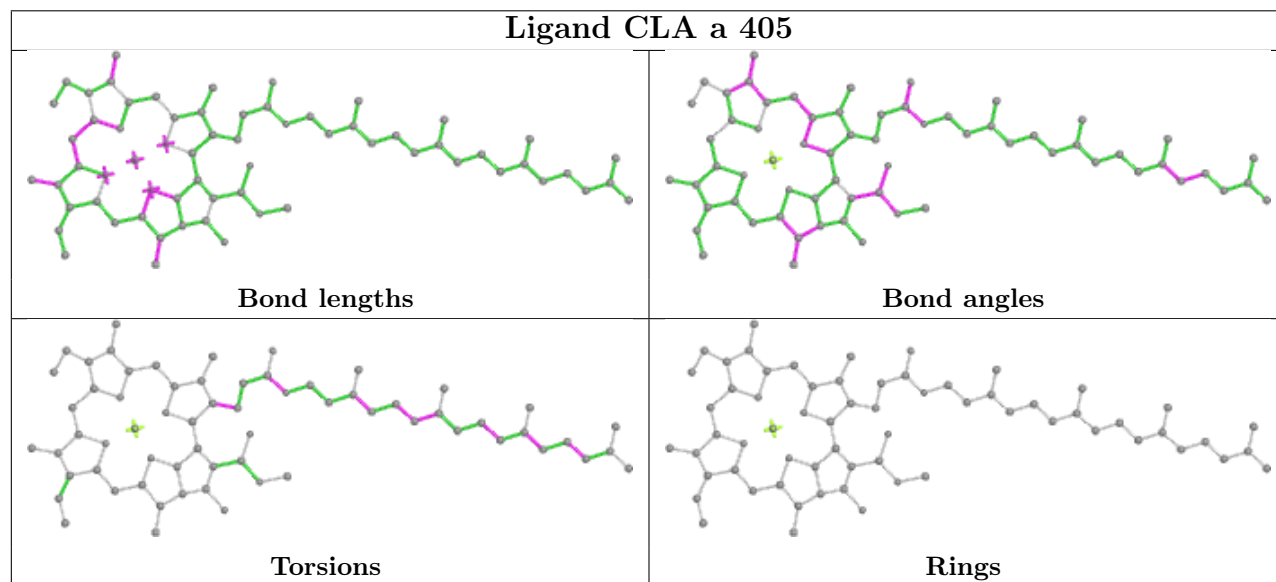
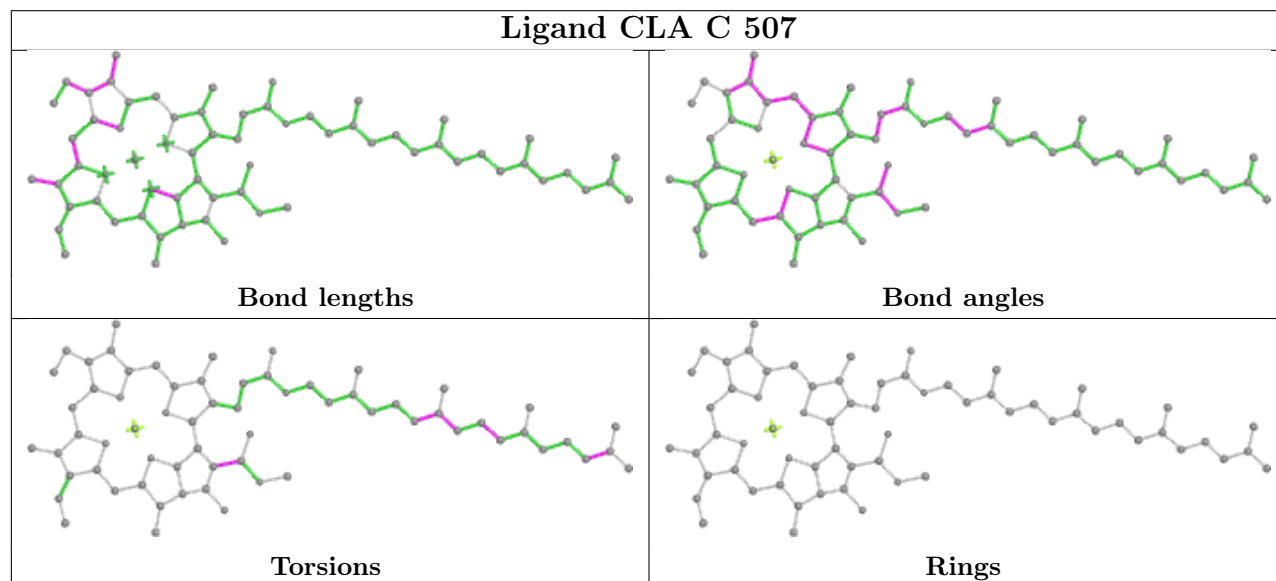
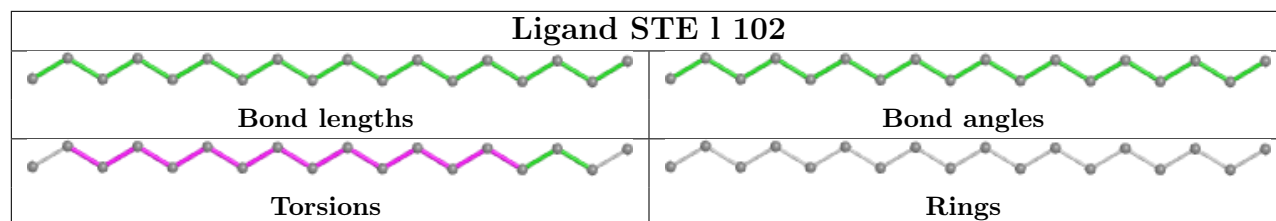


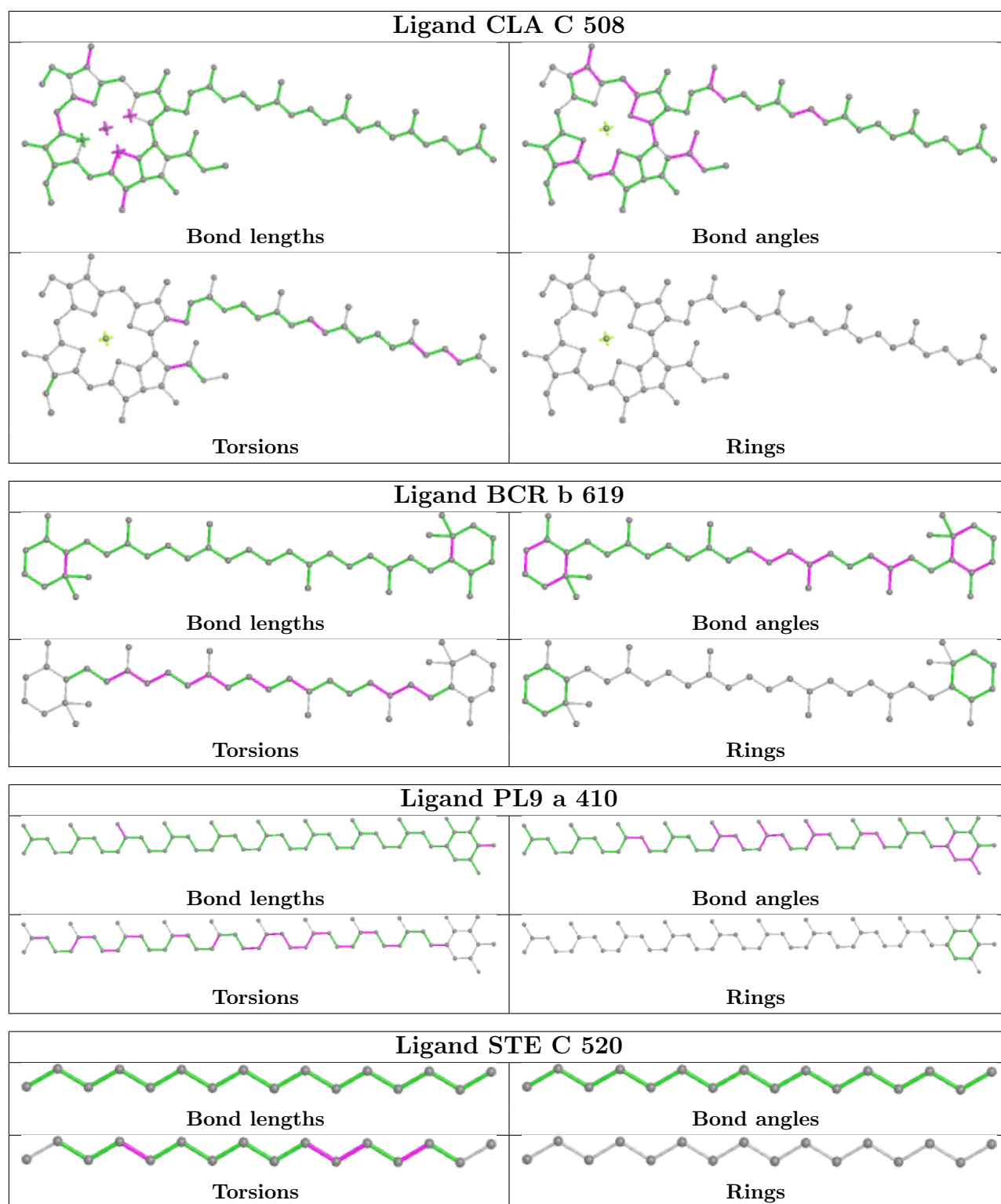


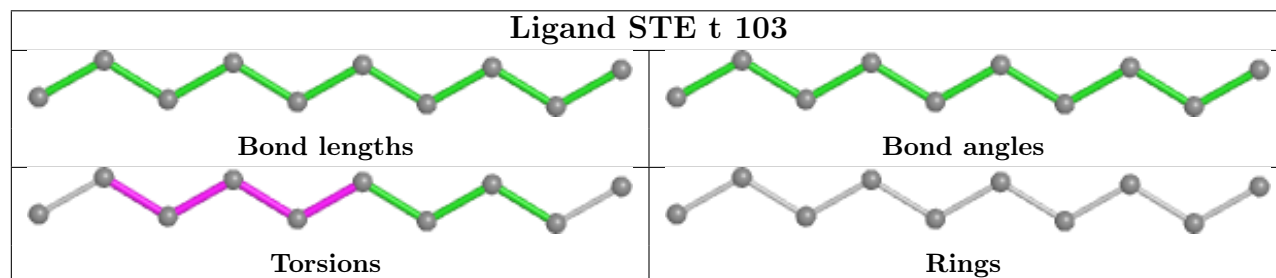
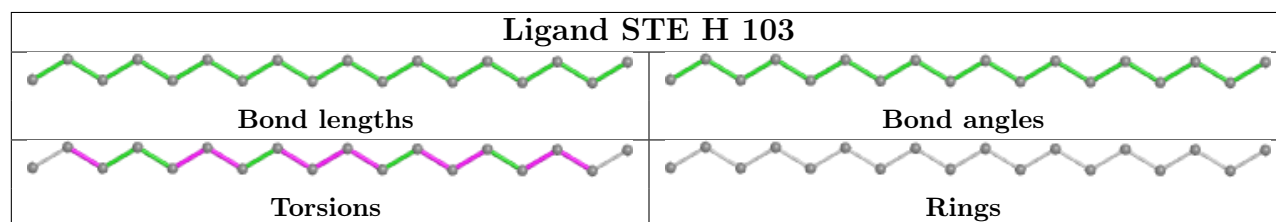
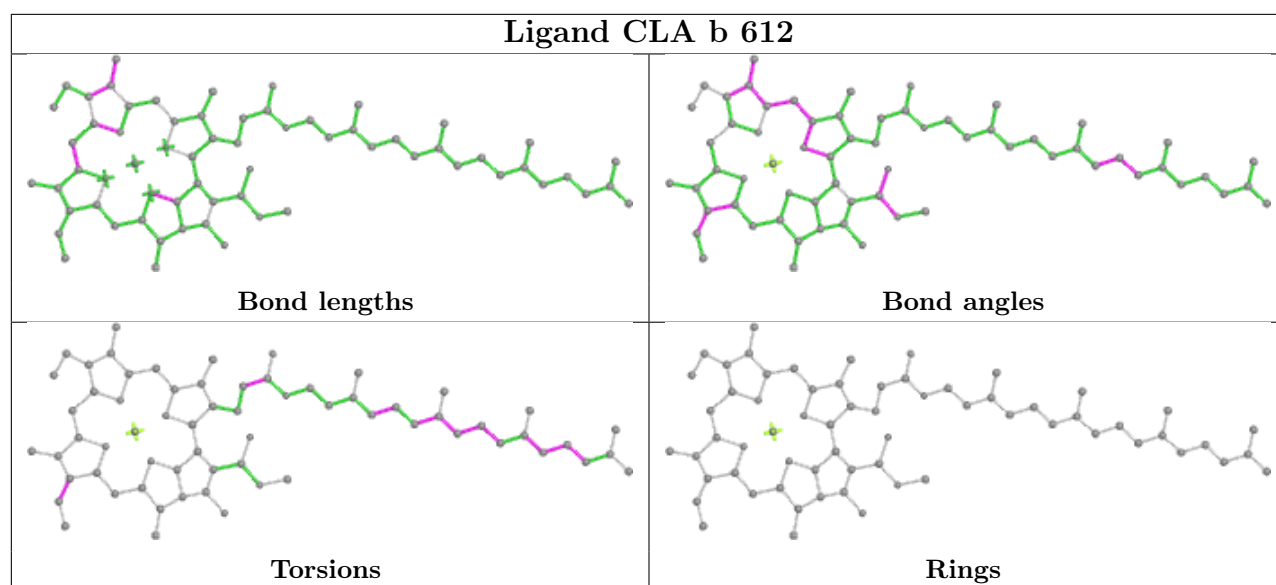


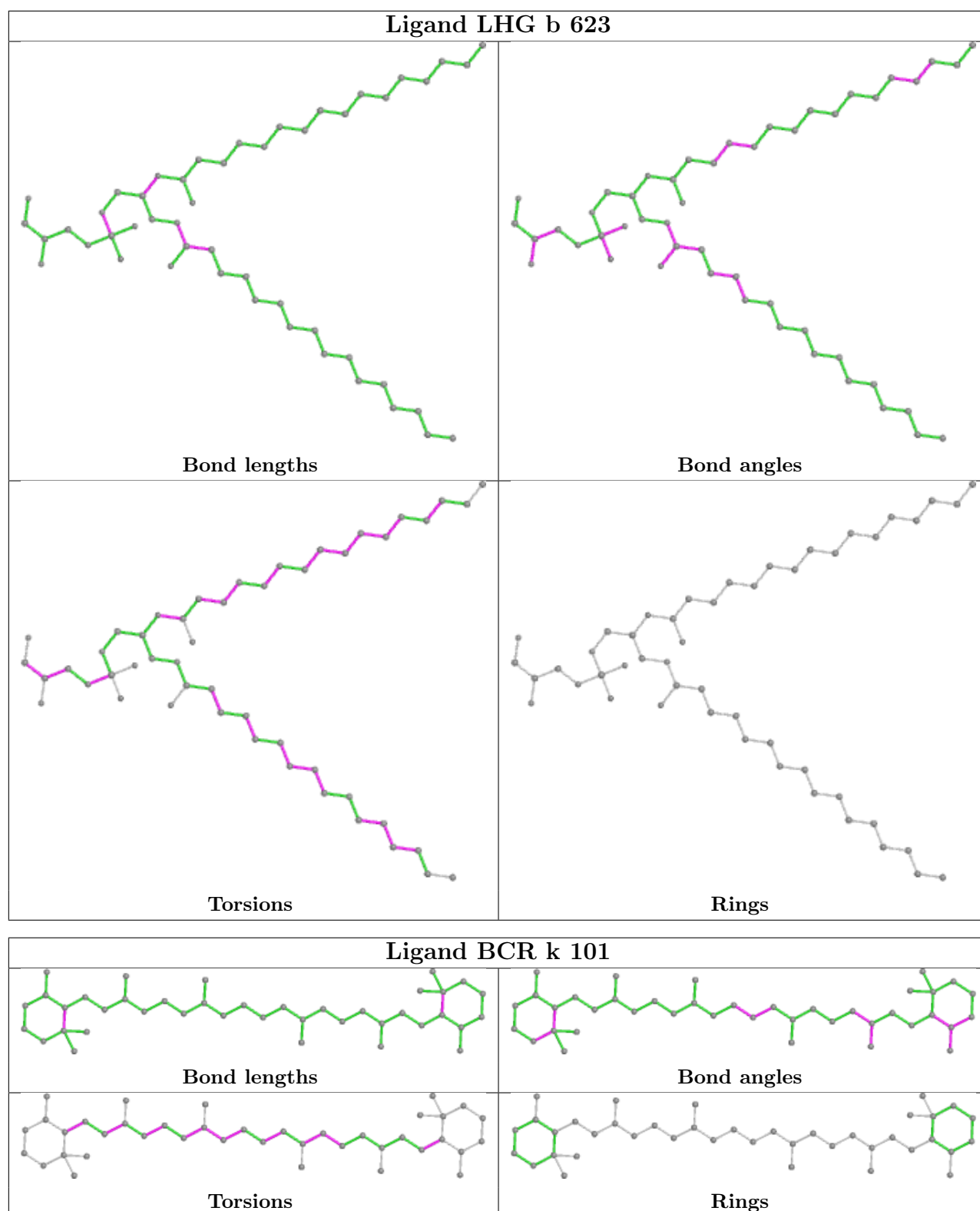


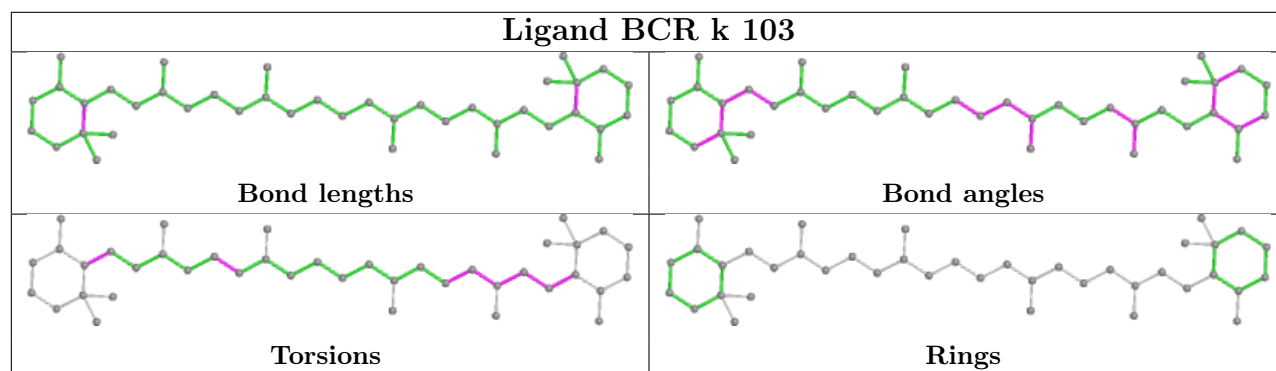
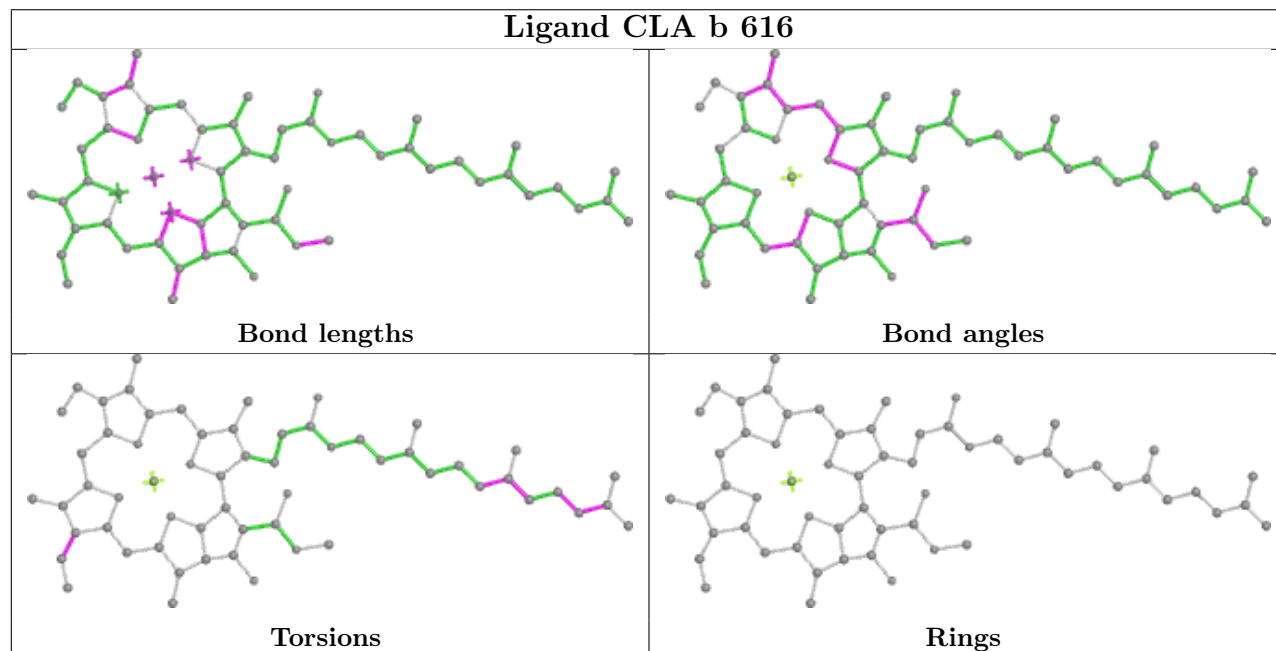
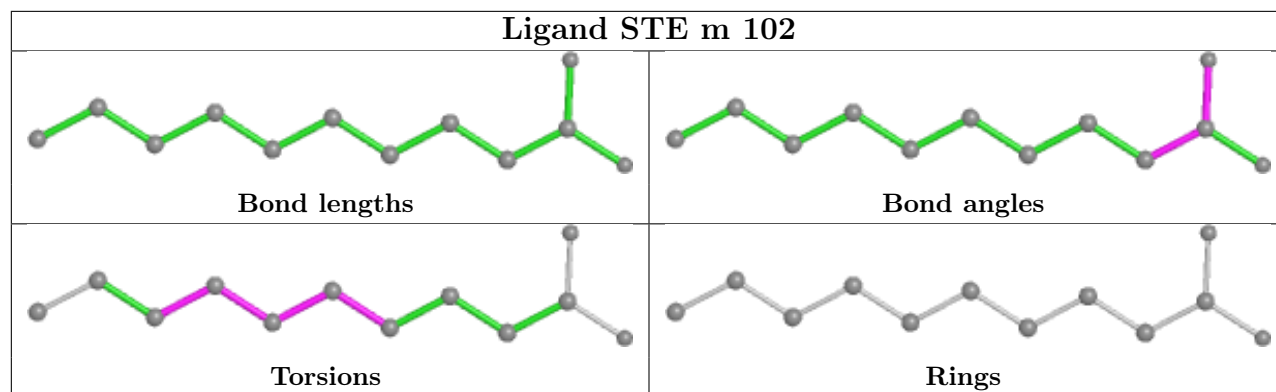


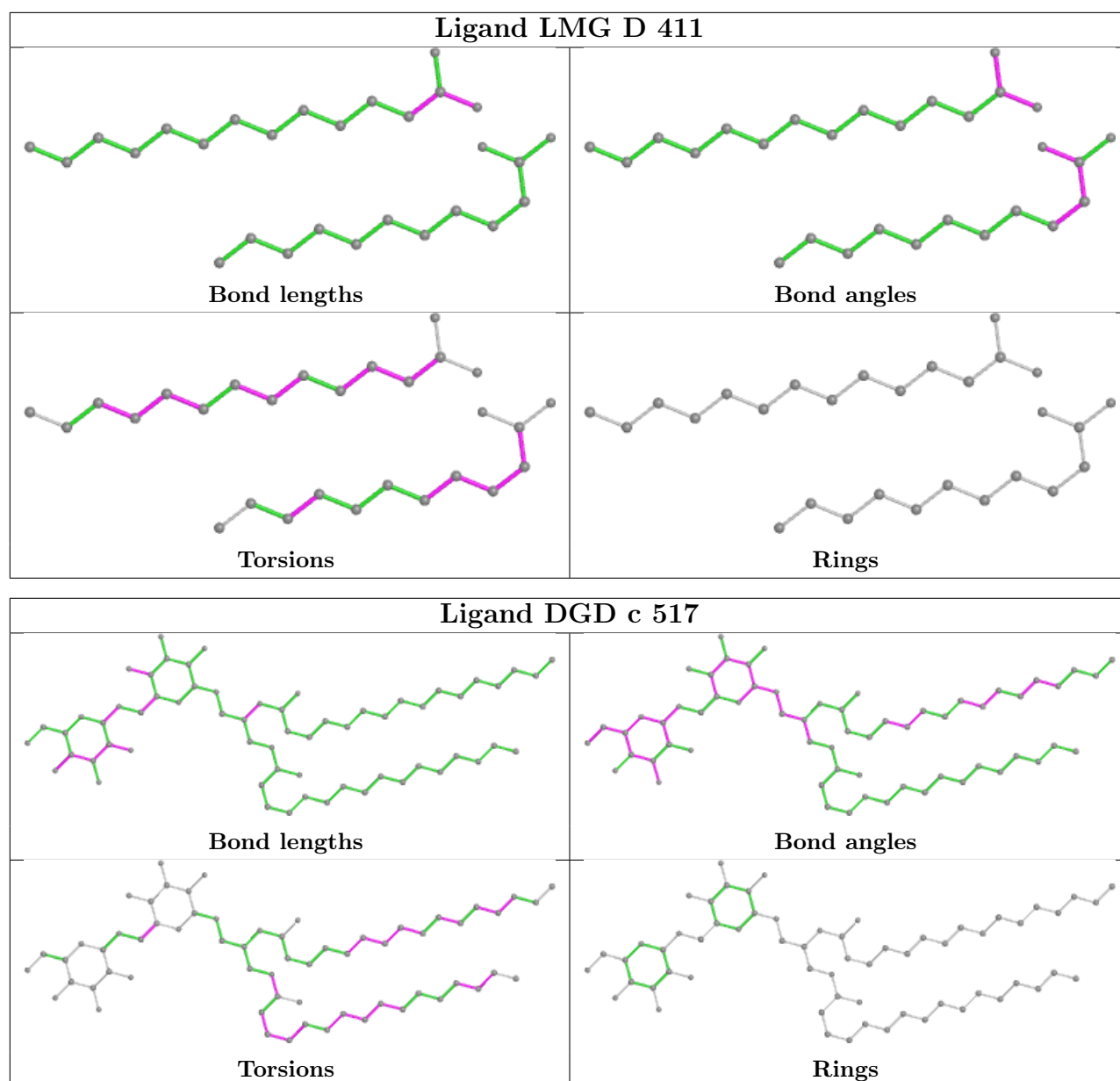




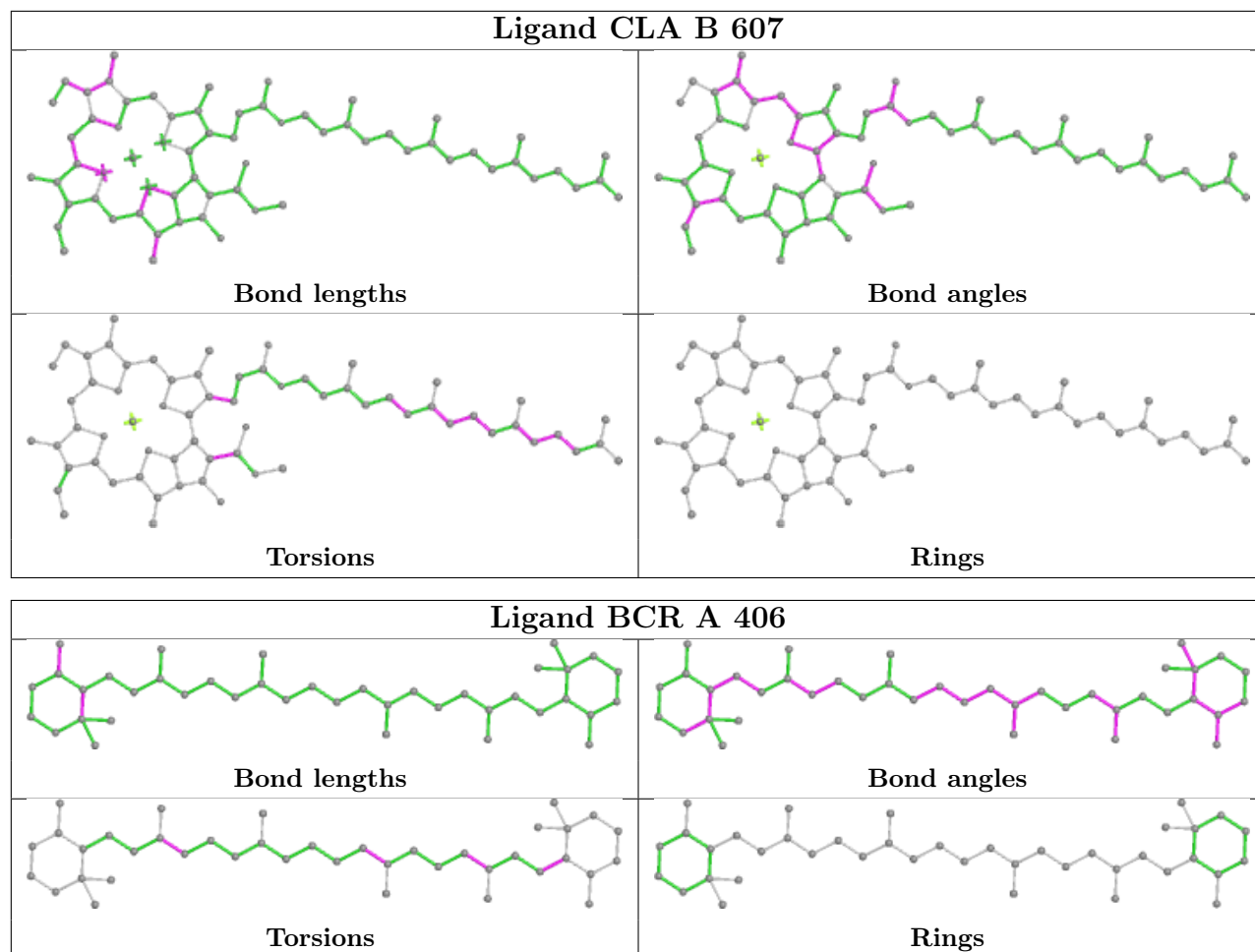


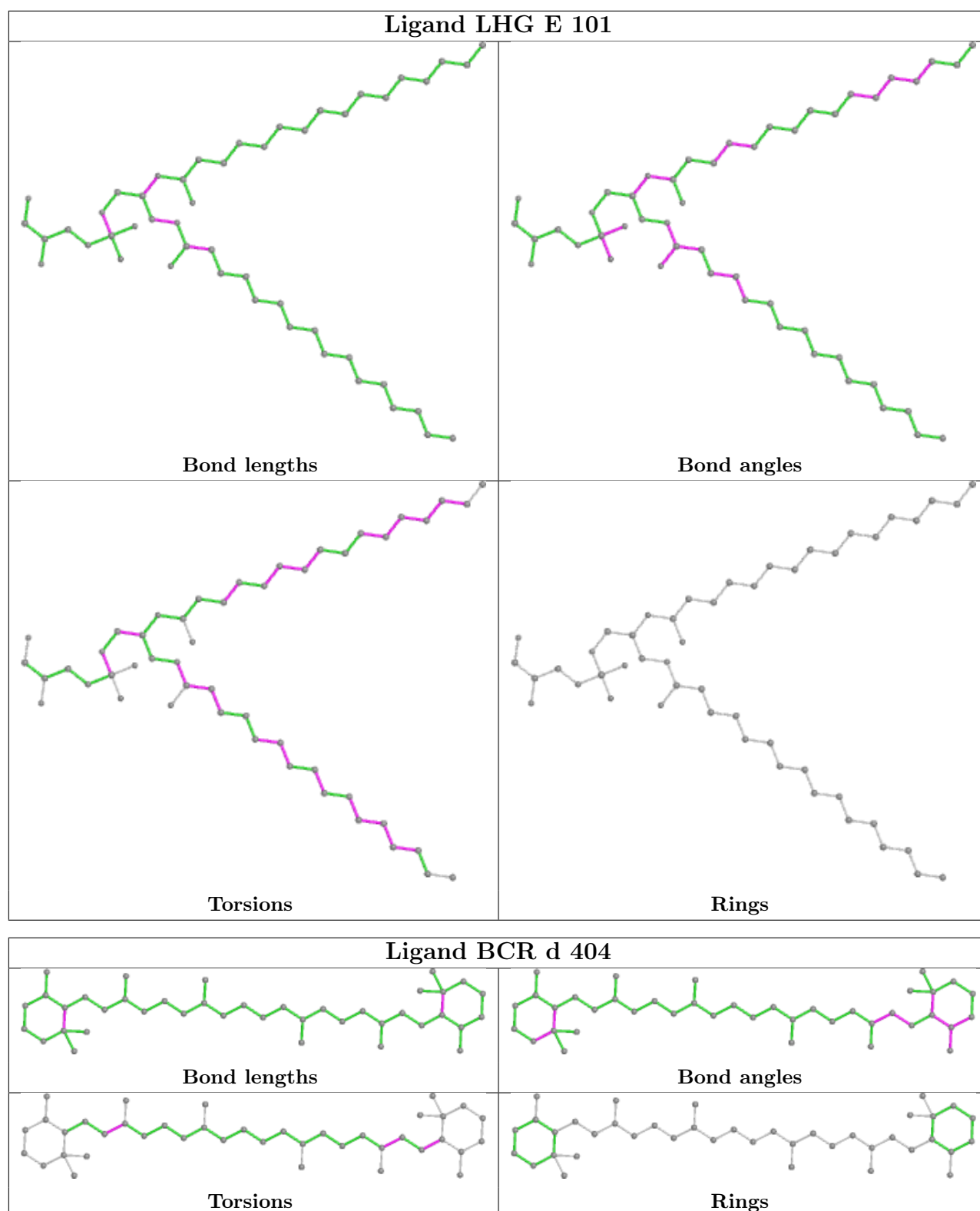


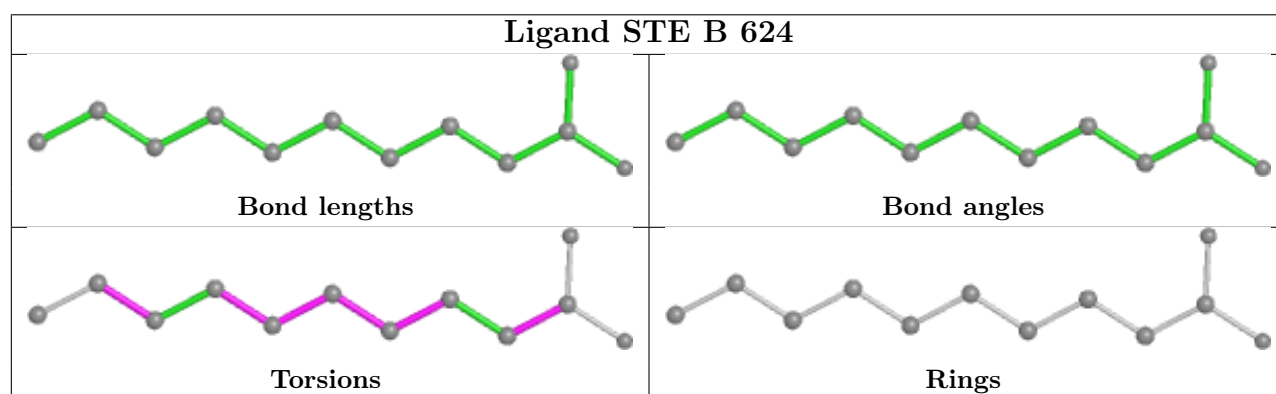
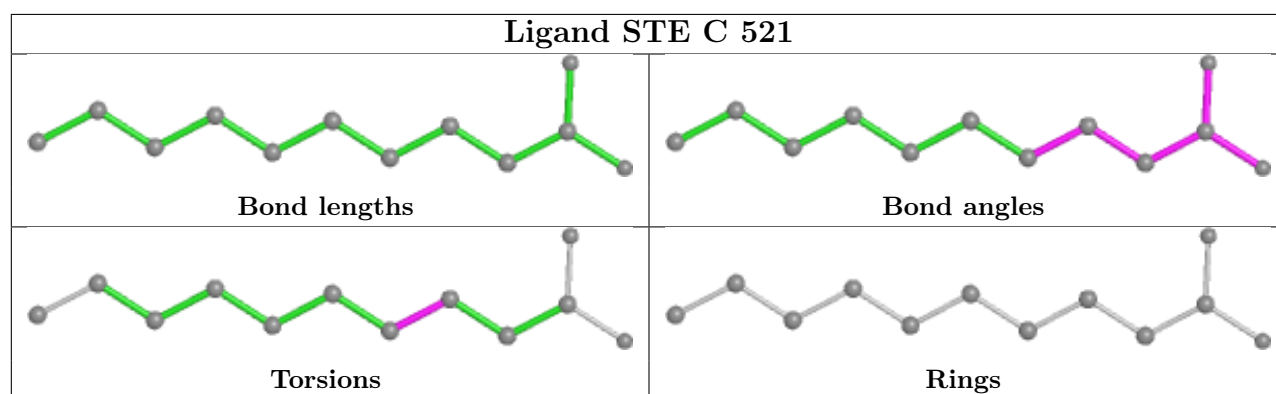
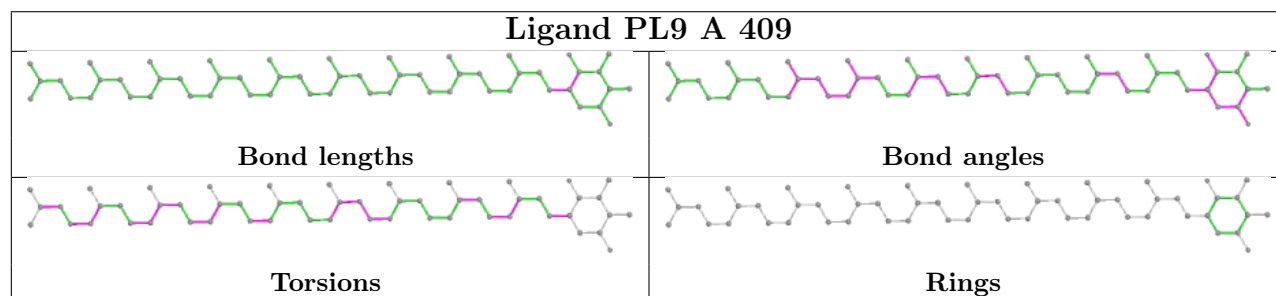
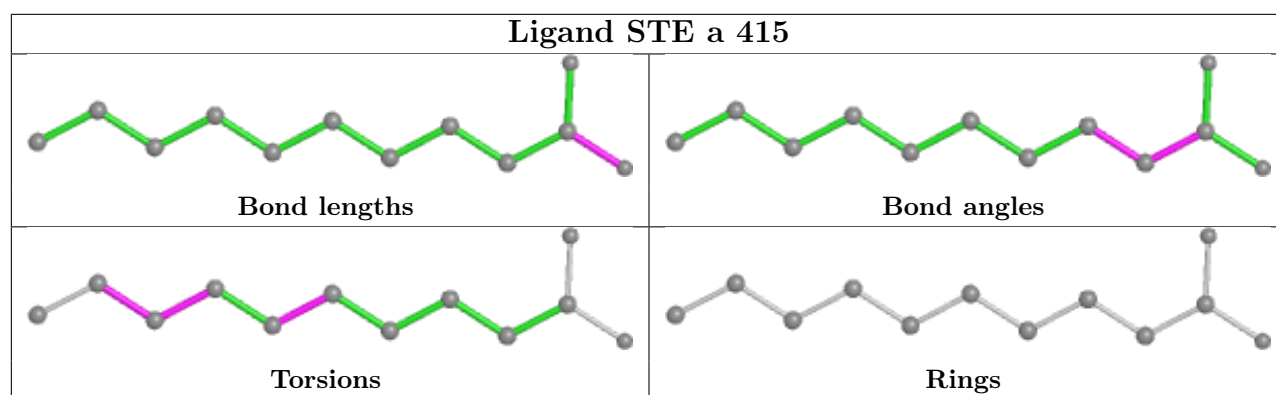


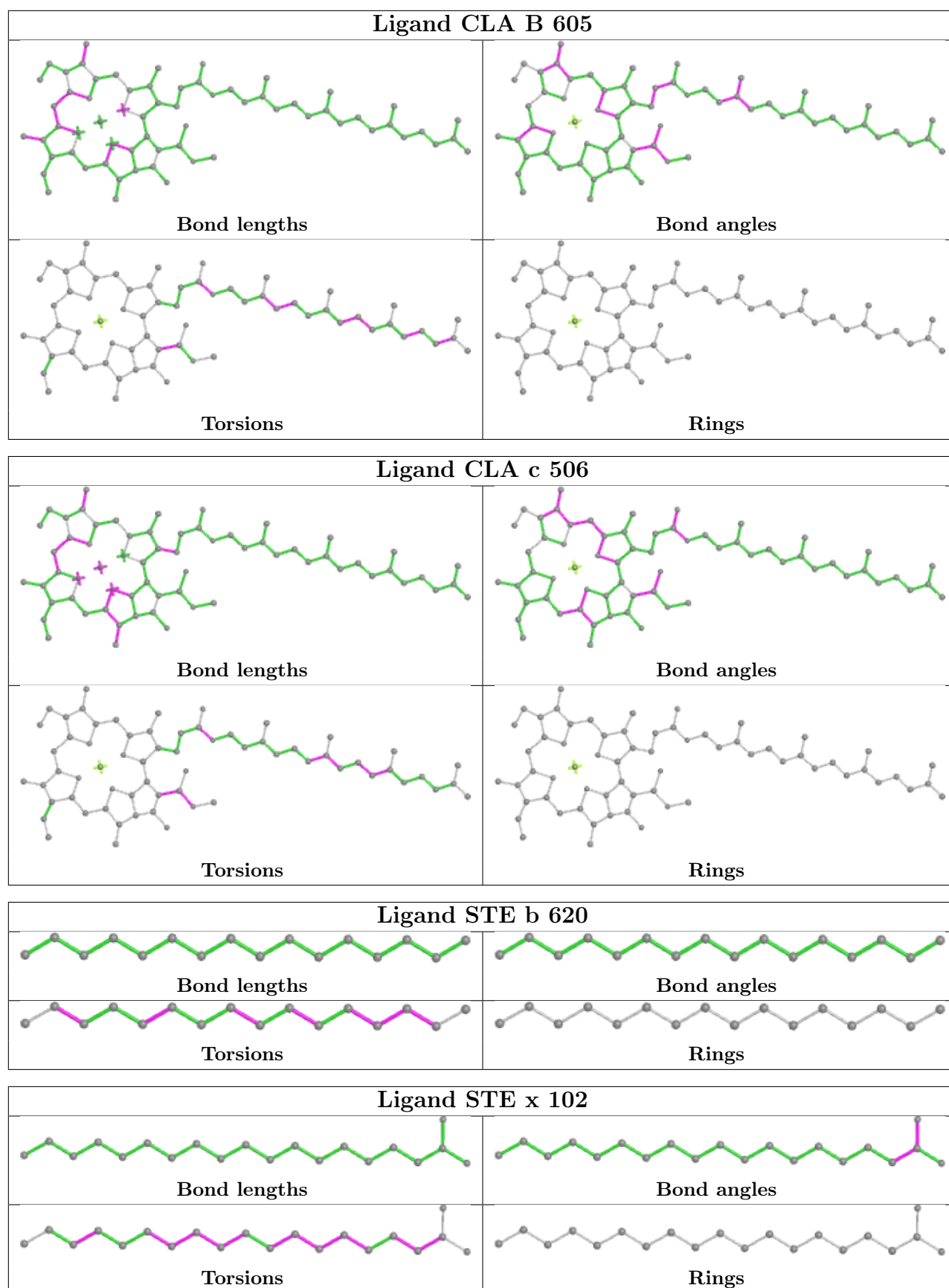


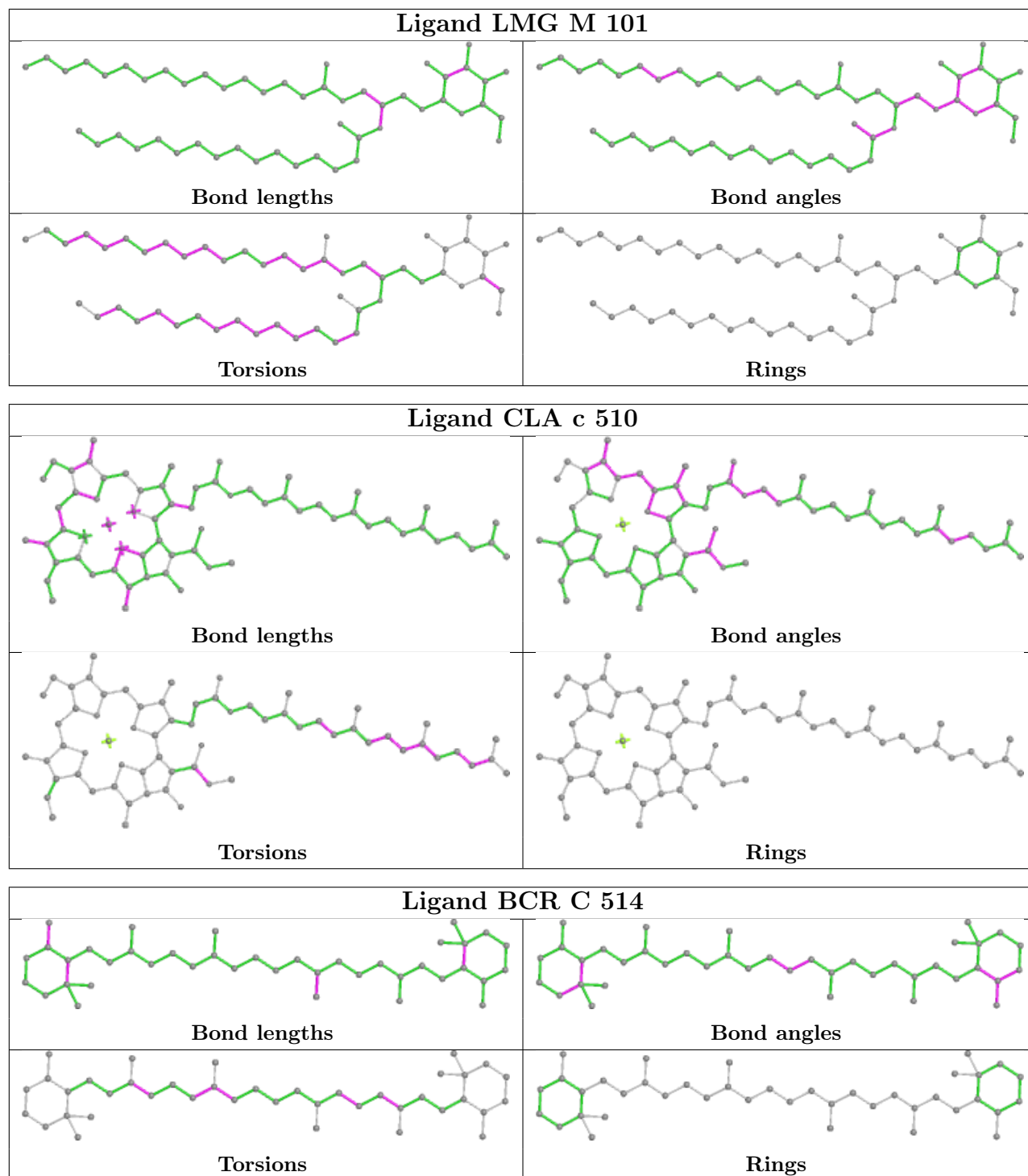


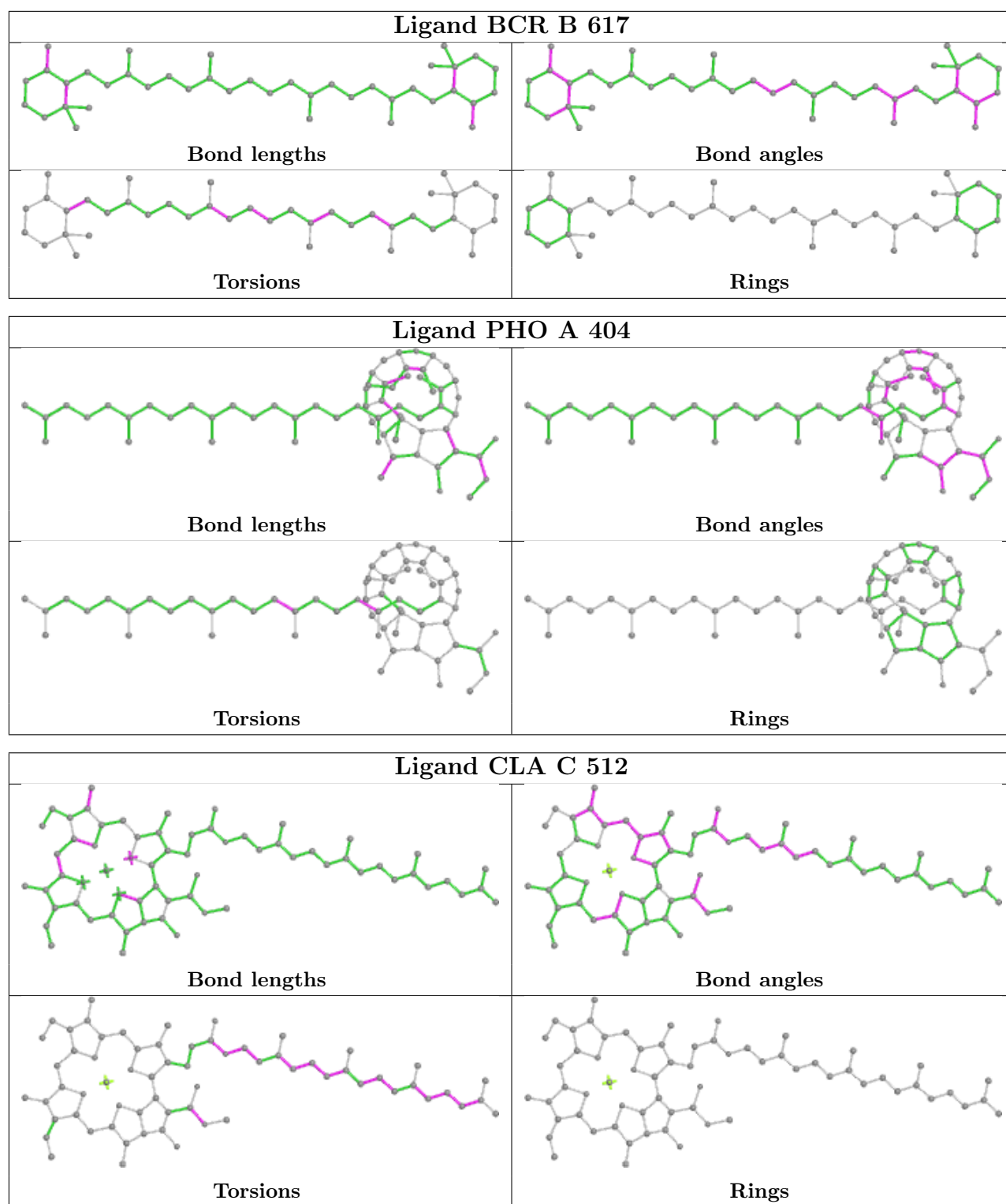


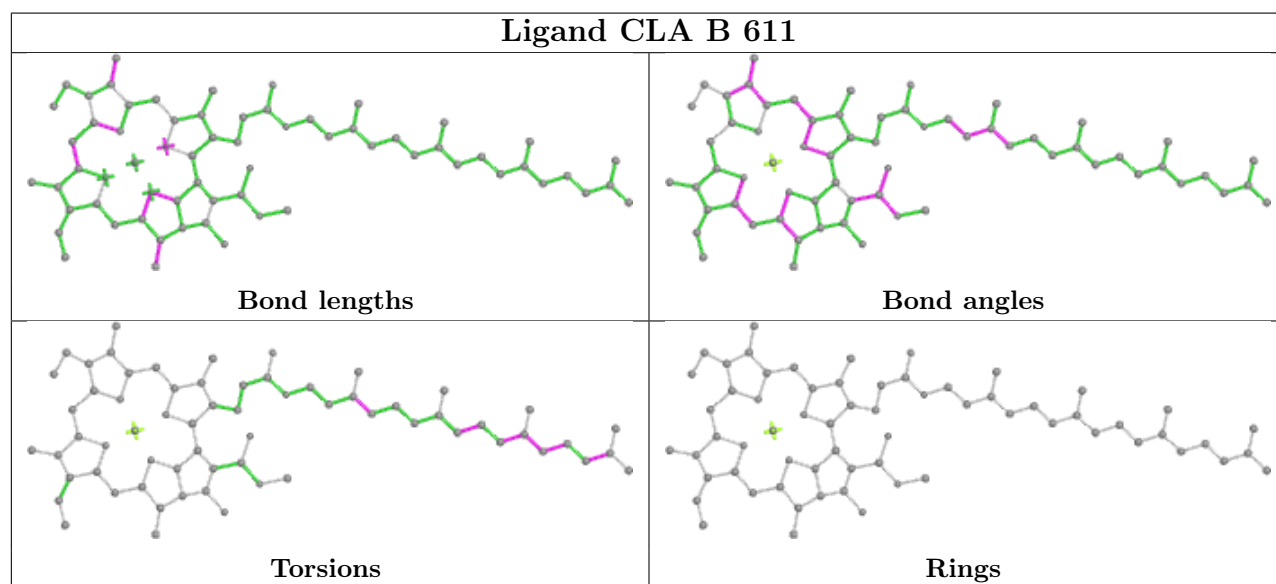
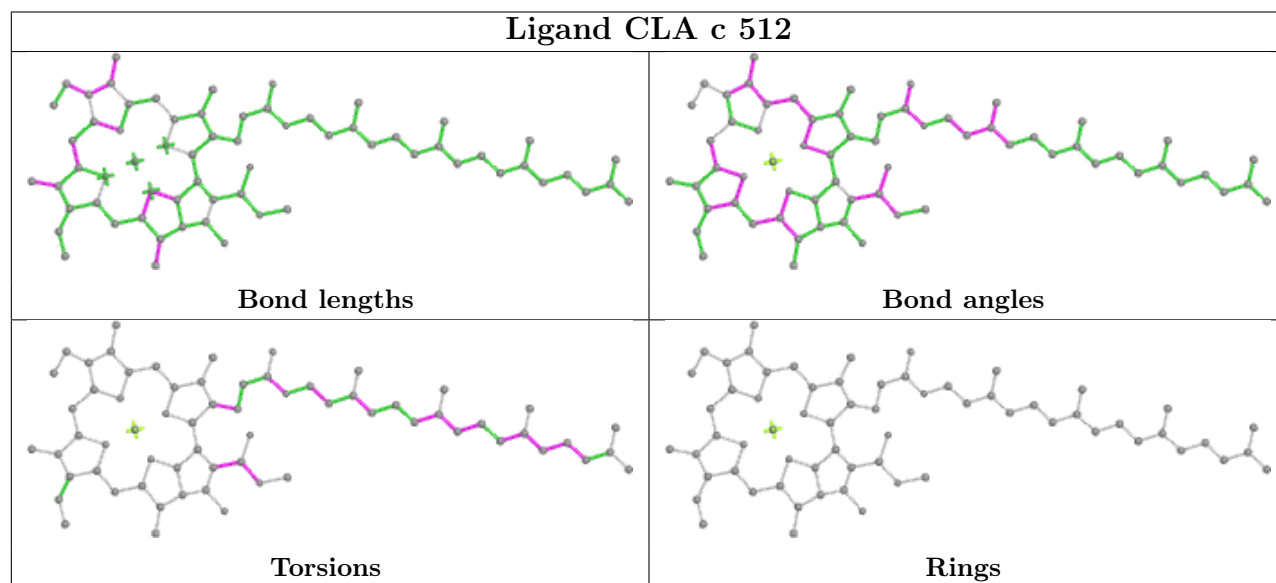
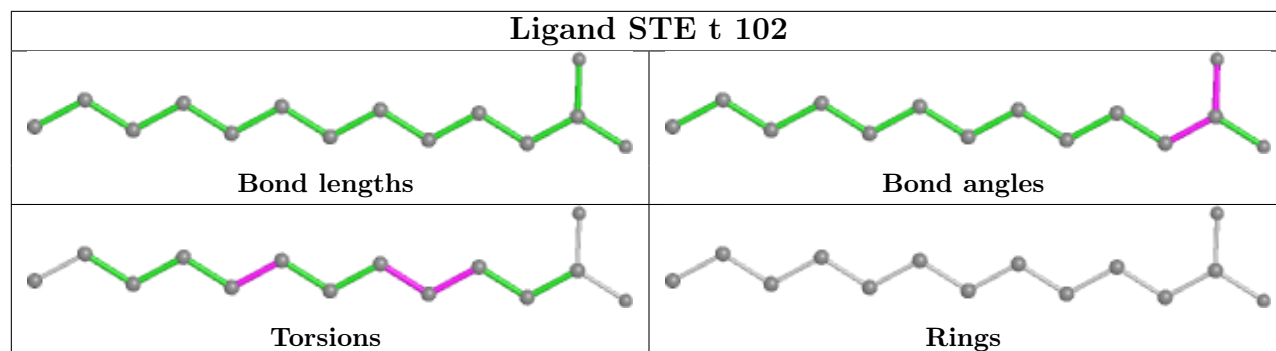


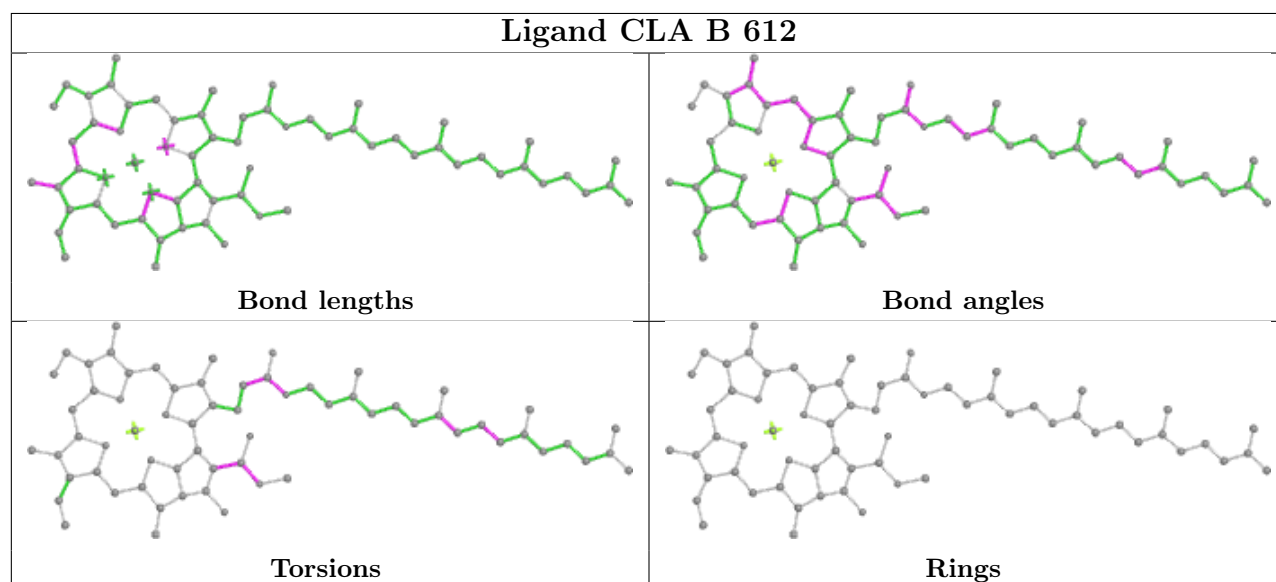
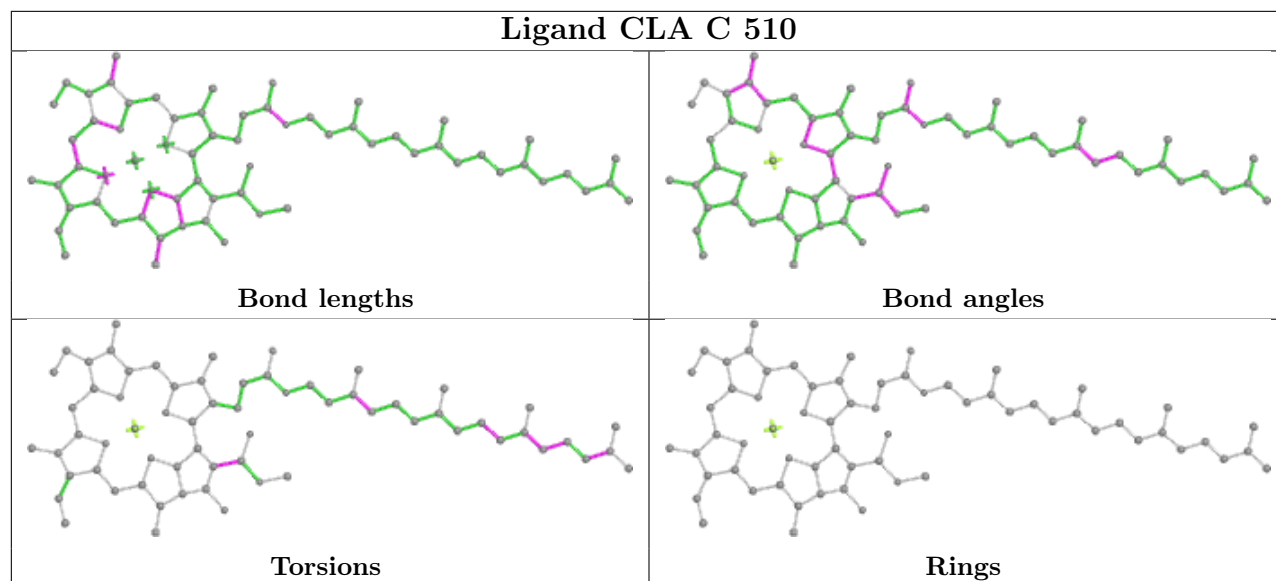
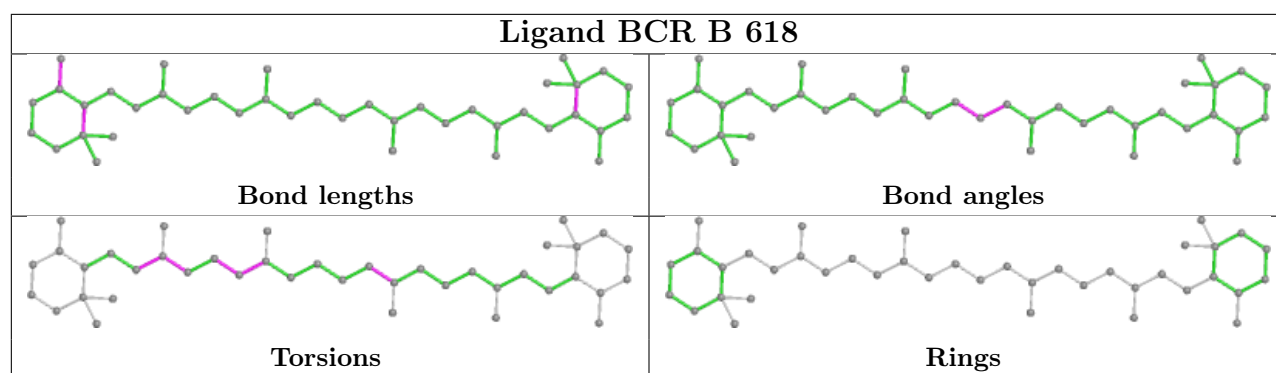




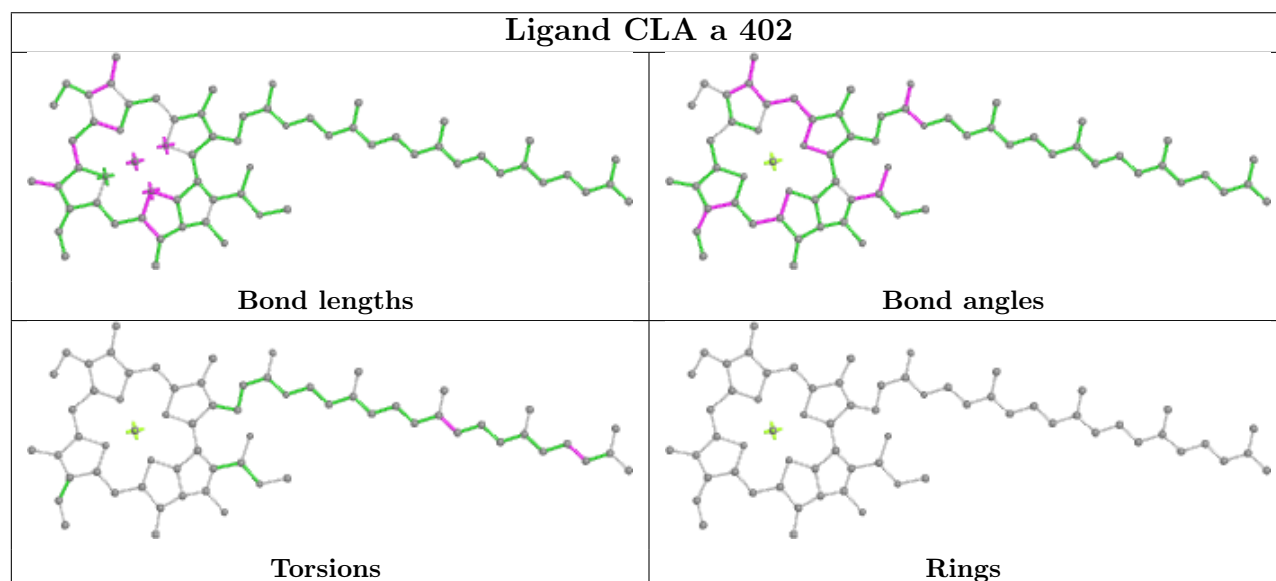
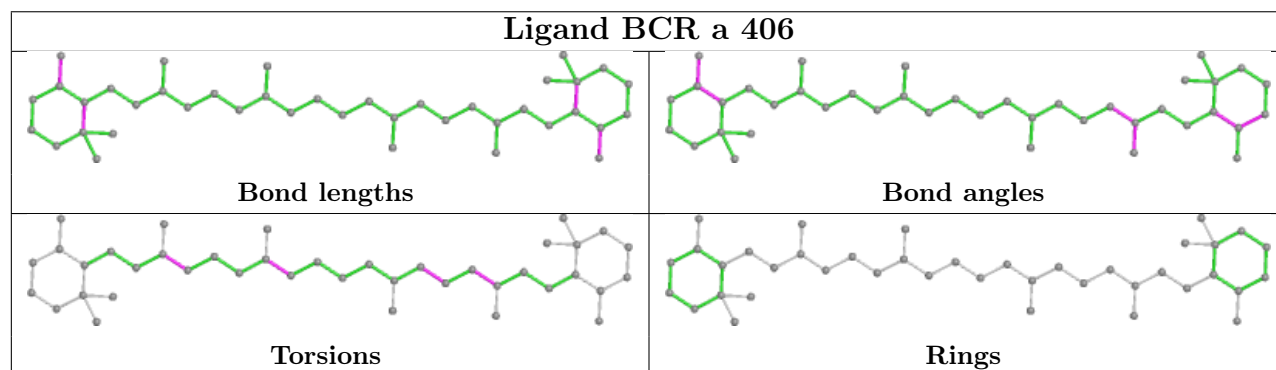
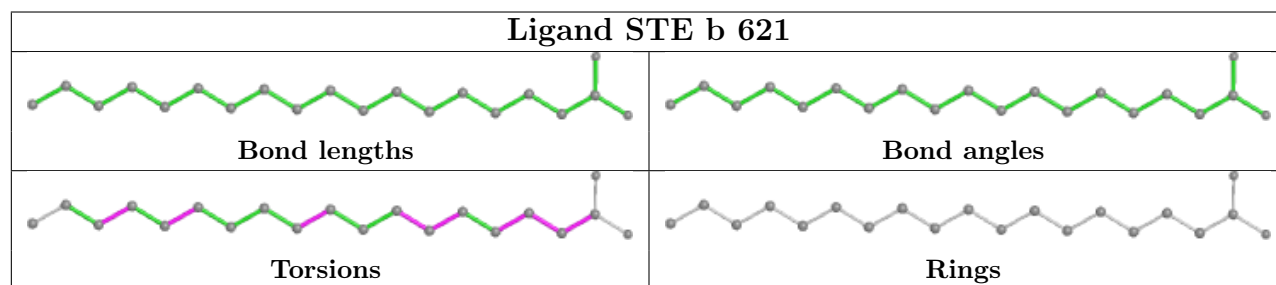
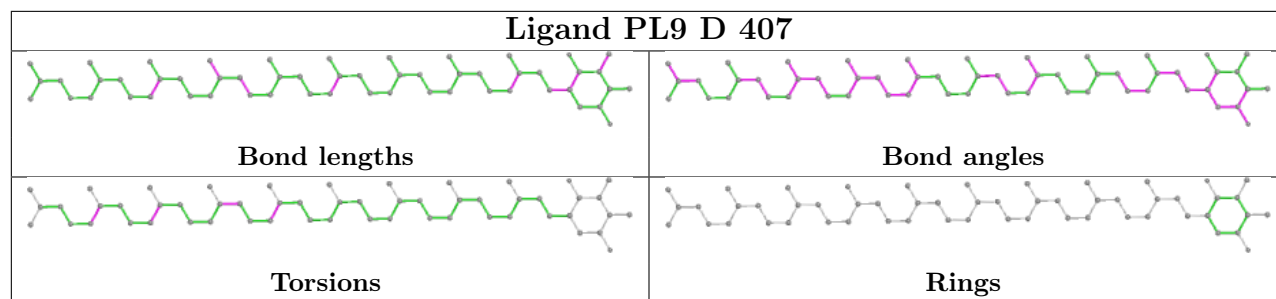


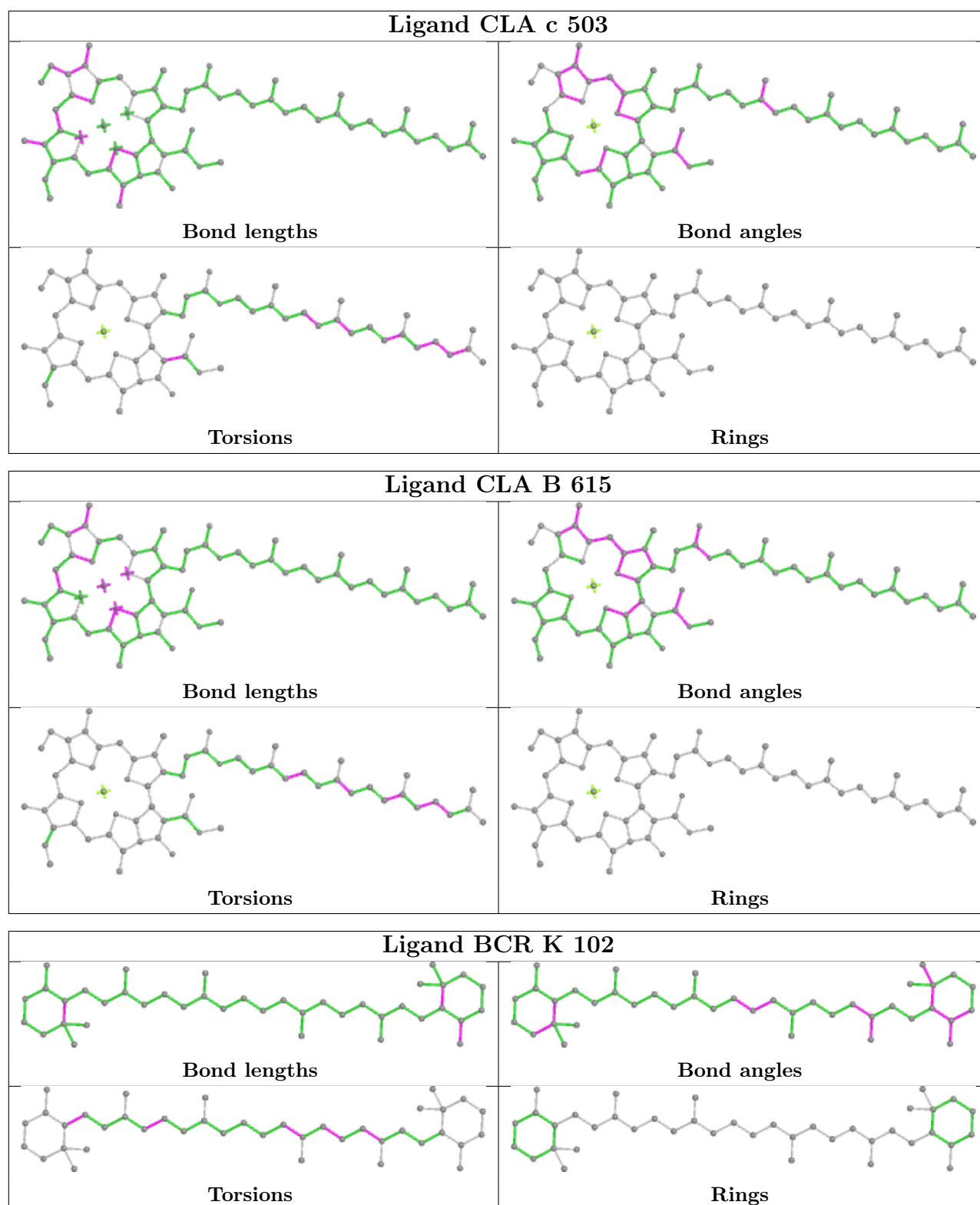


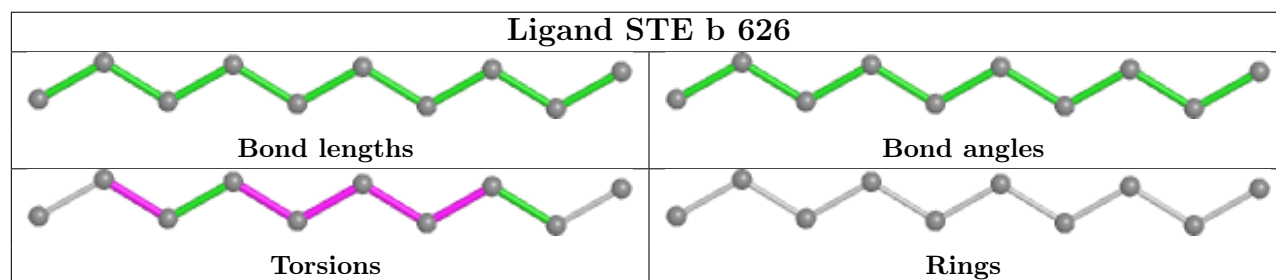
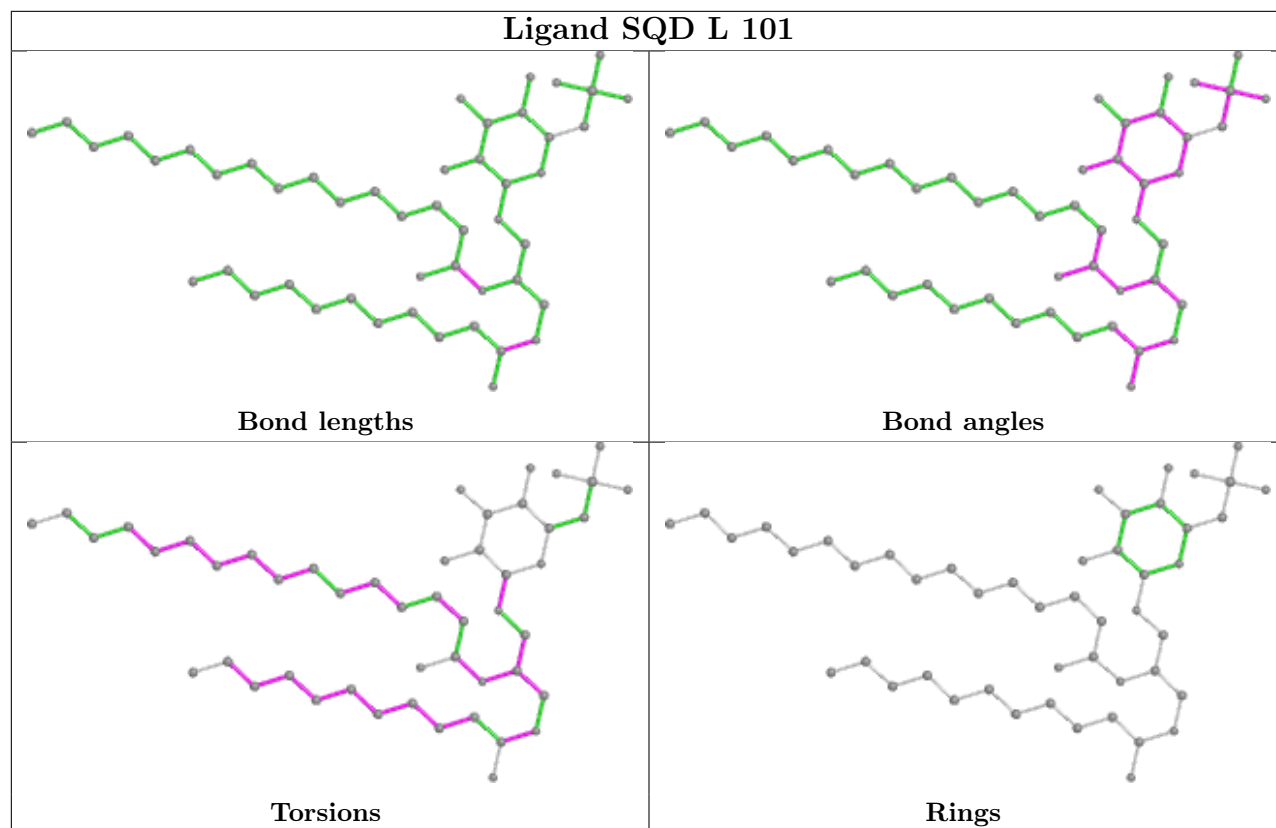
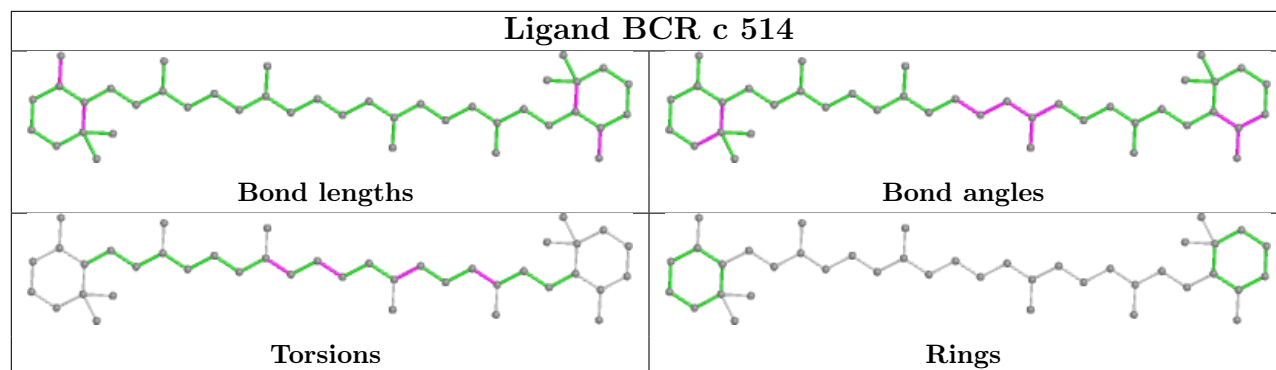


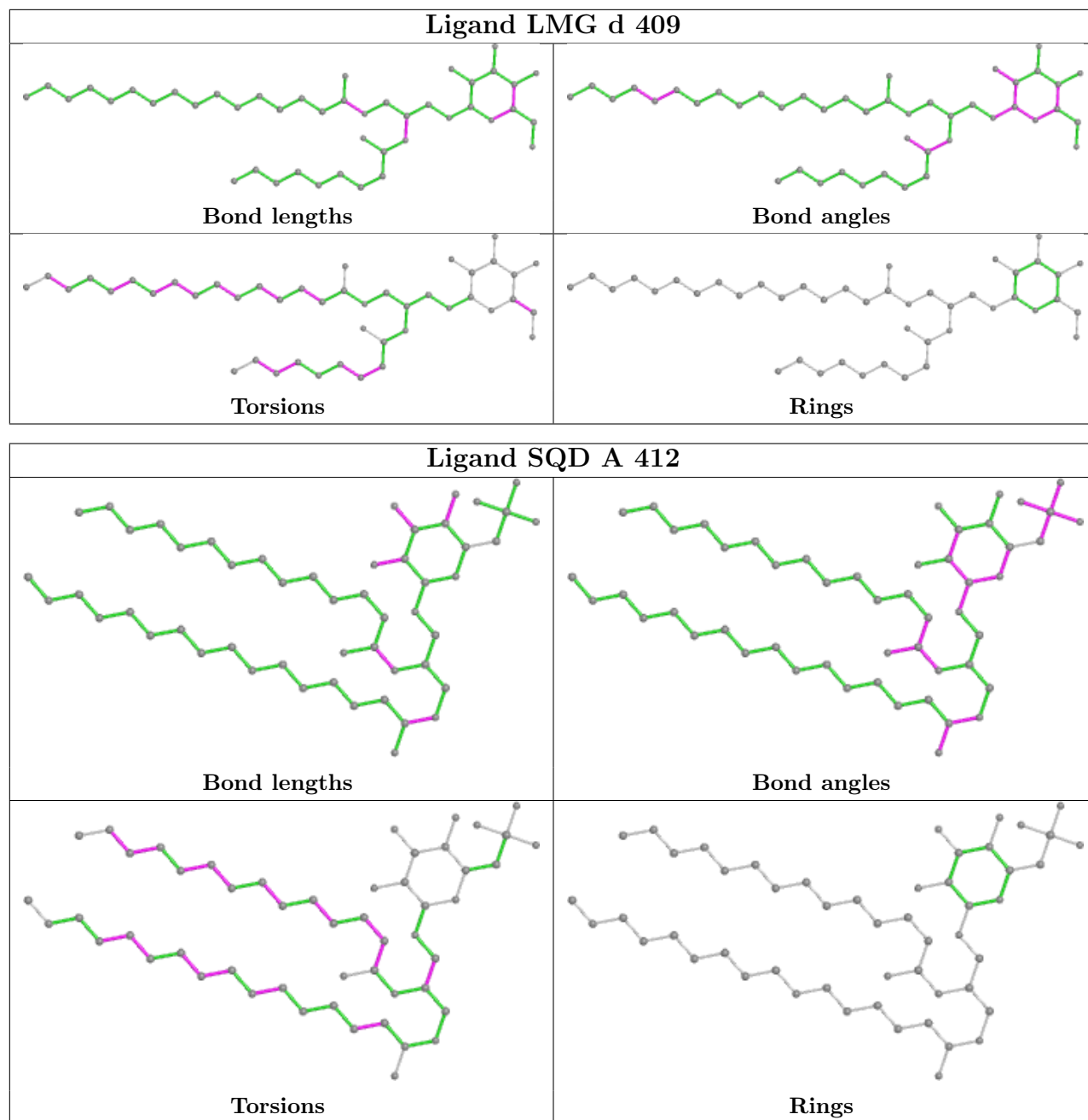


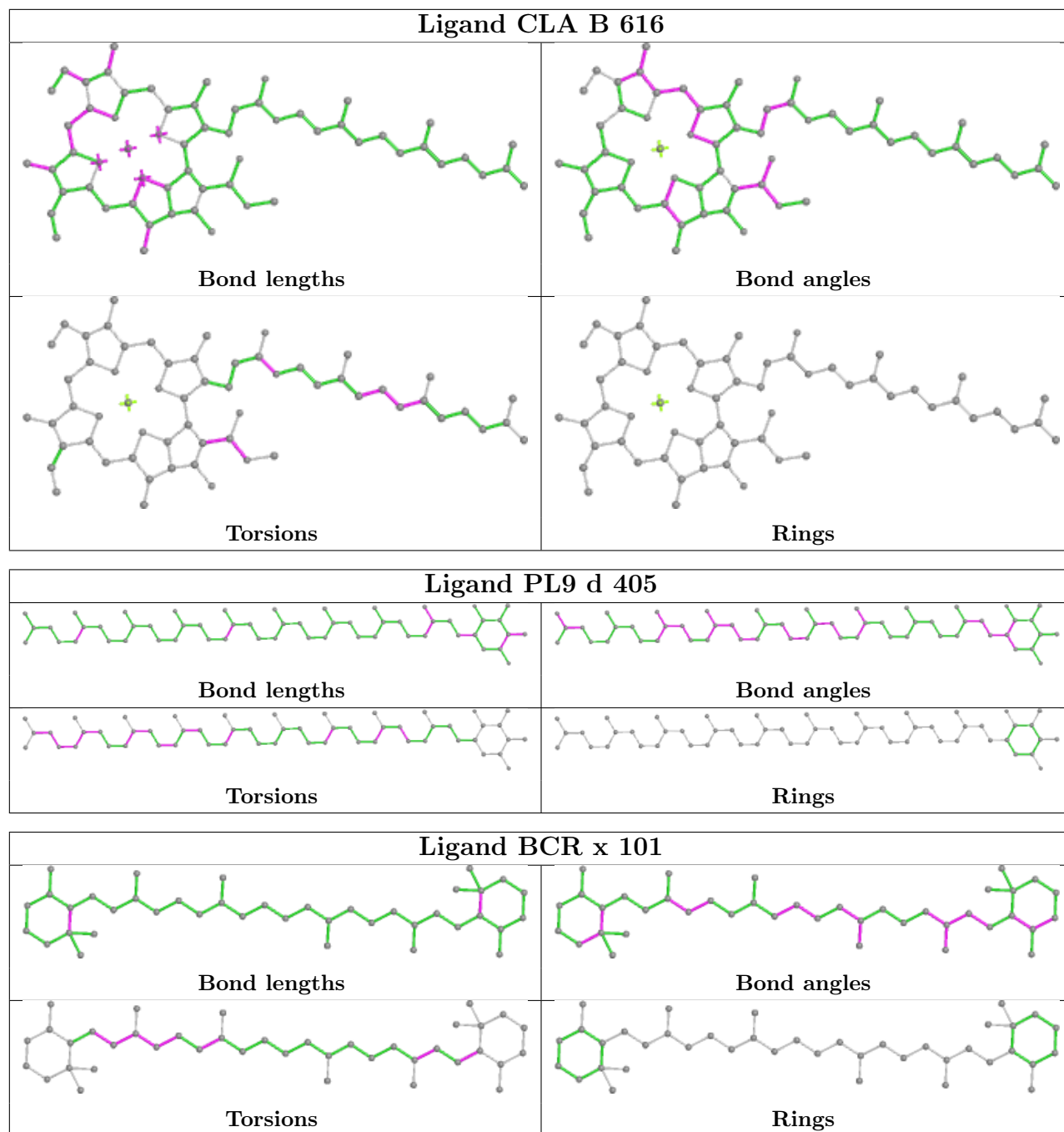


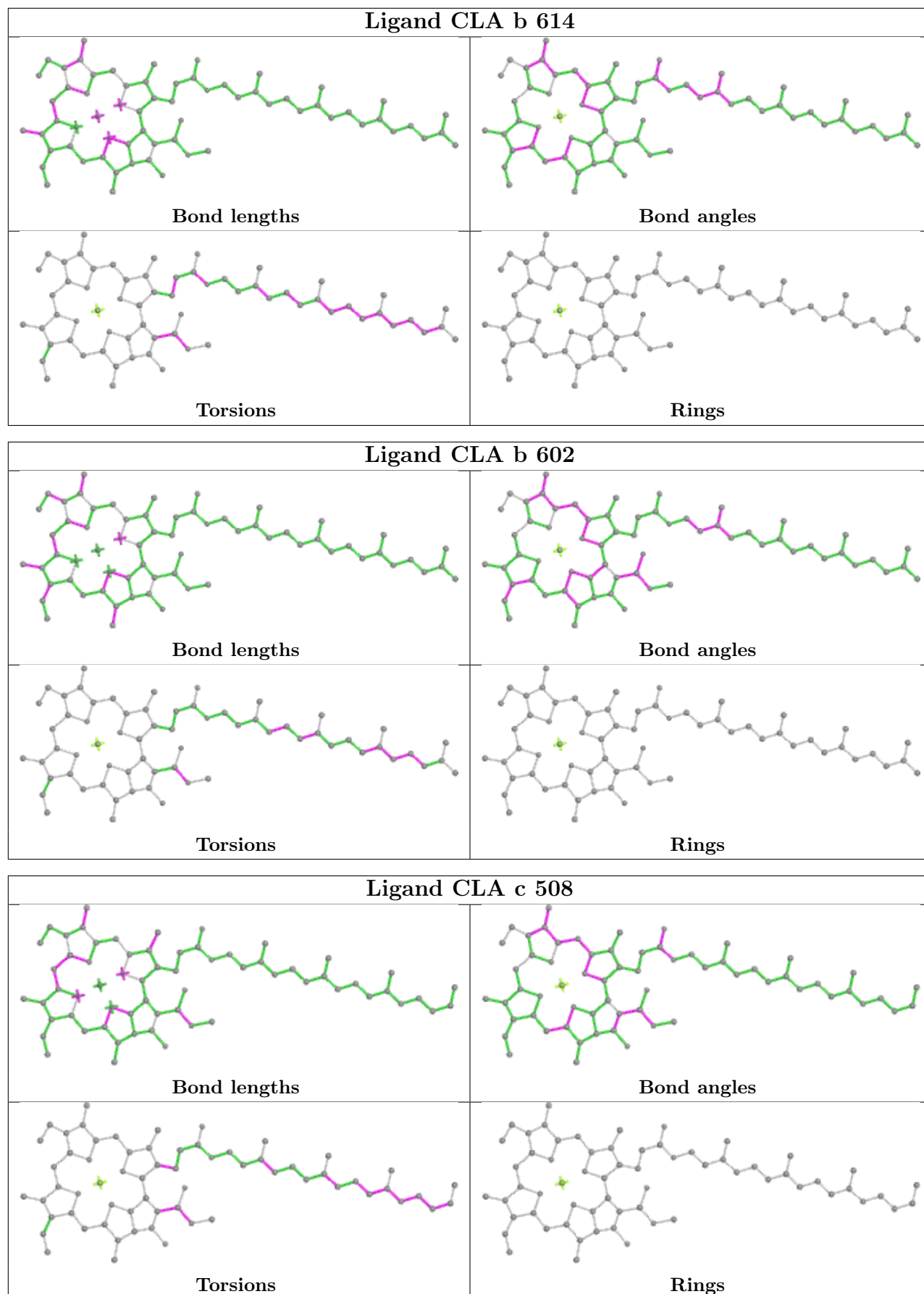


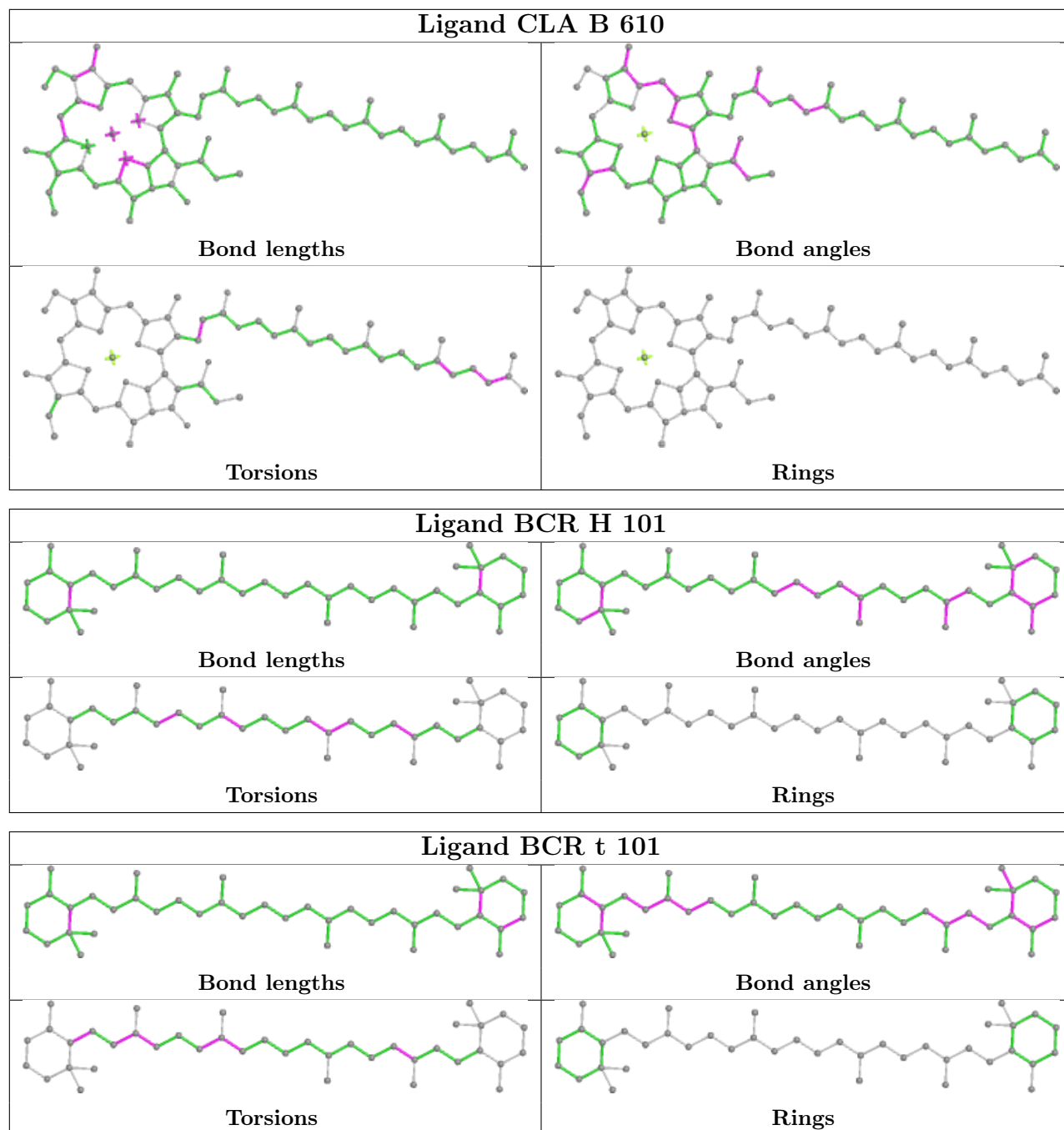


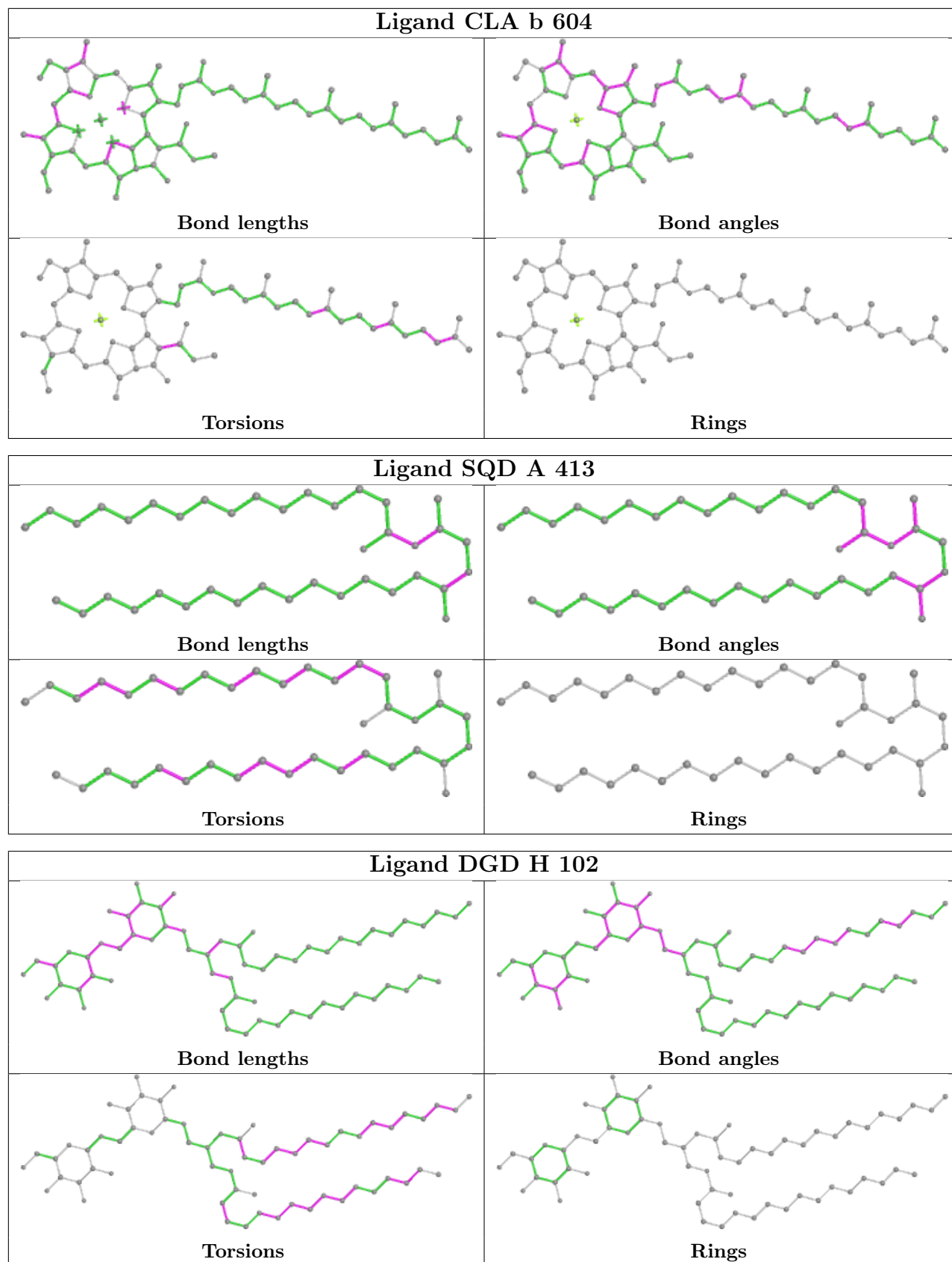




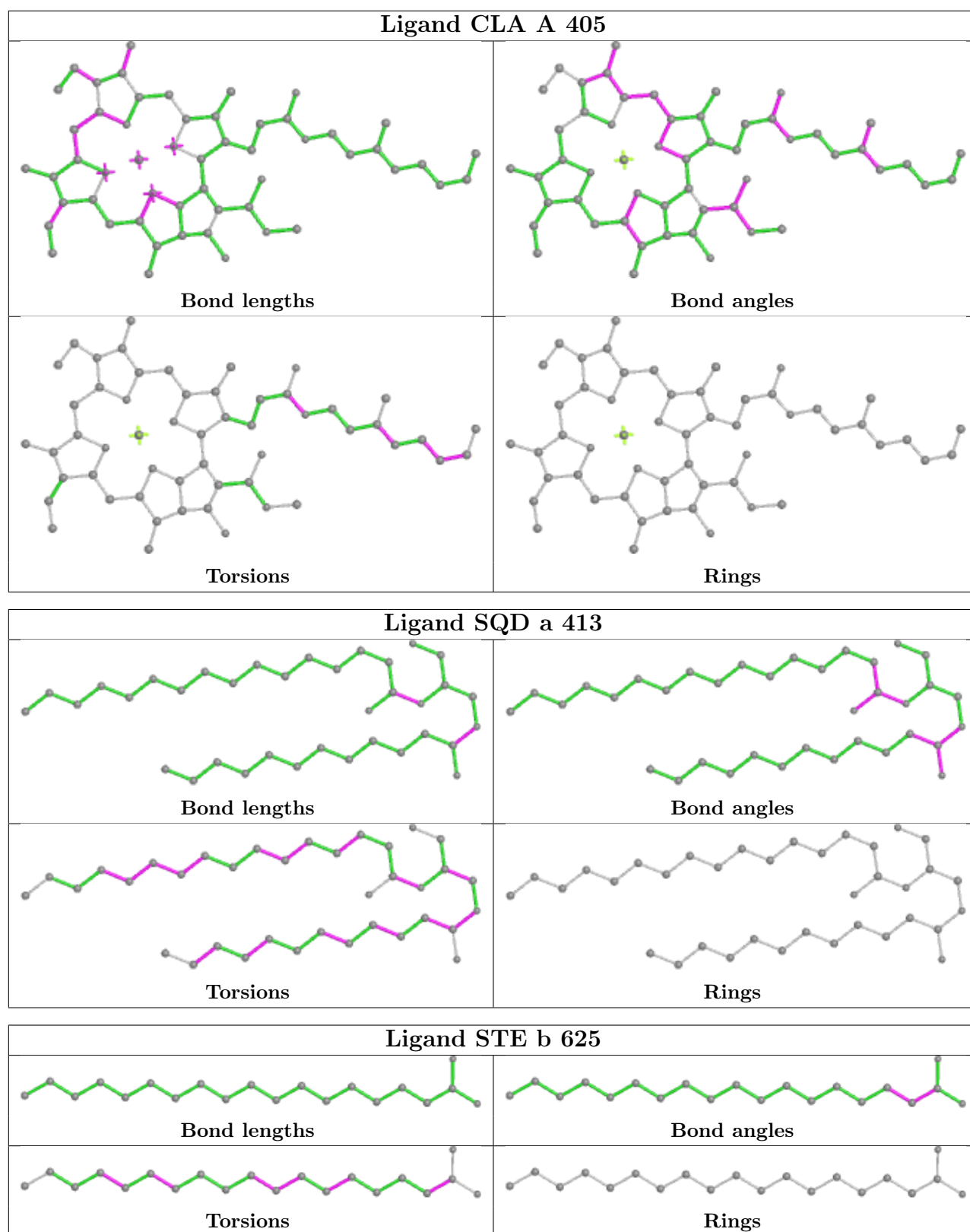


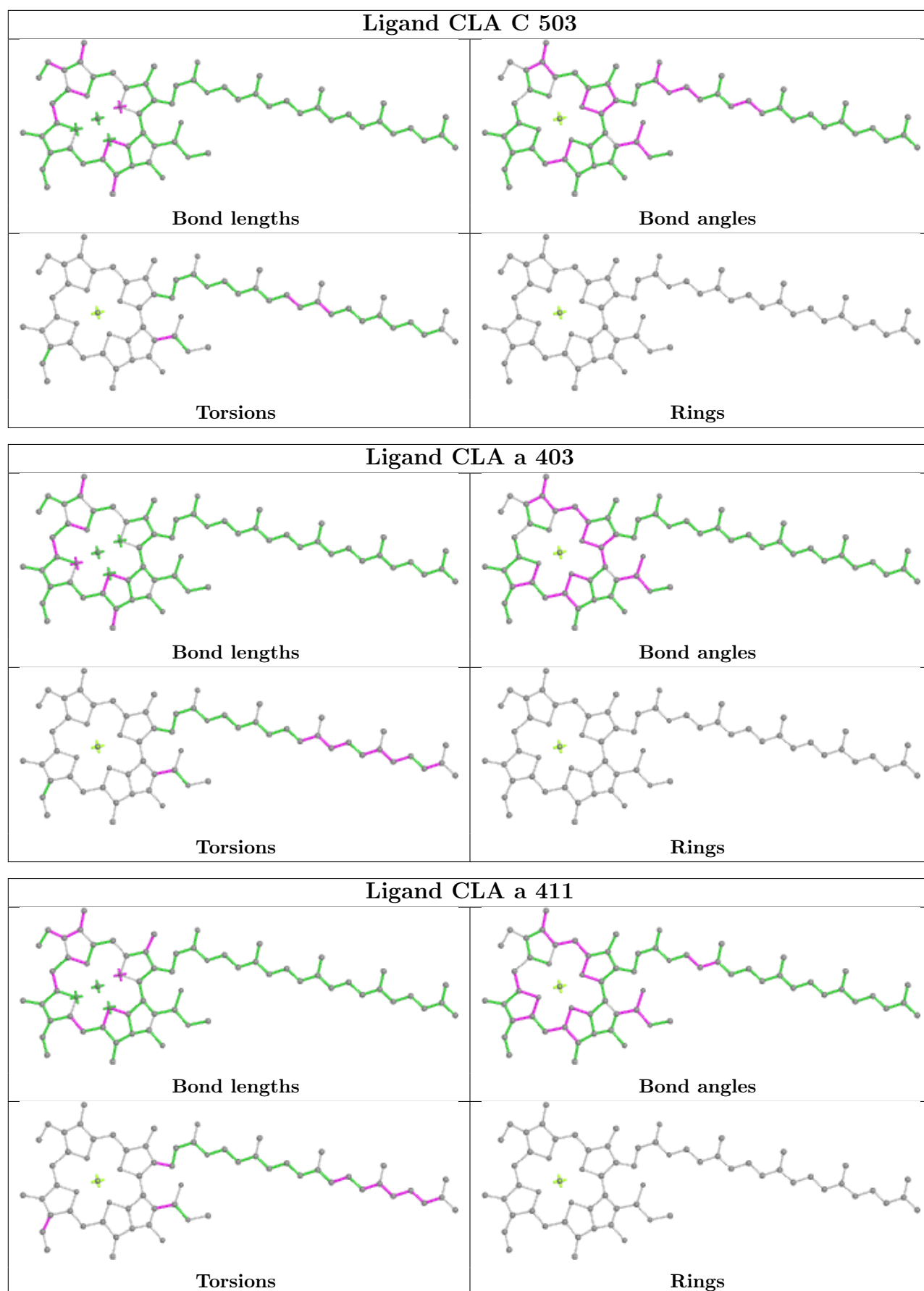


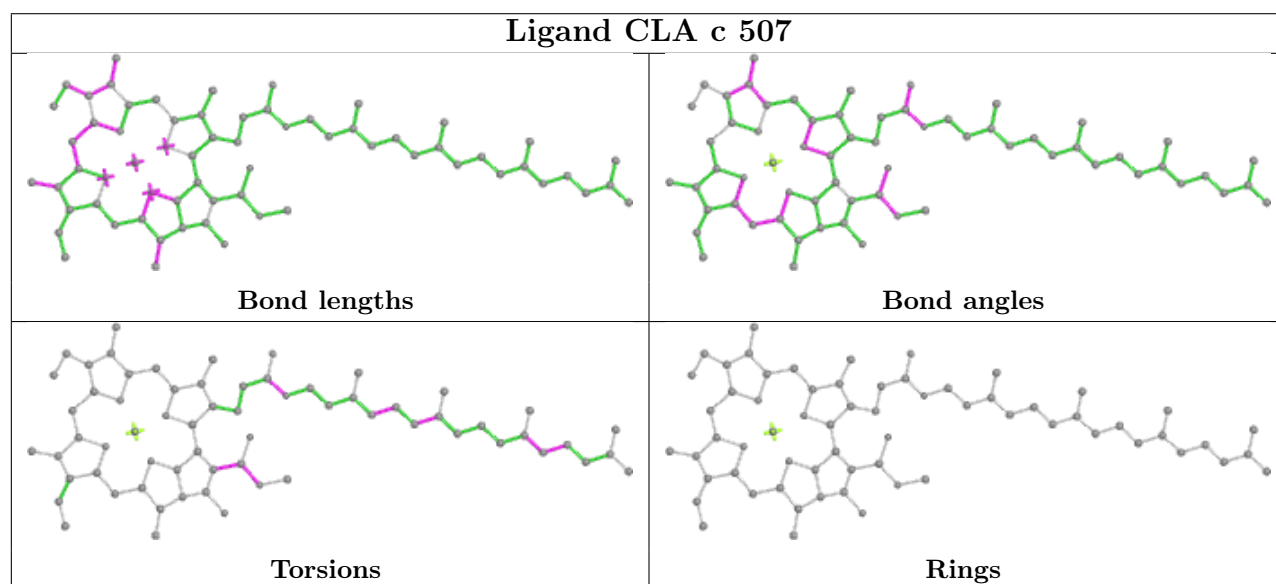
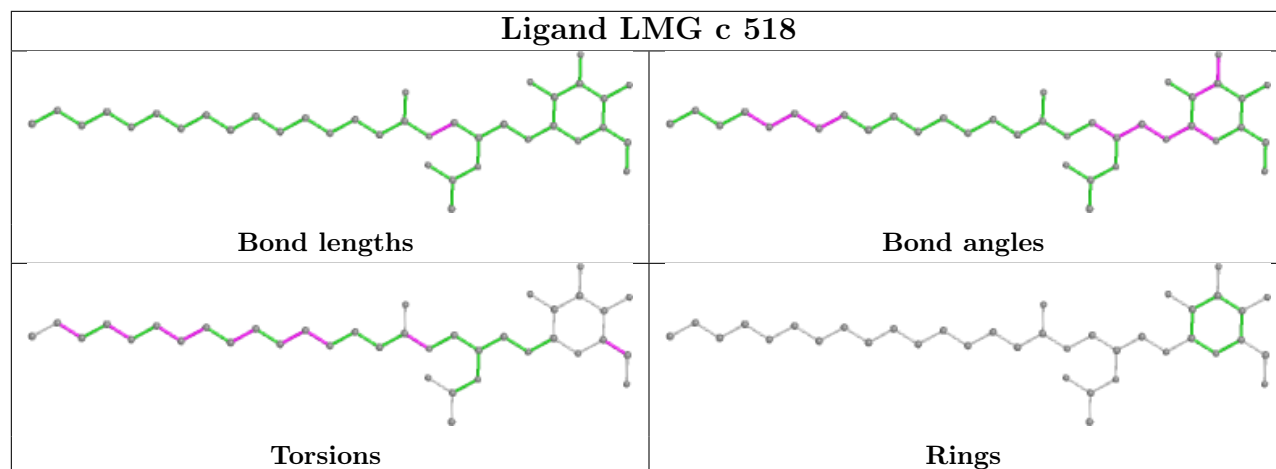
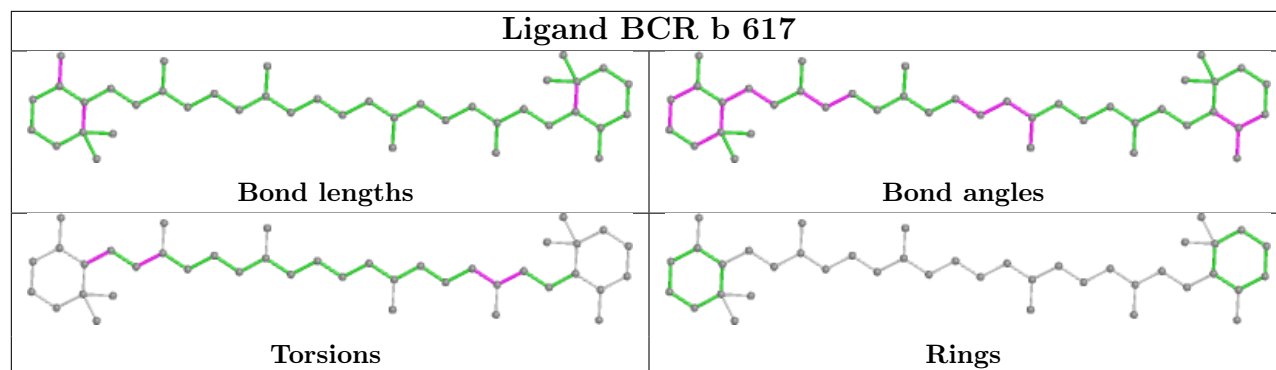


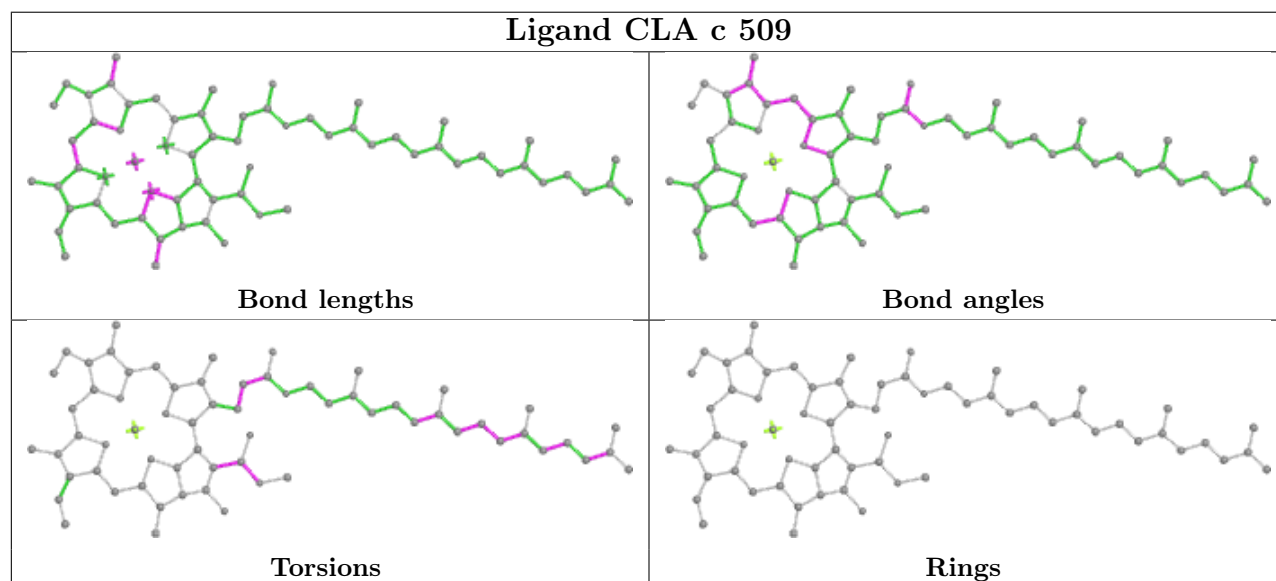
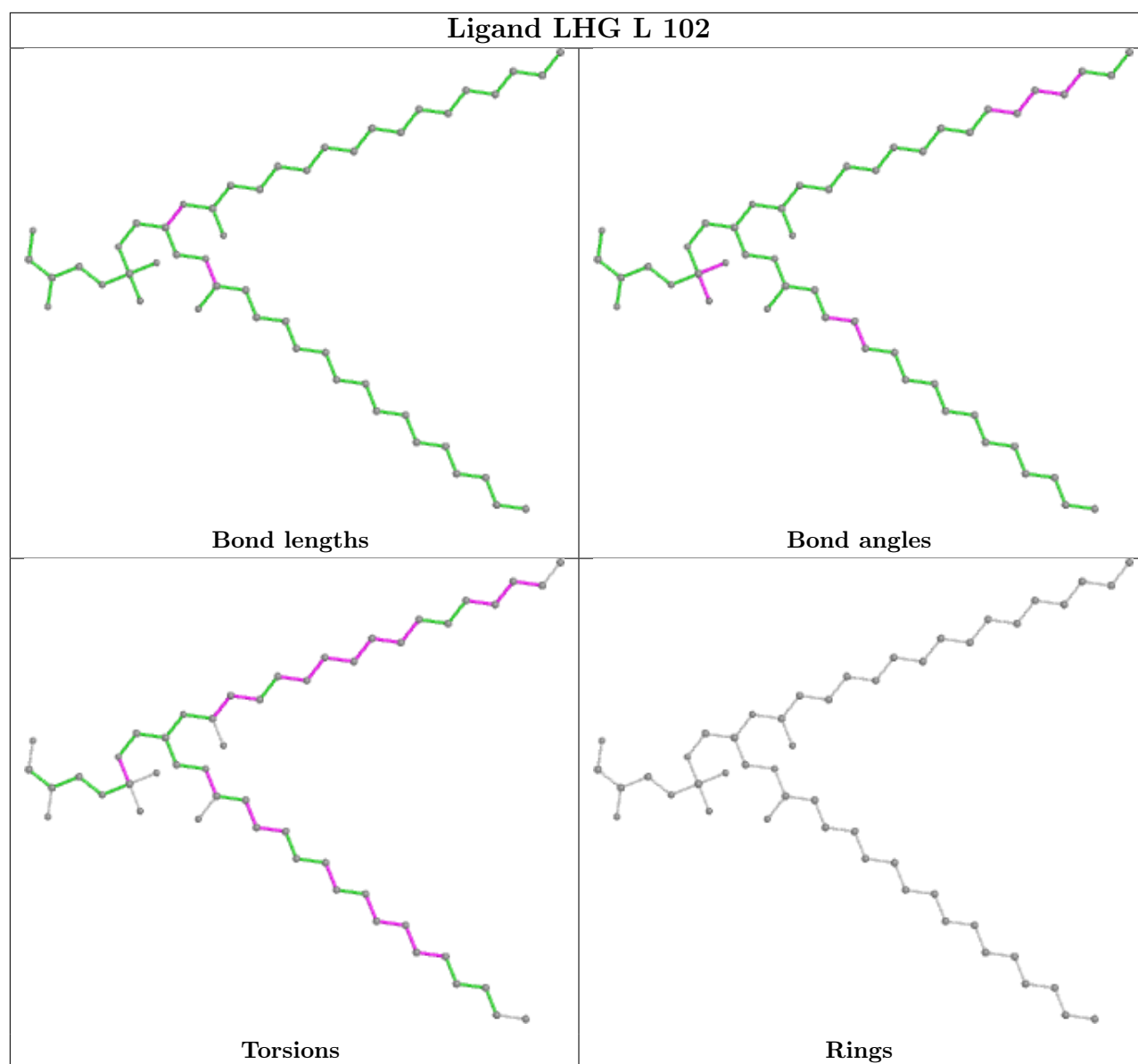


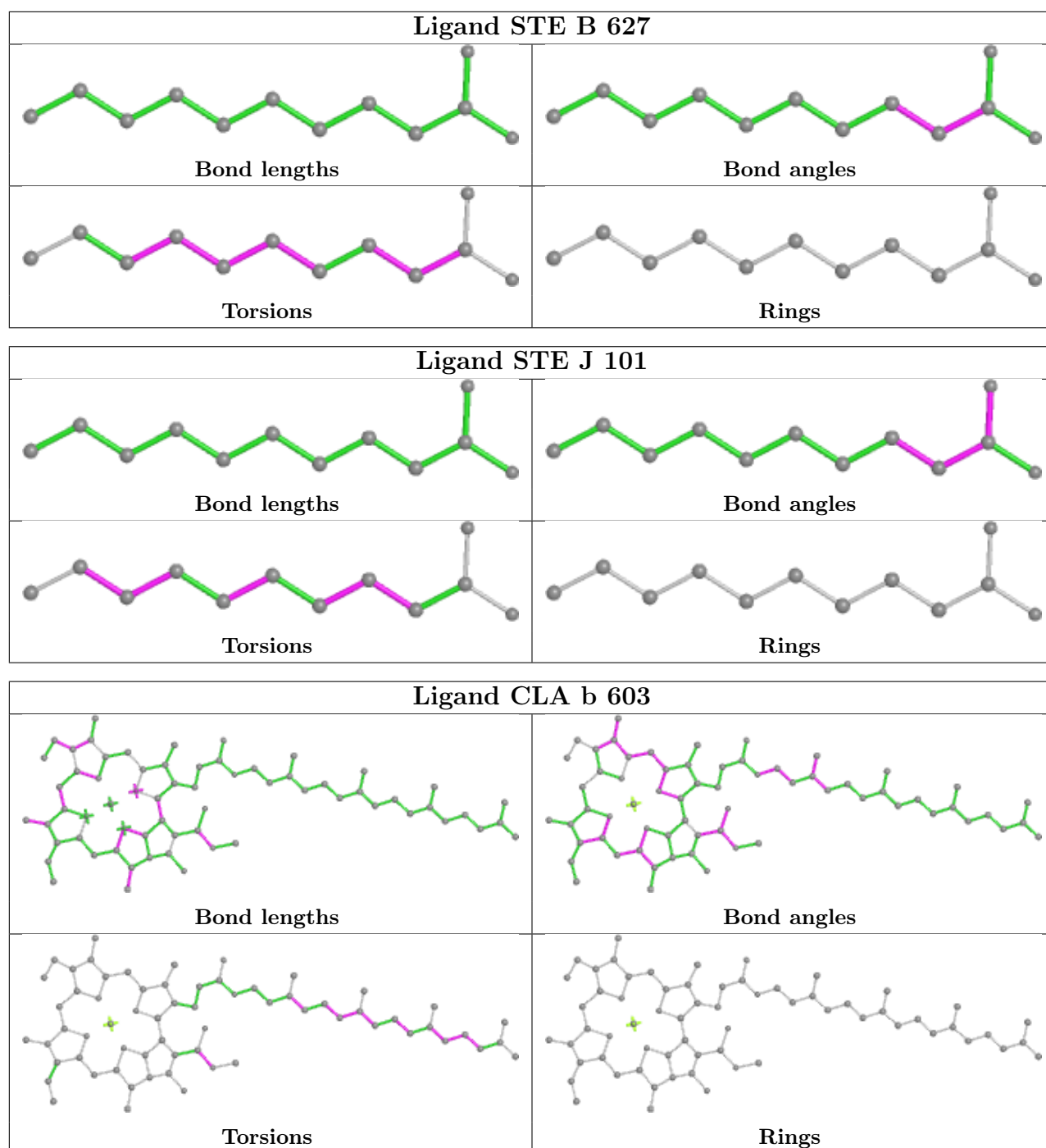


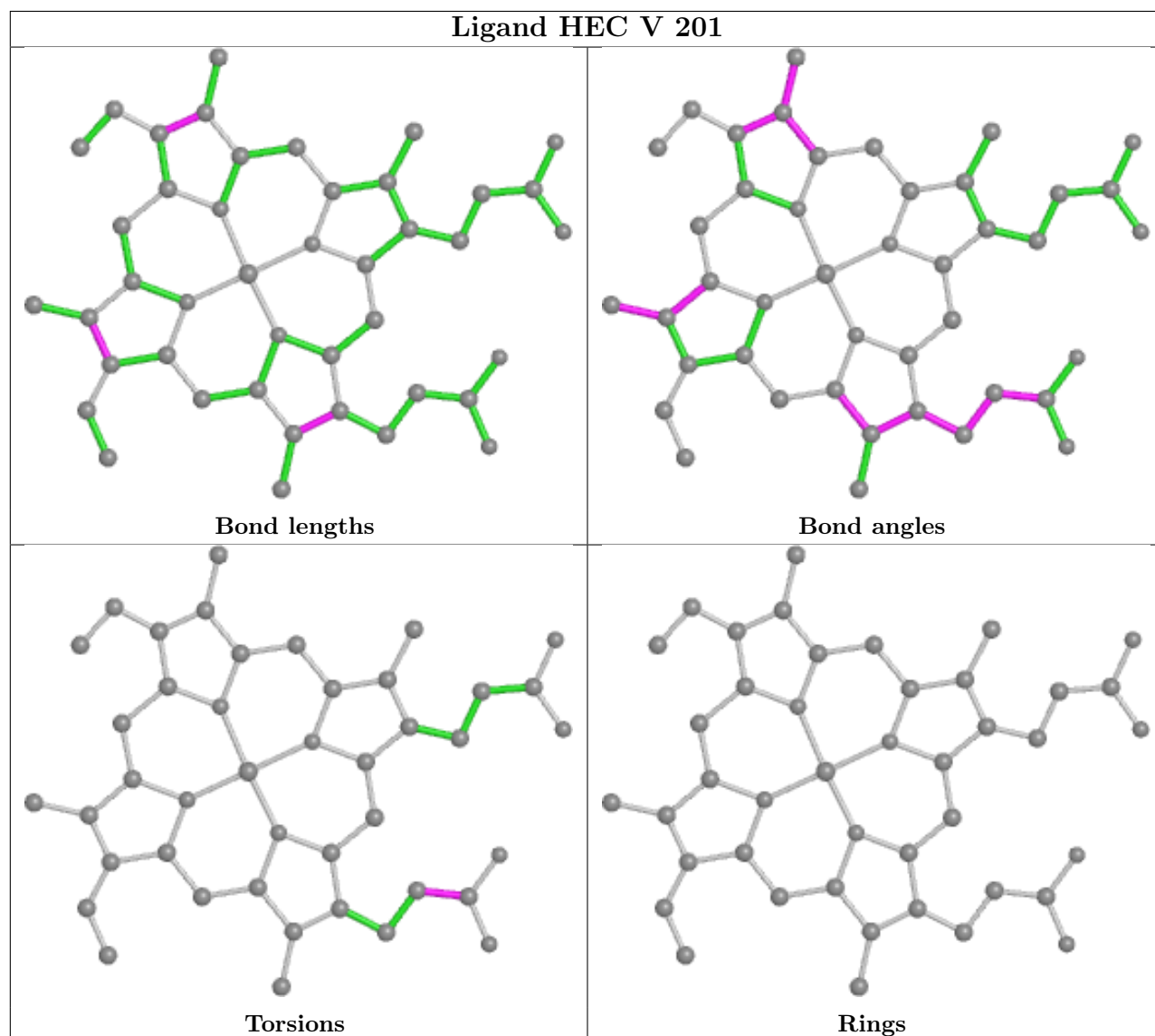
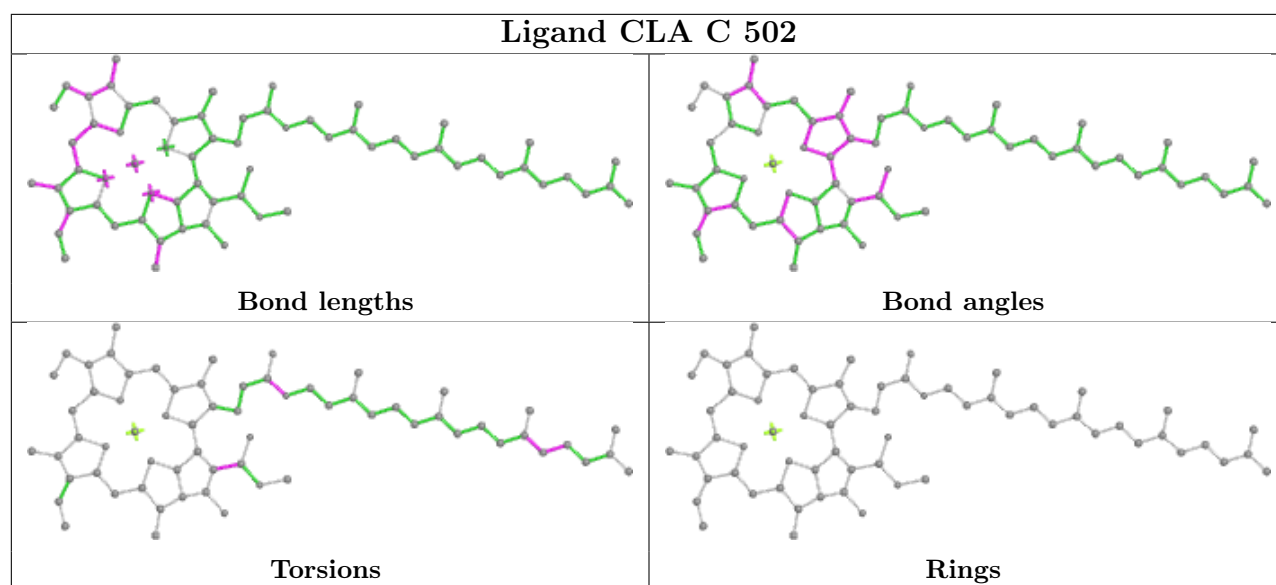


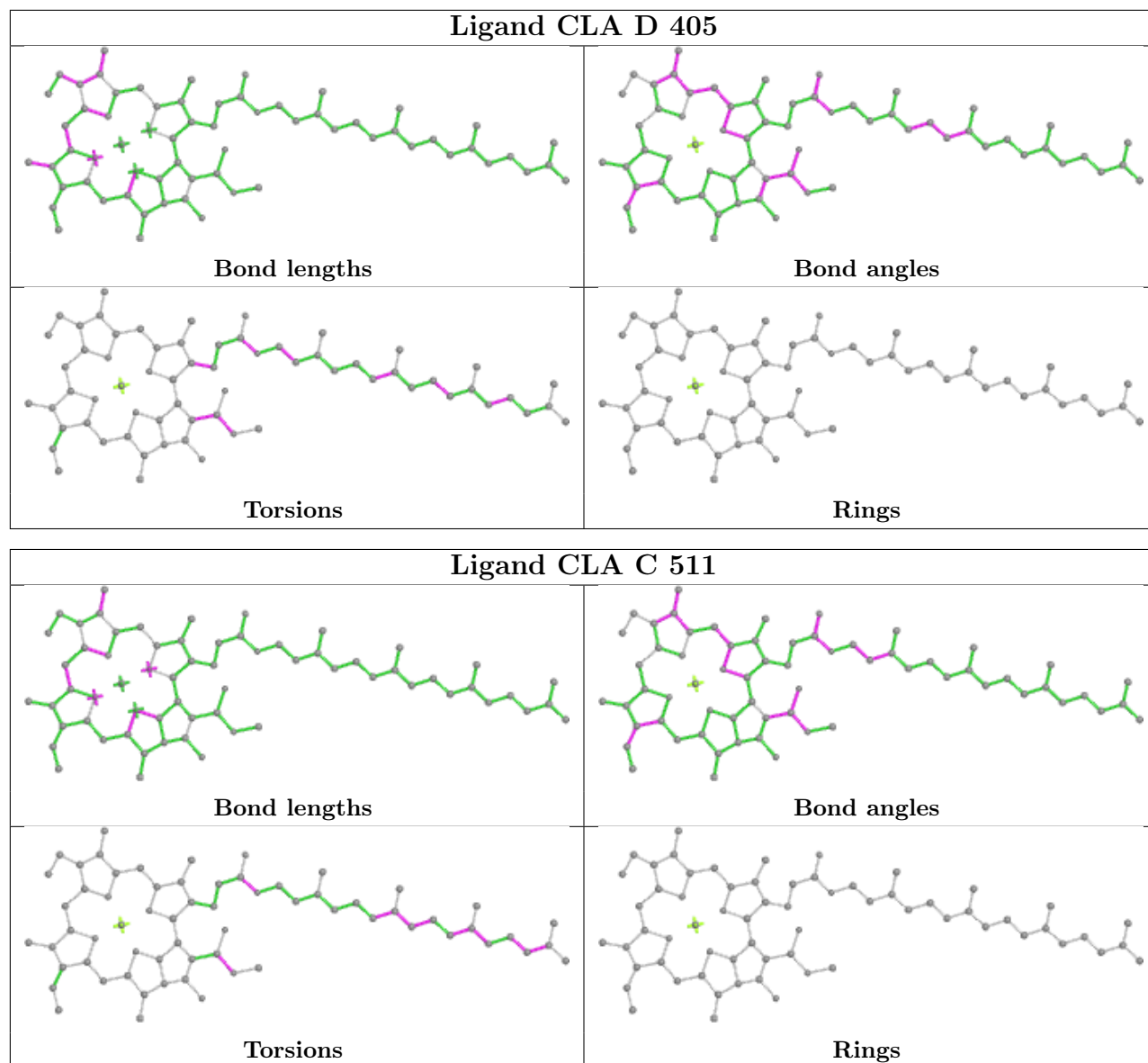


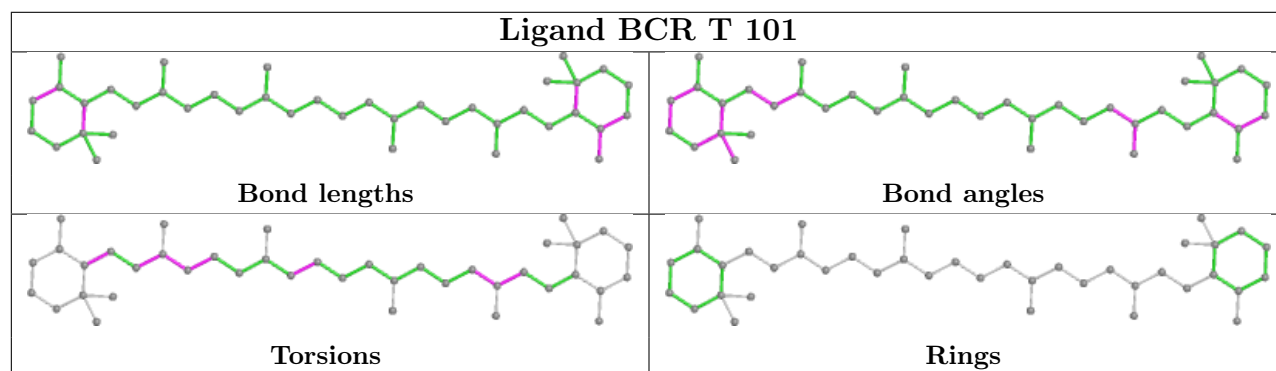
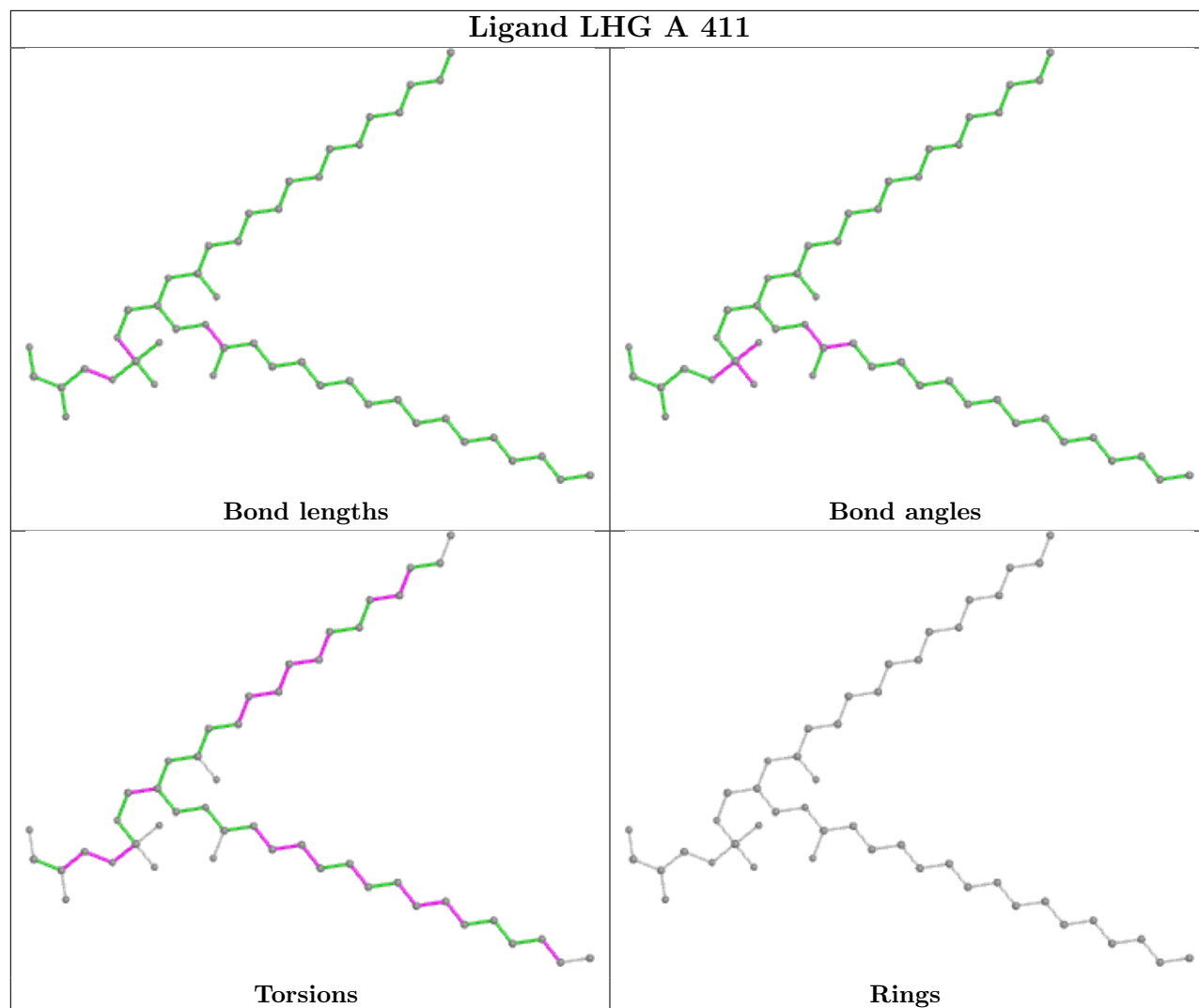




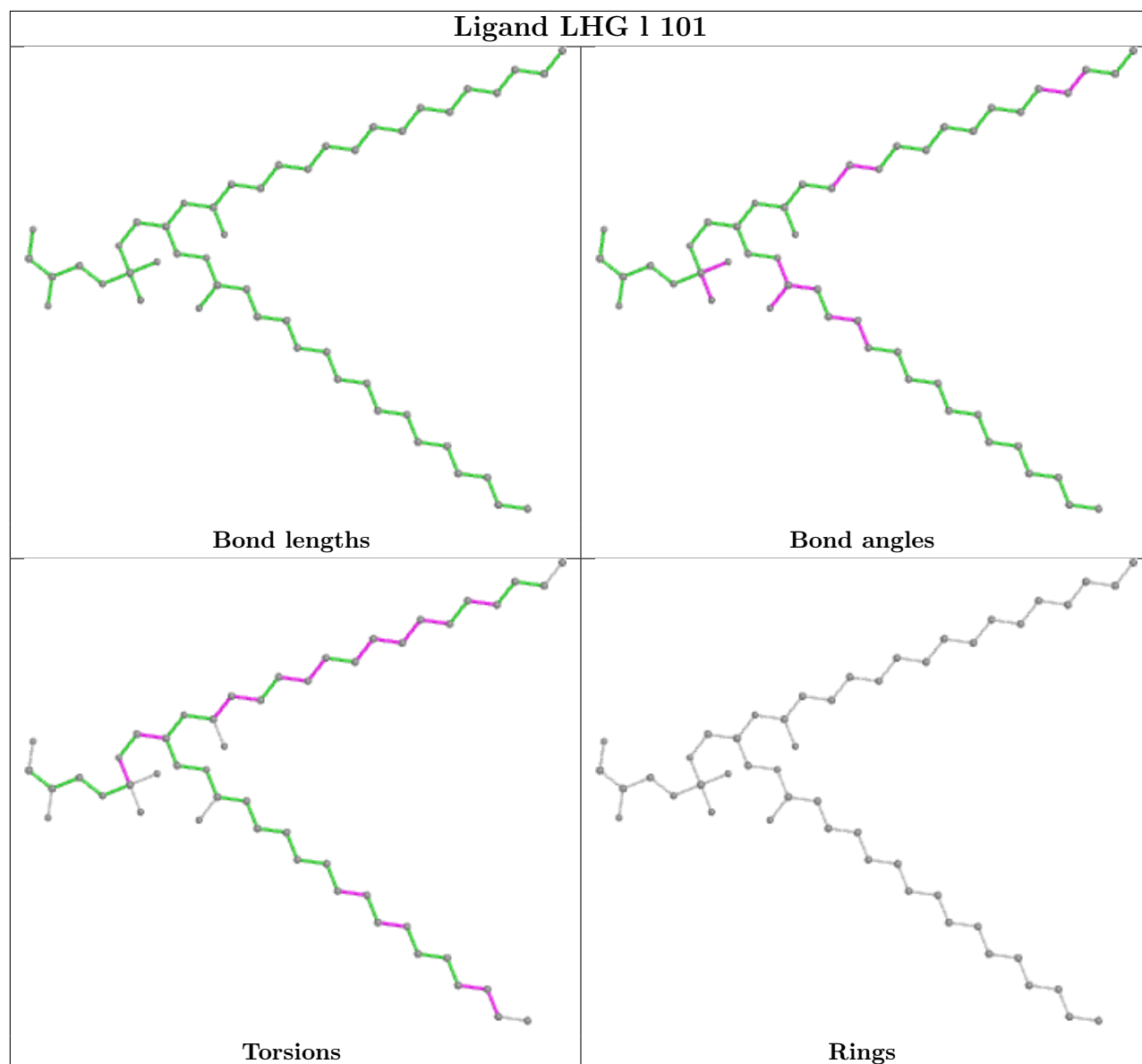
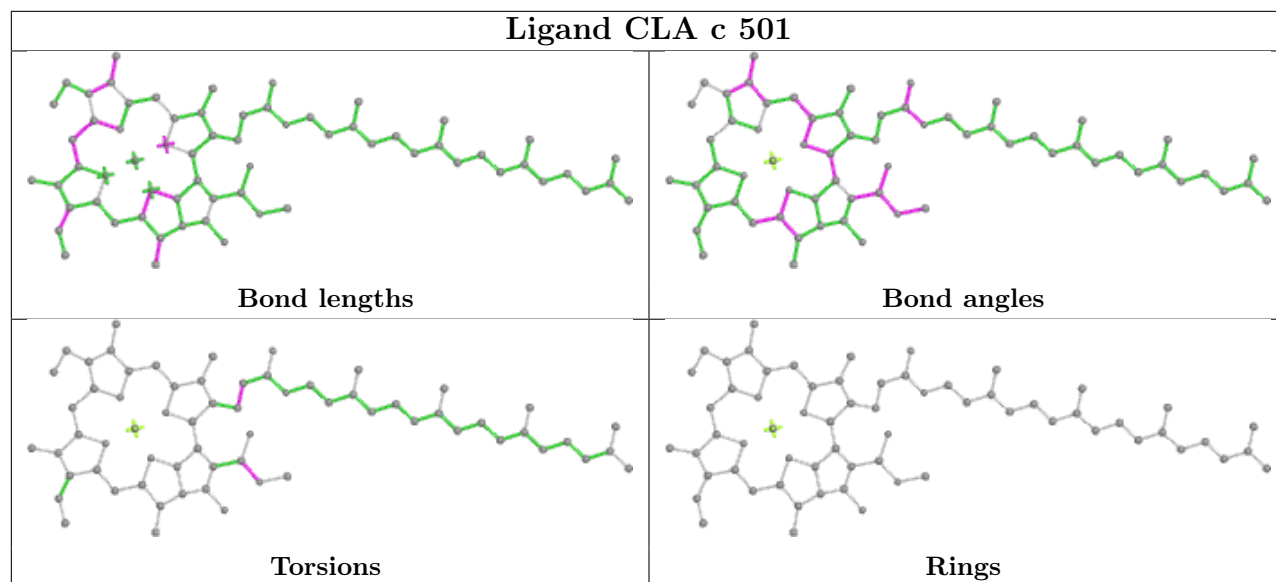


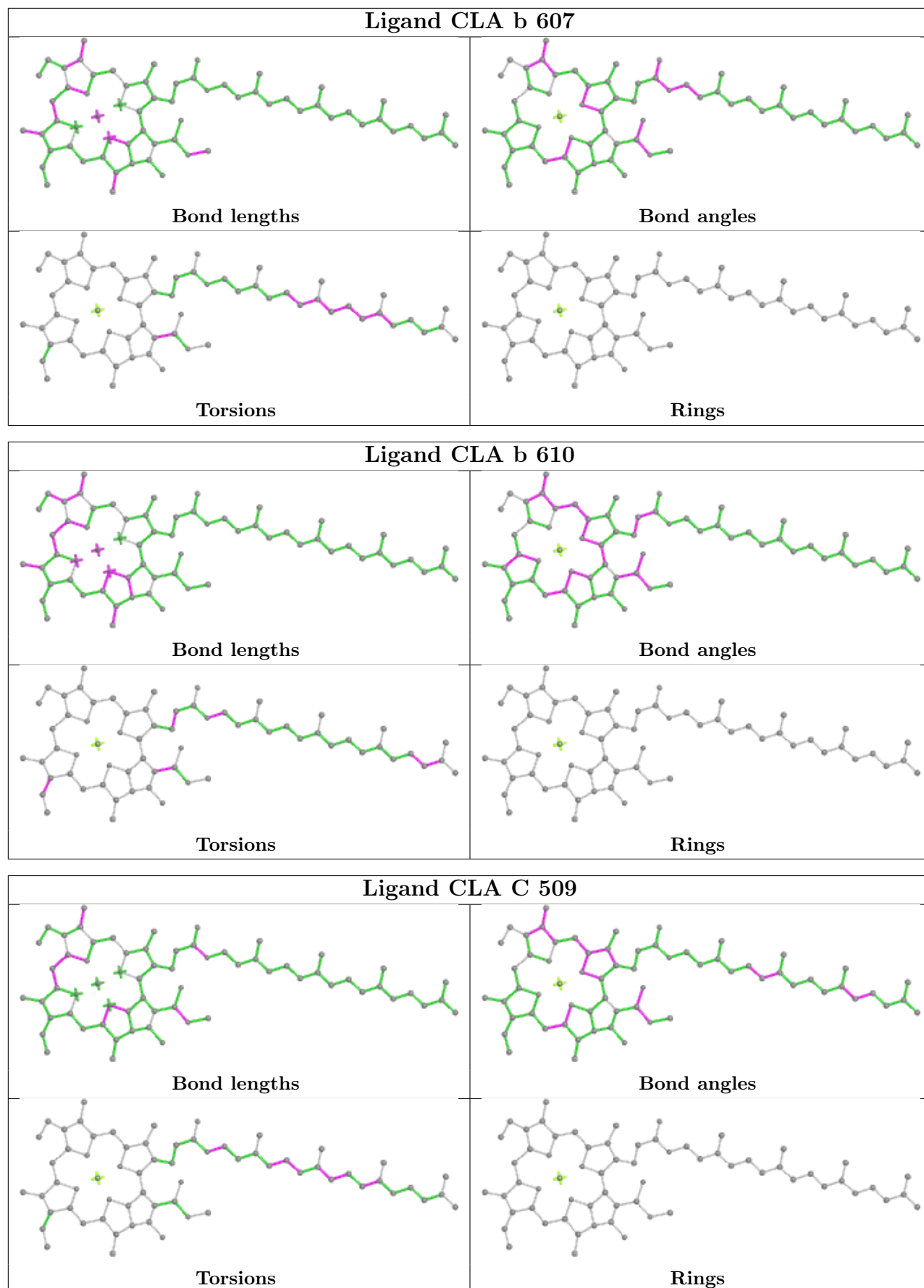


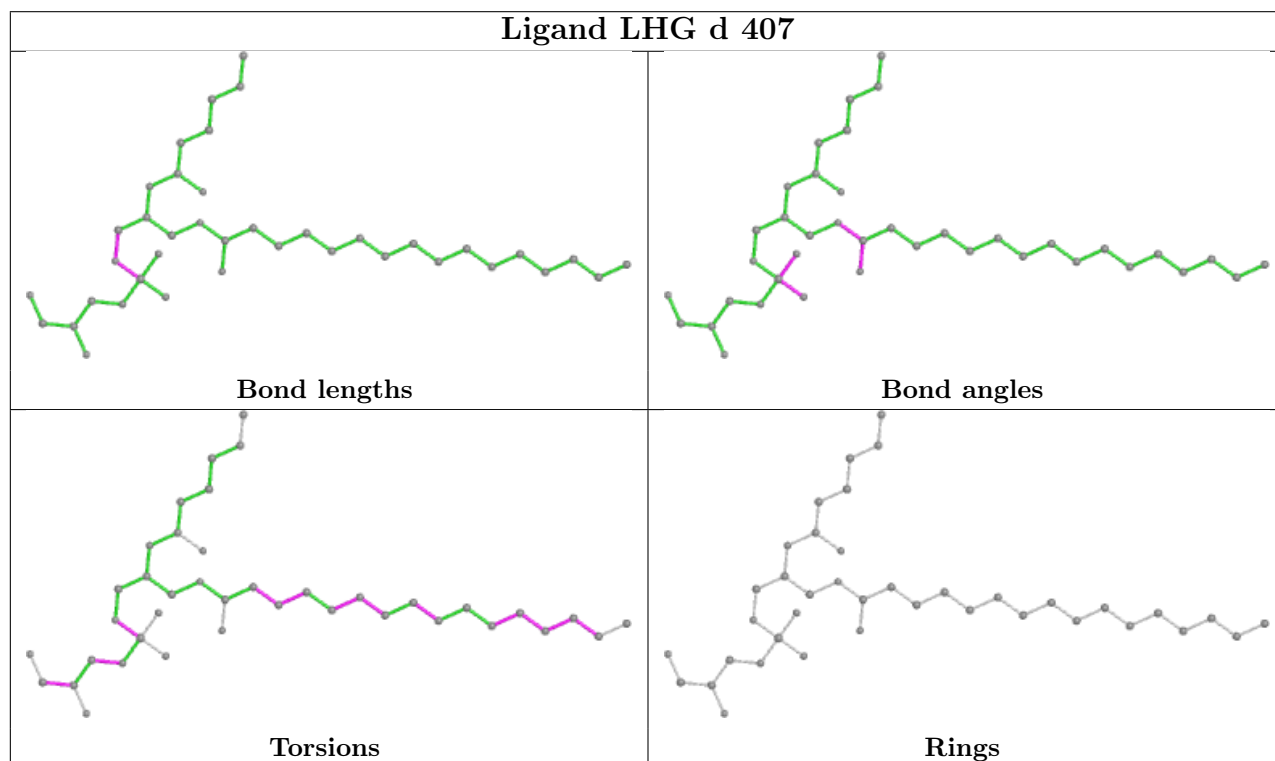
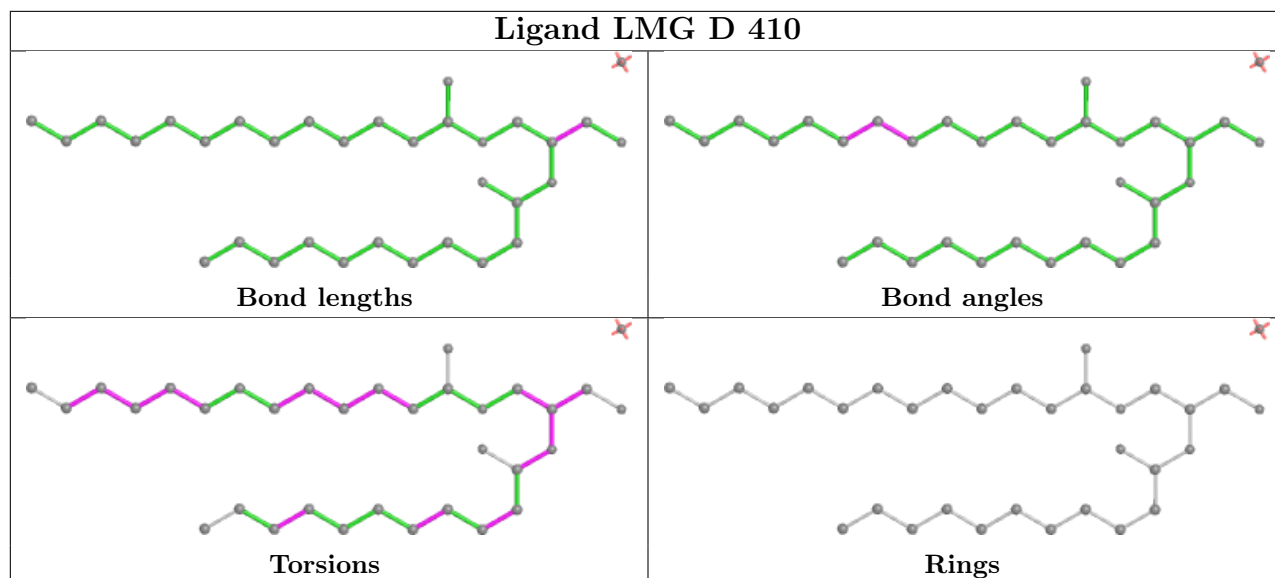


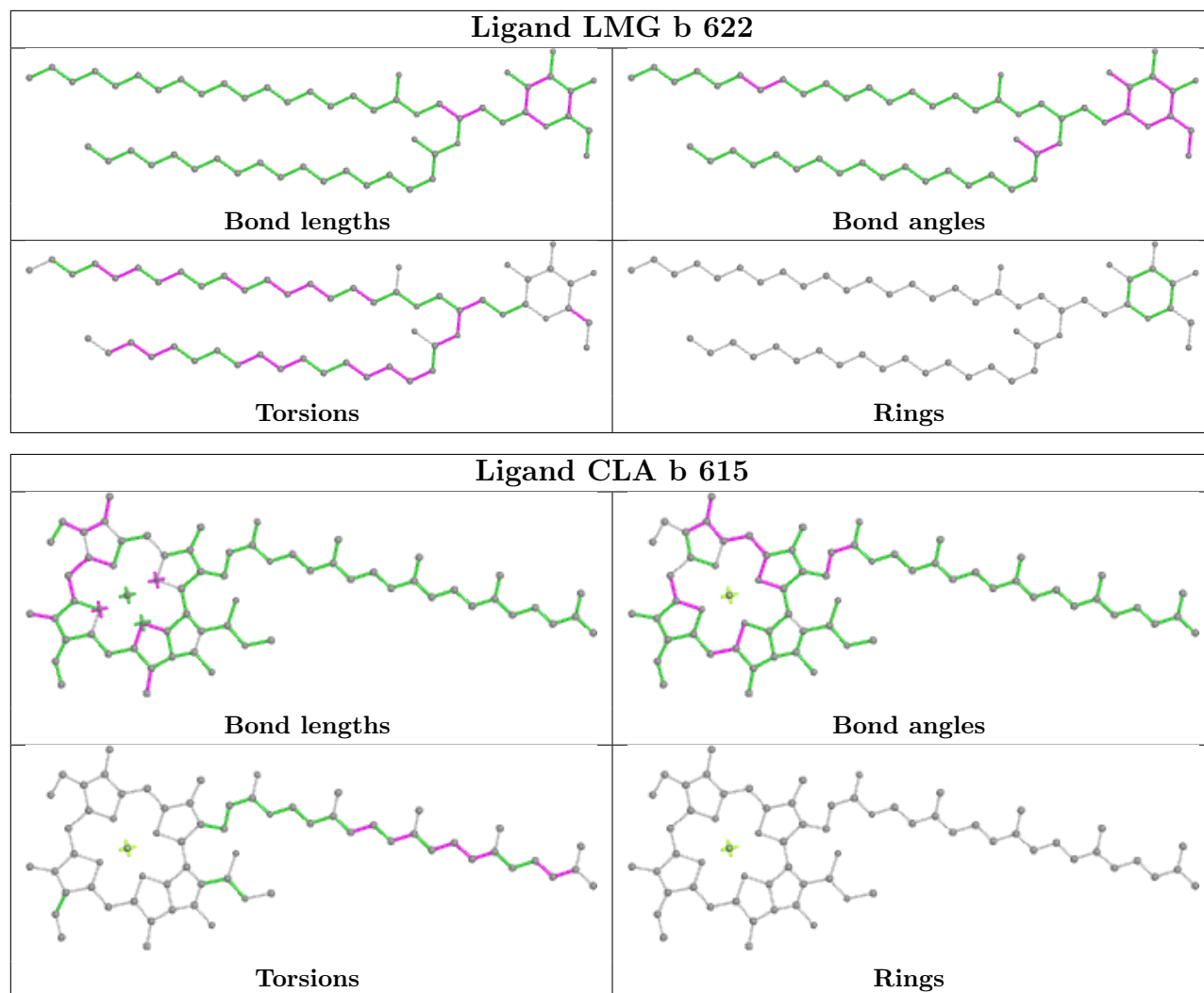


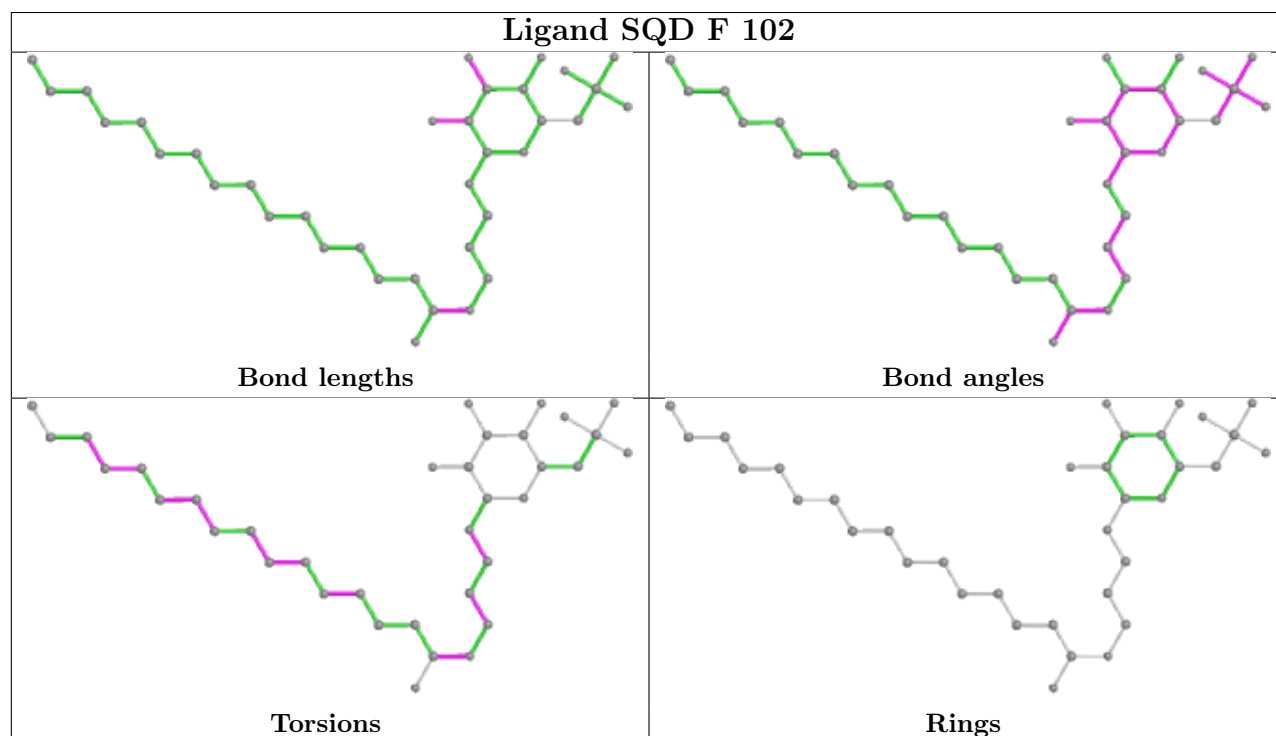
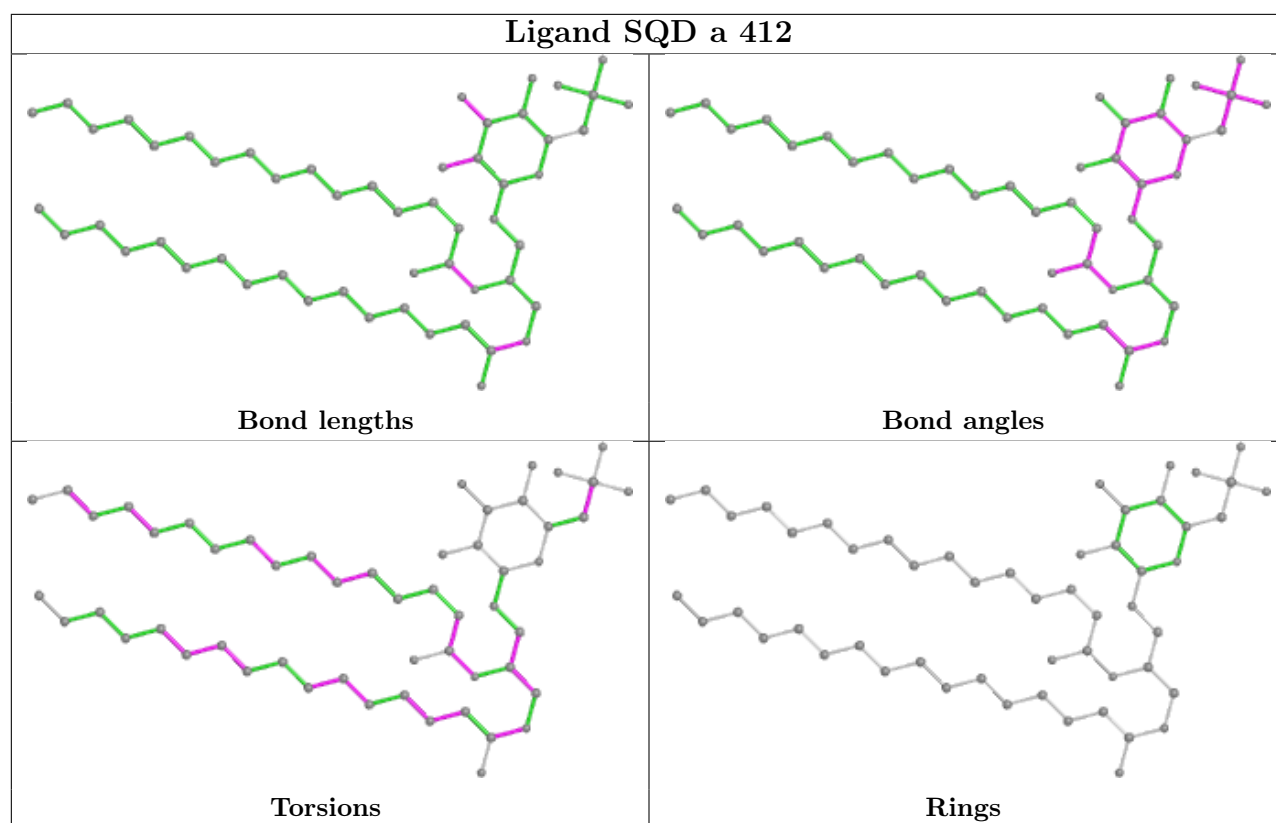


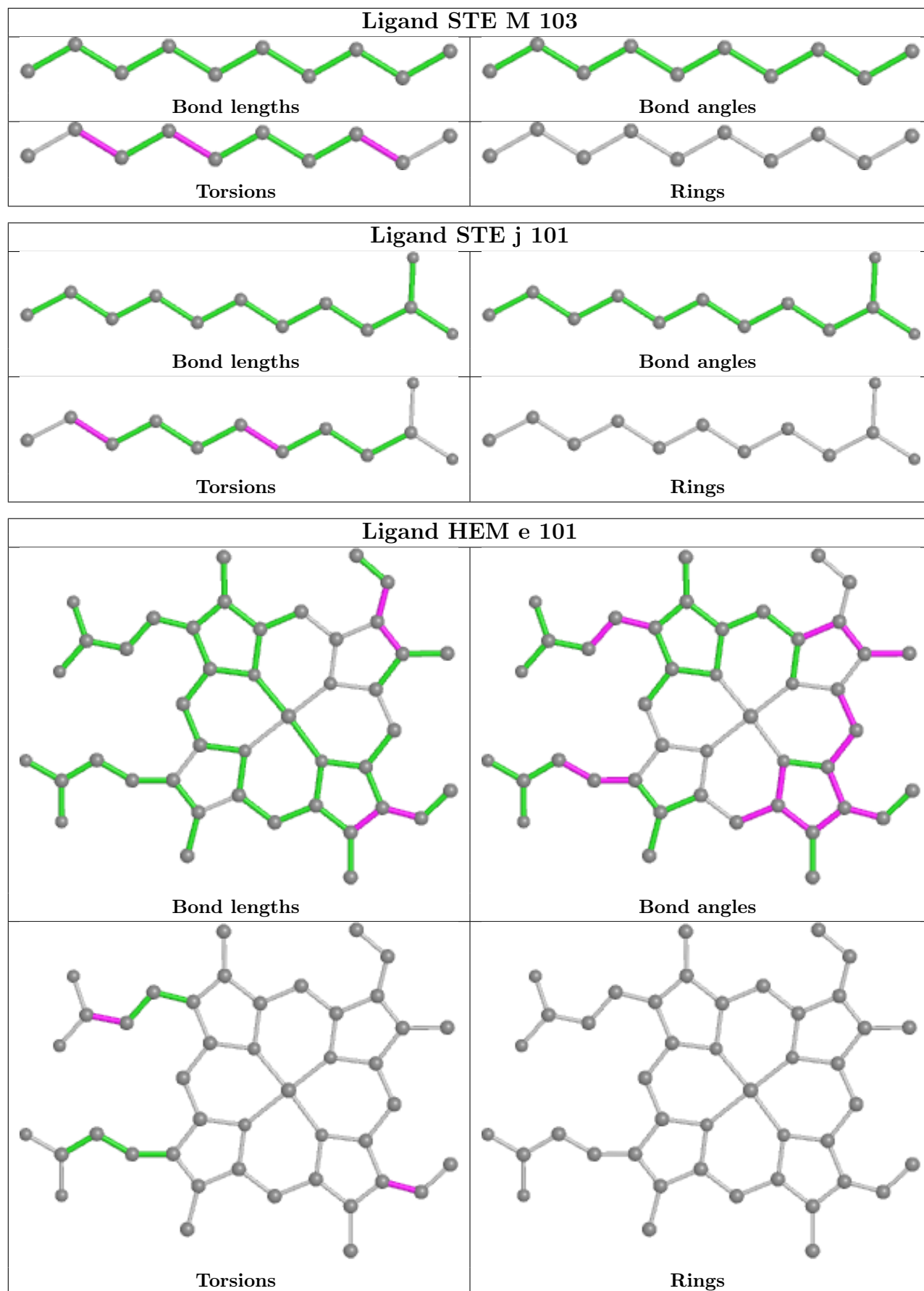


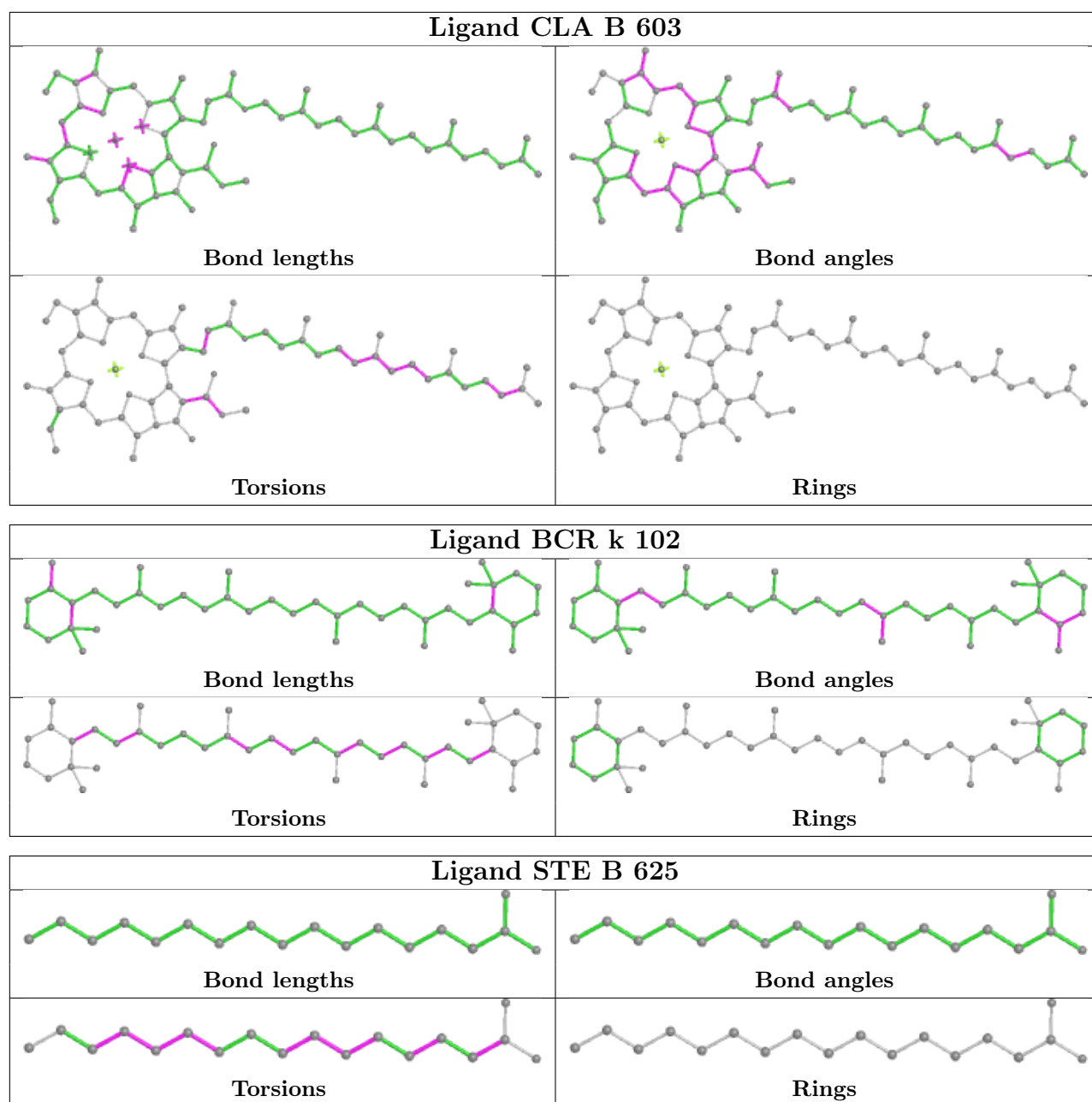












## 5.7 Other polymers [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	334/344 (97%)	-0.44	4 (1%) 79 81	25, 31, 47, 80	0
1	a	334/344 (97%)	-0.47	1 (0%) 94 94	24, 33, 56, 78	0
2	B	505/510 (99%)	-0.41	6 (1%) 79 81	25, 35, 60, 83	0
2	b	505/510 (99%)	-0.23	21 (4%) 36 38	28, 39, 68, 103	0
3	C	442/461 (95%)	-0.33	6 (1%) 75 77	27, 38, 53, 73	0
3	c	451/461 (97%)	-0.26	6 (1%) 77 79	28, 41, 59, 95	0
4	D	341/352 (96%)	-0.40	1 (0%) 94 94	24, 32, 47, 76	0
4	d	341/352 (96%)	-0.31	0 100 100	25, 36, 58, 84	0
5	E	82/84 (97%)	-0.03	3 (3%) 41 44	34, 52, 67, 85	0
5	e	82/84 (97%)	0.18	5 (6%) 21 23	42, 58, 74, 86	0
6	F	34/45 (75%)	-0.51	1 (2%) 51 55	40, 44, 59, 79	0
6	f	34/45 (75%)	-0.25	1 (2%) 51 55	44, 51, 77, 85	0
7	H	65/66 (98%)	-0.06	2 (3%) 49 52	34, 41, 57, 73	0
7	h	63/66 (95%)	0.28	5 (7%) 12 14	41, 51, 61, 65	0
8	I	35/38 (92%)	-0.28	2 (5%) 23 25	35, 41, 64, 77	0
8	i	35/38 (92%)	-0.13	3 (8%) 10 11	33, 41, 75, 84	0
9	J	36/40 (90%)	0.14	4 (11%) 5 5	37, 50, 74, 83	0
9	j	36/40 (90%)	0.11	4 (11%) 5 5	39, 54, 86, 95	0
10	K	37/46 (80%)	0.11	2 (5%) 25 28	45, 52, 69, 78	0
10	k	37/46 (80%)	-0.12	0 100 100	49, 55, 66, 77	0
11	L	37/37 (100%)	-0.48	0 100 100	27, 32, 61, 66	0
11	l	36/37 (97%)	-0.17	3 (8%) 11 12	28, 33, 65, 85	0
12	M	32/36 (88%)	-0.07	1 (3%) 49 52	29, 36, 57, 70	0
12	m	31/36 (86%)	-0.12	1 (3%) 47 50	29, 36, 53, 72	0

*Continued on next page...*



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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
13	O	244/272 (89%)	-0.08	13 (5%) 26 29	28, 43, 76, 124	0
13	o	244/272 (89%)	-0.16	13 (5%) 26 29	28, 41, 78, 126	0
14	R	28/41 (68%)	1.85	14 (50%) 0 0	57, 67, 81, 88	0
14	r	28/41 (68%)	3.67	24 (85%) 0 0	73, 88, 108, 121	0
15	T	29/32 (90%)	-0.46	1 (3%) 45 47	28, 34, 58, 72	0
15	t	29/32 (90%)	-0.26	3 (10%) 6 6	30, 34, 70, 90	0
16	U	97/134 (72%)	-0.29	2 (2%) 63 66	35, 44, 70, 80	0
16	u	97/134 (72%)	-0.45	0 100 100	32, 42, 57, 84	0
17	V	137/163 (84%)	-0.58	0 100 100	33, 42, 56, 73	0
17	v	137/163 (84%)	-0.21	4 (2%) 51 55	34, 48, 67, 81	0
18	X	38/41 (92%)	0.18	3 (7%) 12 14	40, 50, 63, 74	0
18	x	39/41 (95%)	0.49	4 (10%) 6 6	48, 59, 86, 98	0
19	Y	27/46 (58%)	1.45	11 (40%) 0 0	51, 69, 89, 91	0
19	y	30/46 (65%)	0.48	4 (13%) 3 3	58, 74, 88, 97	0
20	Z	62/62 (100%)	0.75	13 (20%) 1 1	52, 67, 104, 118	0
20	z	62/62 (100%)	0.66	10 (16%) 1 1	55, 70, 106, 115	0
All	All	5293/5700 (92%)	-0.21	201 (3%) 40 43	24, 40, 71, 126	0

The worst 5 of 201 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	o	58	ASN	10.7
14	r	14	LEU	7.8
13	o	60	ARG	7.3
14	r	9	LEU	7.0
14	r	10	LEU	6.9

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
12	FME	M	1	10/11	0.92	0.13	41,50,67,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
15	FME	t	1	10/11	0.93	0.10	36,48,66,66	0
15	FME	T	1	10/11	0.94	0.12	31,46,69,69	0
8	FME	i	1	10/11	0.96	0.18	45,54,66,70	0
12	FME	m	1	10/11	0.96	0.14	34,46,59,71	0
8	FME	I	1	10/11	0.98	0.13	41,52,63,68	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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
32	STE	k	104	12/20	0.71	0.26	50,66,81,84	0
32	STE	H	103	18/20	0.72	0.35	47,75,87,88	0
32	STE	a	415	12/20	0.74	0.31	55,69,75,77	0
32	STE	E	102	12/20	0.77	0.27	53,75,86,89	0
32	STE	B	626	16/20	0.77	0.25	47,64,76,87	0
29	SQD	a	413	36/54	0.80	0.19	31,64,84,89	0
27	LMG	c	520	48/55	0.80	0.25	41,73,104,109	0
32	STE	l	102	18/20	0.80	0.18	36,53,83,90	0
32	STE	C	520	16/20	0.81	0.17	42,56,79,79	0
32	STE	b	624	16/20	0.81	0.18	51,66,80,83	0
27	LMG	D	410	33/55	0.82	0.19	38,56,80,83	0
27	LMG	b	622	55/55	0.82	0.30	49,75,94,103	0
32	STE	B	625	18/20	0.83	0.16	43,59,73,74	0
32	STE	b	625	20/20	0.83	0.18	42,65,80,84	0
28	LHG	e	102	42/49	0.83	0.26	58,82,104,116	0
22	CLA	C	512	65/65	0.83	0.20	37,55,85,90	0
27	LMG	d	408	23/55	0.84	0.23	43,66,82,84	0
32	STE	I	101	15/20	0.84	0.14	45,59,81,82	0
32	STE	c	519	20/20	0.84	0.23	43,61,86,98	0
32	STE	M	104	15/20	0.84	0.18	44,60,84,86	0
30	DGD	B	623	44/66	0.84	0.16	39,56,75,85	0
32	STE	x	102	20/20	0.84	0.22	36,60,76,80	0
28	LHG	E	101	49/49	0.85	0.23	54,79,113,119	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
24	BCR	H	101	40/40	0.85	0.16	31,48,62,70	0
24	BCR	x	101	40/40	0.85	0.16	38,57,78,80	0
22	CLA	b	601	65/65	0.86	0.19	44,68,89,105	0
32	STE	J	101	12/20	0.86	0.17	46,60,71,71	0
30	DGD	A	414	66/66	0.86	0.18	42,65,81,89	0
26	PL9	A	409	55/55	0.86	0.23	37,69,85,88	0
29	SQD	A	413	39/54	0.86	0.18	42,60,87,91	0
22	CLA	c	512	65/65	0.87	0.17	46,59,87,93	0
27	LMG	a	414	49/55	0.87	0.16	37,58,84,101	0
32	STE	d	410	17/20	0.87	0.15	42,58,69,78	0
24	BCR	k	102	40/40	0.87	0.14	45,65,75,78	0
32	STE	b	621	20/20	0.87	0.20	40,56,70,73	0
29	SQD	f	101	41/54	0.87	0.23	62,86,110,115	0
32	STE	B	620	17/20	0.88	0.18	36,50,66,67	0
32	STE	b	620	16/20	0.88	0.18	35,53,66,76	0
22	CLA	B	601	65/65	0.88	0.15	36,63,90,96	0
26	PL9	a	410	55/55	0.88	0.19	40,66,87,94	0
27	LMG	A	410	48/55	0.88	0.14	41,57,75,87	0
32	STE	b	626	10/20	0.88	0.28	43,55,61,65	0
27	LMG	C	518	48/55	0.88	0.19	40,74,93,101	0
24	BCR	K	101	40/40	0.88	0.14	43,57,72,82	0
24	BCR	d	404	40/40	0.88	0.16	36,54,84,98	0
22	CLA	C	513	65/65	0.88	0.20	42,63,92,95	0
22	CLA	c	513	65/65	0.88	0.21	43,67,103,109	0
32	STE	B	624	12/20	0.89	0.10	41,57,67,77	0
32	STE	j	101	12/20	0.89	0.15	42,60,73,77	0
29	SQD	L	101	49/54	0.89	0.14	41,59,89,101	0
24	BCR	k	103	40/40	0.89	0.19	44,58,69,74	0
29	SQD	B	622	54/54	0.89	0.15	36,61,87,102	0
32	STE	C	521	12/20	0.90	0.11	37,48,57,59	0
22	CLA	a	405	65/65	0.90	0.14	21,38,87,98	0
22	CLA	c	508	64/65	0.90	0.17	29,45,85,98	0
22	CLA	d	403	65/65	0.90	0.16	36,53,90,95	0
24	BCR	k	101	40/40	0.90	0.17	42,60,76,77	0
27	LMG	D	411	28/55	0.90	0.15	33,52,63,64	0
32	STE	B	627	12/20	0.90	0.38	51,65,84,84	0
32	STE	C	519	12/20	0.90	0.13	42,57,69,73	0
32	STE	t	103	10/20	0.90	0.18	32,61,69,71	0
27	LMG	M	101	51/55	0.90	0.13	32,52,68,73	0
27	LMG	D	408	51/55	0.91	0.19	29,58,82,92	0
32	STE	D	412	20/20	0.91	0.13	32,53,69,70	0
32	STE	M	102	15/20	0.91	0.14	38,51,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
32	STE	M	103	10/20	0.91	0.16	38,48,56,65	0
32	STE	m	102	12/20	0.91	0.17	51,64,80,84	0
22	CLA	c	502	65/65	0.91	0.16	31,49,64,70	0
22	CLA	D	405	65/65	0.91	0.14	25,47,98,106	0
27	LMG	m	101	51/55	0.92	0.13	35,54,68,80	0
24	BCR	D	406	40/40	0.92	0.14	31,46,83,87	0
22	CLA	B	615	65/65	0.92	0.14	28,40,71,75	0
22	CLA	B	616	60/65	0.92	0.15	28,44,86,98	0
30	DGD	C	516	62/66	0.92	0.15	35,55,105,118	0
22	CLA	b	616	60/65	0.92	0.14	28,47,91,95	0
22	CLA	C	502	65/65	0.92	0.14	33,45,64,76	0
24	BCR	B	619	40/40	0.93	0.12	28,46,64,68	0
22	CLA	C	507	65/65	0.93	0.15	28,46,61,63	0
22	CLA	c	503	65/65	0.93	0.17	37,48,61,71	0
22	CLA	c	506	65/65	0.93	0.14	30,54,99,106	0
24	BCR	K	102	40/40	0.93	0.17	40,55,71,75	0
30	DGD	C	517	62/66	0.93	0.14	30,53,74,86	0
30	DGD	c	516	62/66	0.93	0.14	33,56,93,101	0
30	DGD	h	101	62/66	0.93	0.13	30,51,63,69	0
24	BCR	Z	101	40/40	0.93	0.16	40,58,72,79	0
24	BCR	b	617	40/40	0.93	0.13	28,47,58,59	0
27	LMG	c	518	37/55	0.93	0.14	44,65,82,88	0
22	CLA	c	507	65/65	0.93	0.16	30,48,66,67	0
22	CLA	b	602	65/65	0.93	0.16	27,47,66,77	0
22	CLA	c	510	65/65	0.93	0.16	31,50,66,74	0
22	CLA	c	511	65/65	0.93	0.14	40,55,73,77	0
22	CLA	b	606	65/65	0.93	0.12	28,43,75,79	0
22	CLA	b	615	65/65	0.93	0.14	27,42,65,68	0
32	STE	t	102	14/20	0.93	0.12	36,53,59,60	0
22	CLA	C	511	65/65	0.93	0.14	35,52,66,77	0
24	BCR	B	618	40/40	0.93	0.11	26,39,53,56	0
22	CLA	C	505	65/65	0.94	0.15	26,43,71,76	0
22	CLA	C	506	65/65	0.94	0.13	27,49,99,103	0
22	CLA	a	403	65/65	0.94	0.15	26,43,91,102	0
30	DGD	H	102	62/66	0.94	0.11	31,47,60,62	0
22	CLA	B	604	65/65	0.94	0.14	24,36,70,78	0
30	DGD	c	517	62/66	0.94	0.14	32,54,90,96	0
22	CLA	c	505	65/65	0.94	0.17	30,44,71,73	0
27	LMG	d	409	44/55	0.94	0.15	36,56,83,89	0
24	BCR	C	514	40/40	0.94	0.12	28,44,57,62	0
26	PL9	D	407	55/55	0.94	0.12	24,37,51,53	0
22	CLA	C	508	65/65	0.94	0.12	33,47,100,108	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
29	SQD	A	412	52/54	0.94	0.17	33,59,86,89	0
22	CLA	B	606	65/65	0.94	0.12	24,39,76,81	0
22	CLA	B	614	65/65	0.94	0.16	25,40,76,85	0
22	CLA	c	509	65/65	0.94	0.20	36,51,70,74	0
29	SQD	a	412	54/54	0.94	0.17	45,65,85,89	0
22	CLA	b	609	65/65	0.94	0.15	31,48,72,76	0
22	CLA	b	614	65/65	0.94	0.15	27,42,77,88	0
24	BCR	b	619	40/40	0.94	0.10	32,49,67,74	0
22	CLA	C	509	65/65	0.95	0.18	26,49,67,72	0
22	CLA	C	510	65/65	0.95	0.14	30,46,68,74	0
22	CLA	B	603	65/65	0.95	0.16	20,36,62,63	0
22	CLA	A	405	54/65	0.95	0.12	22,37,67,72	0
22	CLA	C	501	65/65	0.95	0.13	23,37,53,58	0
24	BCR	T	101	40/40	0.95	0.09	29,43,62,64	0
22	CLA	c	504	60/65	0.95	0.12	34,49,80,87	0
22	CLA	A	403	65/65	0.95	0.14	22,37,83,96	0
28	LHG	A	411	47/49	0.95	0.13	31,51,76,89	0
28	LHG	B	621	49/49	0.95	0.12	31,47,65,80	0
24	BCR	b	618	40/40	0.95	0.10	29,42,53,59	0
28	LHG	b	623	49/49	0.95	0.13	34,52,68,73	0
22	CLA	C	503	65/65	0.95	0.14	33,46,56,58	0
24	BCR	c	514	40/40	0.95	0.12	30,45,60,69	0
22	CLA	C	504	59/65	0.95	0.12	29,47,84,88	0
22	CLA	B	609	65/65	0.95	0.12	28,39,58,68	0
29	SQD	F	102	36/54	0.95	0.17	44,73,93,97	0
22	CLA	B	610	65/65	0.95	0.15	21,36,46,49	0
22	CLA	b	604	65/65	0.95	0.14	25,41,77,86	0
22	CLA	B	613	65/65	0.95	0.15	21,37,68,77	0
22	CLA	b	608	65/65	0.95	0.15	30,46,66,76	0
22	CLA	B	602	65/65	0.95	0.17	26,41,57,65	0
22	CLA	b	610	65/65	0.95	0.18	27,40,51,61	0
30	DGD	C	515	62/66	0.95	0.13	23,43,80,92	0
26	PL9	d	405	55/55	0.95	0.12	24,38,48,52	0
23	PHO	a	404	64/64	0.95	0.13	22,34,42,44	0
24	BCR	A	406	40/40	0.95	0.10	26,38,50,52	0
30	DGD	c	515	62/66	0.95	0.12	26,45,79,86	0
24	BCR	B	617	40/40	0.95	0.12	27,42,58,64	0
22	CLA	b	611	65/65	0.95	0.14	22,35,55,64	0
22	CLA	b	613	65/65	0.95	0.15	25,38,75,78	0
22	CLA	a	411	65/65	0.96	0.12	23,34,52,56	0
24	BCR	t	101	40/40	0.96	0.09	27,42,57,58	0
22	CLA	B	608	65/65	0.96	0.13	25,37,55,61	0

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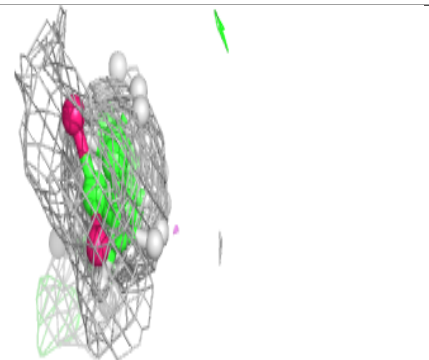
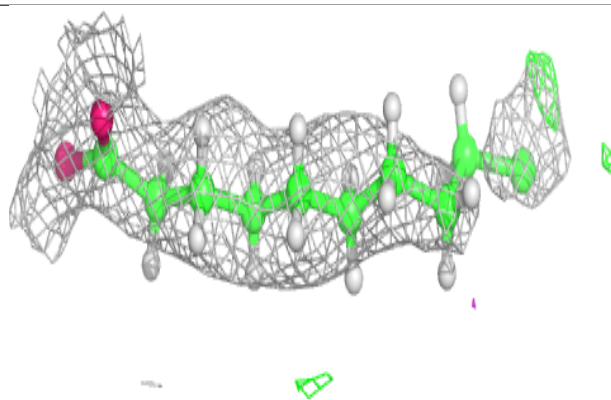
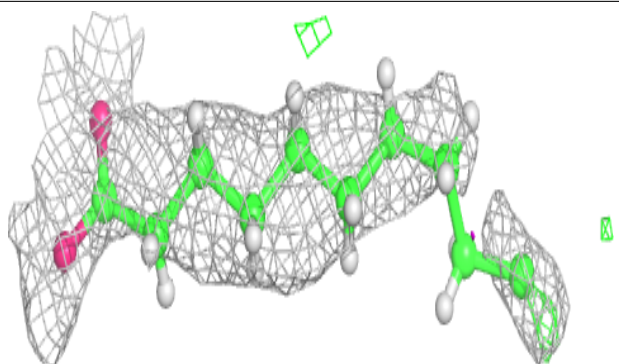
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
22	CLA	b	612	65/65	0.96	0.17	21,37,49,59	0
22	CLA	D	403	65/65	0.96	0.12	21,33,56,65	0
22	CLA	b	603	65/65	0.96	0.14	24,40,68,75	0
22	CLA	D	404	65/65	0.96	0.11	22,33,50,57	0
28	LHG	l	101	49/49	0.96	0.11	25,47,57,73	0
22	CLA	b	605	65/65	0.96	0.13	23,38,51,57	0
22	CLA	c	501	65/65	0.96	0.14	28,45,56,61	0
22	CLA	d	402	65/65	0.96	0.12	23,36,60,64	0
24	BCR	a	406	40/40	0.96	0.10	22,38,51,55	0
22	CLA	A	402	65/65	0.96	0.11	21,31,44,62	0
23	PHO	A	404	64/64	0.96	0.12	19,31,42,44	0
23	PHO	D	401	64/64	0.96	0.12	23,35,45,49	0
22	CLA	b	607	65/65	0.96	0.13	22,39,66,74	0
23	PHO	d	401	64/64	0.96	0.11	29,42,51,60	0
22	CLA	B	607	65/65	0.96	0.11	20,36,61,68	0
22	CLA	B	612	65/65	0.96	0.15	22,35,49,58	0
34	HEM	F	101	43/43	0.96	0.13	40,49,68,72	0
34	HEM	e	101	43/43	0.96	0.12	48,59,78,79	0
22	CLA	a	402	65/65	0.97	0.10	22,33,46,56	0
28	LHG	d	406	49/49	0.97	0.10	27,44,56,65	0
28	LHG	d	407	39/49	0.97	0.10	34,50,70,73	0
22	CLA	B	611	65/65	0.97	0.14	21,33,52,55	0
28	LHG	D	409	49/49	0.97	0.10	25,43,55,61	0
22	CLA	B	605	65/65	0.97	0.14	23,35,52,55	0
28	LHG	L	102	49/49	0.97	0.10	29,43,57,69	0
35	HEC	V	201	43/43	0.97	0.14	27,37,46,49	0
33	BCT	D	402	4/4	0.98	0.18	28,32,35,42	0
35	HEC	v	201	43/43	0.98	0.12	33,41,51,58	0
21	FE2	a	401	1/1	0.99	0.09	37,37,37,37	0
25	CL	A	407	1/1	0.99	0.07	34,34,34,34	0
25	CL	a	407	1/1	0.99	0.06	32,32,32,32	0
33	BCT	a	409	4/4	0.99	0.20	33,34,45,51	0
25	CL	a	408	1/1	0.99	0.06	32,32,32,32	0
31	OEX	A	415	10/10	0.99	0.13	26,29,33,36	0
31	OEX	a	416	10/10	0.99	0.12	24,30,33,33	0
21	FE2	A	401	1/1	0.99	0.08	29,29,29,29	0
25	CL	A	408	1/1	1.00	0.04	30,30,30,30	0

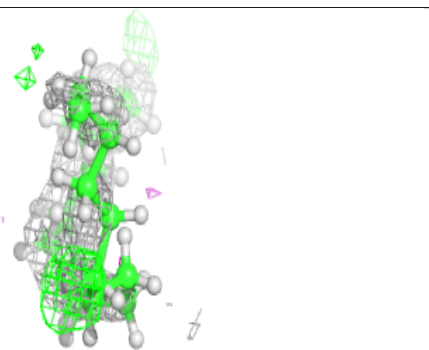
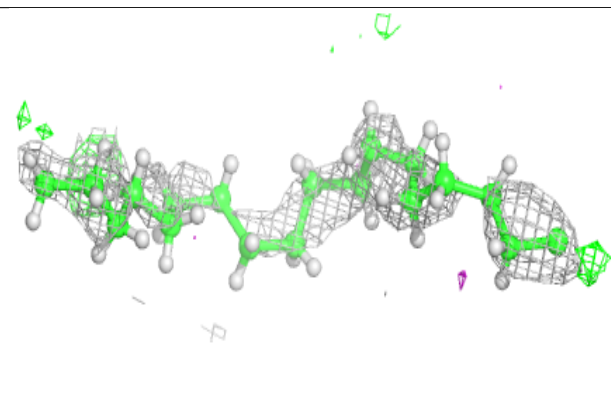
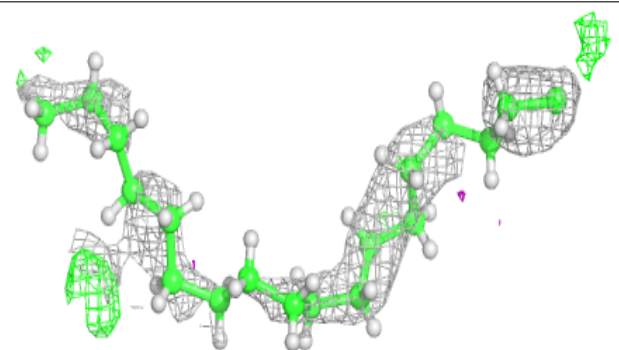
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around STE k 104:**

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

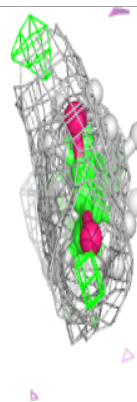
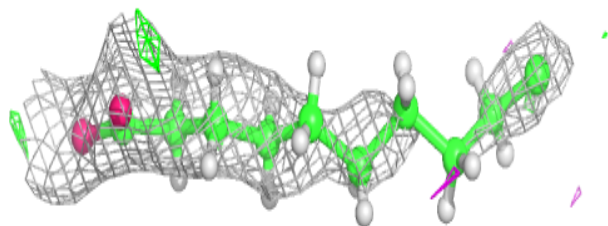
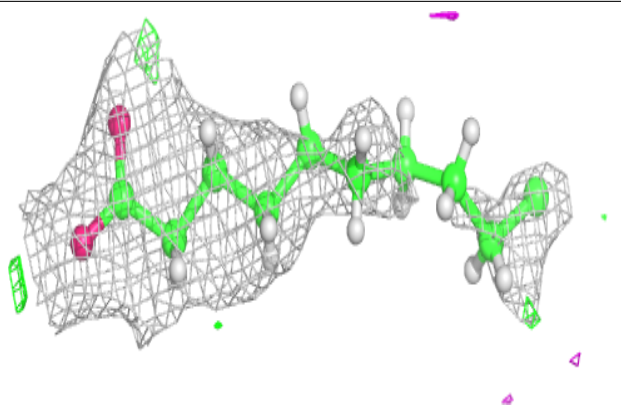
**Electron density around STE H 103:**

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

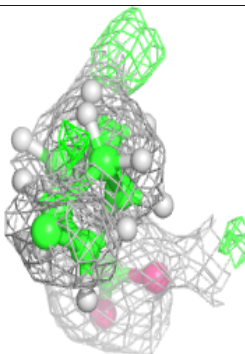
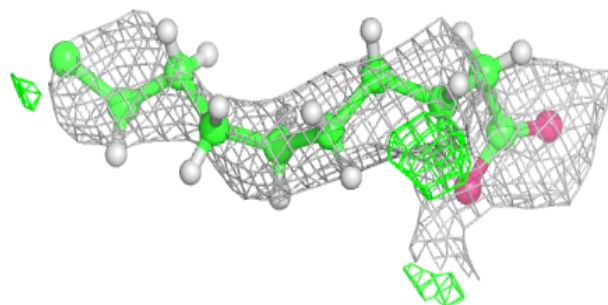
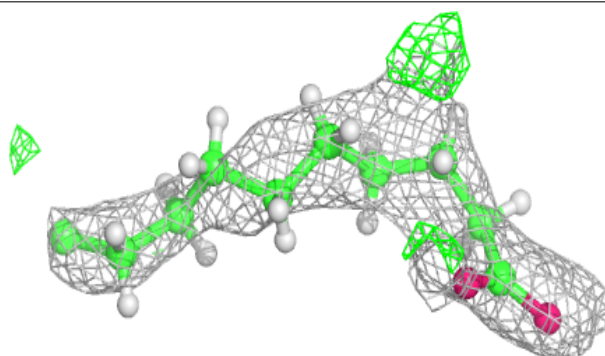


**Electron density around STE a 415:**

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

**Electron density around STE E 102:**

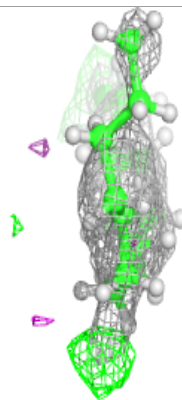
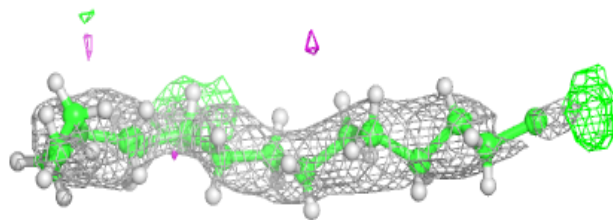
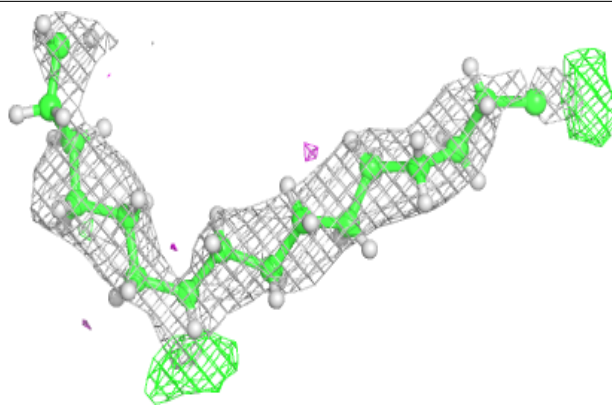
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





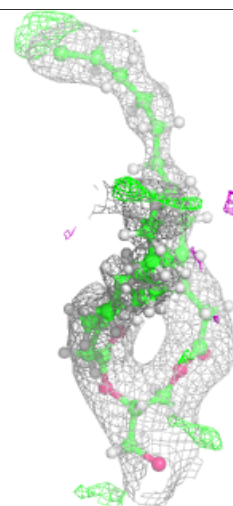
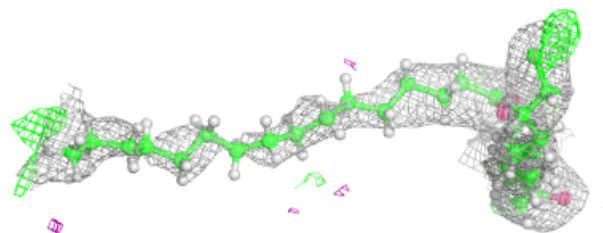
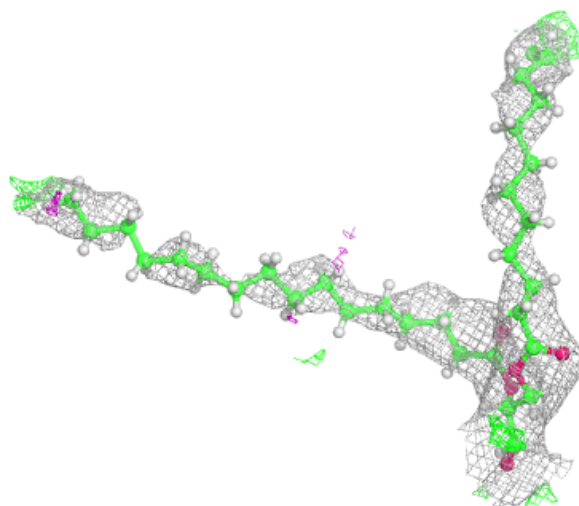
**Electron density around STE B 626:**

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



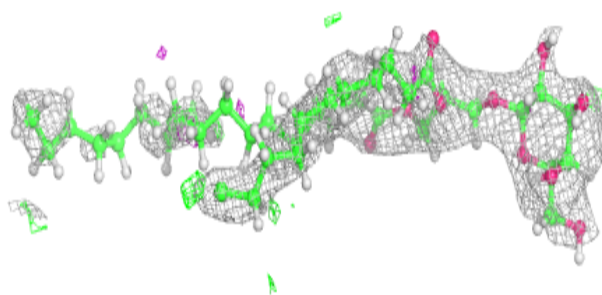
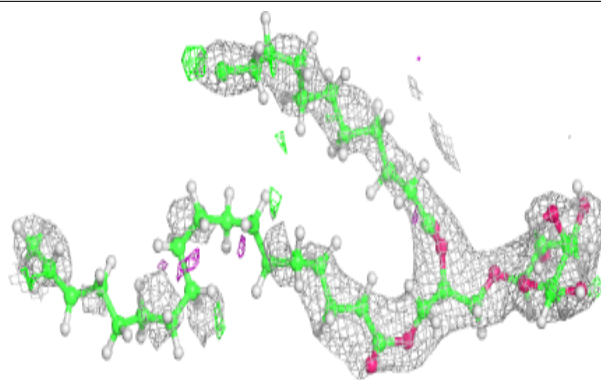
**Electron density around SQD a 413:**

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

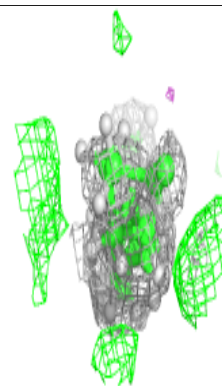
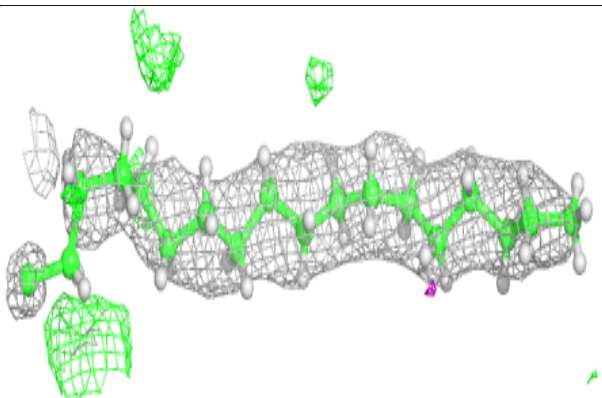
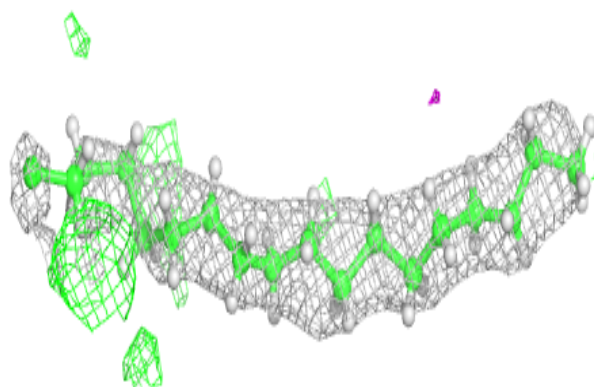


**Electron density around LMG c 520:**

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

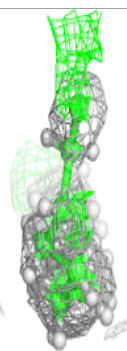
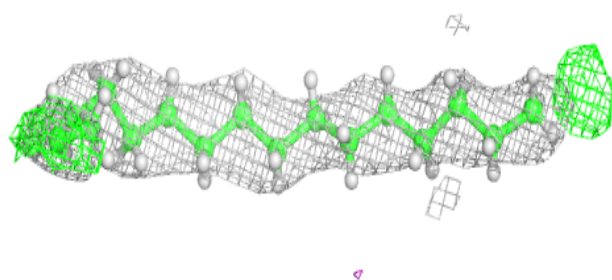
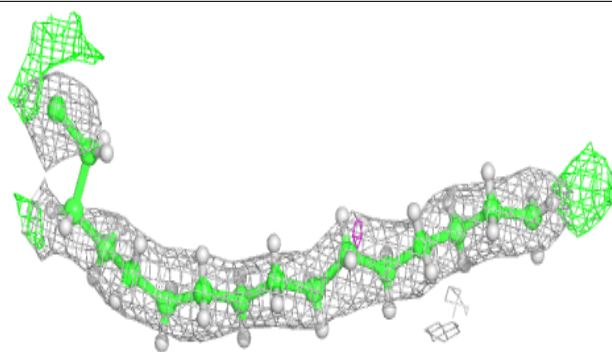
**Electron density around STE 1 102:**

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

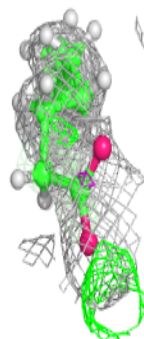
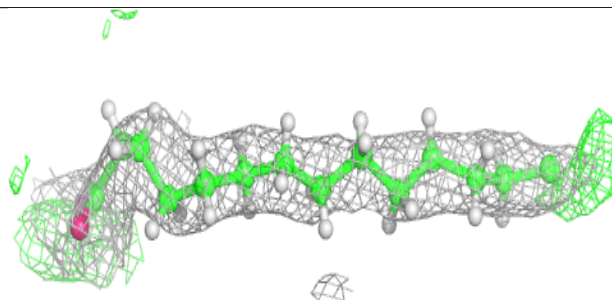
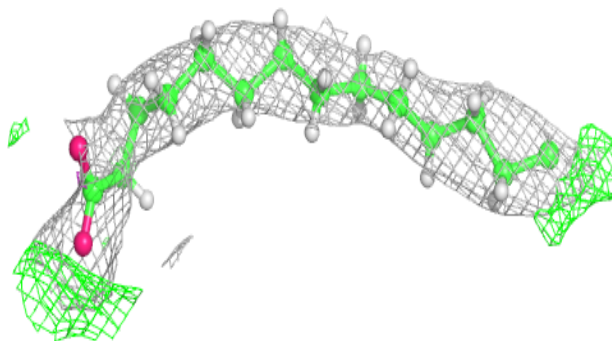


**Electron density around STE C 520:**

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

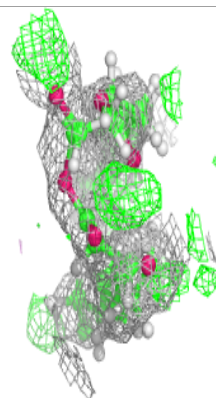
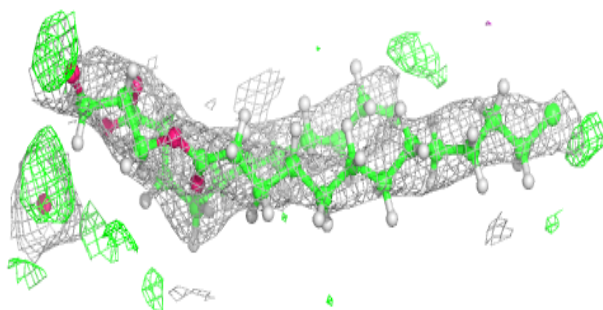
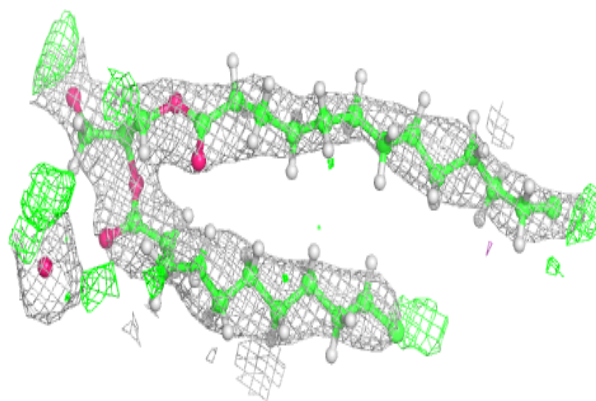
**Electron density around STE b 624:**

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

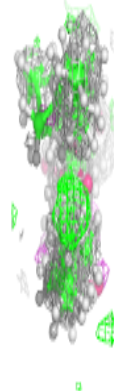
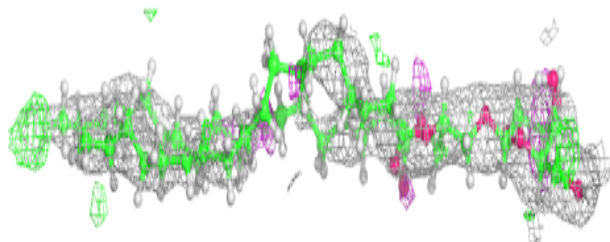
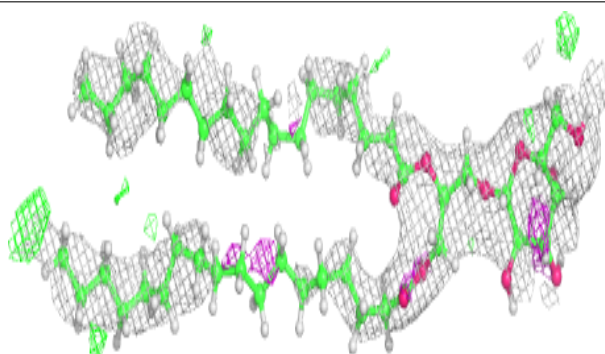


**Electron density around LMG D 410:**

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

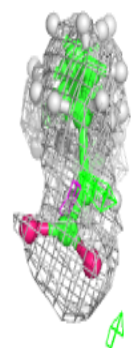
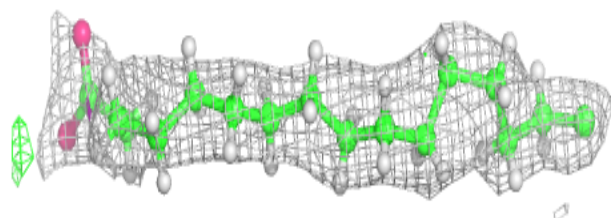
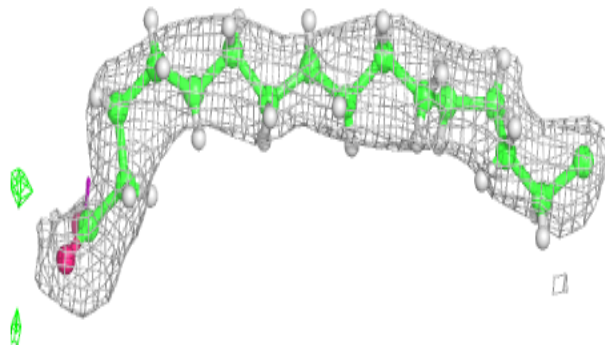
**Electron density around LMG b 622:**

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

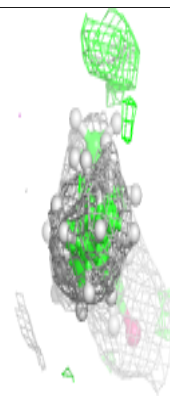
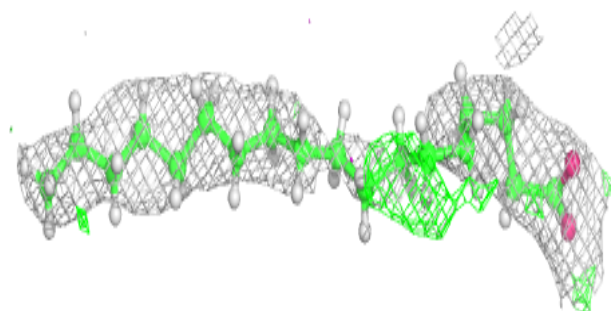
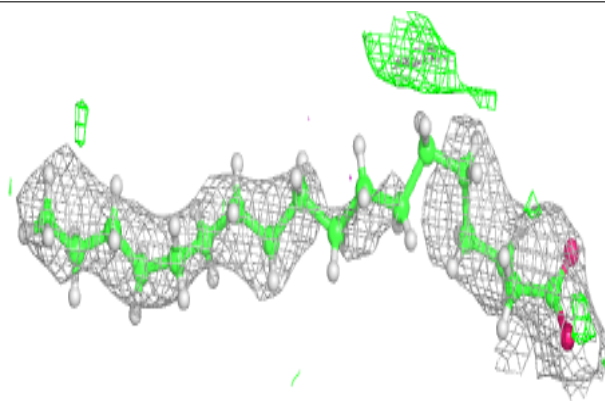


**Electron density around STE B 625:**

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

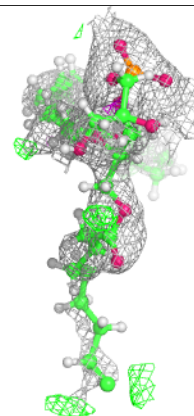
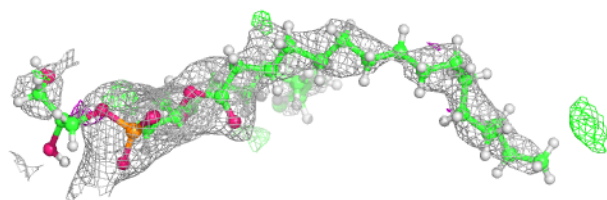
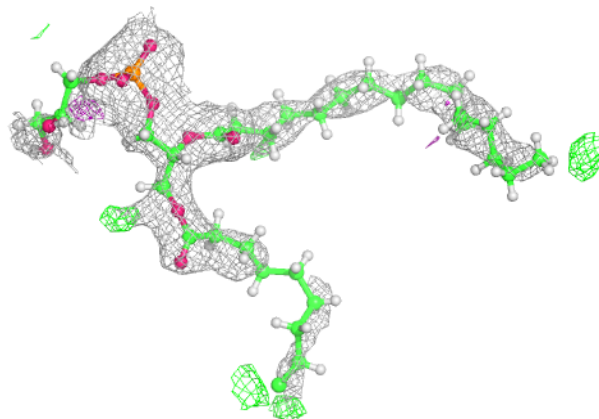
**Electron density around STE b 625:**

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



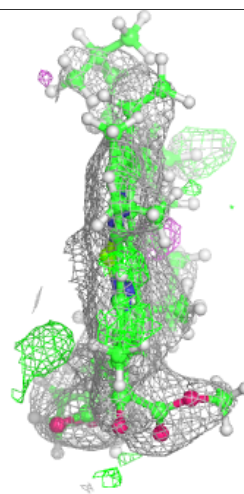
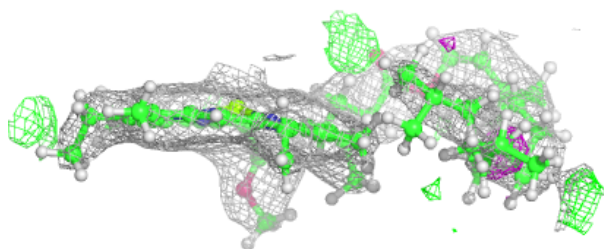
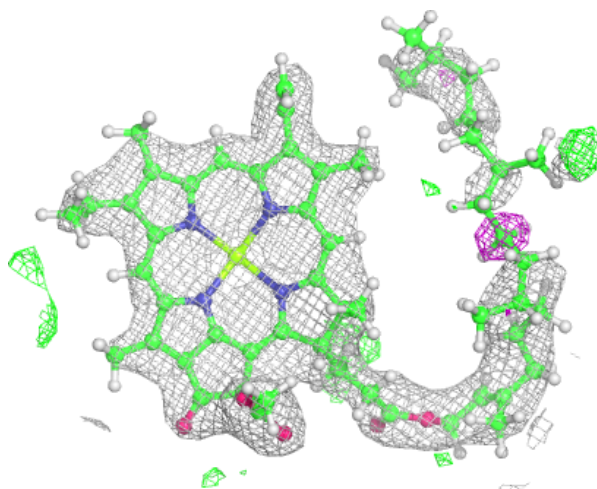
**Electron density around LHG e 102:**

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

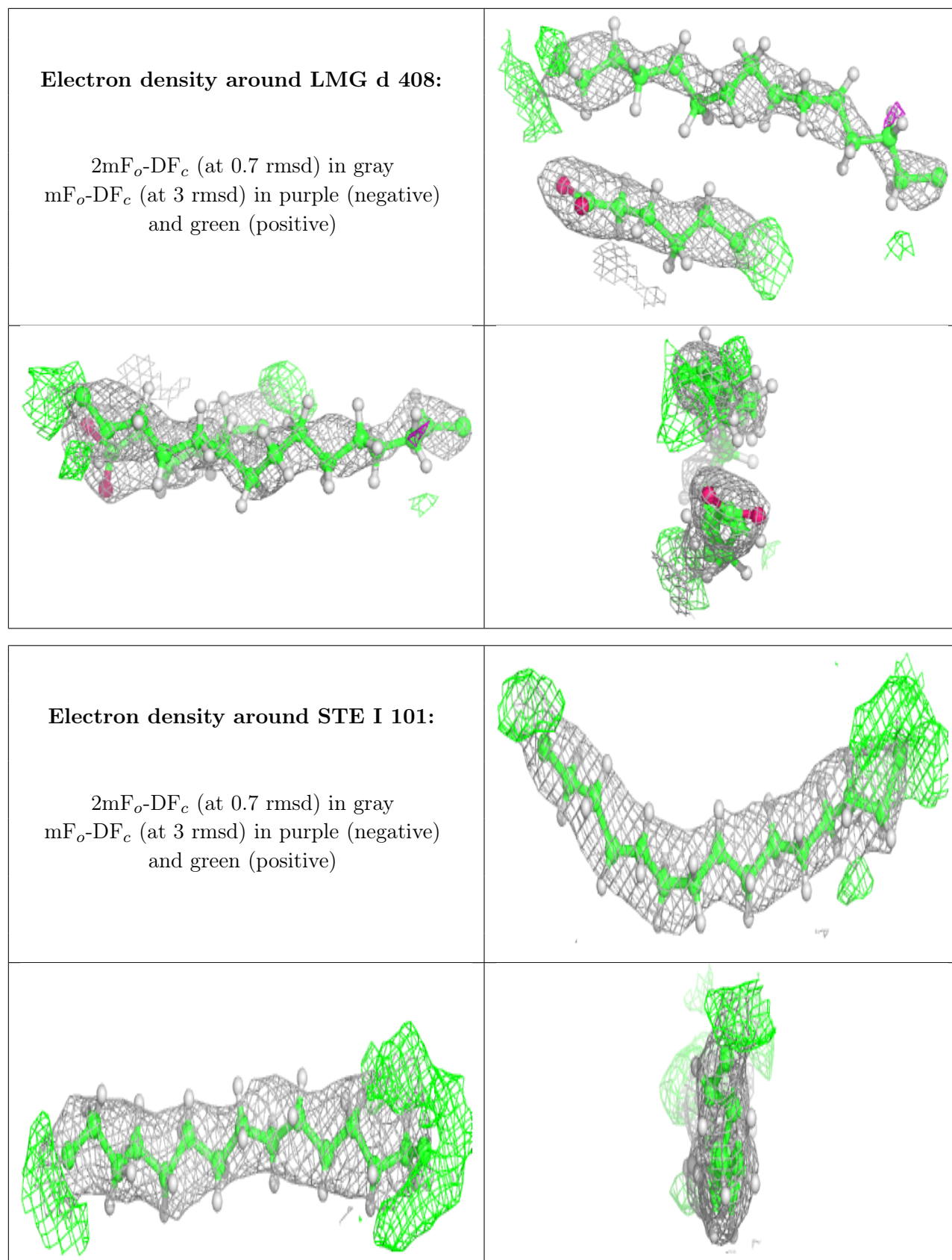


**Electron density around CLA C 512:**

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

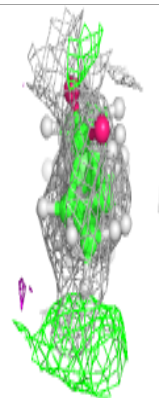
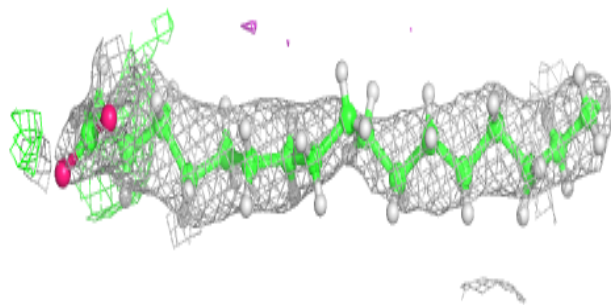
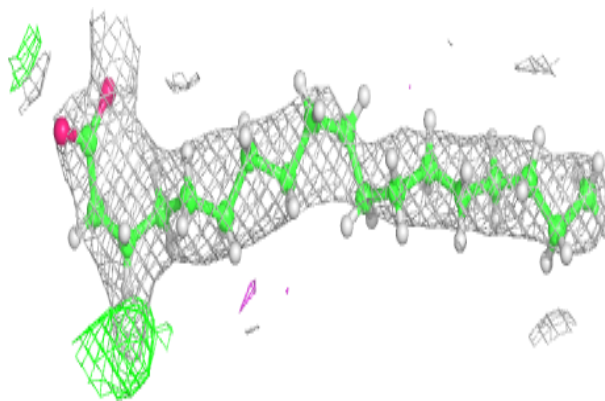




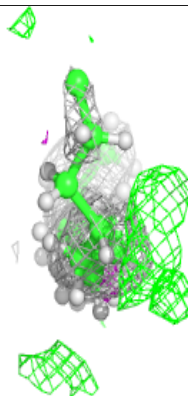
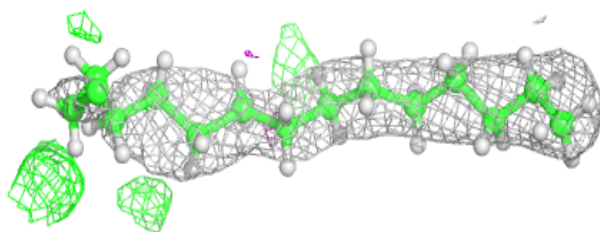
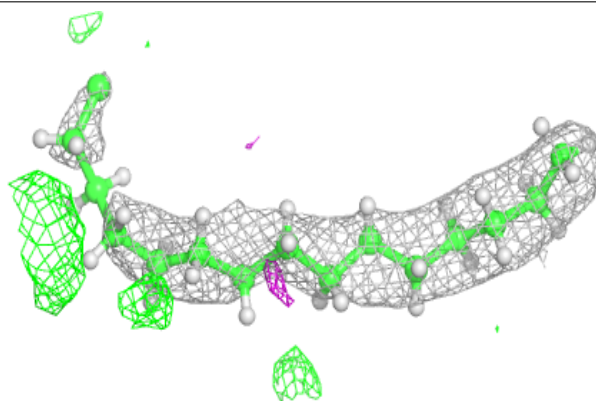


**Electron density around STE c 519:**

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

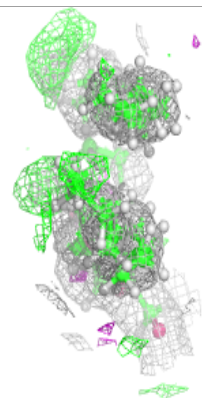
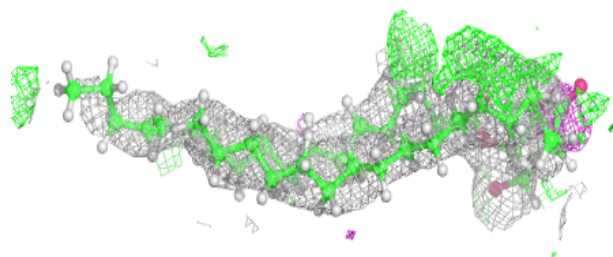
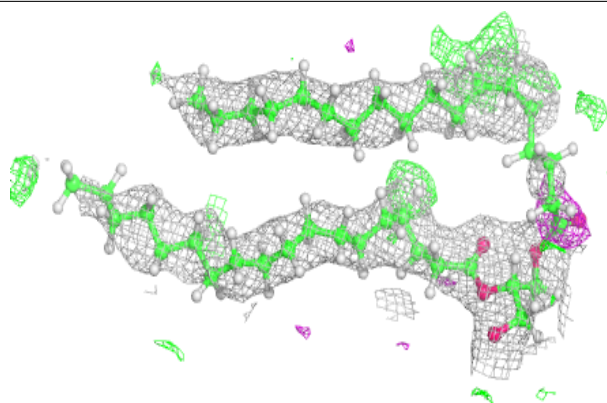
**Electron density around STE M 104:**

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

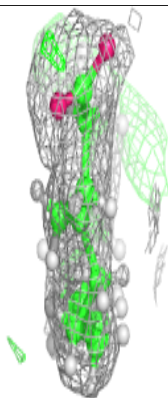
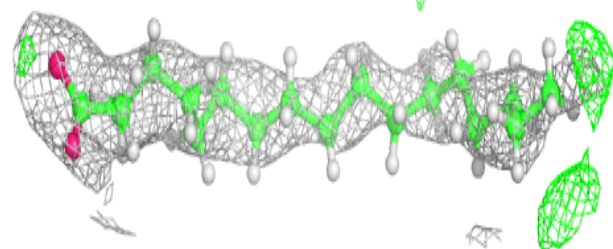
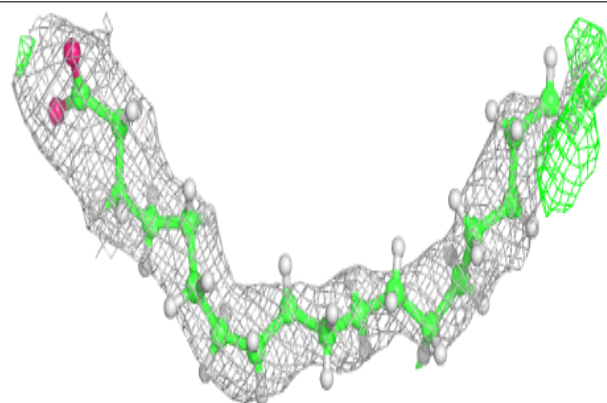


**Electron density around DGD B 623:**

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

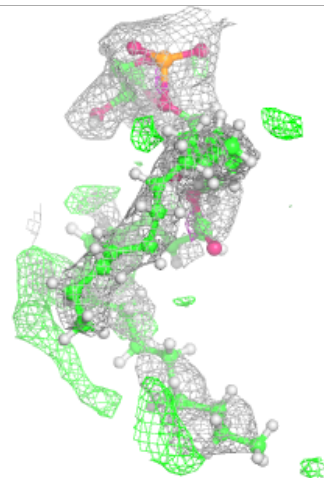
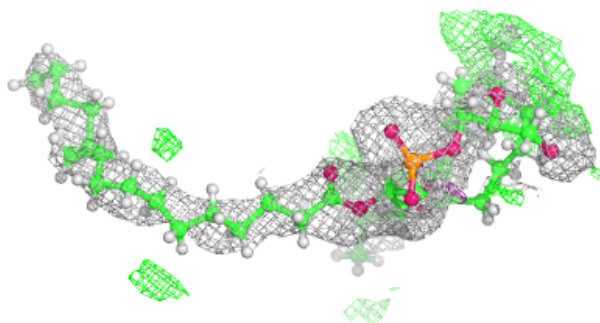
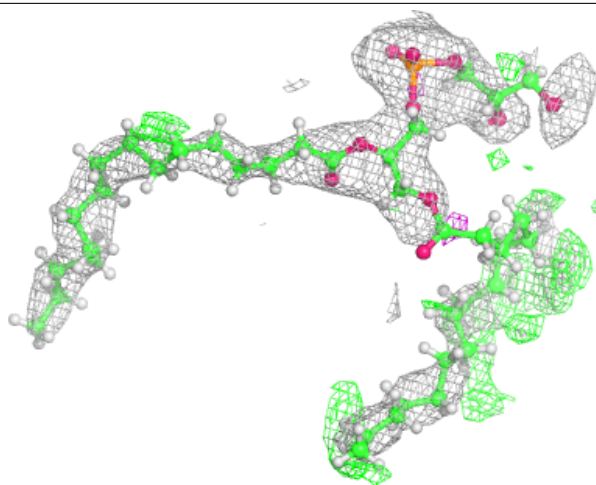
**Electron density around STE x 102:**

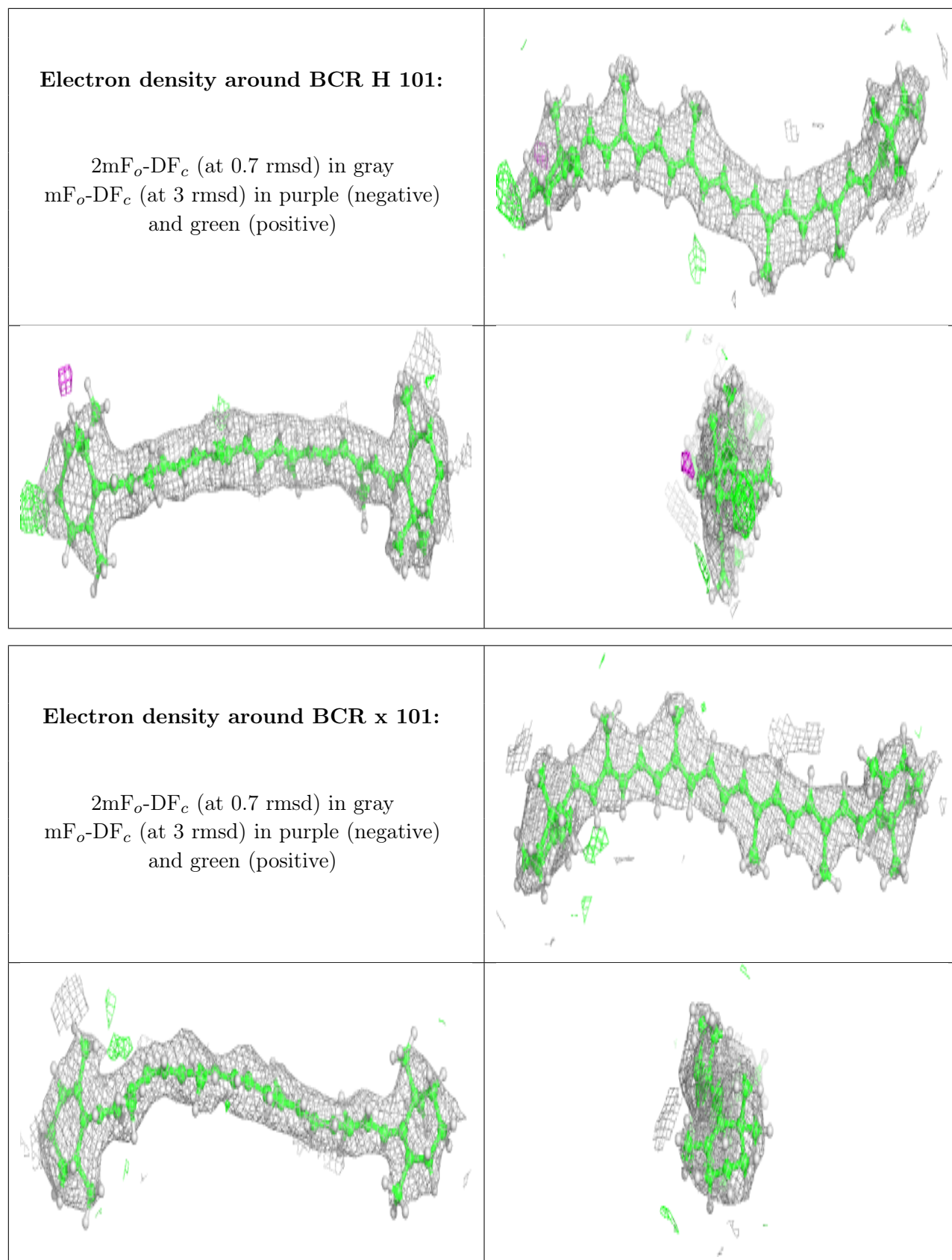
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around LHG E 101:**

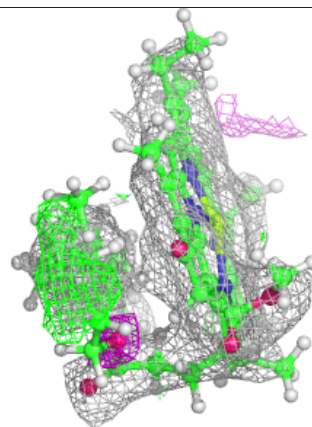
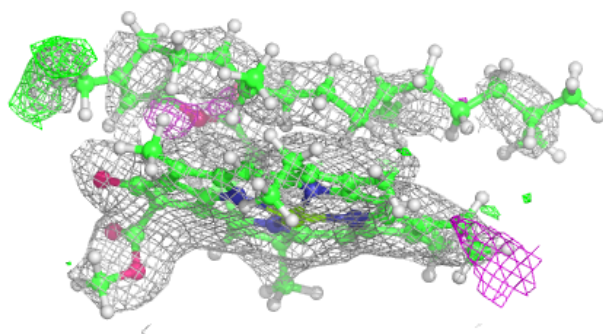
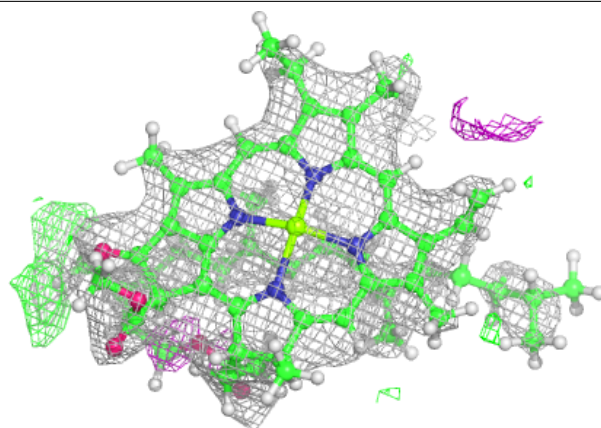
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



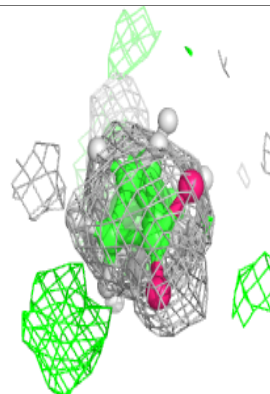
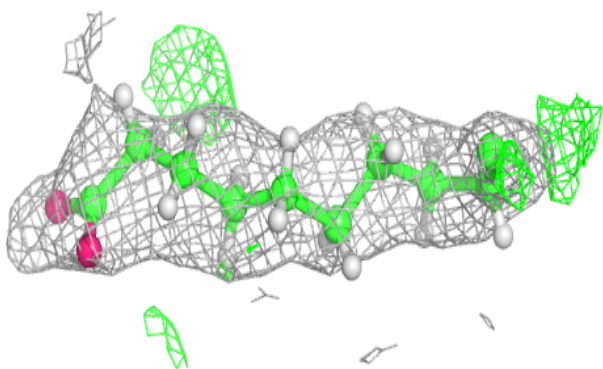
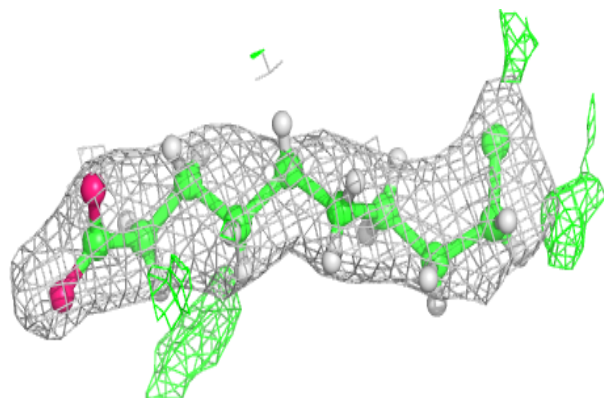


**Electron density around CLA b 601:**

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

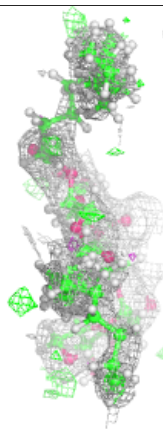
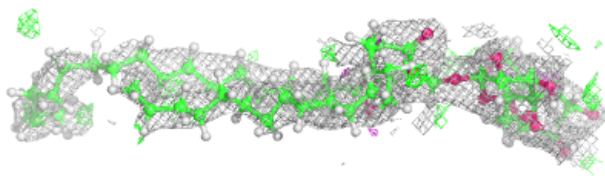
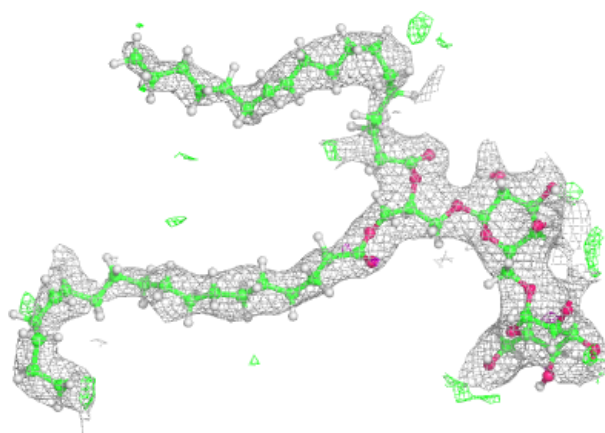
**Electron density around STE J 101:**

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

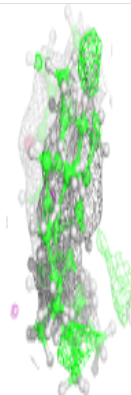
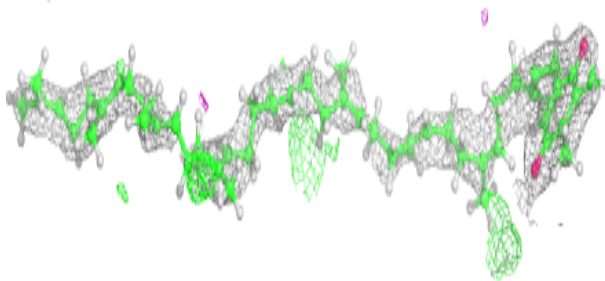
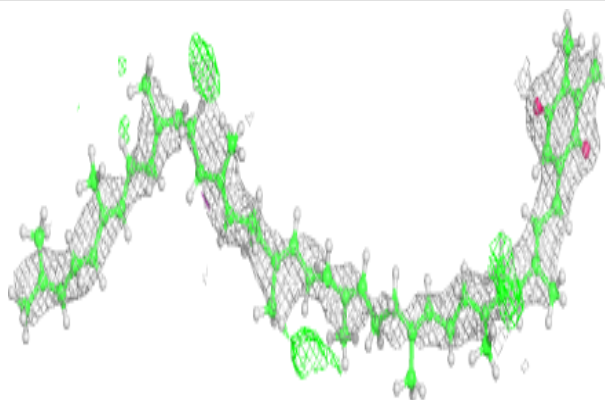


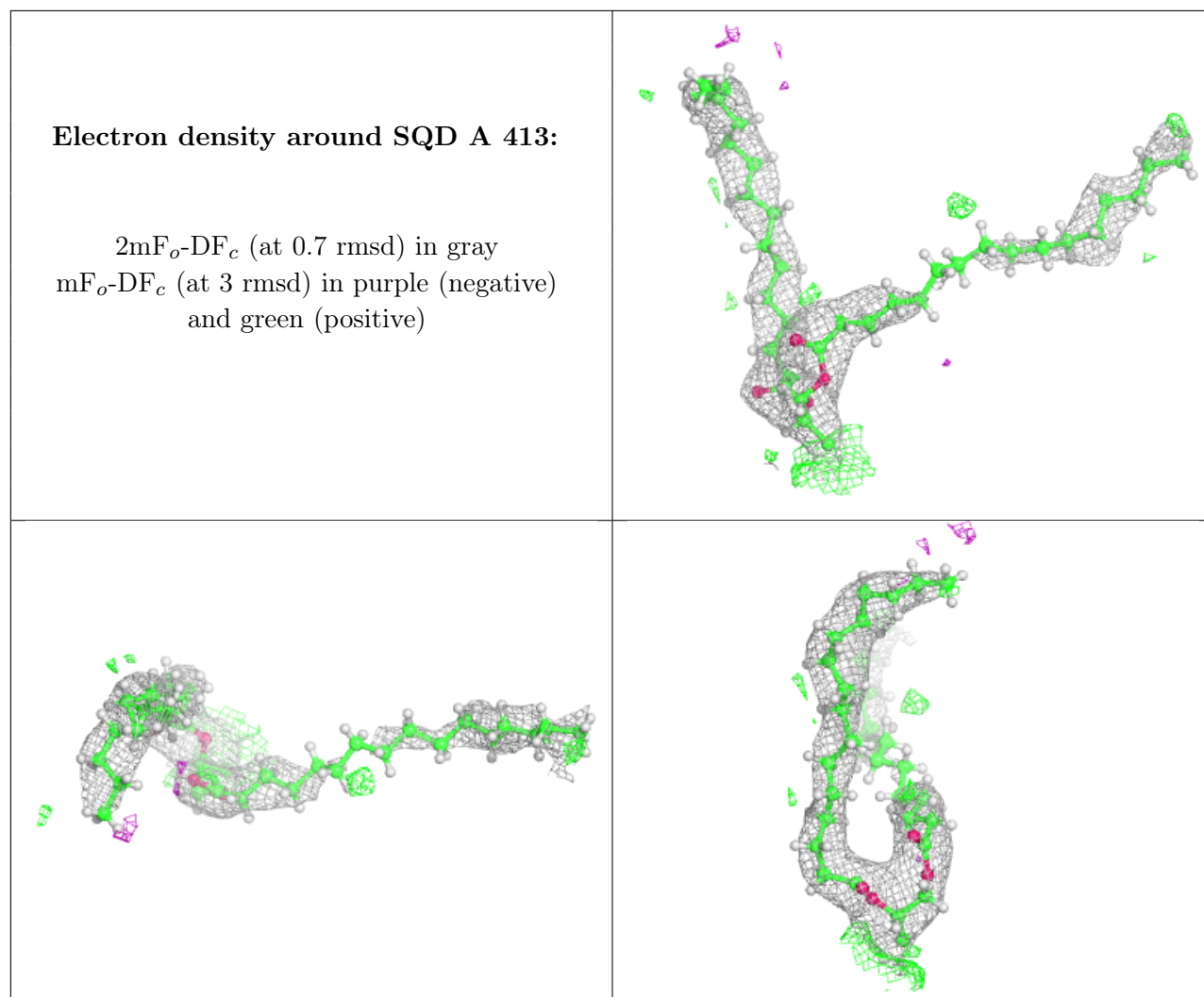
**Electron density around DGD A 414:**

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

**Electron density around PL9 A 409:**

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

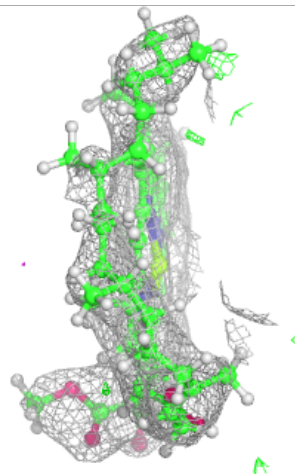
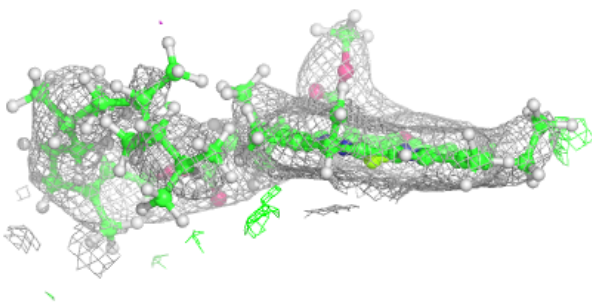
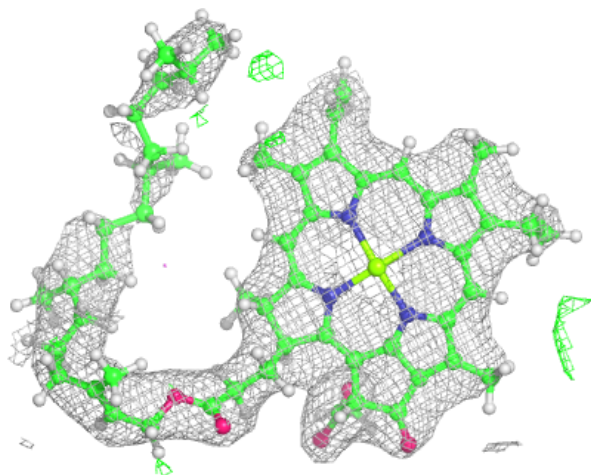






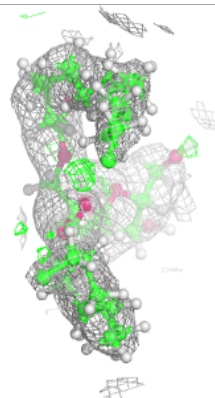
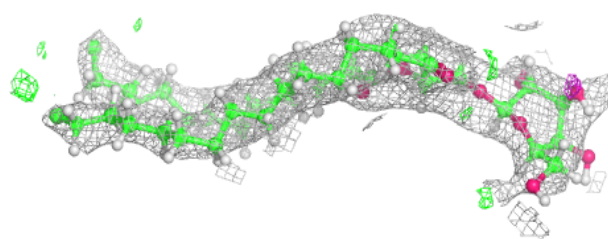
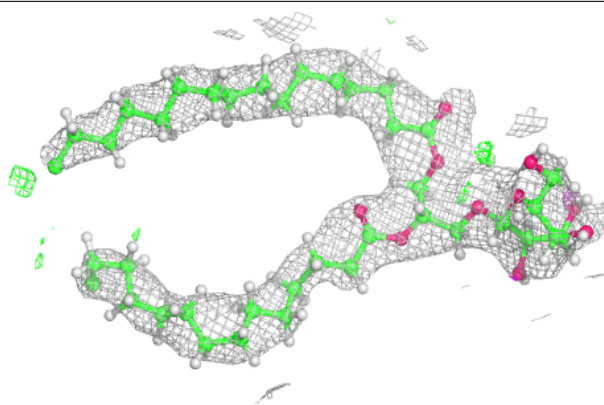
**Electron density around CLA c 512:**

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

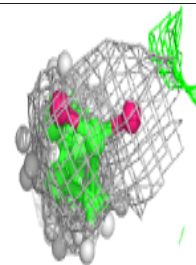
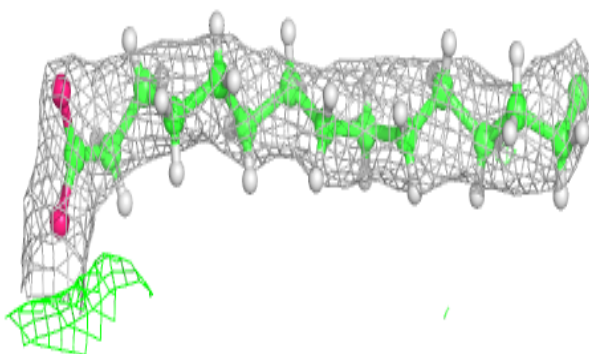
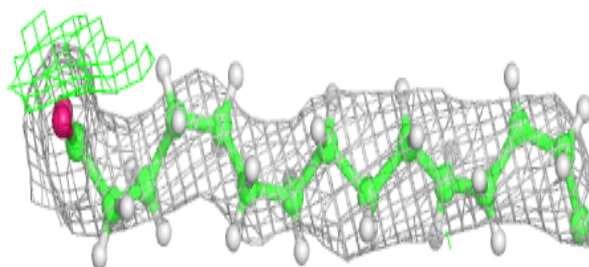


**Electron density around LMG a 414:**

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

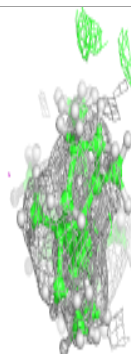
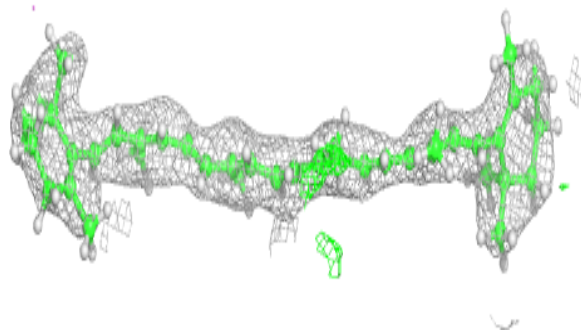
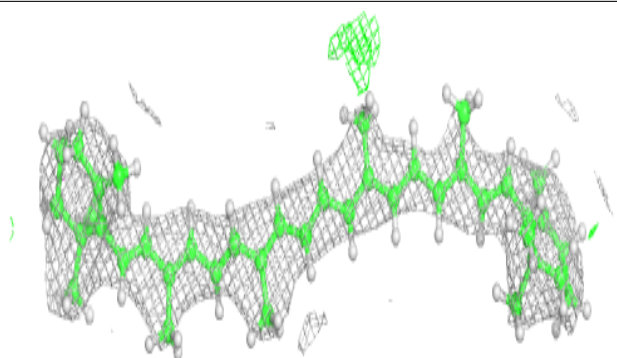
**Electron density around STE d 410:**

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

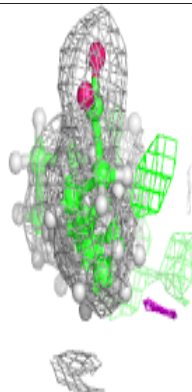
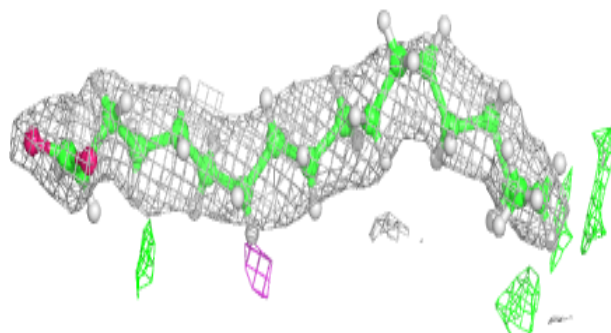
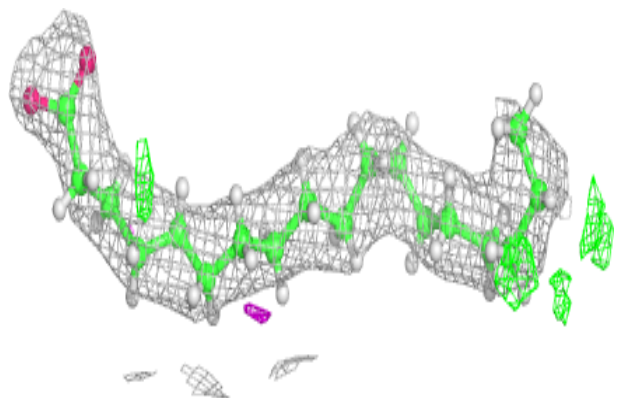


**Electron density around BCR k 102:**

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

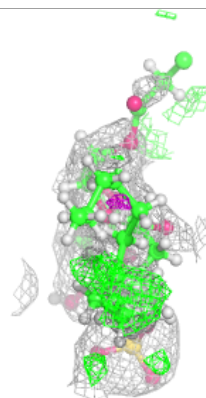
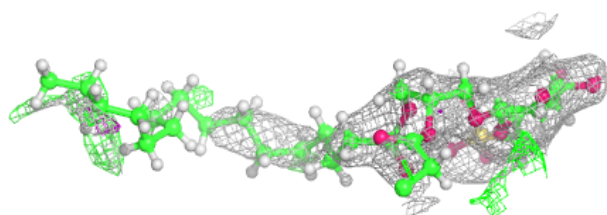
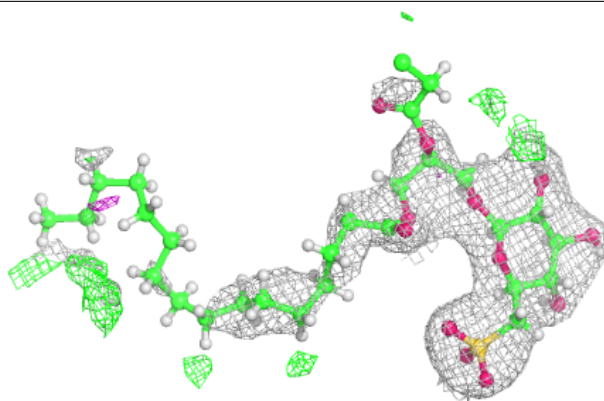
**Electron density around STE b 621:**

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

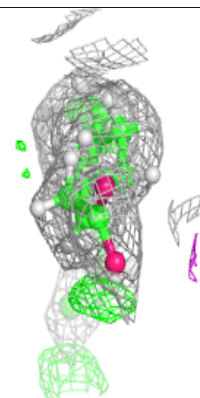
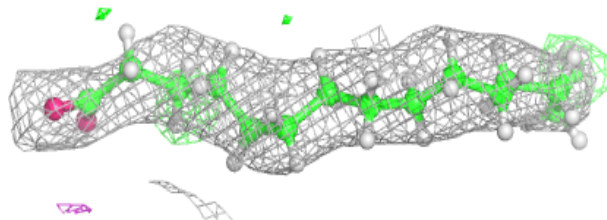
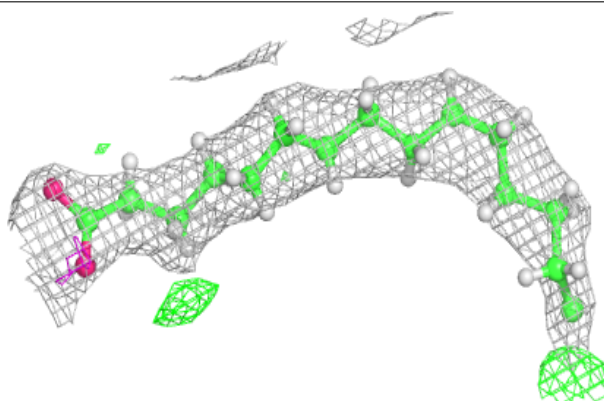


**Electron density around SQD f 101:**

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

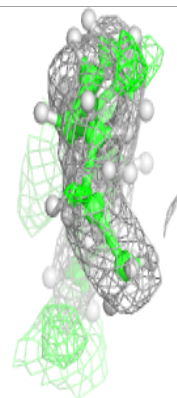
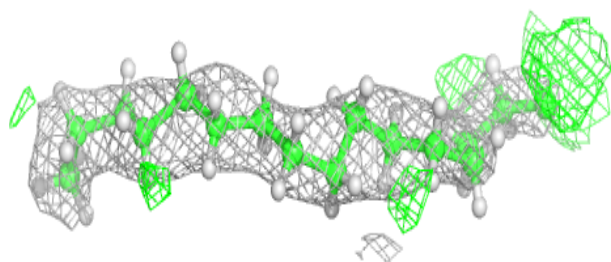
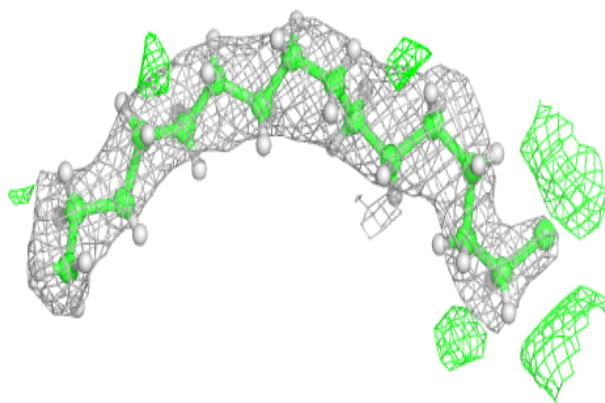
**Electron density around STE B 620:**

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

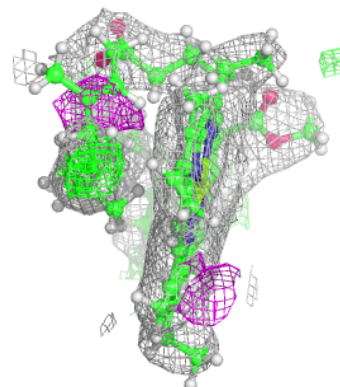
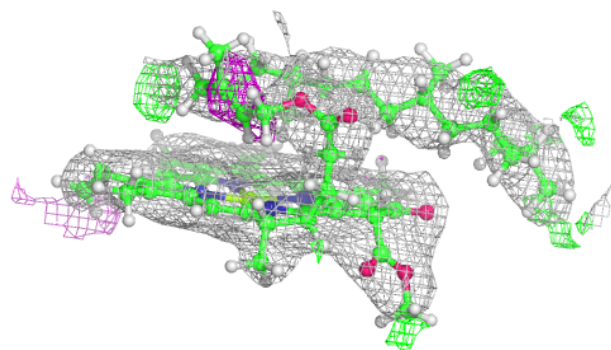
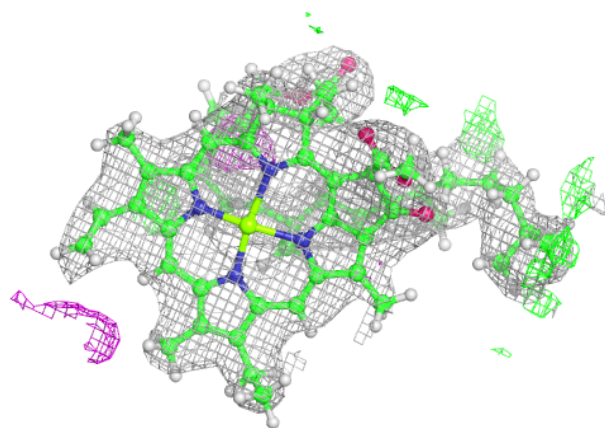


**Electron density around STE b 620:**

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

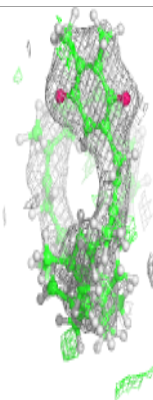
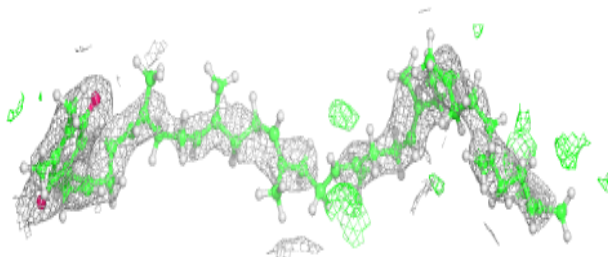
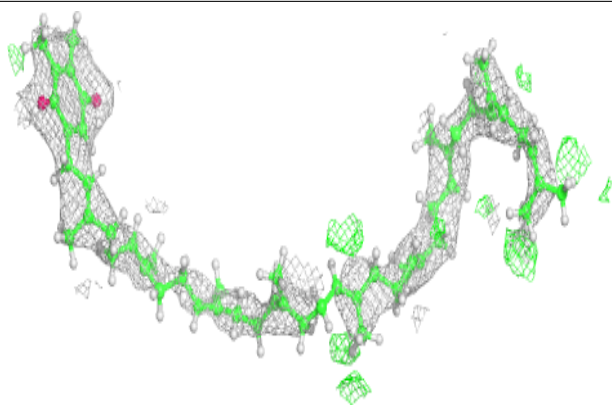
**Electron density around CLA B 601:**

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

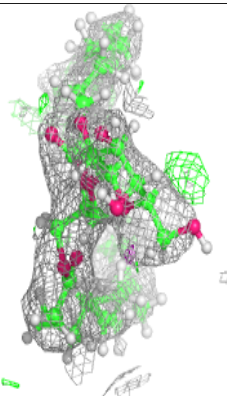
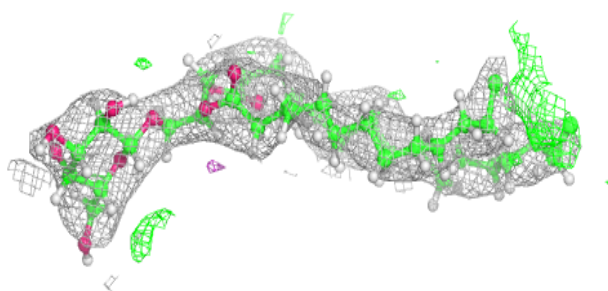
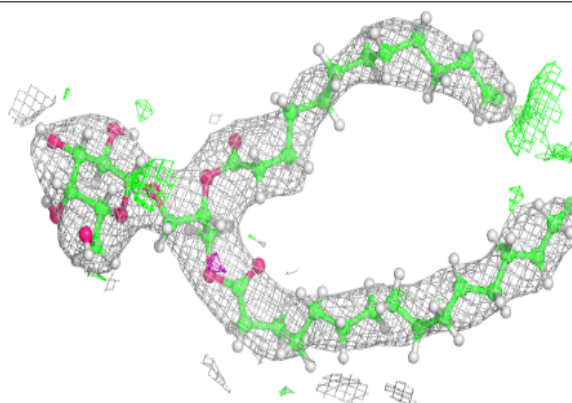


**Electron density around PL9 a 410:**

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

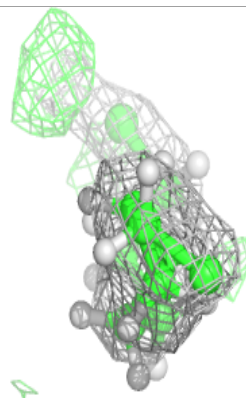
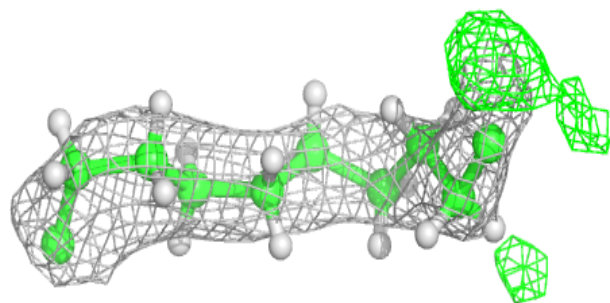
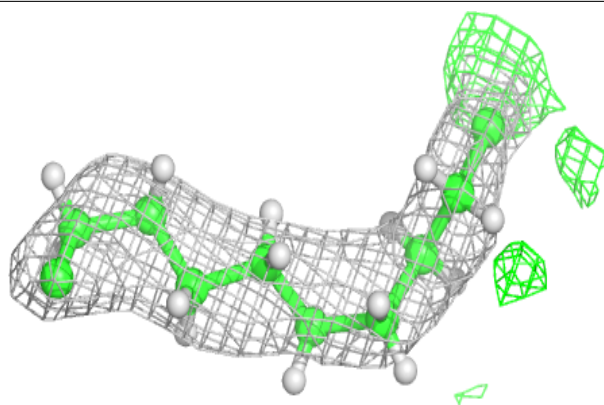
**Electron density around LMG A 410:**

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



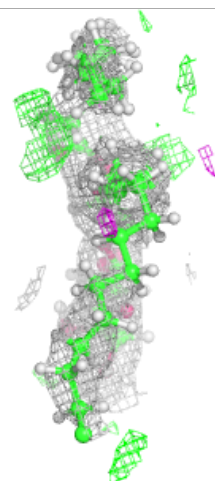
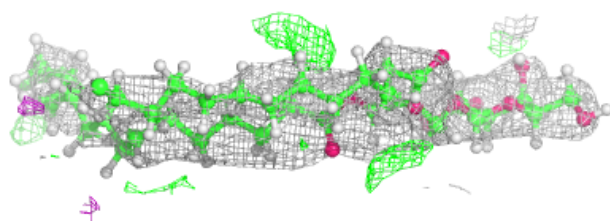
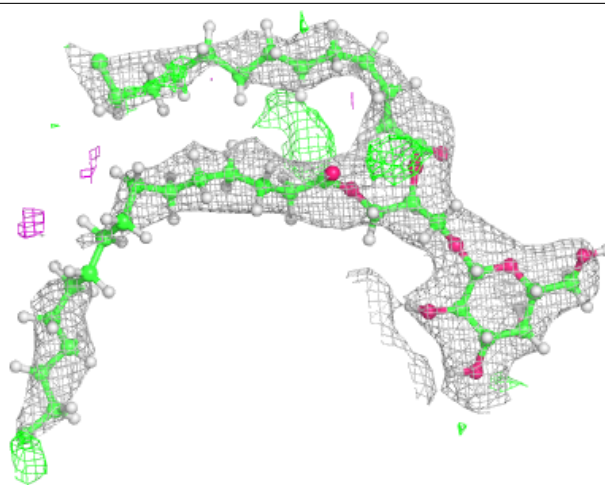
**Electron density around STE b 626:**

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

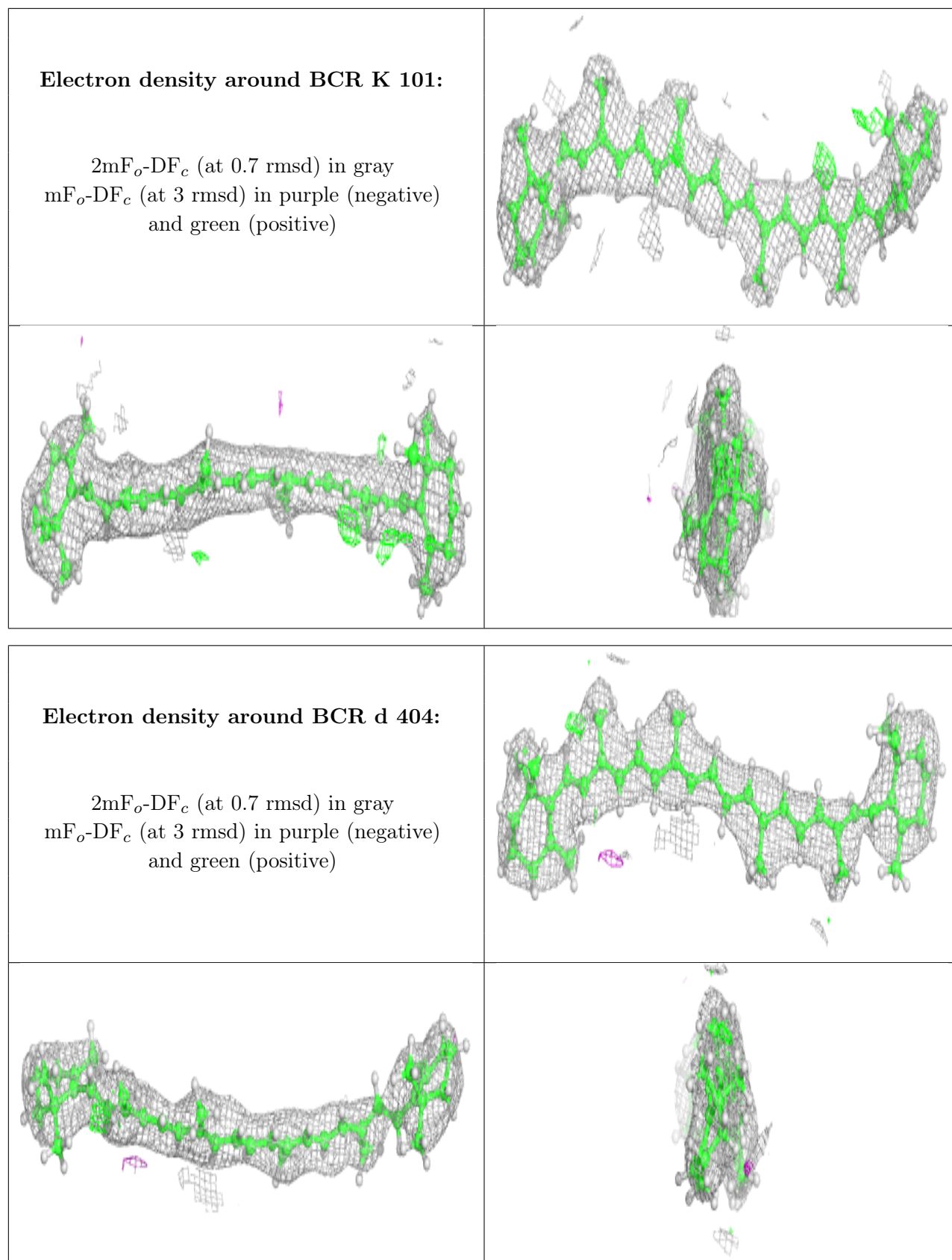


**Electron density around LMG C 518:**

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

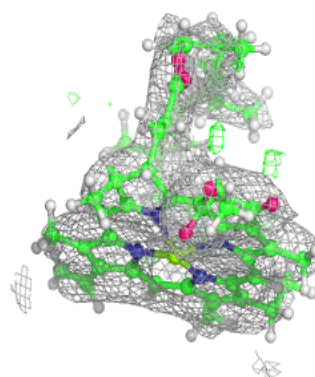
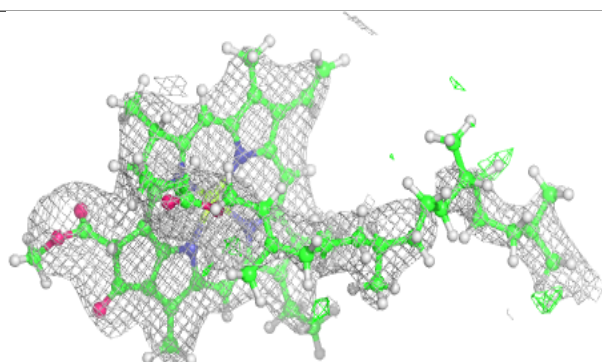
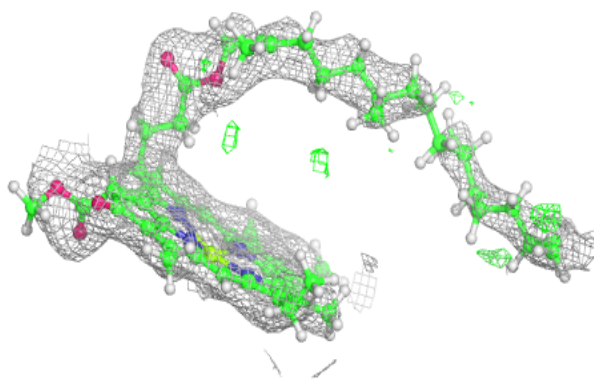




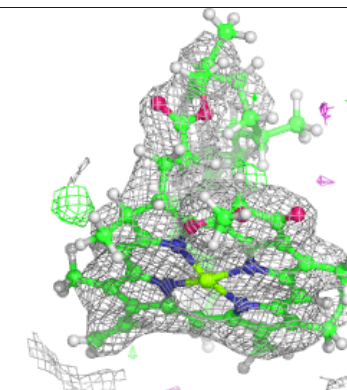
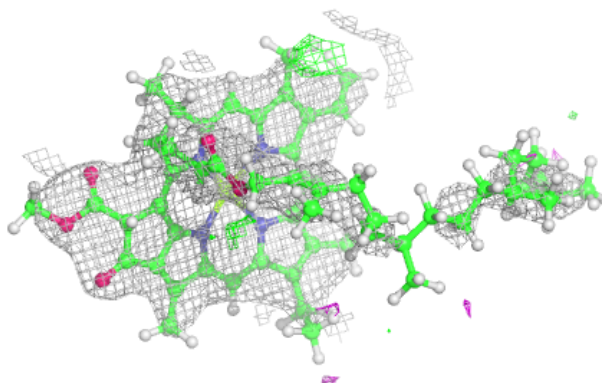
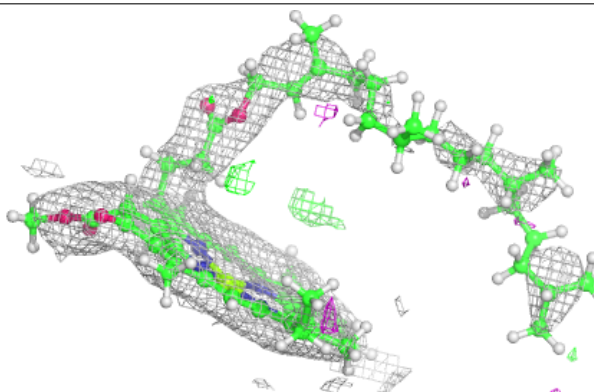


**Electron density around CLA C 513:**

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

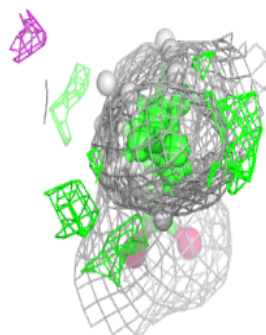
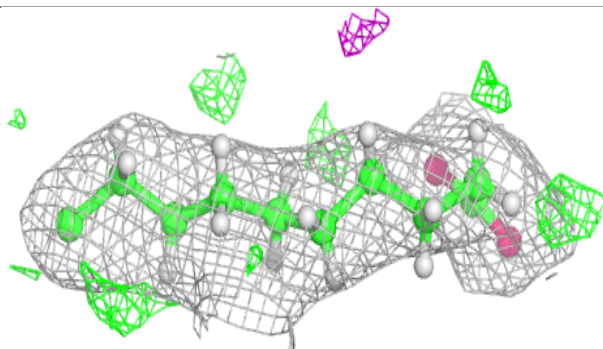
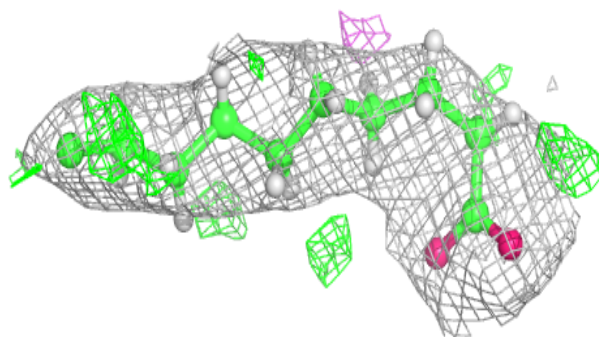
**Electron density around CLA c 513:**

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

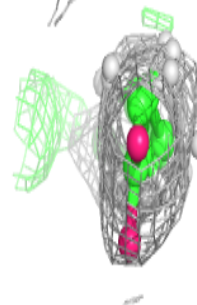
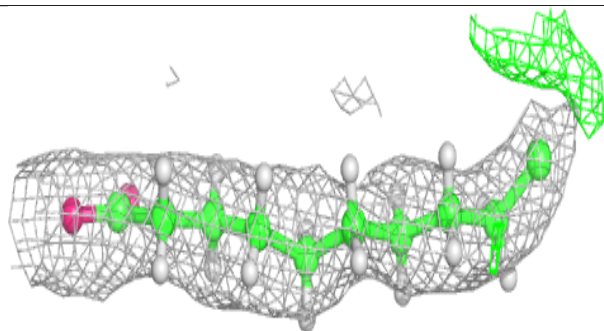
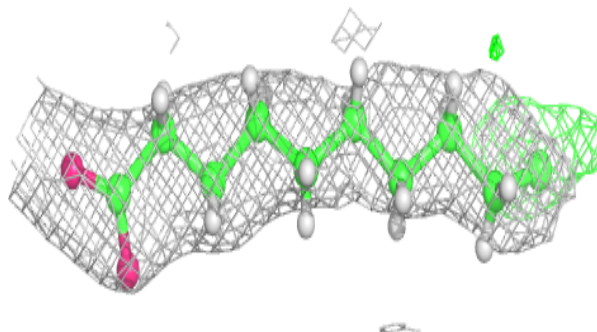


**Electron density around STE B 624:**

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

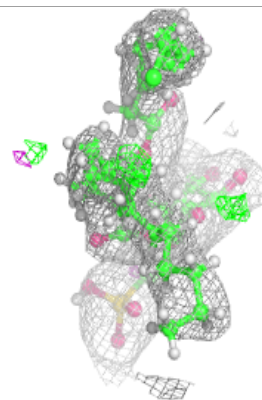
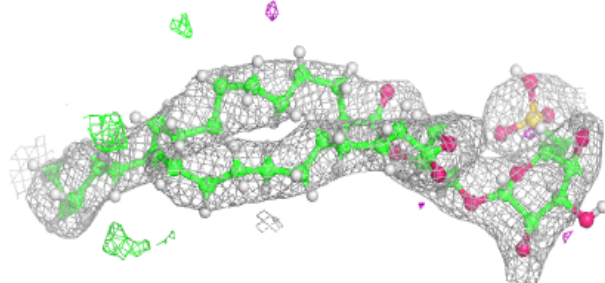
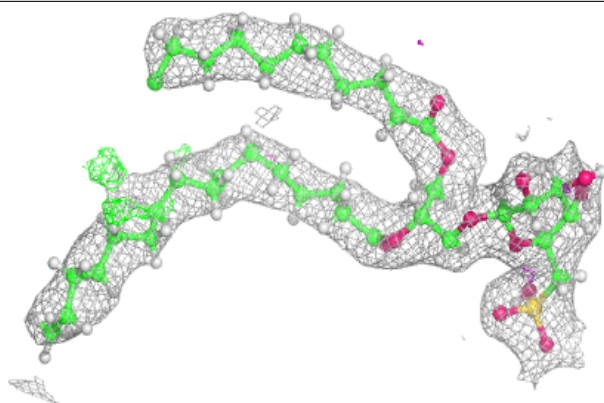
**Electron density around STE j 101:**

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

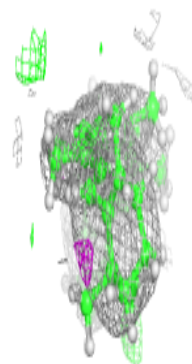
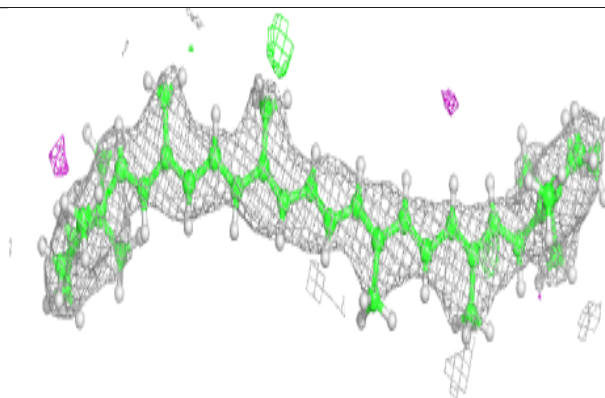
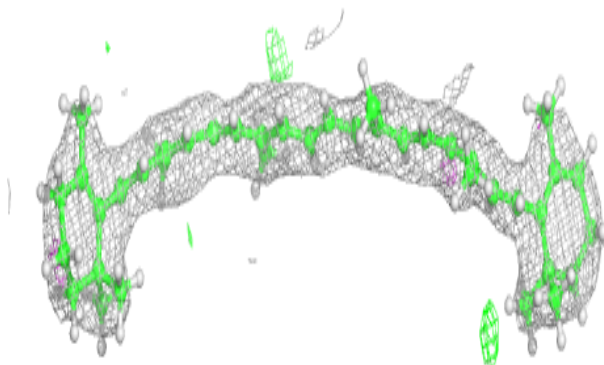


**Electron density around SQD L 101:**

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

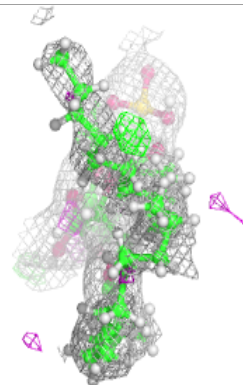
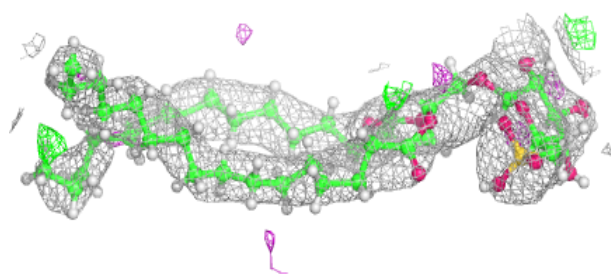
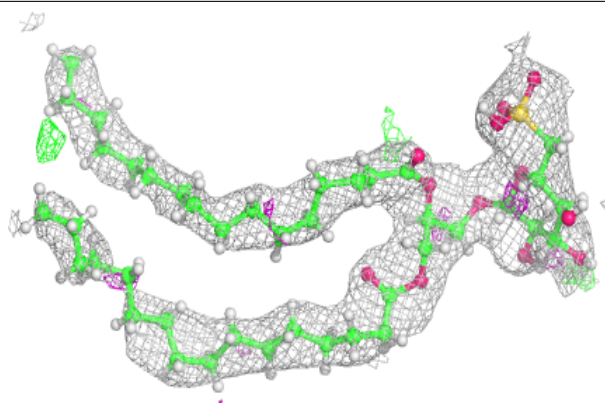
**Electron density around BCR k 103:**

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

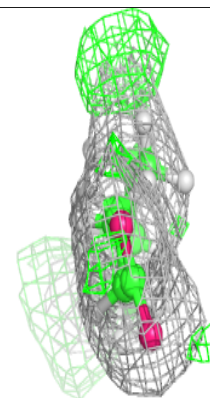
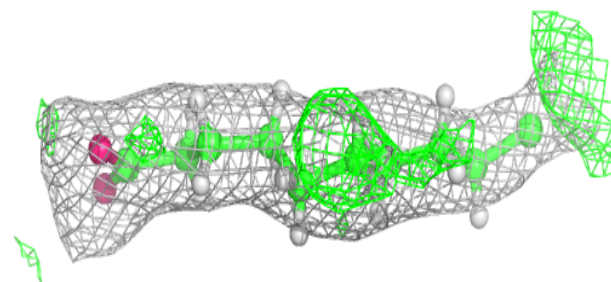
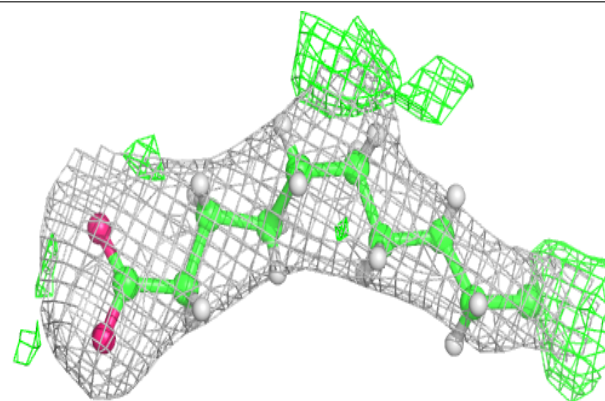


**Electron density around SQD B 622:**

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

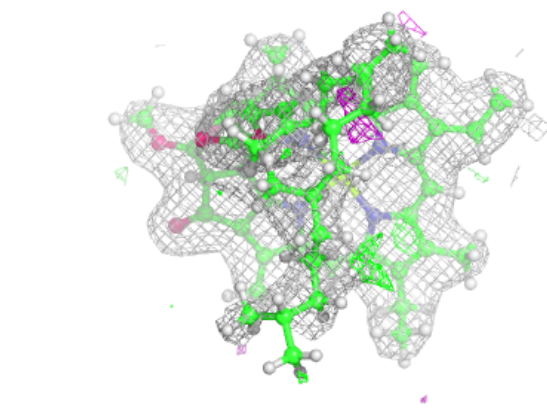
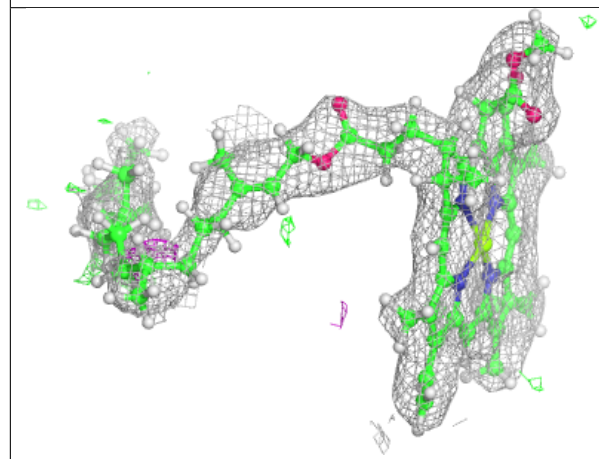
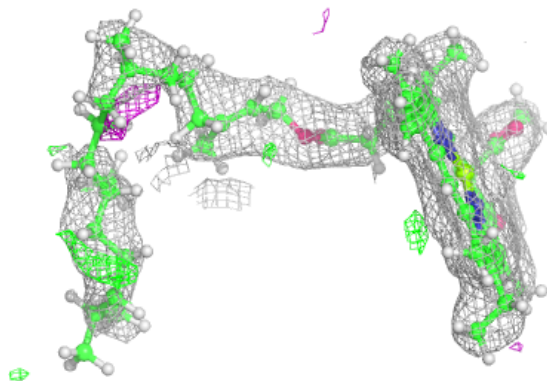
**Electron density around STE C 521:**

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

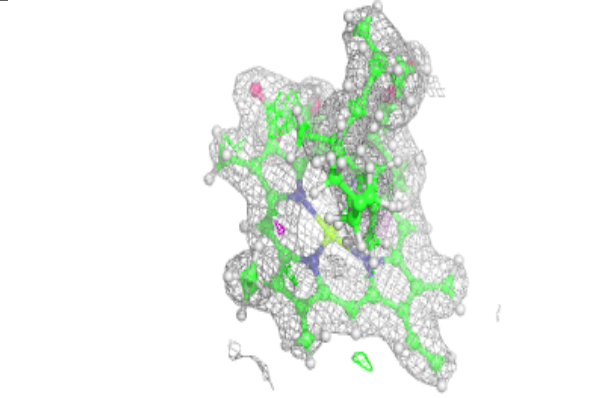
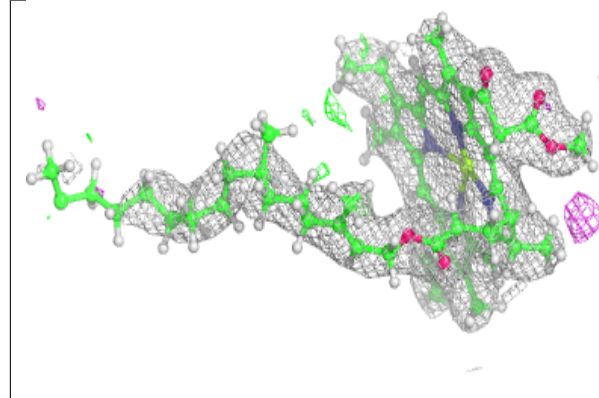
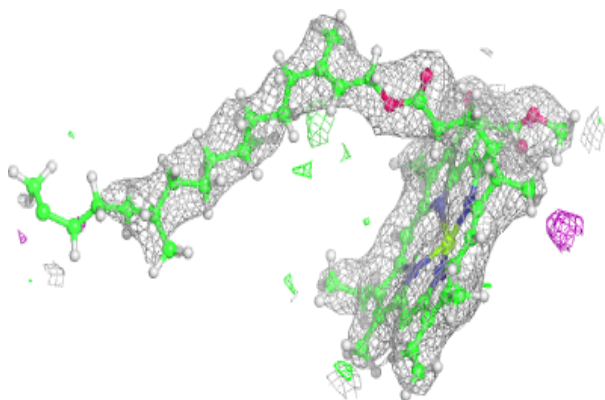


**Electron density around CLA a 405:**

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

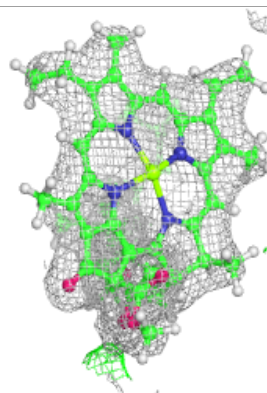
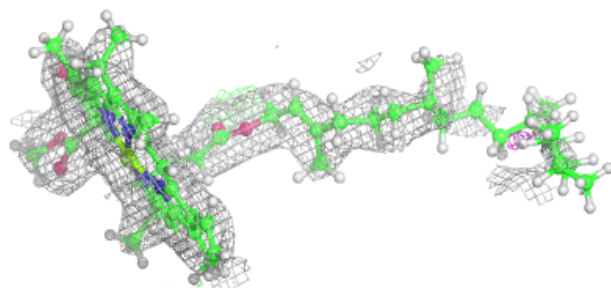
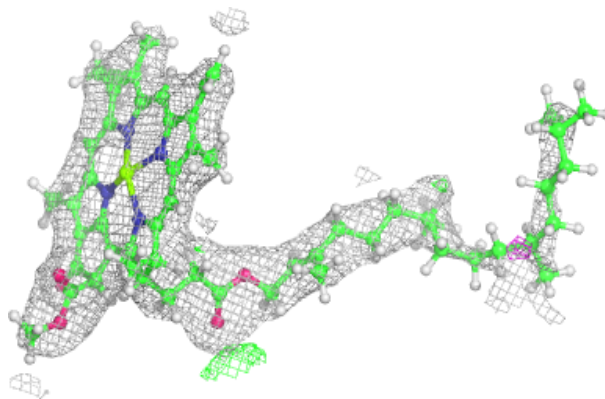
**Electron density around CLA c 508:**

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

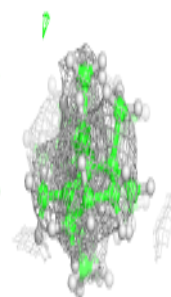
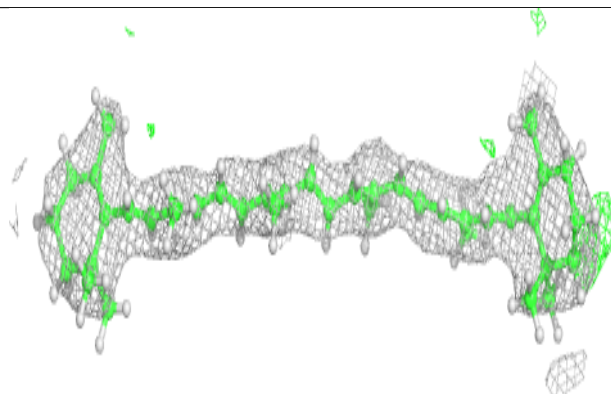
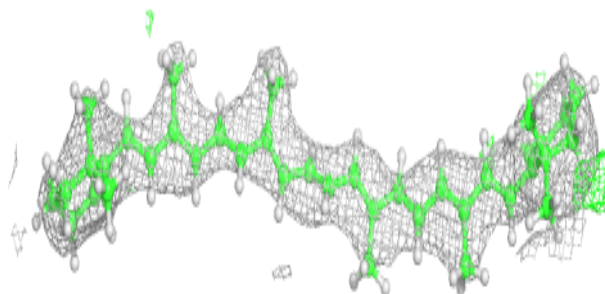


**Electron density around CLA d 403:**

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

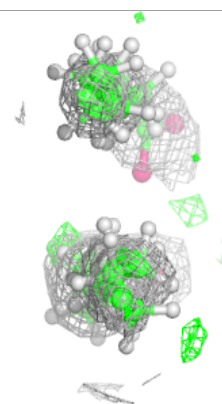
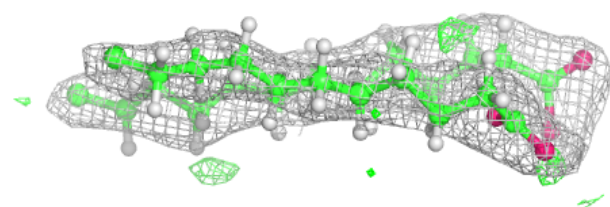
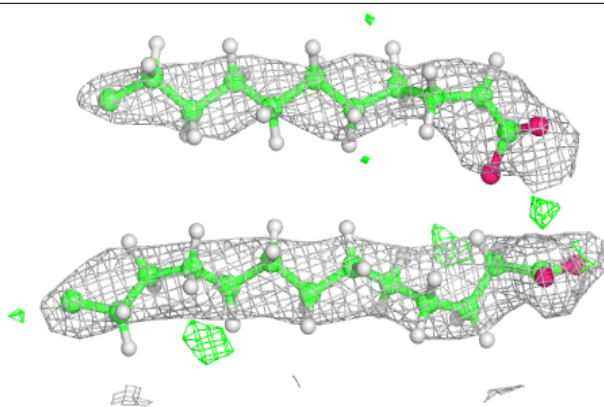
**Electron density around BCR k 101:**

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

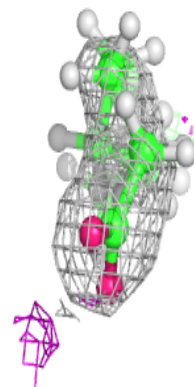
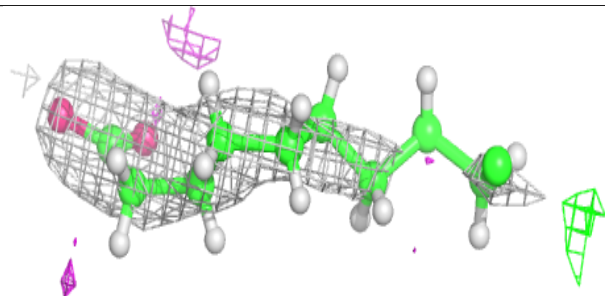
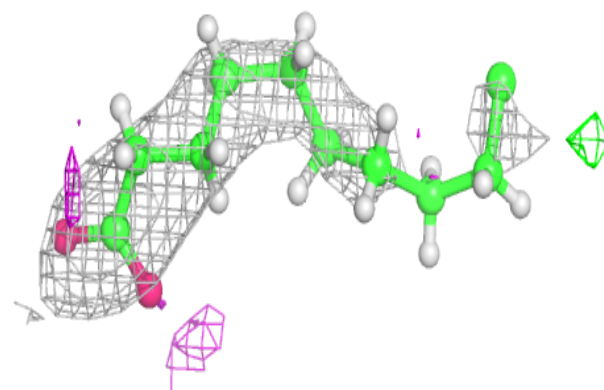


**Electron density around LMG D 411:**

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

**Electron density around STE B 627:**

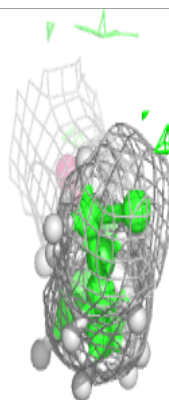
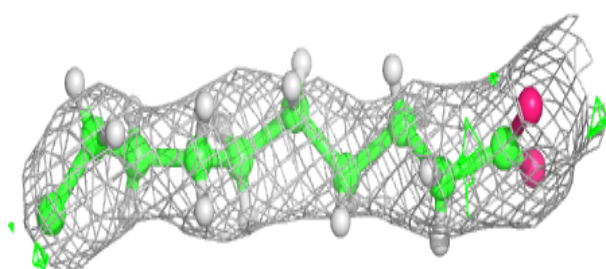
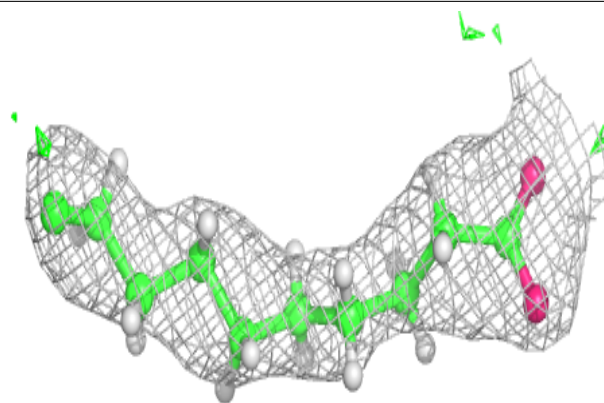
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



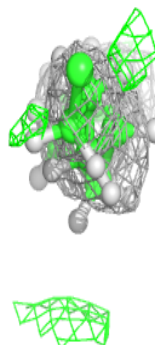
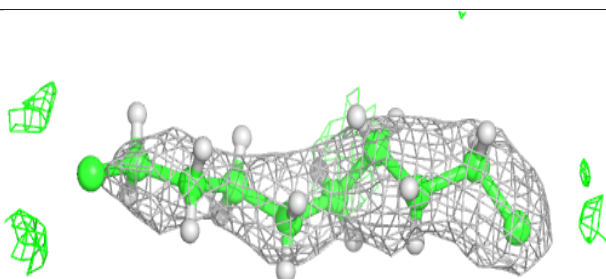
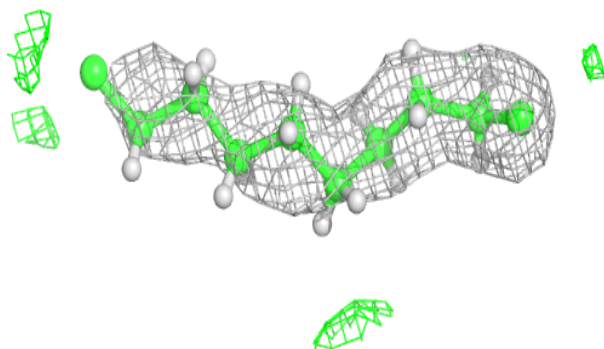


**Electron density around STE C 519:**

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

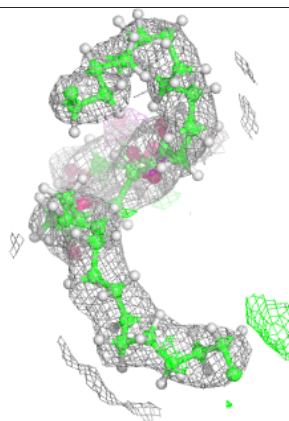
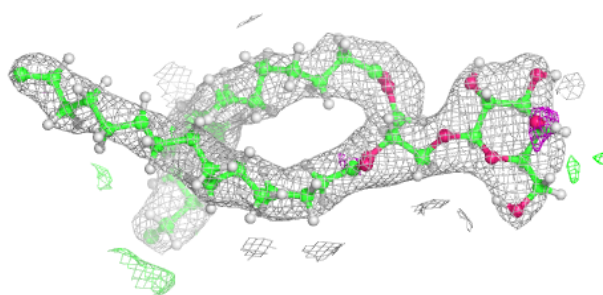
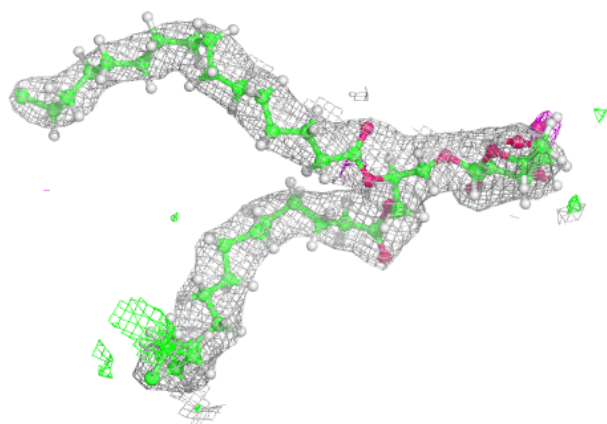
**Electron density around STE t 103:**

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

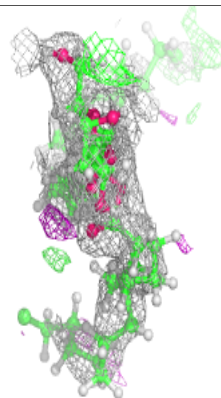
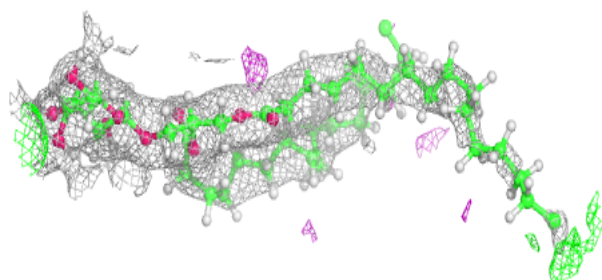
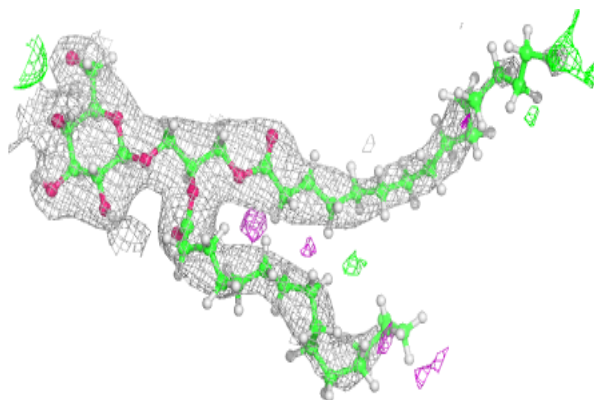


**Electron density around LMG M 101:**

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

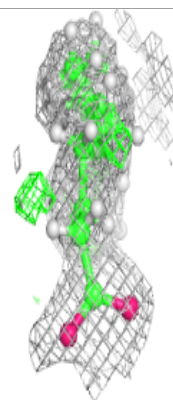
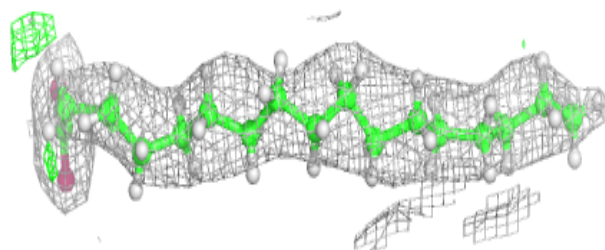
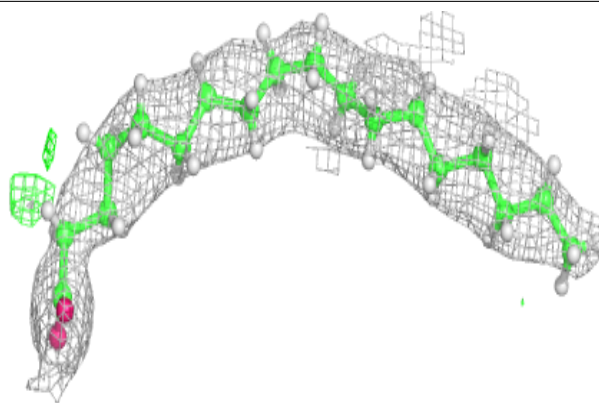
**Electron density around LMG D 408:**

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

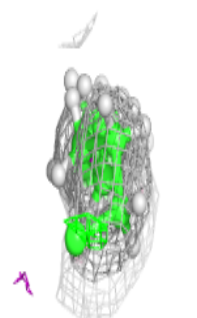
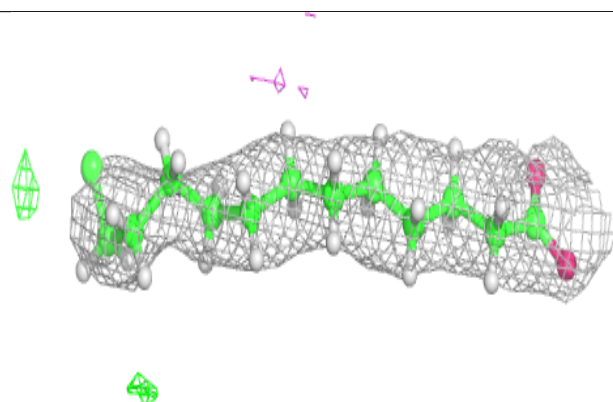
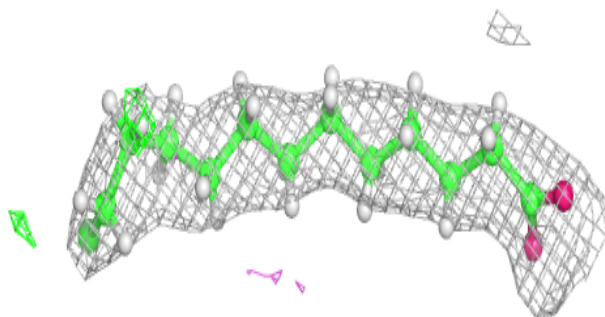


**Electron density around STE D 412:**

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

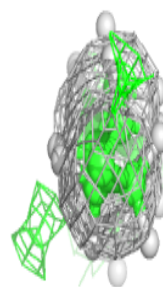
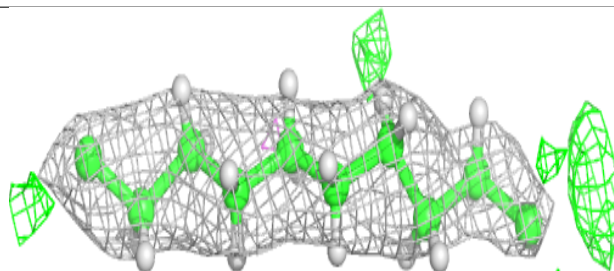
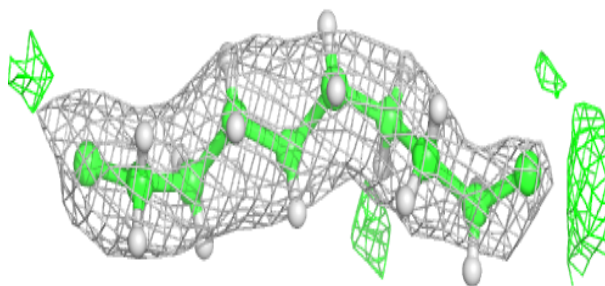
**Electron density around STE M 102:**

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

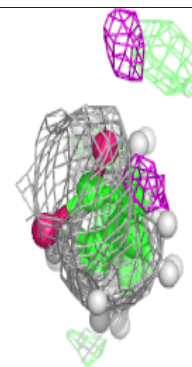
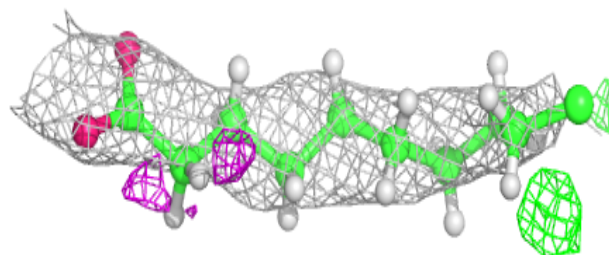
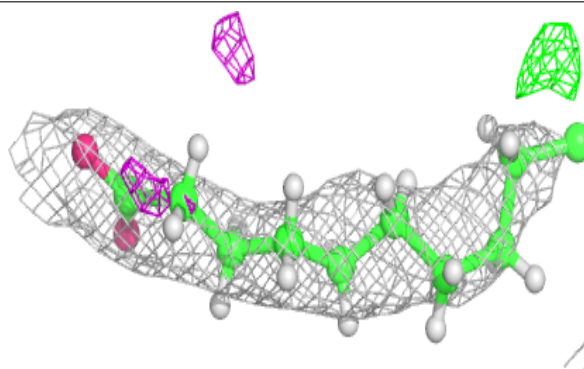


**Electron density around STE M 103:**

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

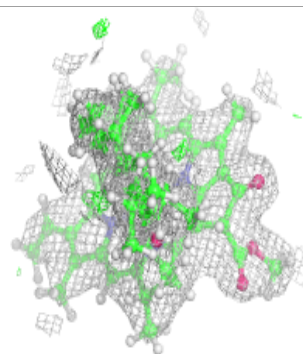
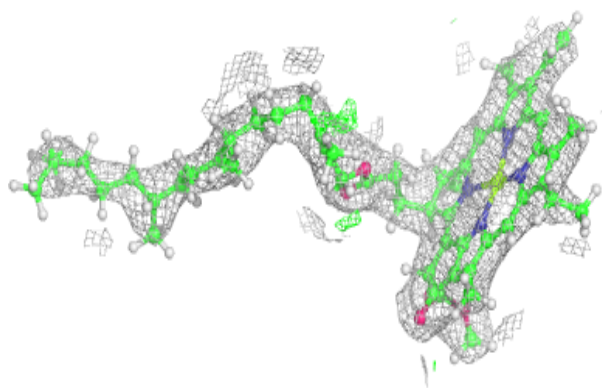
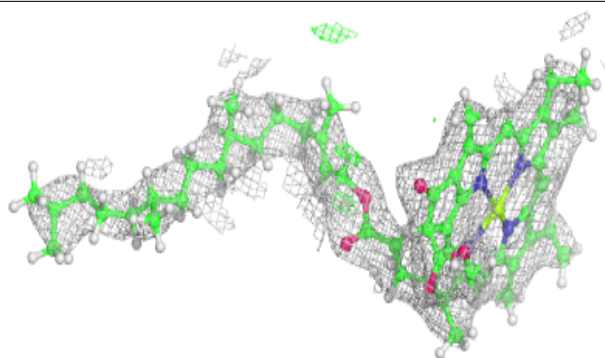
**Electron density around STE m 102:**

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

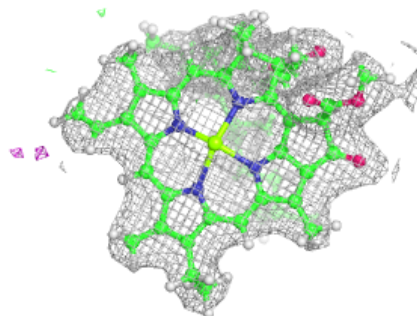
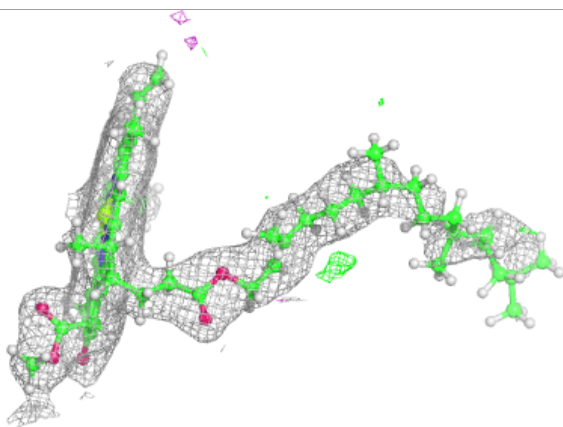
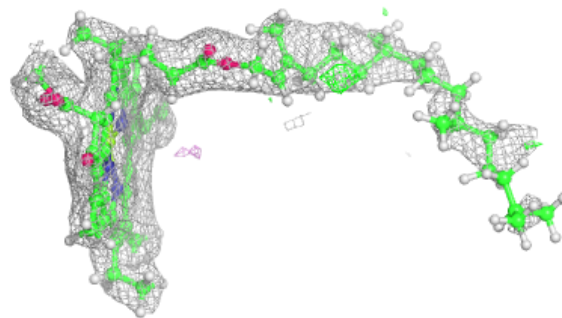


**Electron density around CLA c 502:**

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

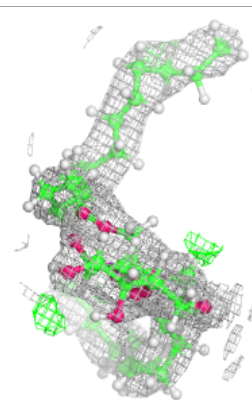
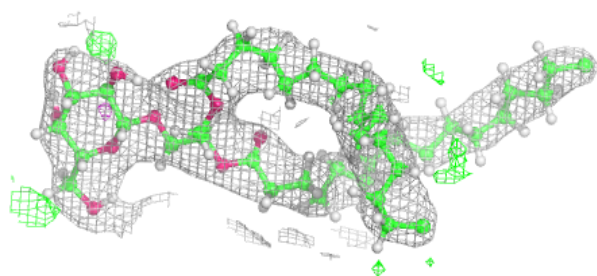
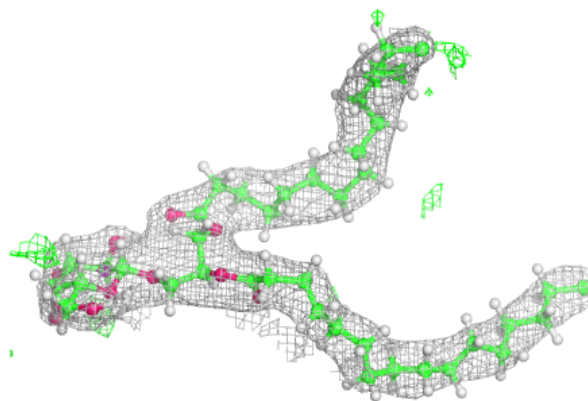
**Electron density around CLA D 405:**

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

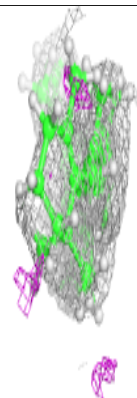
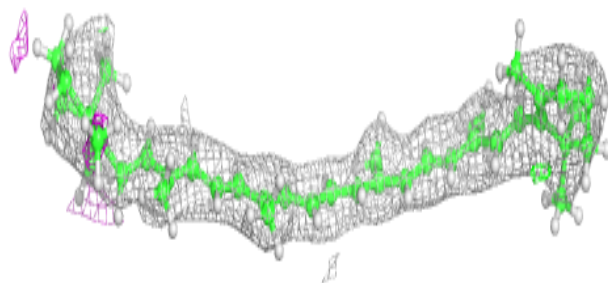
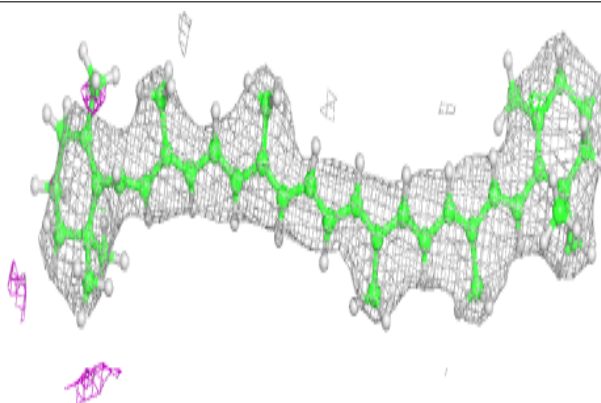


**Electron density around LMG m 101:**

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

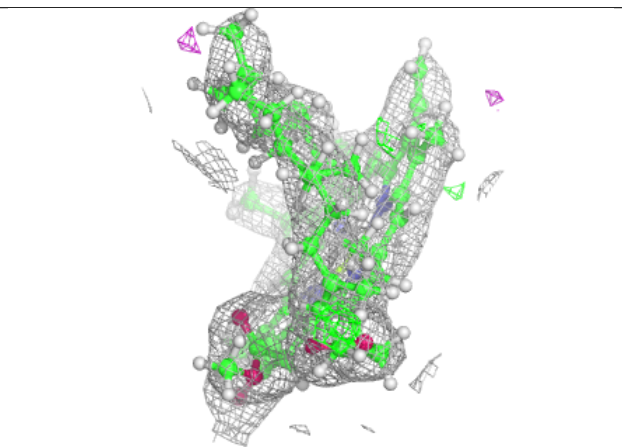
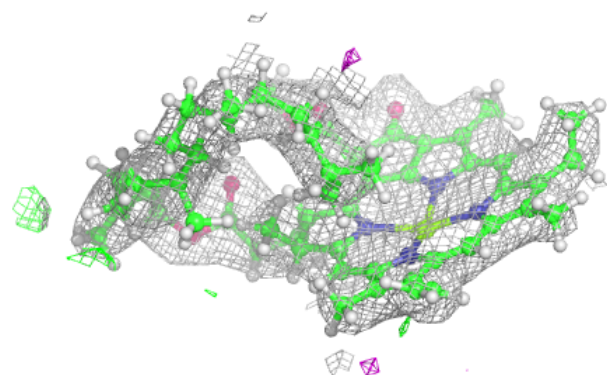
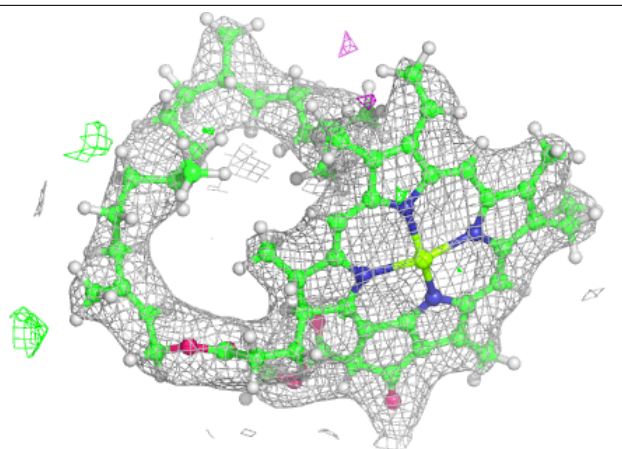
**Electron density around BCR D 406:**

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



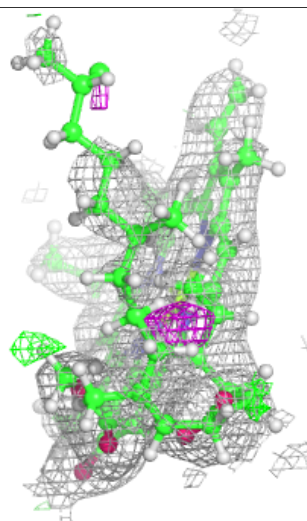
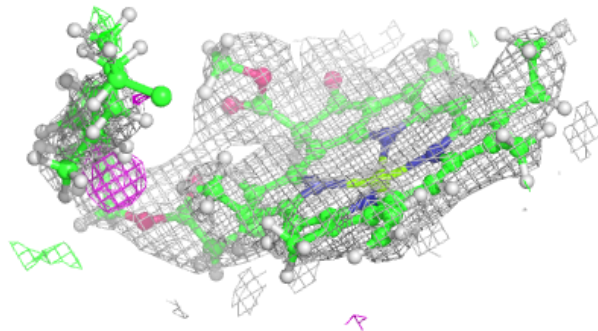
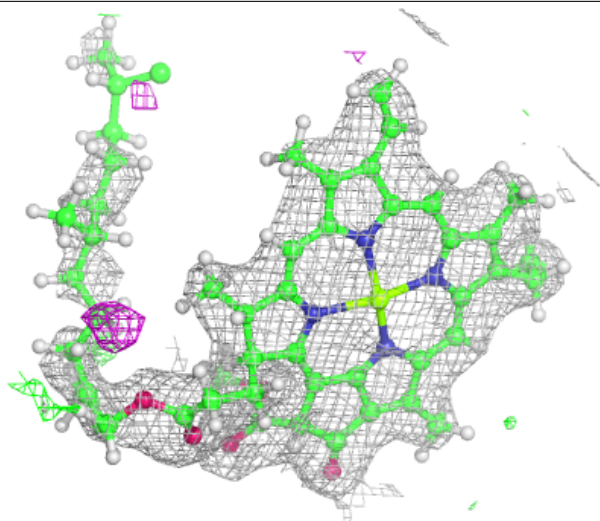
**Electron density around CLA B 615:**

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

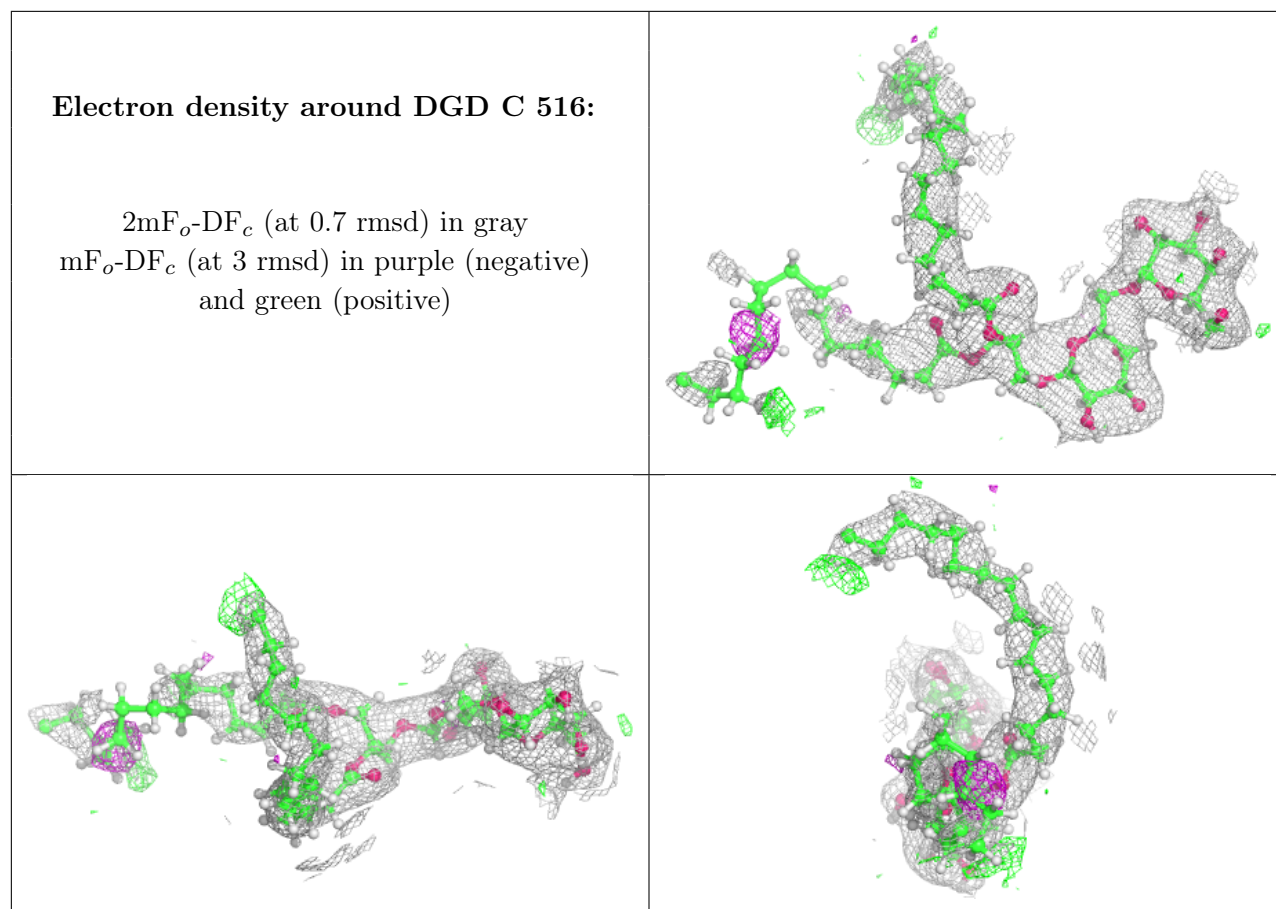


**Electron density around CLA B 616:**

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

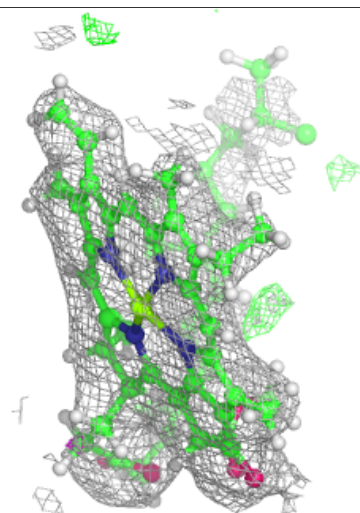
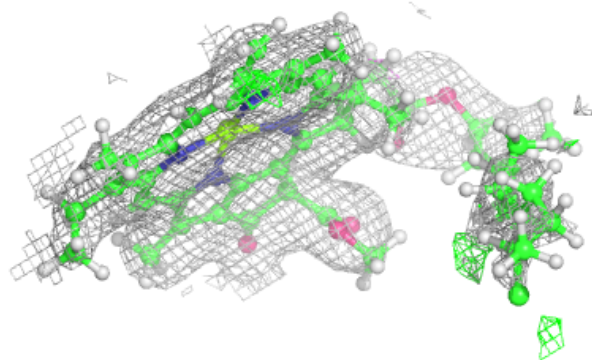
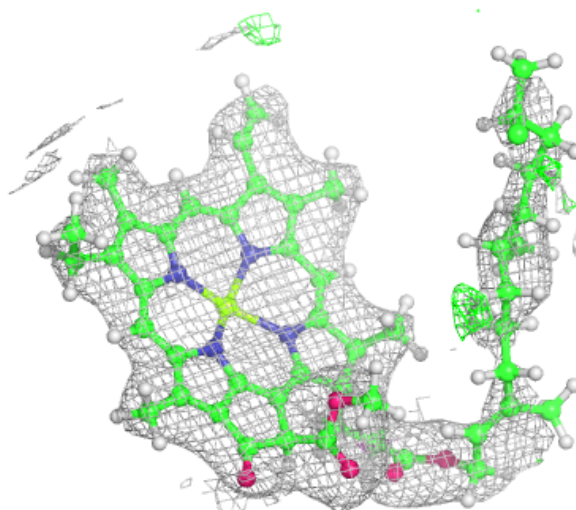






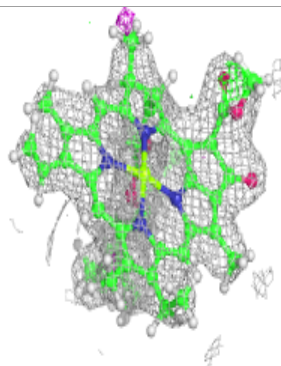
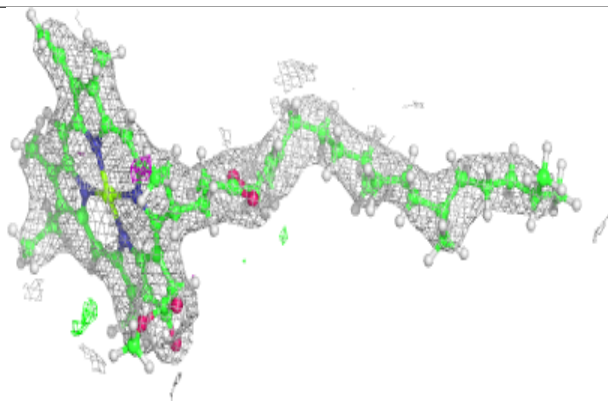
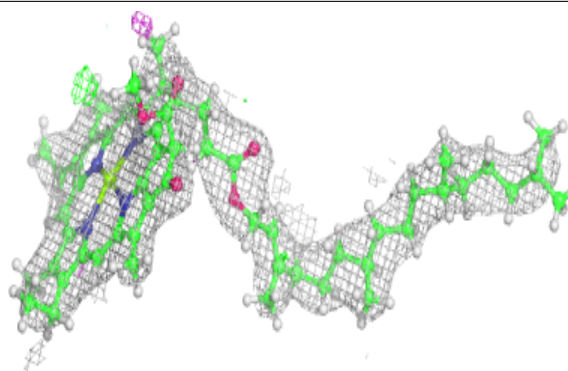
**Electron density around CLA b 616:**

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

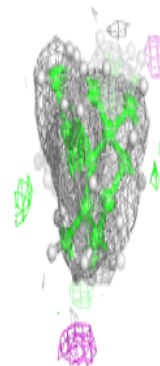
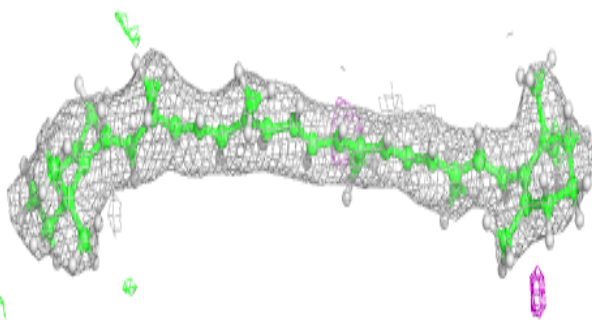
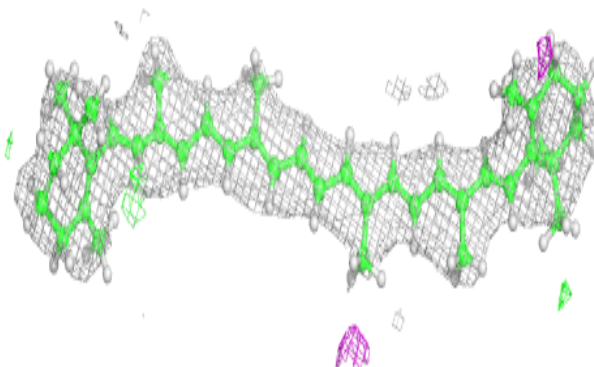


**Electron density around CLA C 502:**

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

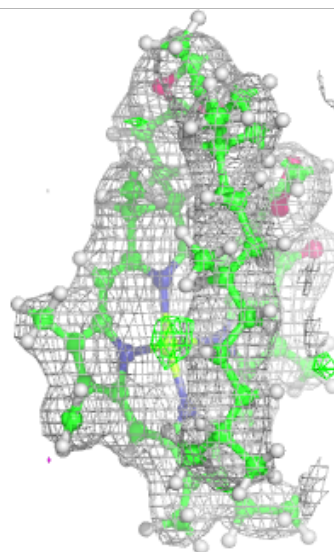
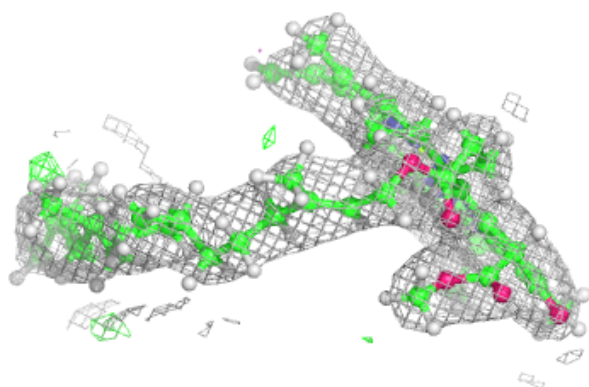
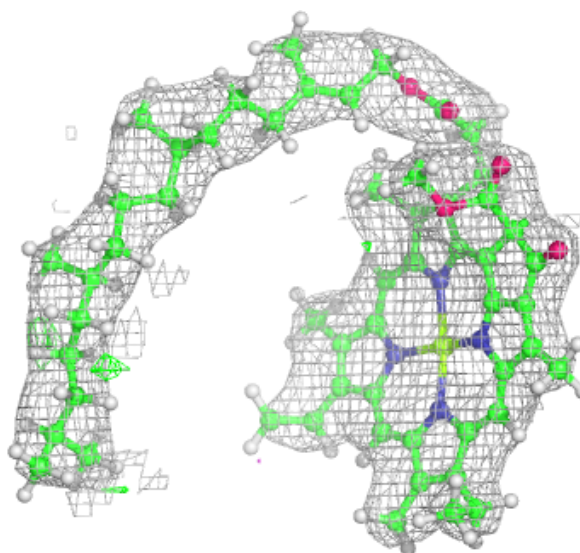
**Electron density around BCR B 619:**

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



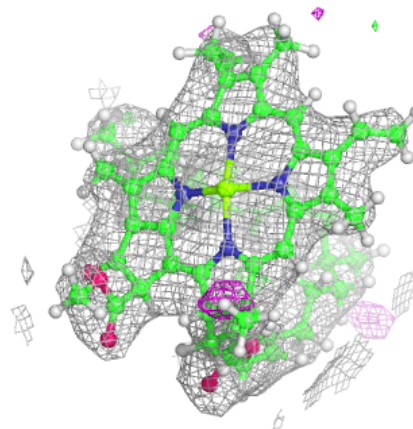
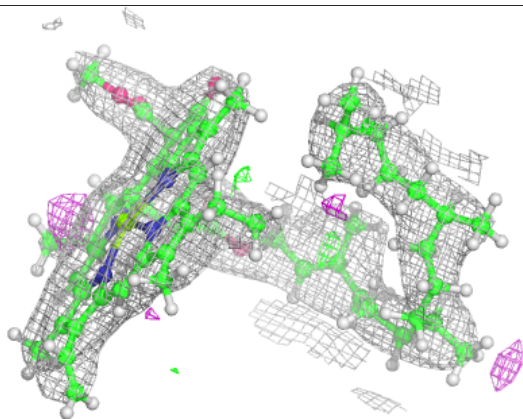
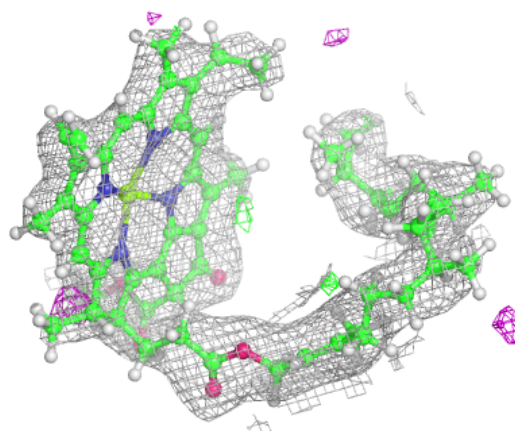
**Electron density around CLA C 507:**

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



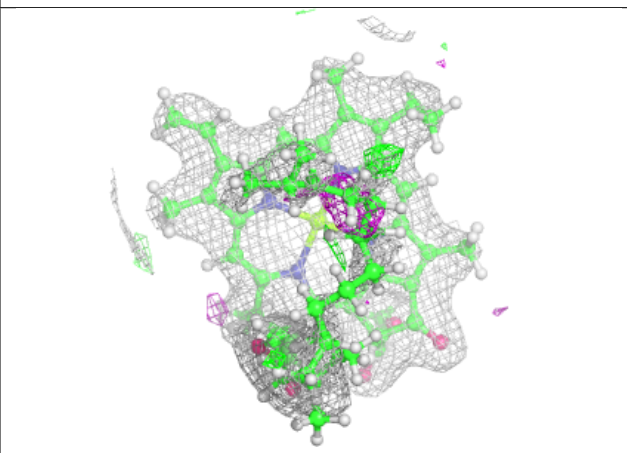
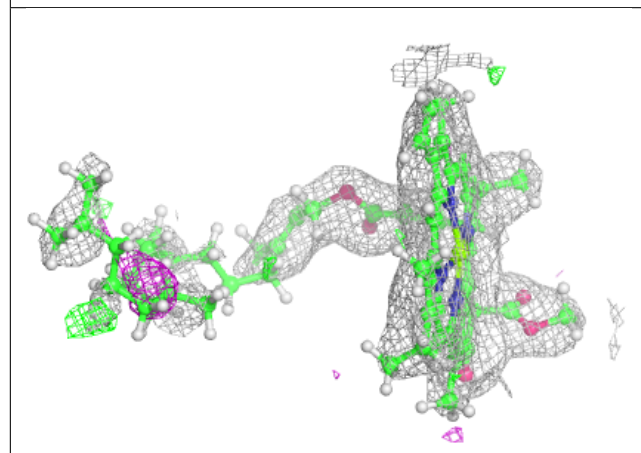
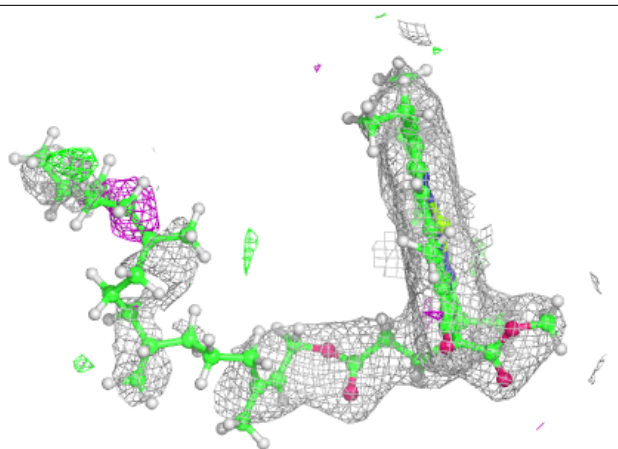
**Electron density around CLA c 503:**

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

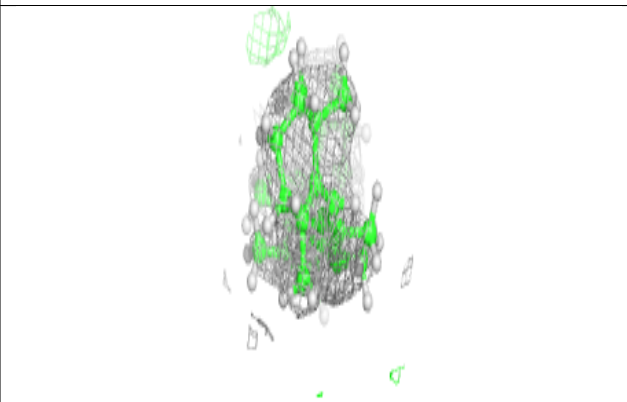
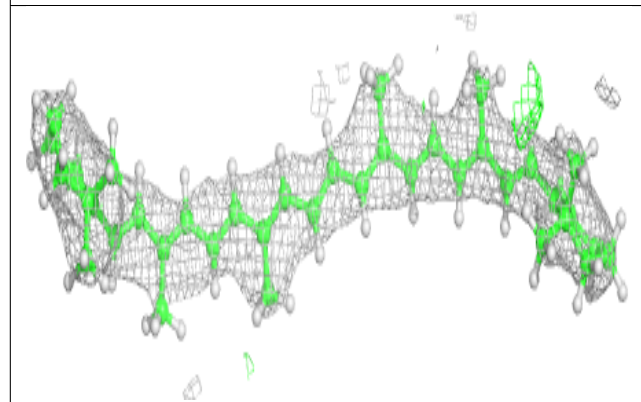
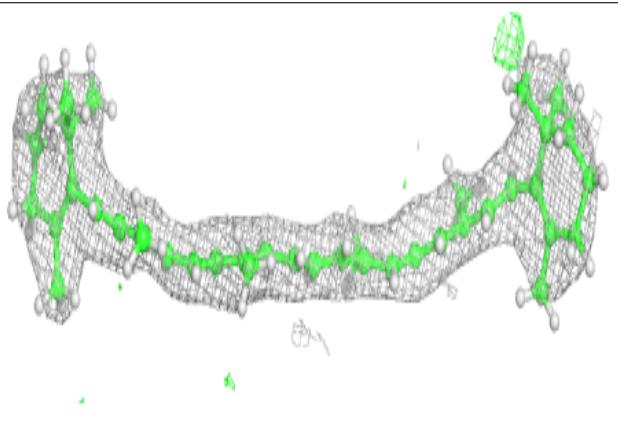


**Electron density around CLA c 506:**

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

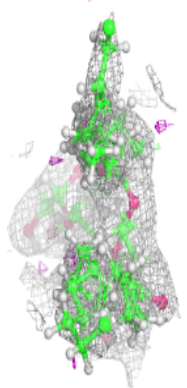
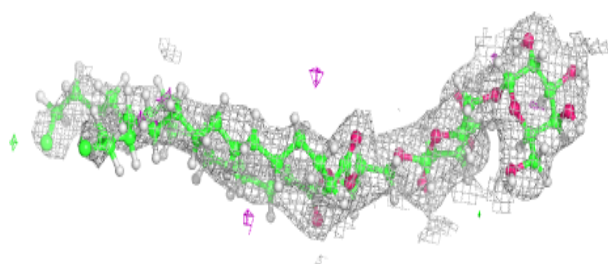
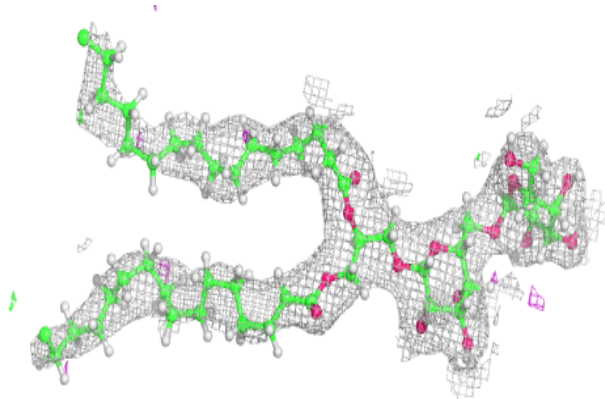
**Electron density around BCR K 102:**

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

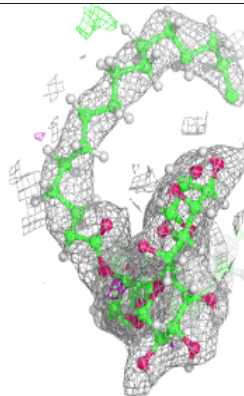
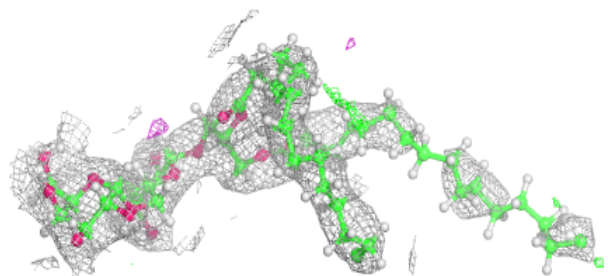
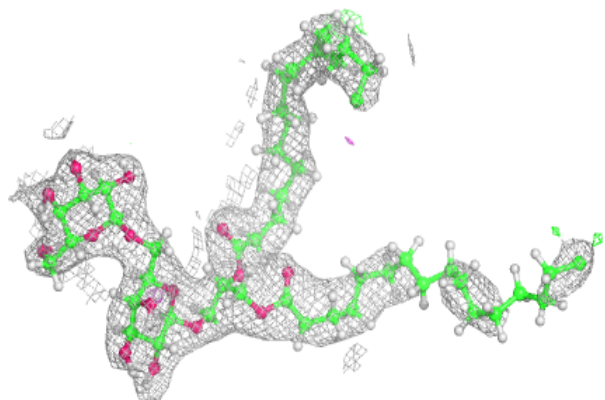


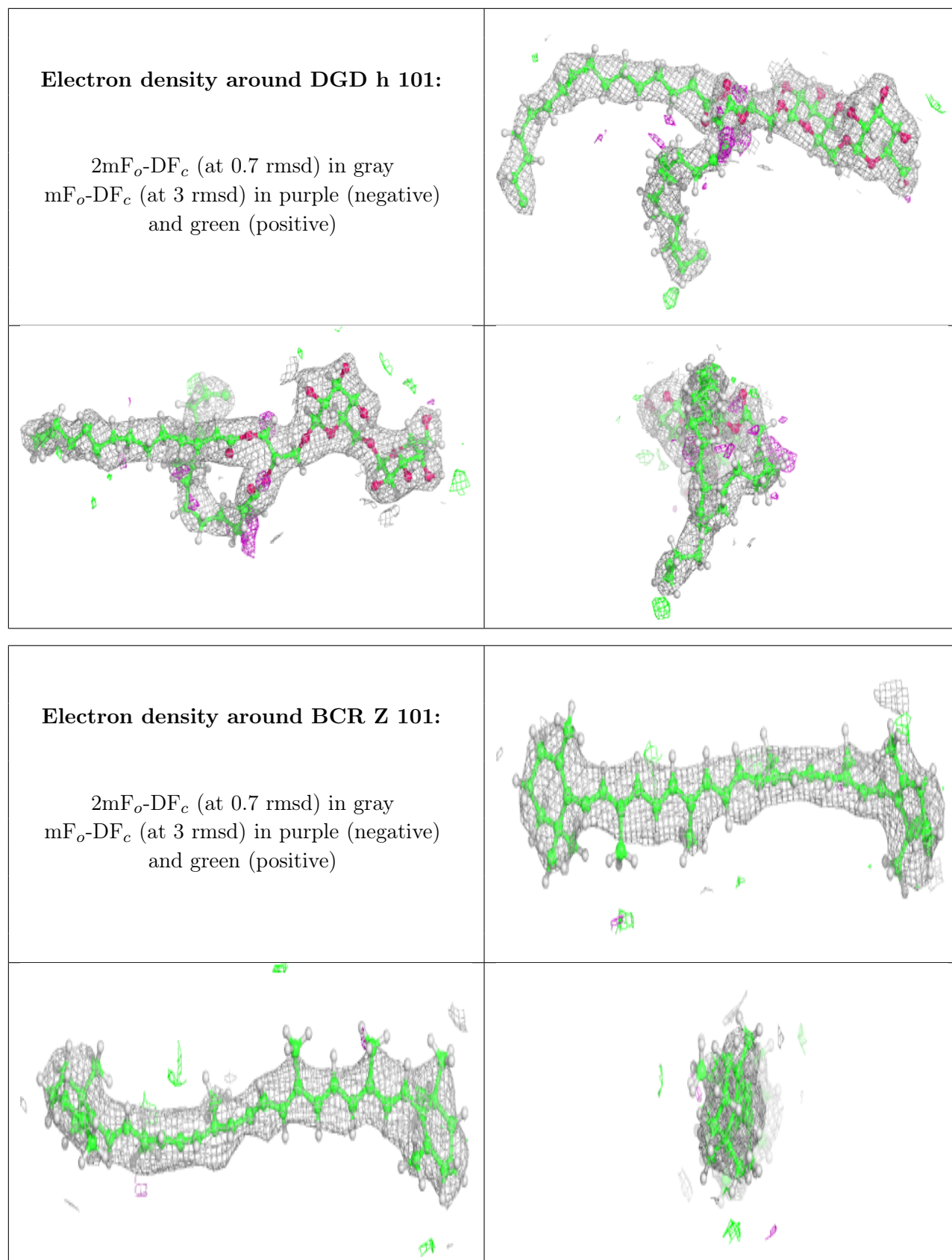
**Electron density around DGD C 517:**

$2mF_o-DF_c$  (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:**

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

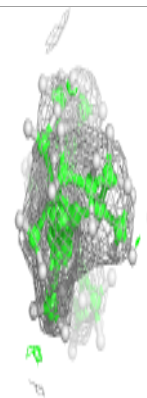
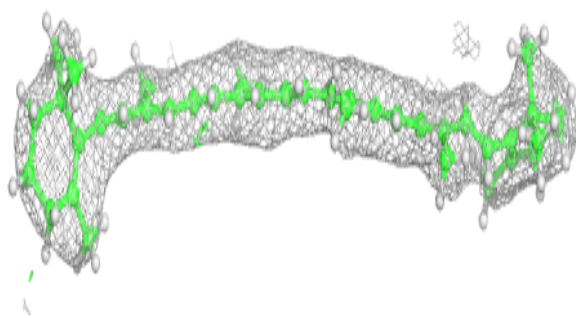
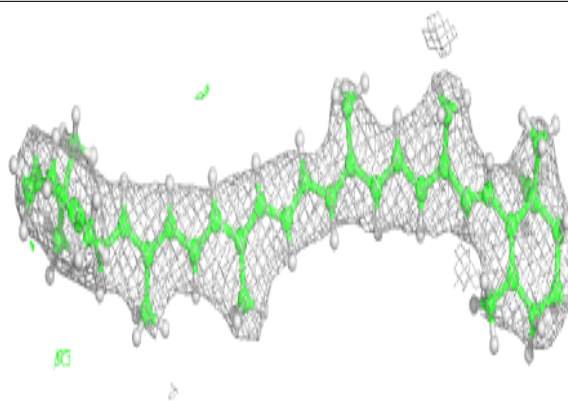




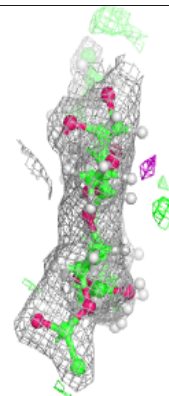
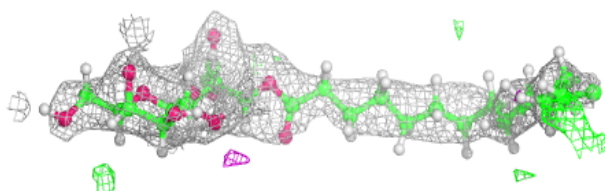
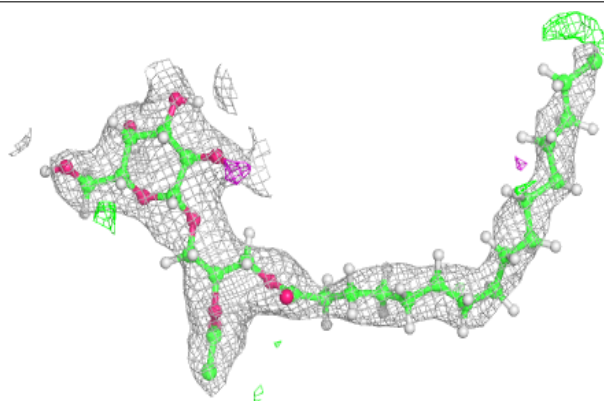


**Electron density around BCR b 617:**

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

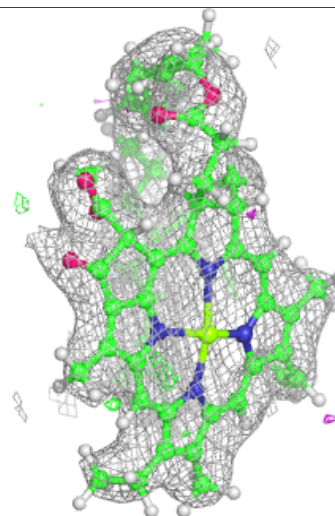
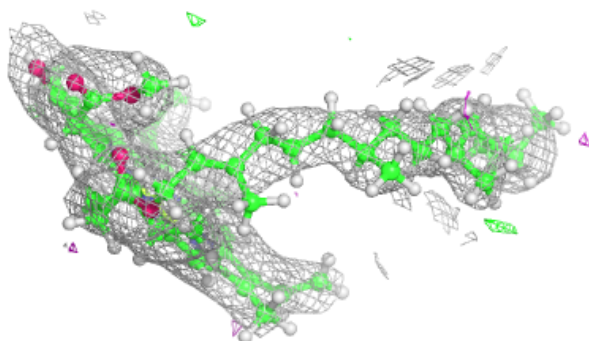
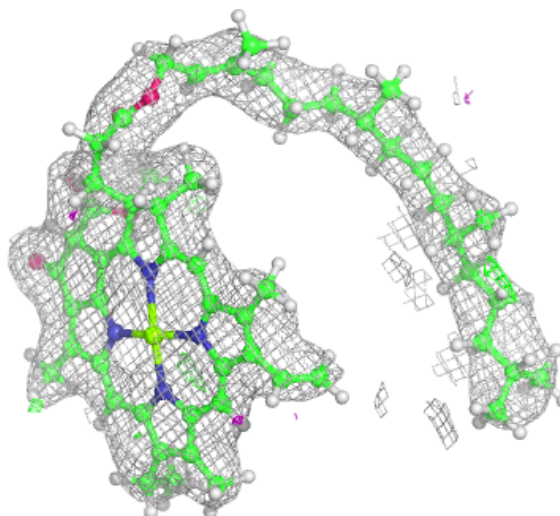
**Electron density around LMG c 518:**

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



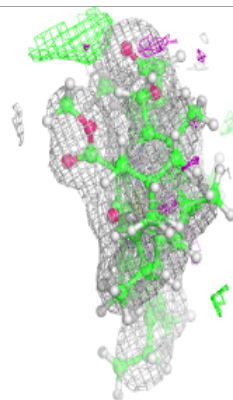
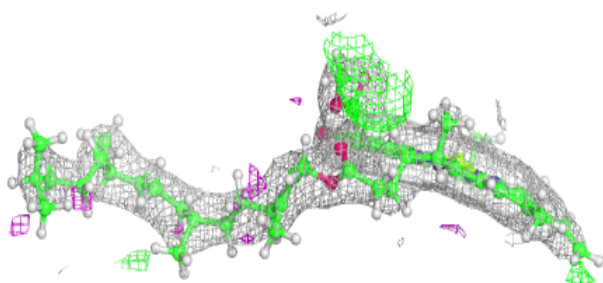
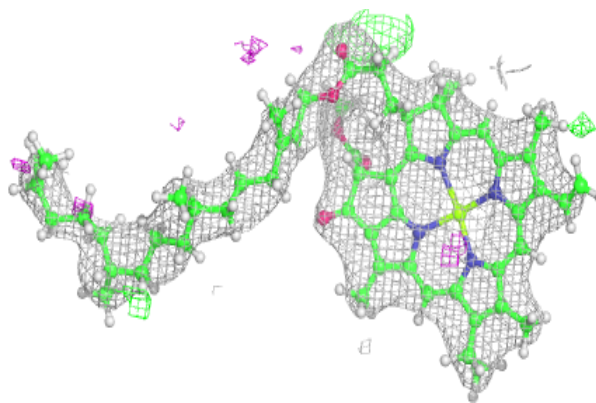
**Electron density around CLA c 507:**

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

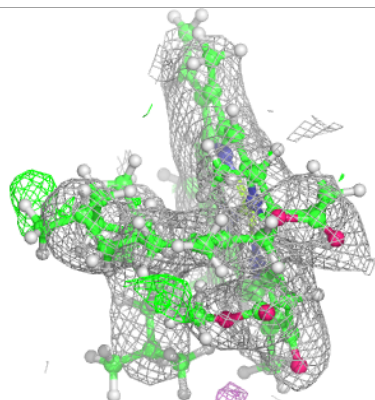
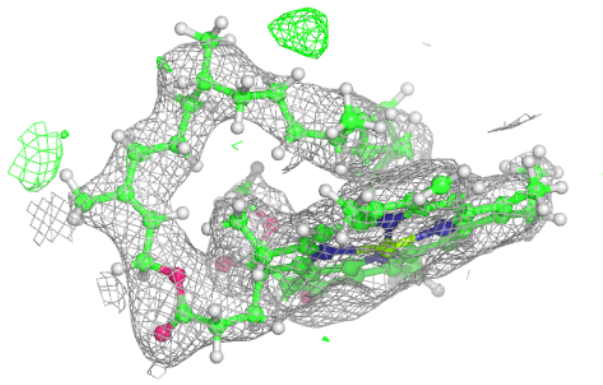
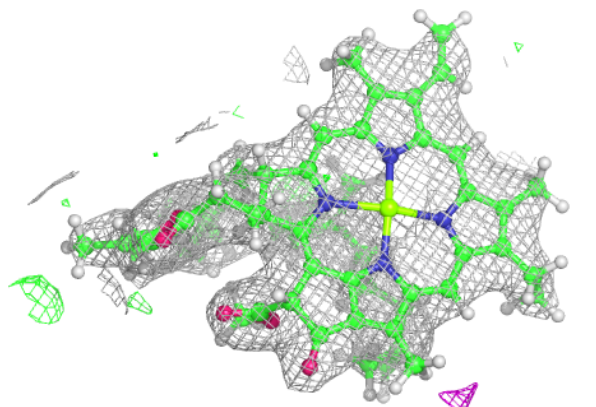


**Electron density around CLA b 602:**

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

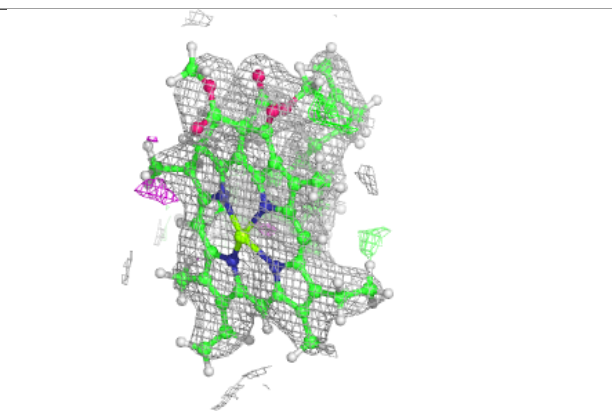
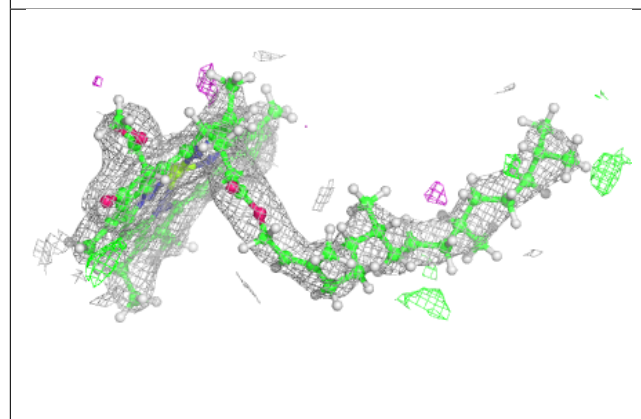
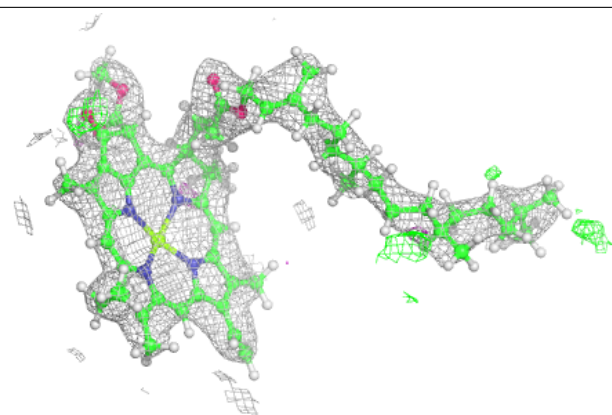
**Electron density around CLA c 510:**

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

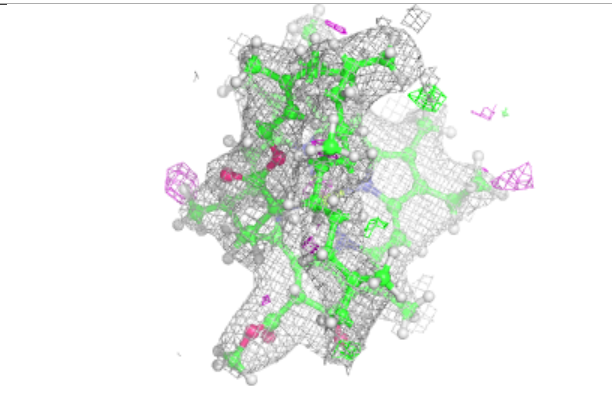
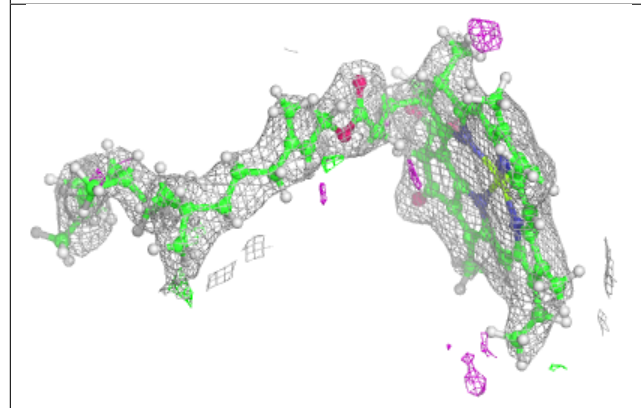
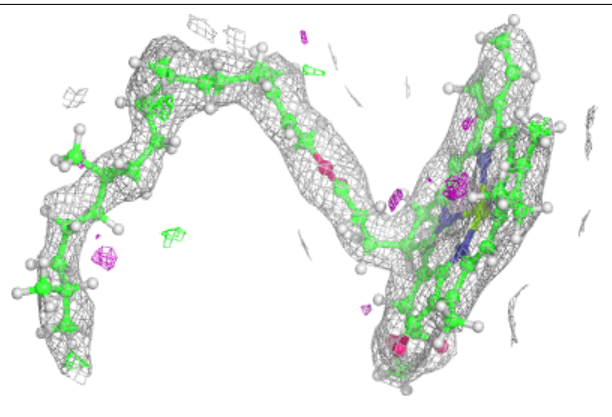


**Electron density around CLA c 511:**

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

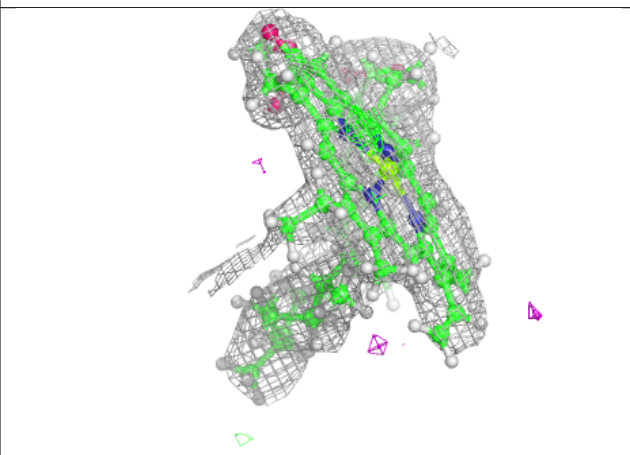
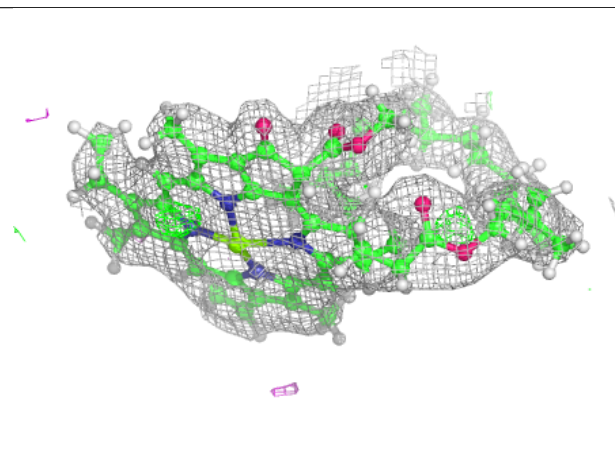
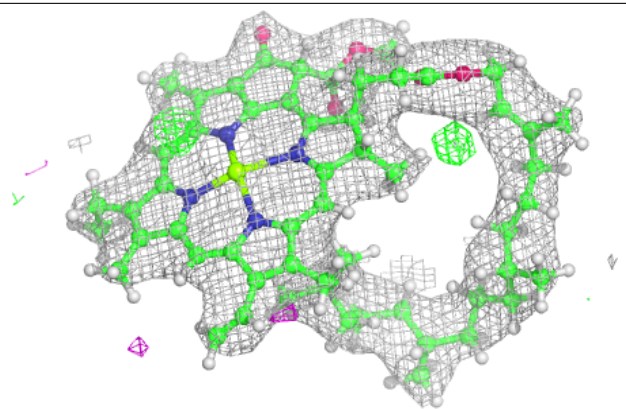
**Electron density around CLA b 606:**

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

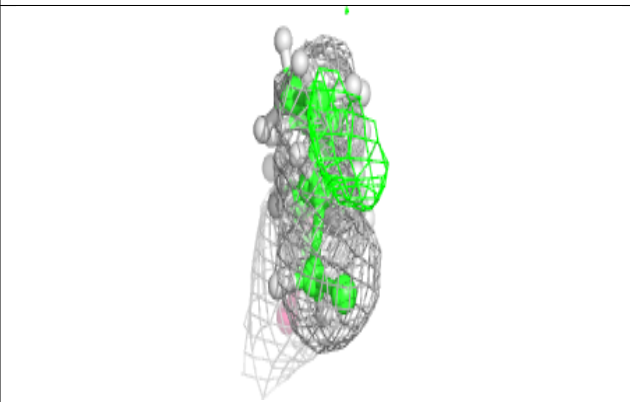
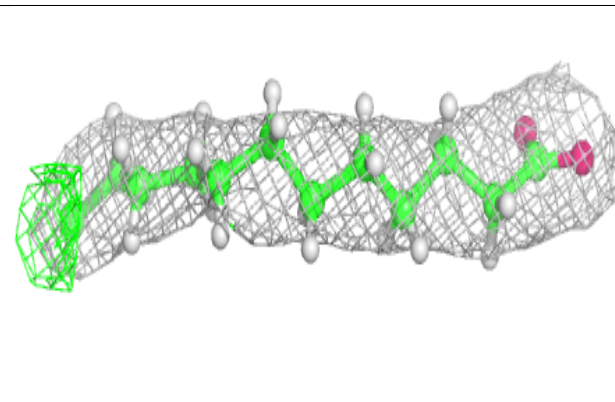
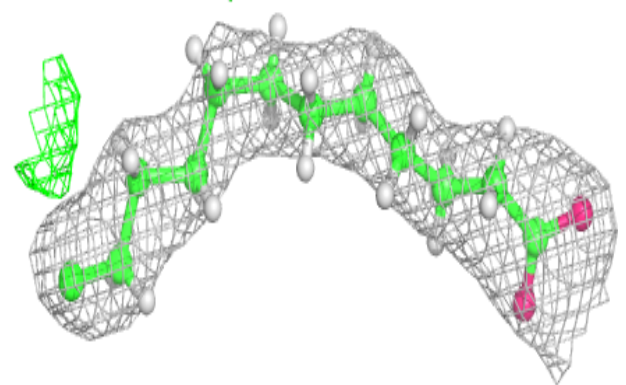


**Electron density around CLA b 615:**

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

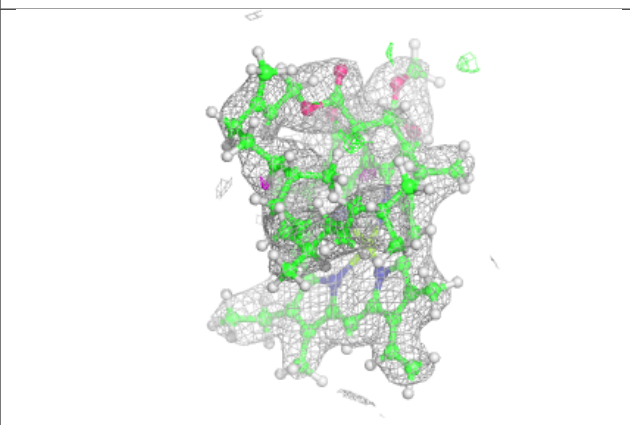
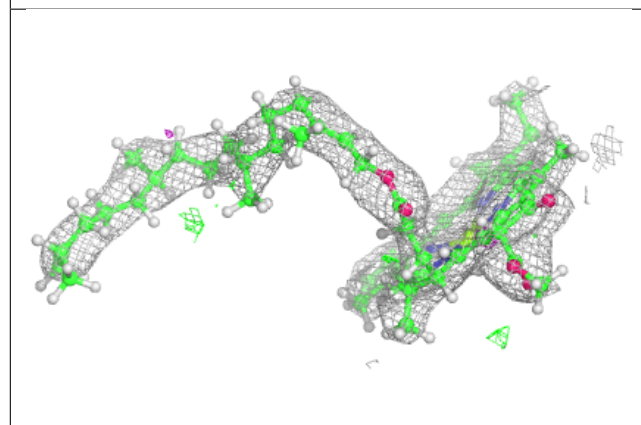
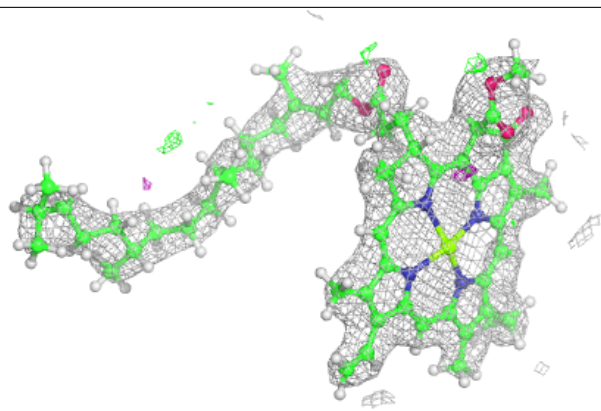
**Electron density around STE t 102:**

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

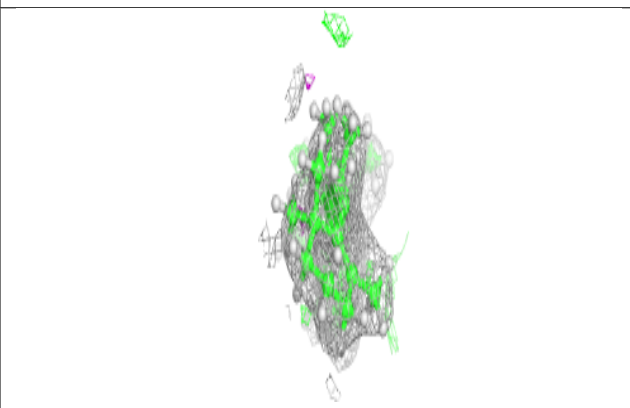
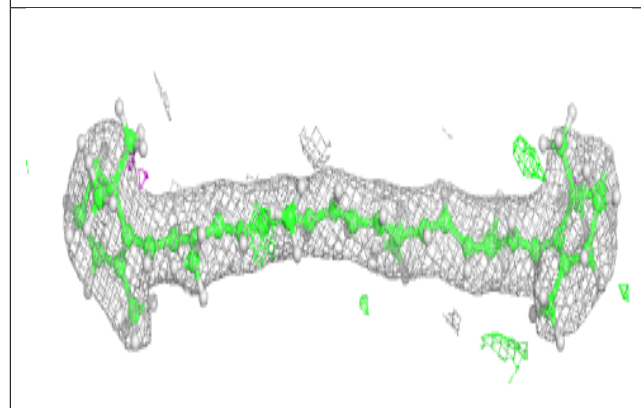
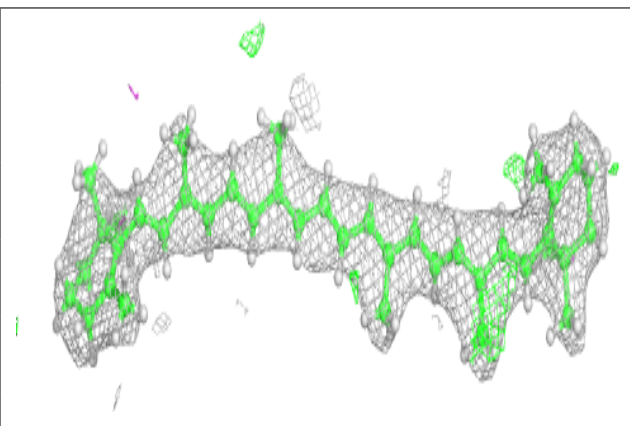


**Electron density around CLA C 511:**

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

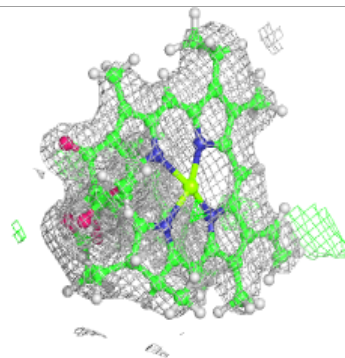
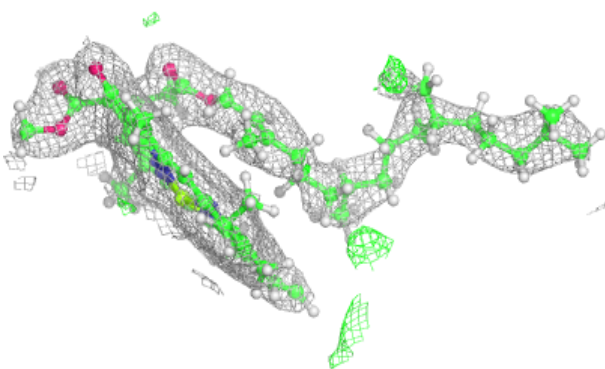
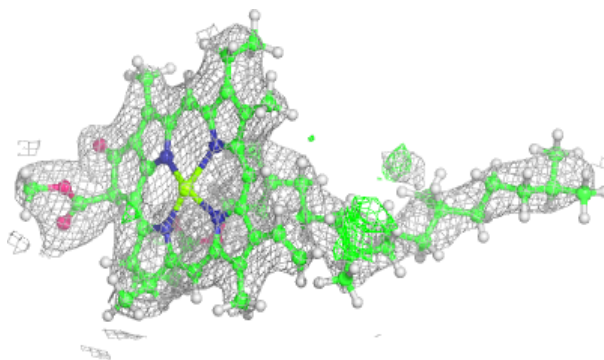
**Electron density around BCR B 618:**

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

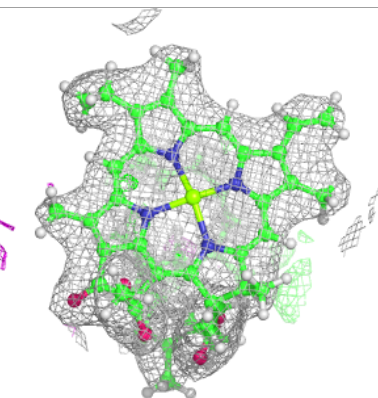
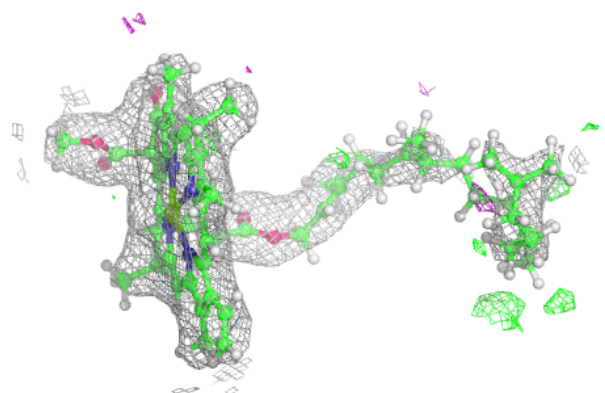
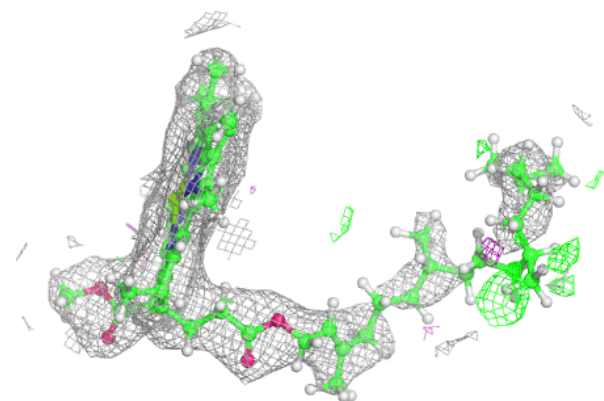


**Electron density around CLA C 505:**

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

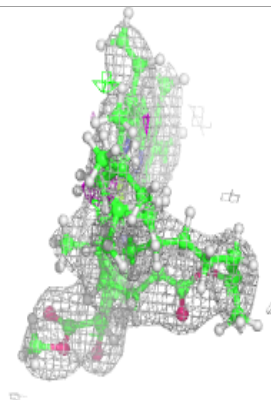
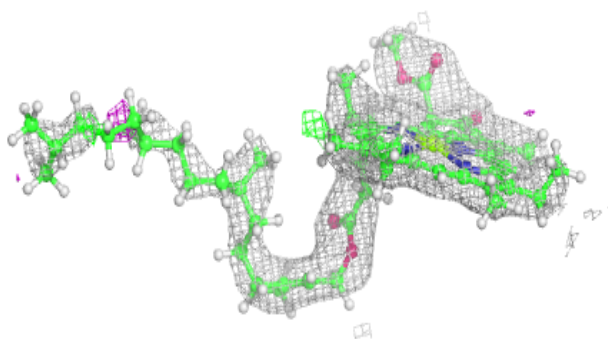
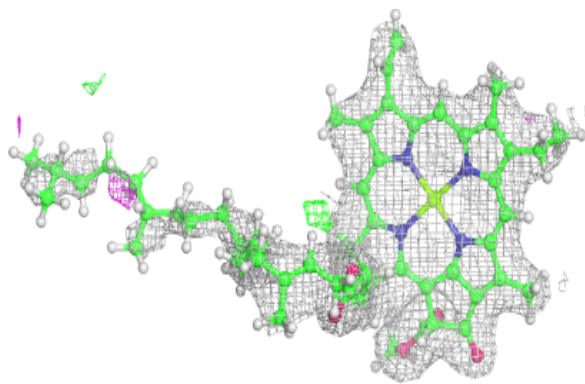
**Electron density around CLA C 506:**

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

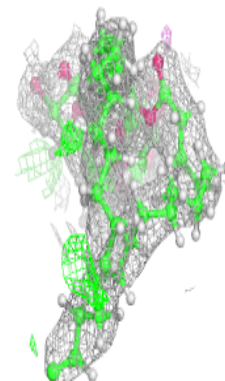
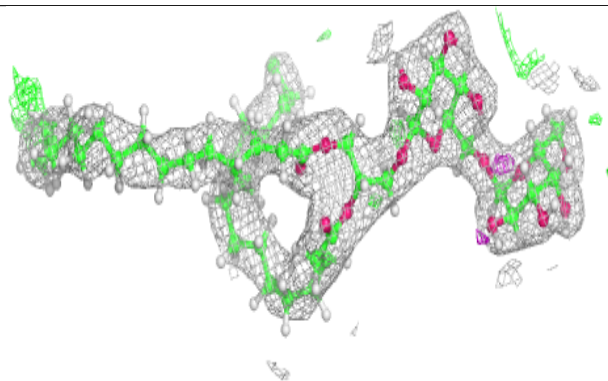
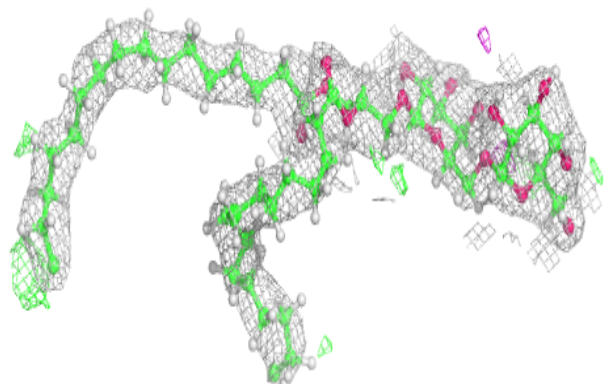


**Electron density around CLA a 403:**

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

**Electron density around DGD H 102:**

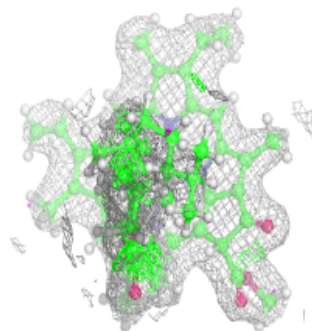
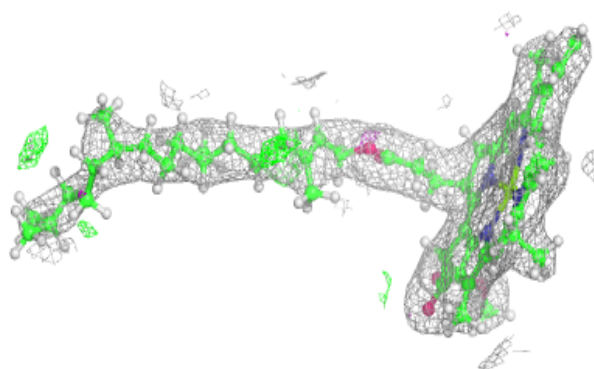
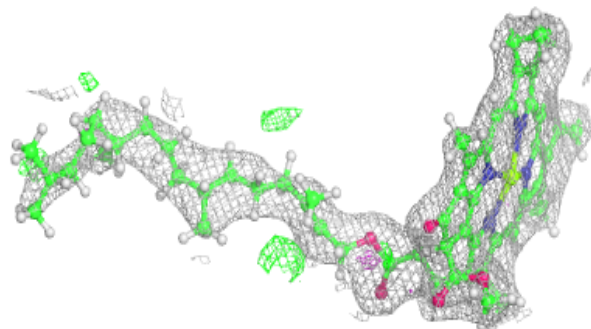
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



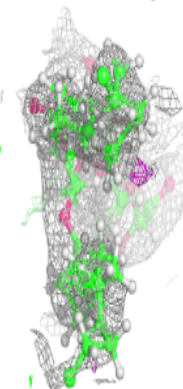
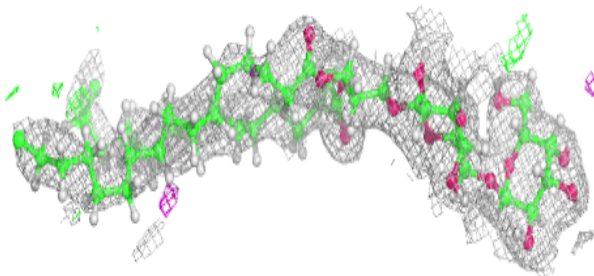
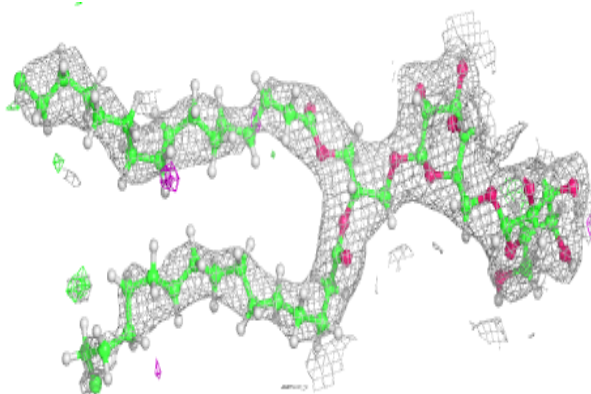


**Electron density around CLA B 604:**

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

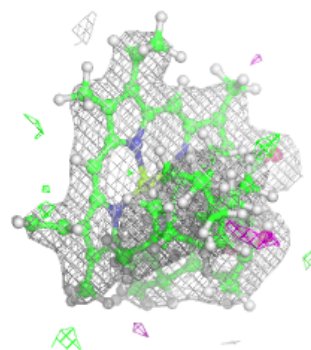
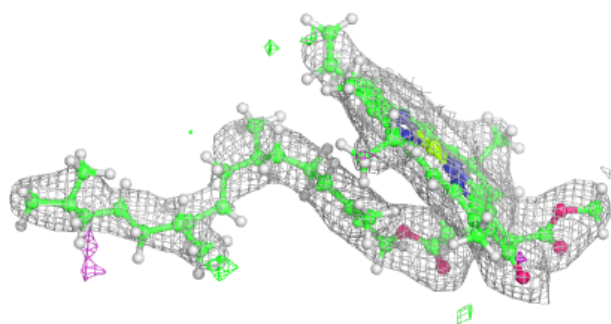
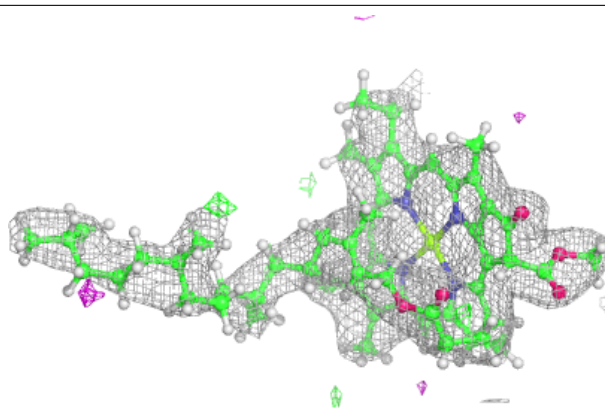
**Electron density around DGD c 517:**

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

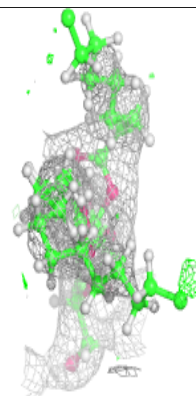
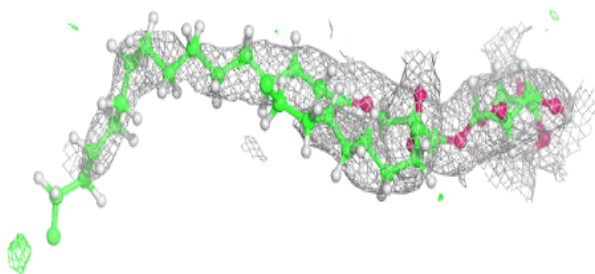
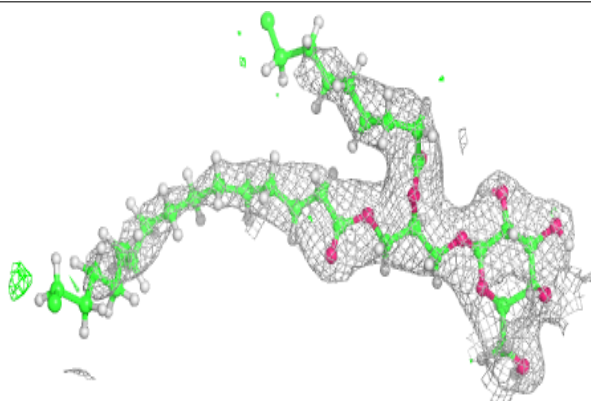


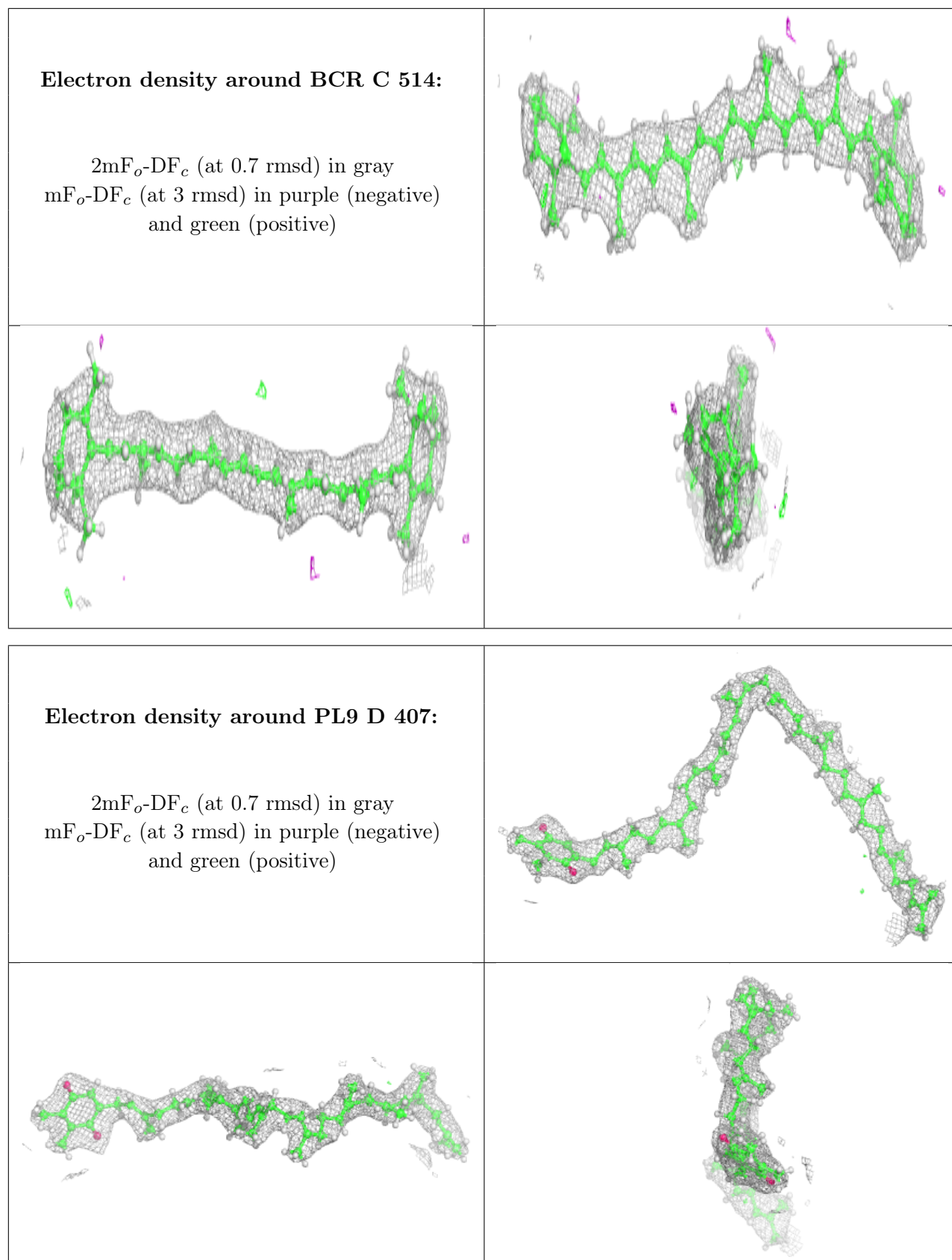
**Electron density around CLA c 505:**

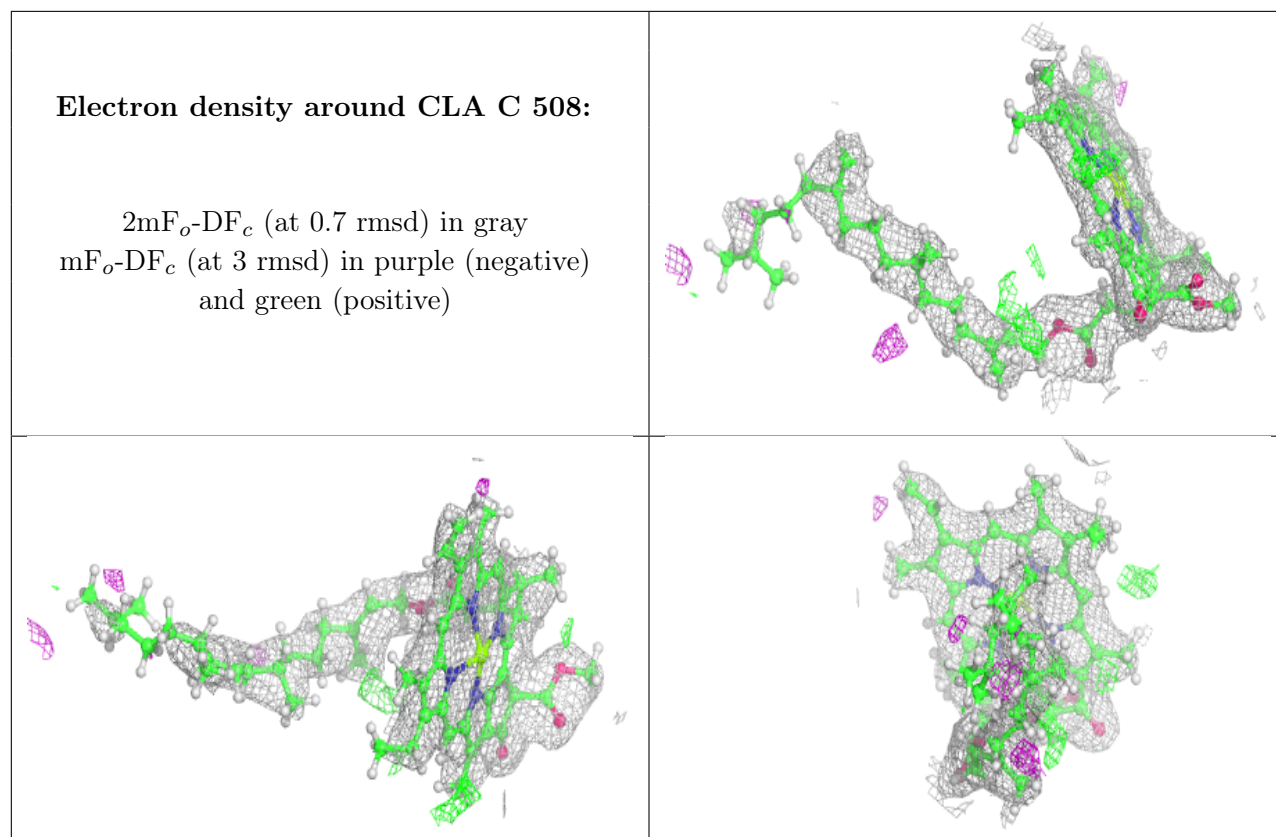
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

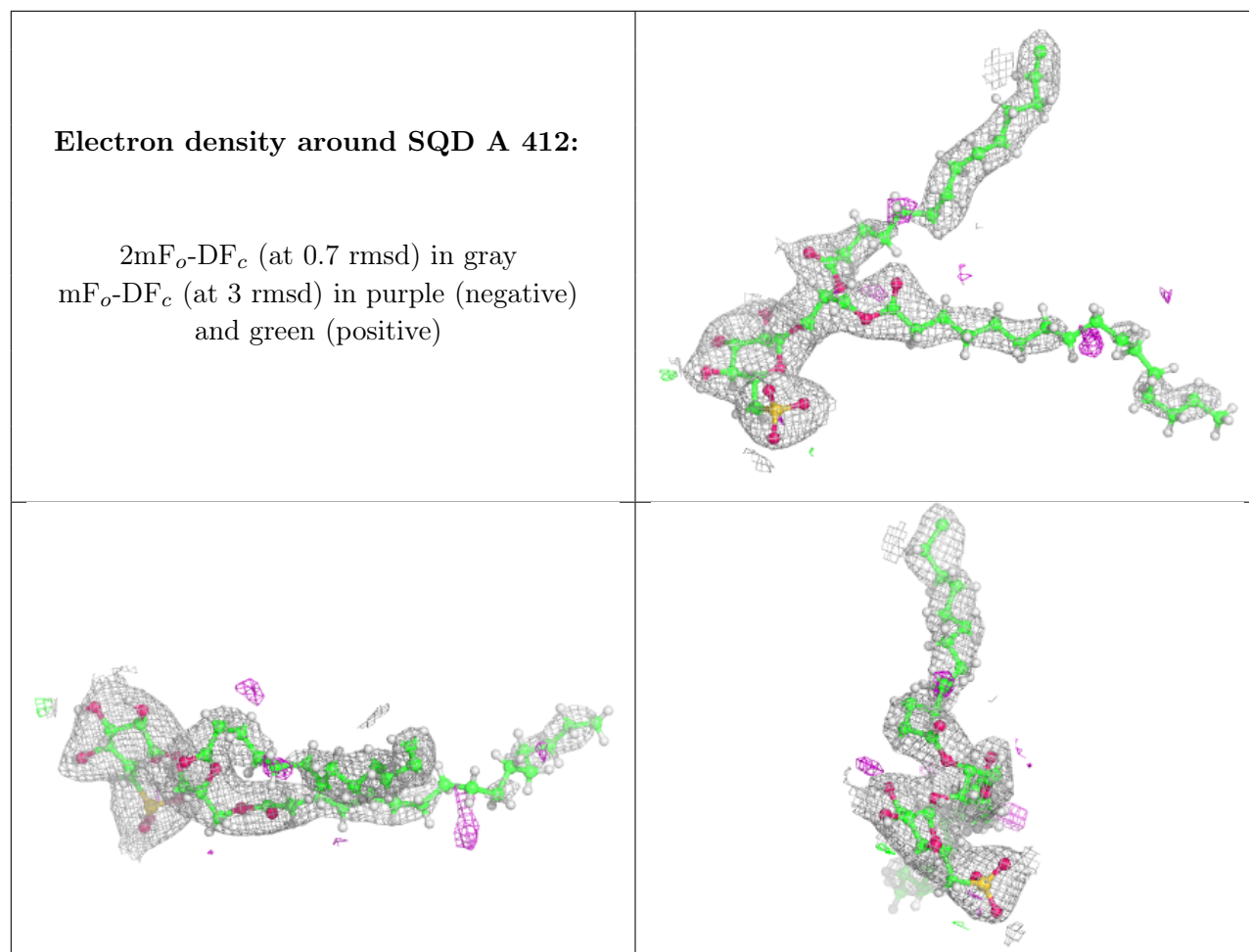
**Electron density around LMG d 409:**

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



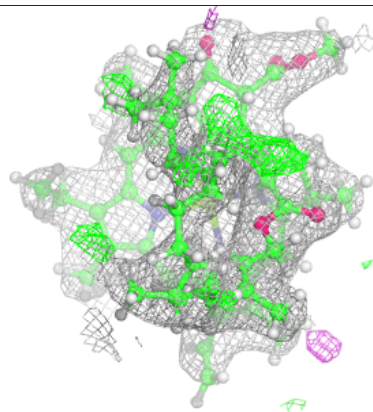
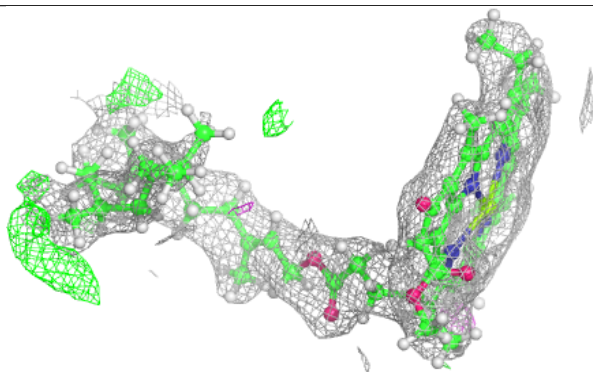
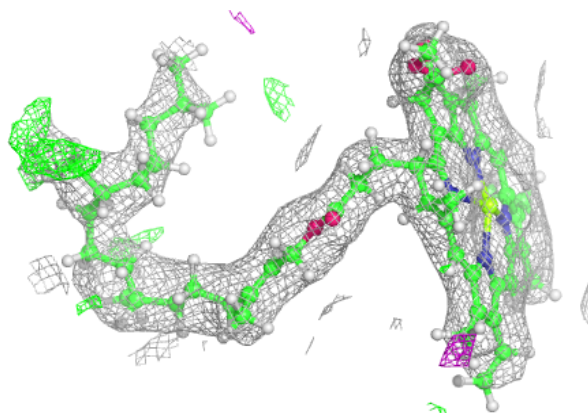




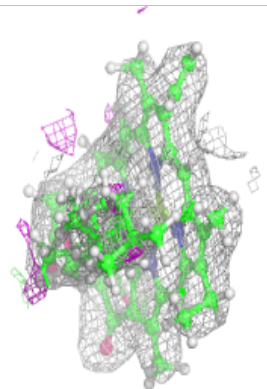
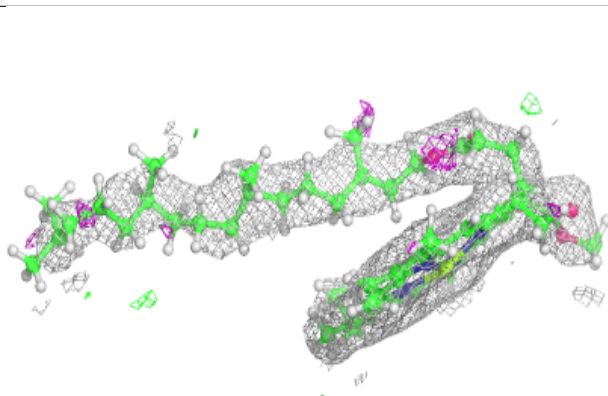
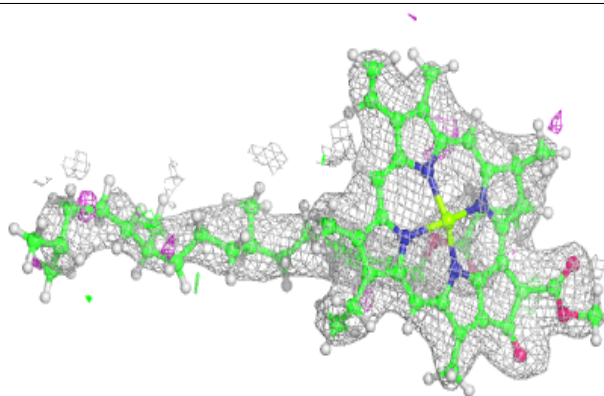


**Electron density around CLA B 606:**

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

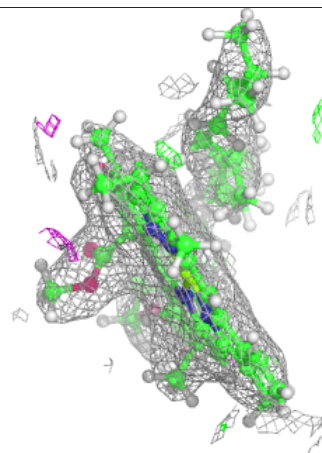
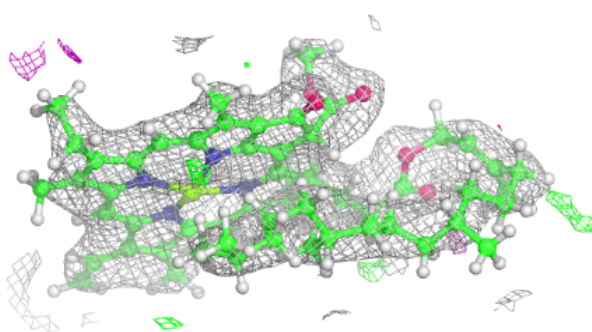
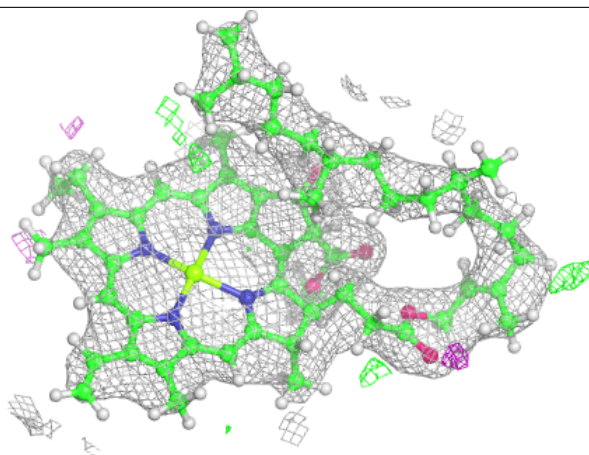
**Electron density around CLA B 614:**

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



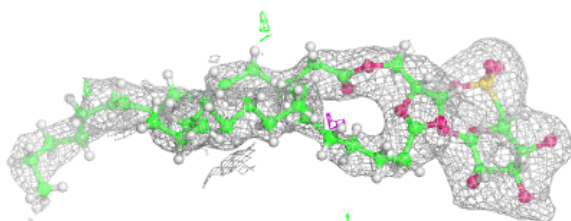
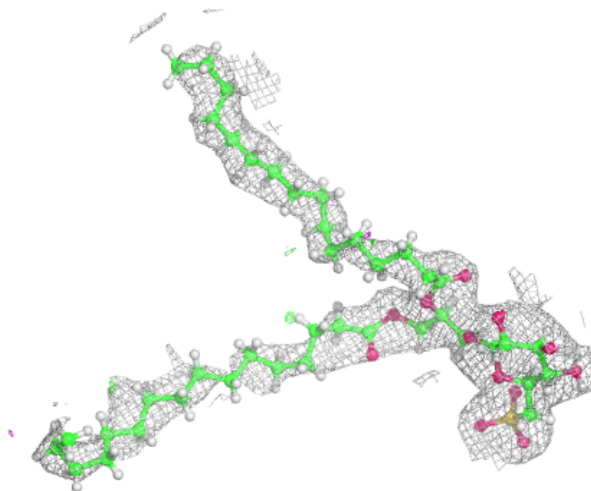
**Electron density around CLA c 509:**

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



**Electron density around SQD a 412:**

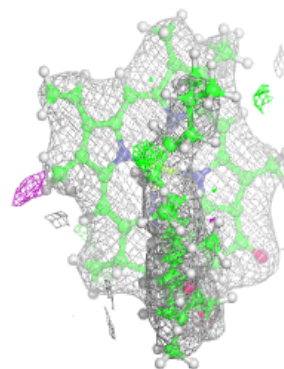
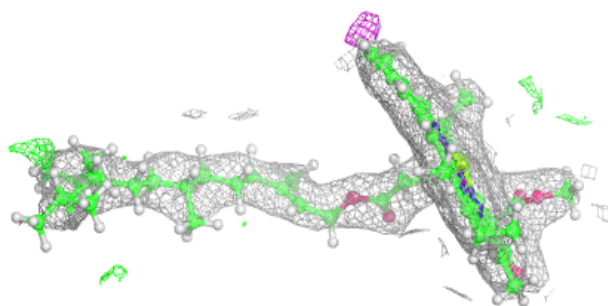
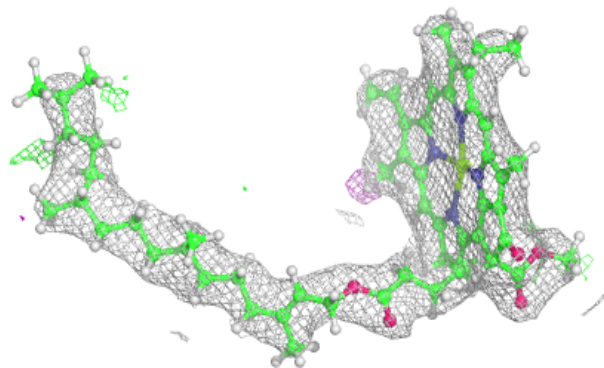
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



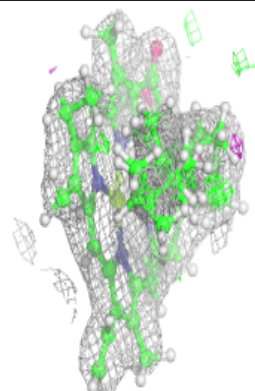
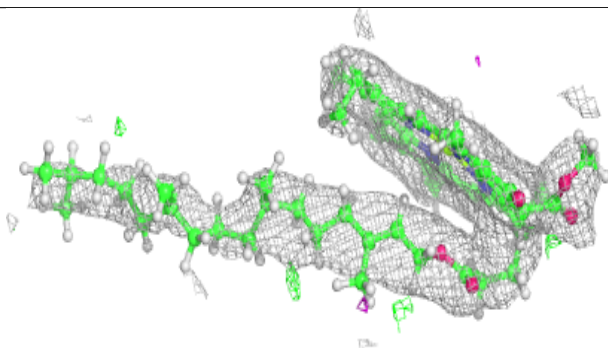
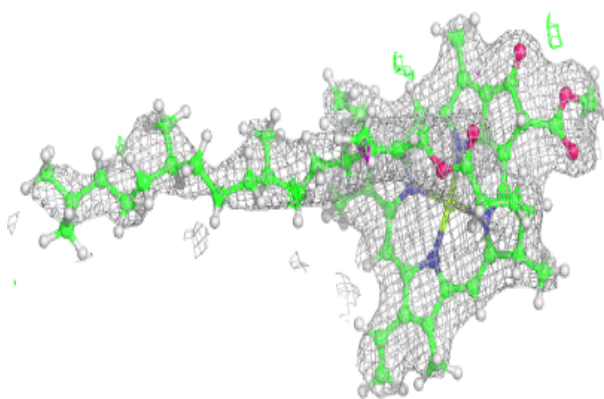


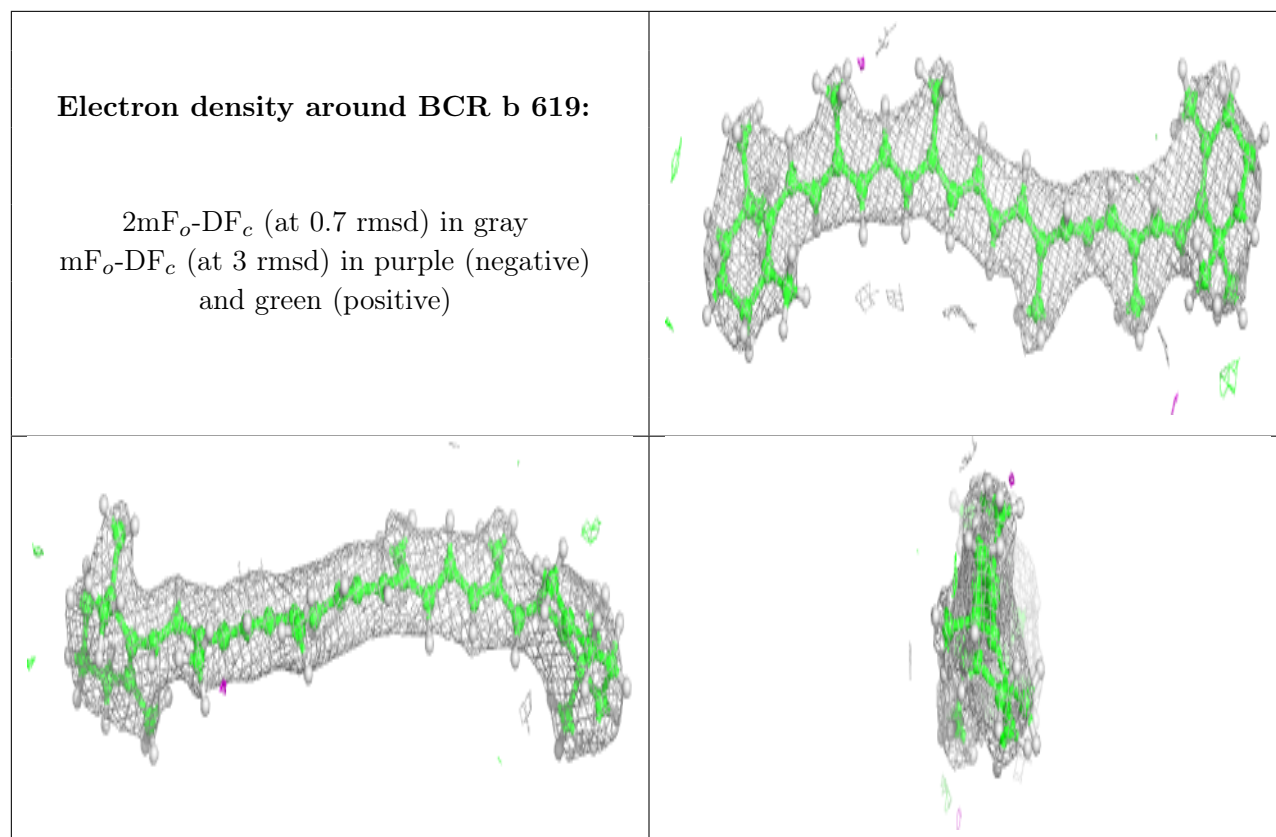
**Electron density around CLA b 609:**

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

**Electron density around CLA b 614:**

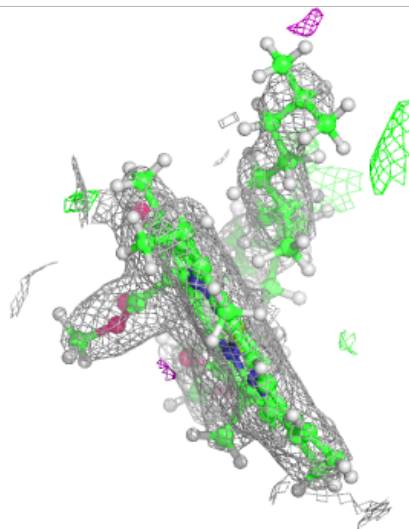
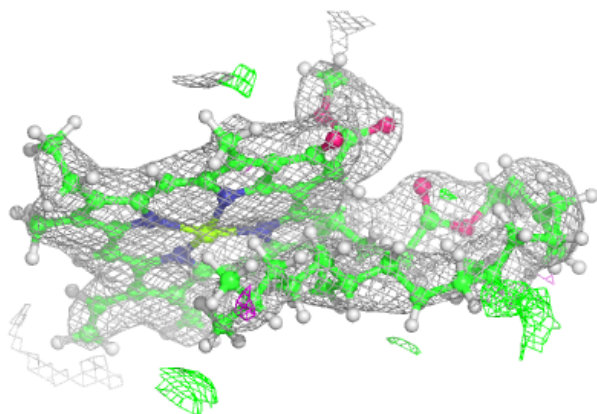
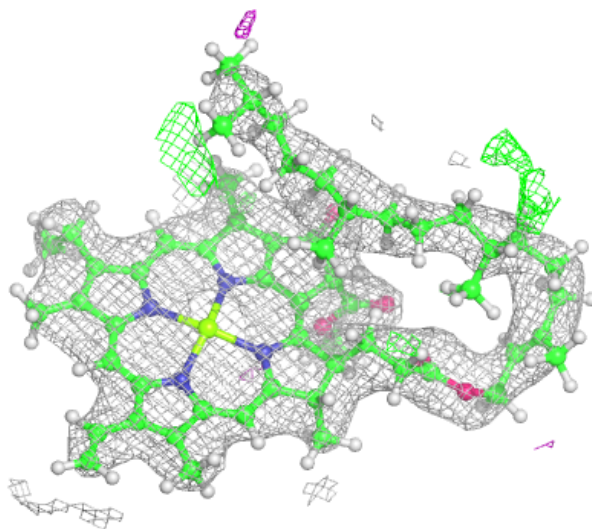
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





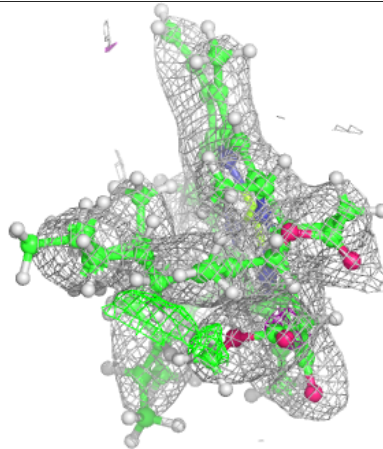
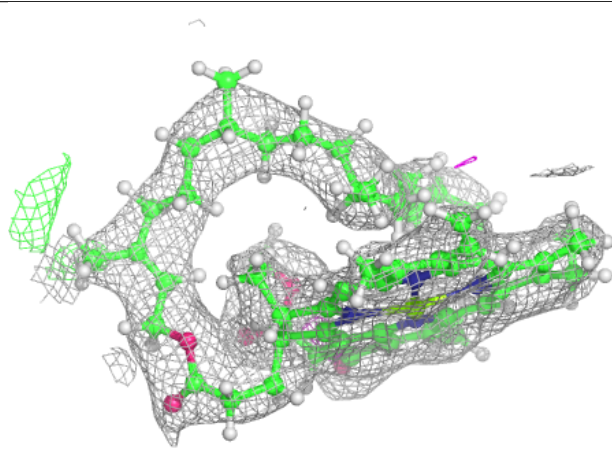
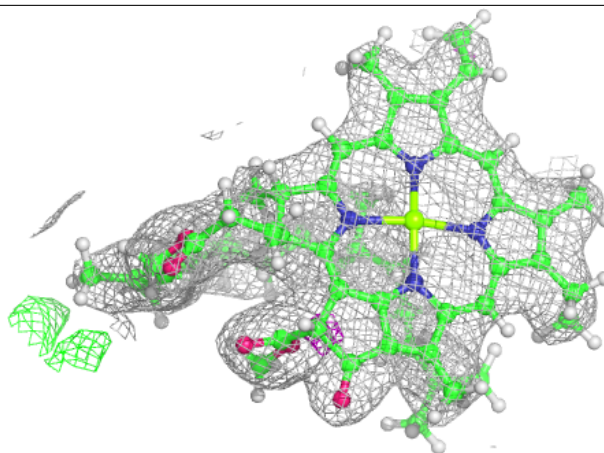
**Electron density around CLA C 509:**

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

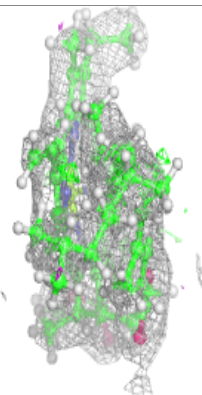
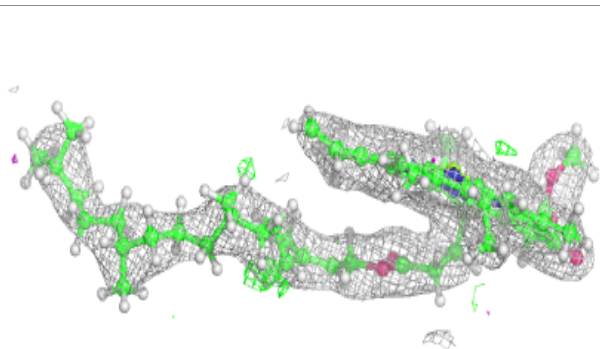
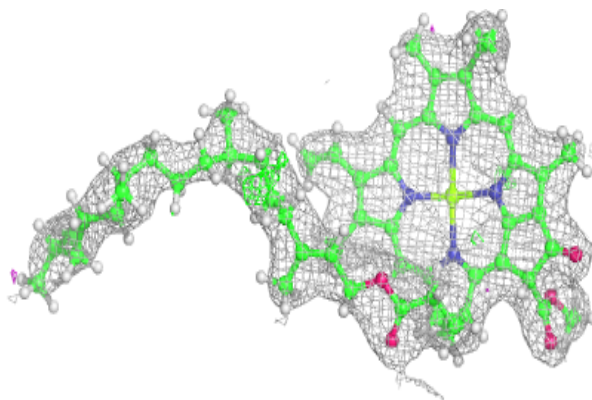


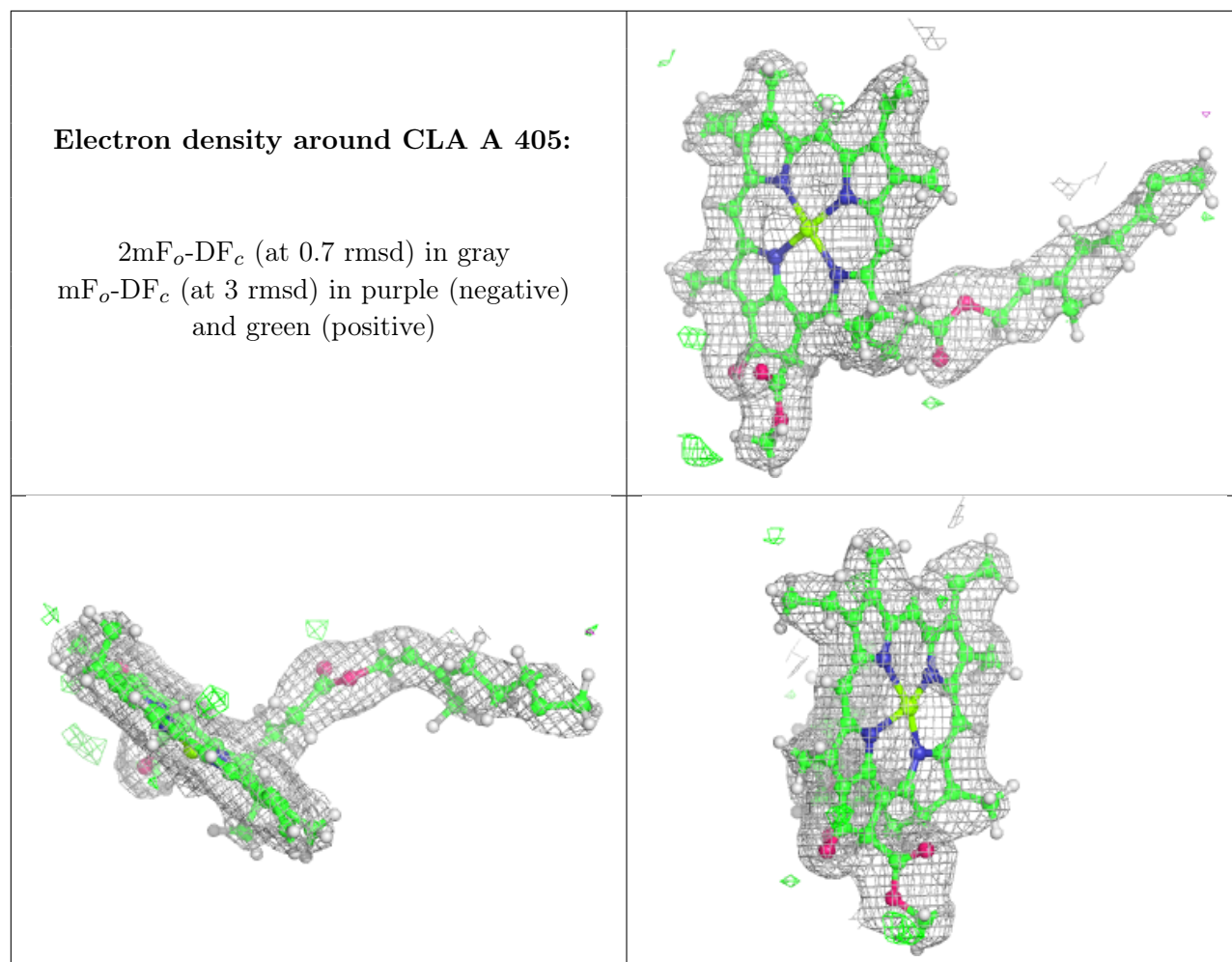
**Electron density around CLA C 510:**

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

**Electron density around CLA B 603:**

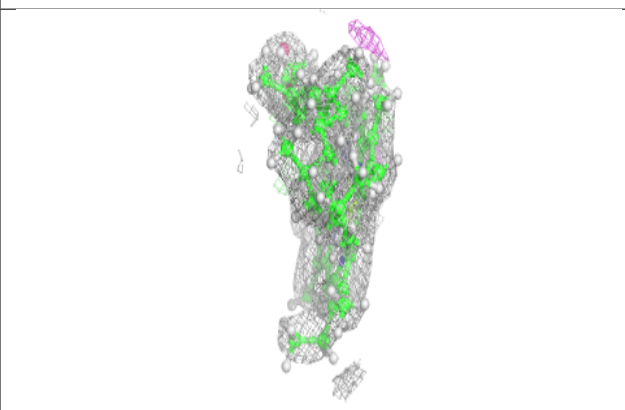
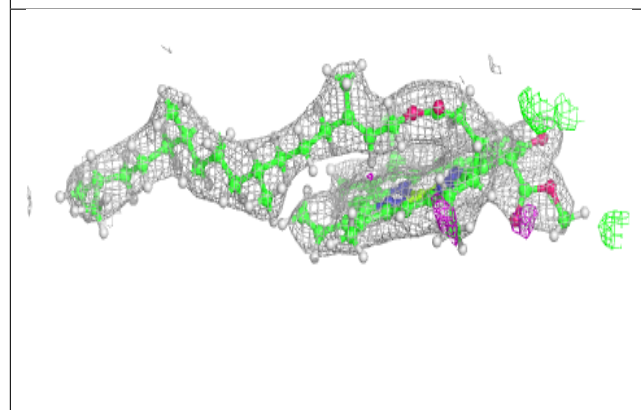
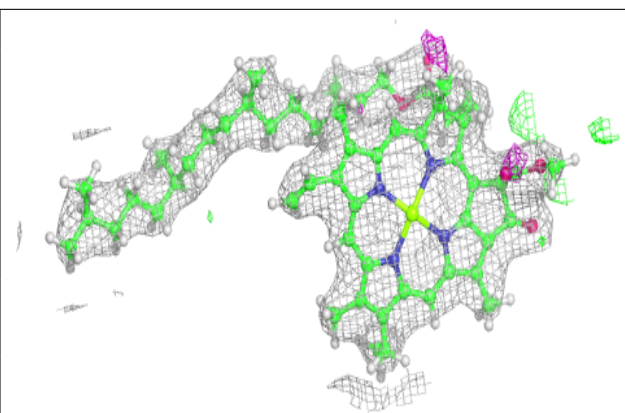
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



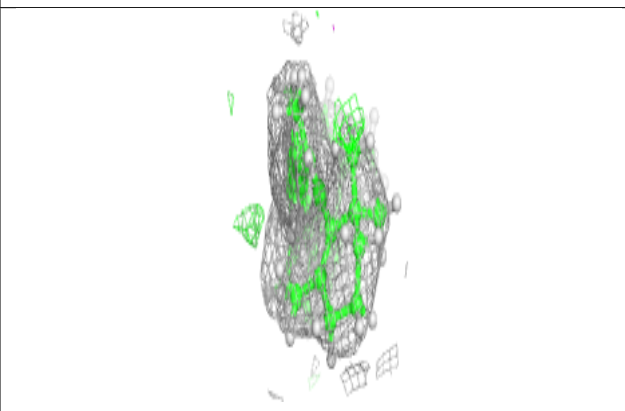
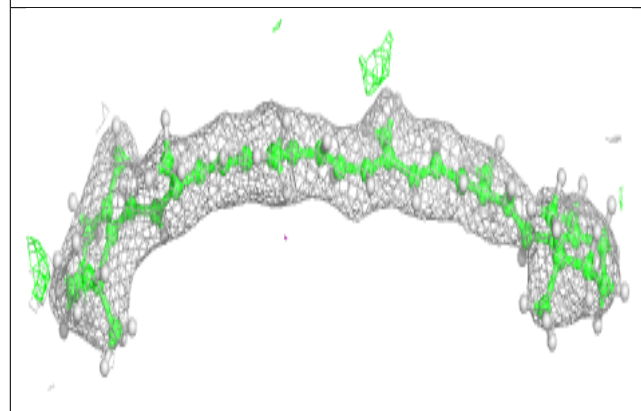
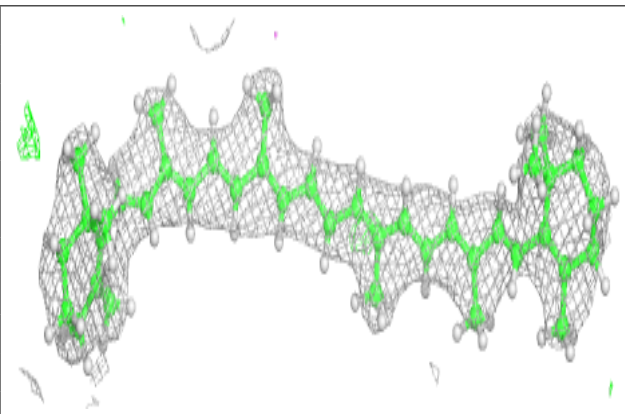


**Electron density around CLA C 501:**

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

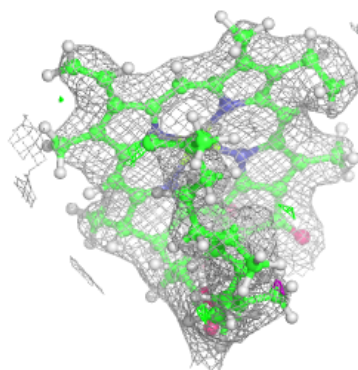
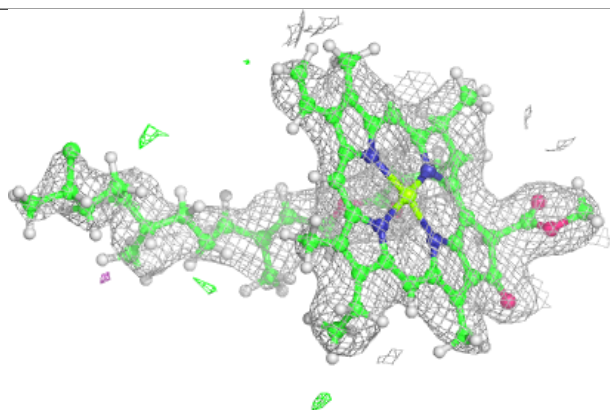
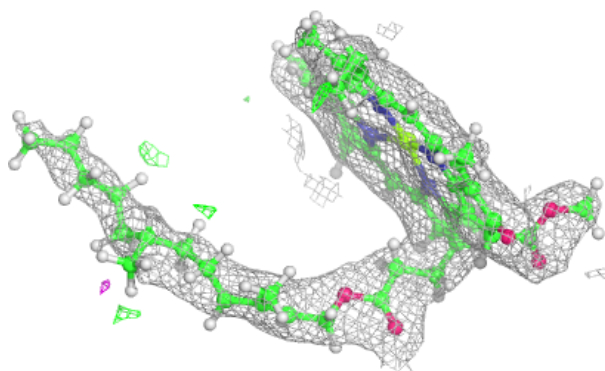
**Electron density around BCR T 101:**

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

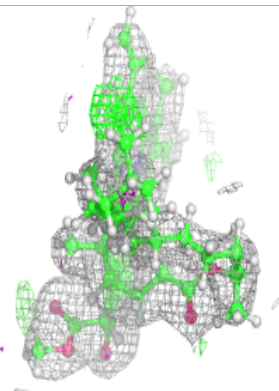
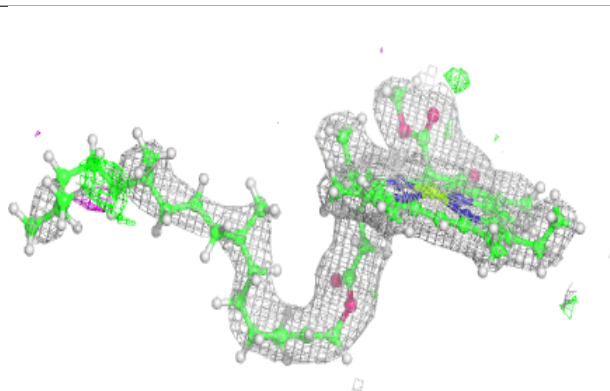
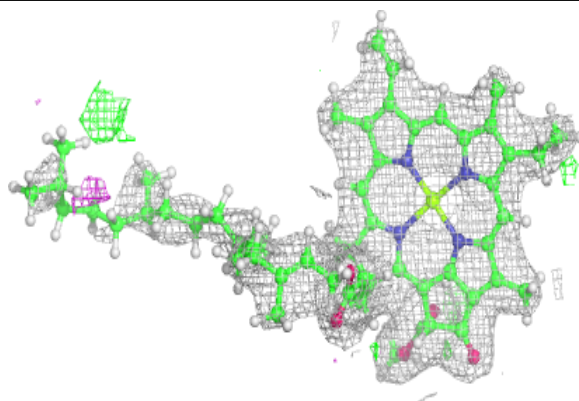


**Electron density around CLA c 504:**

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

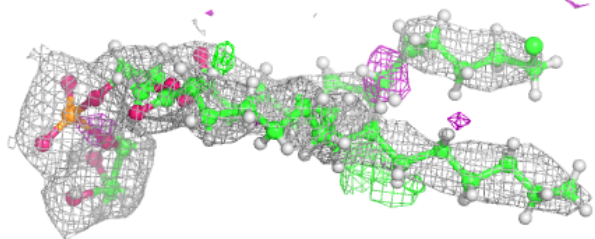
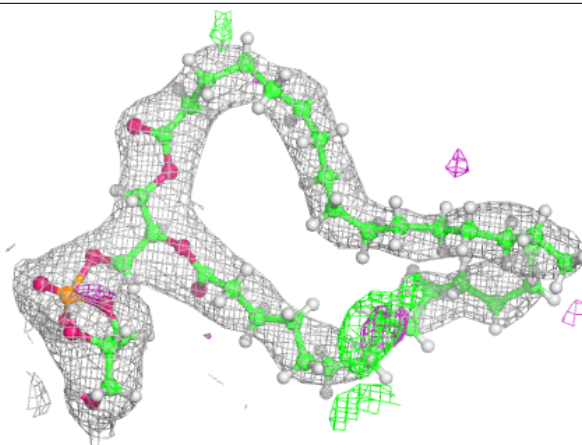
**Electron density around CLA A 403:**

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

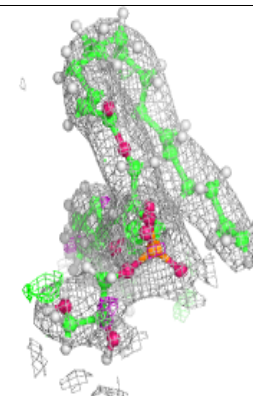
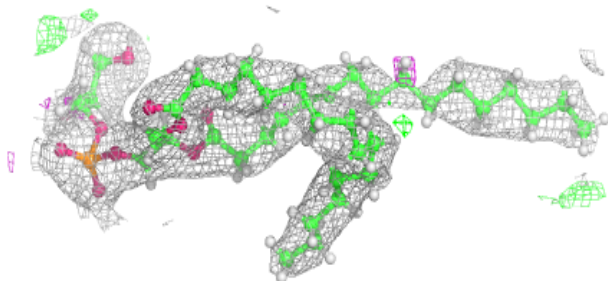
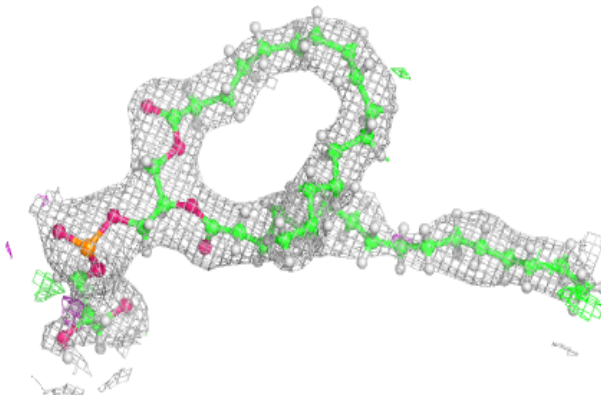


**Electron density around LHG A 411:**

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

**Electron density around LHG B 621:**

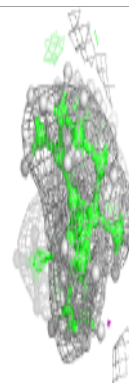
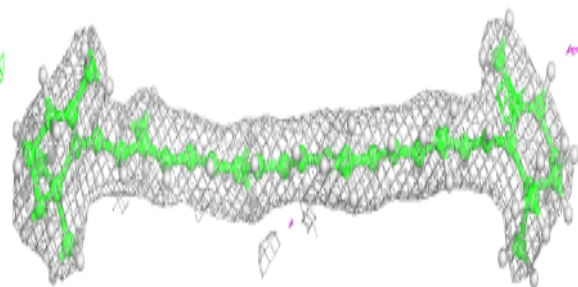
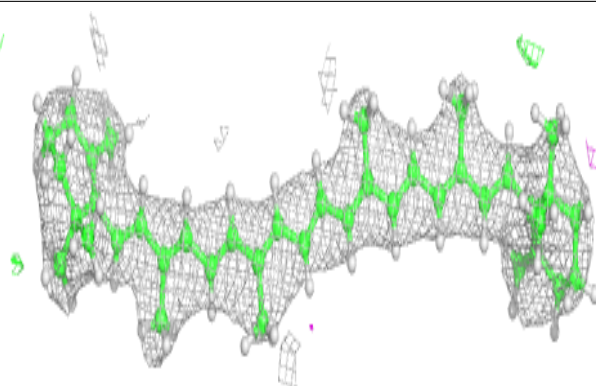
$2mF_o-DF_c$  (at 0.7 rnsd) in gray  
 $mF_o-DF_c$  (at 3 rnsd) in purple (negative)  
and green (positive)



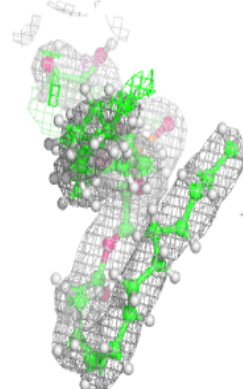
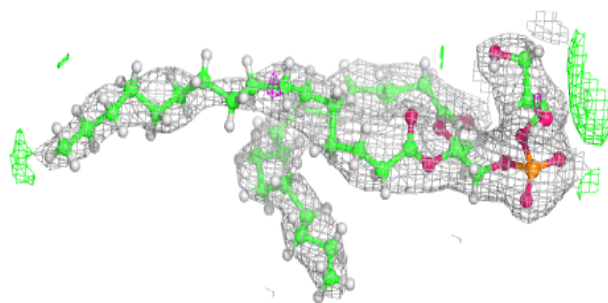
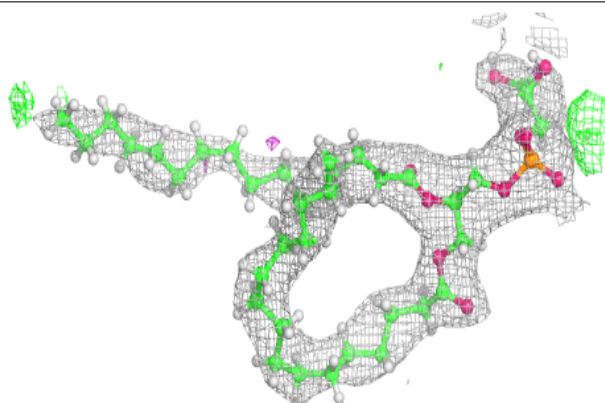


**Electron density around BCR b 618:**

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

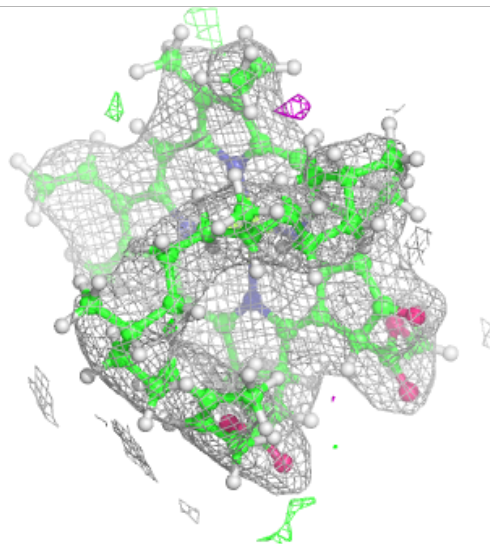
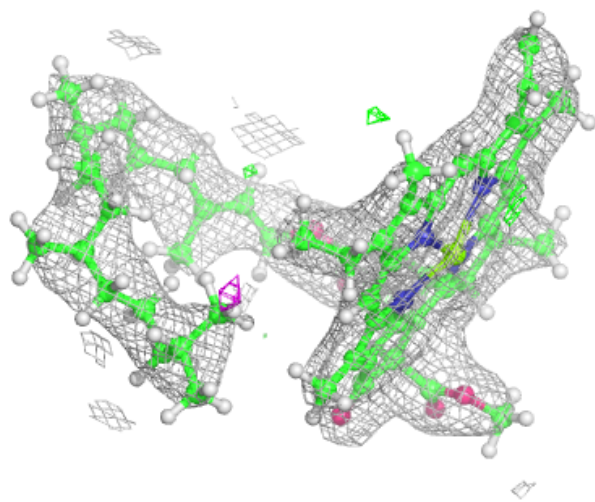
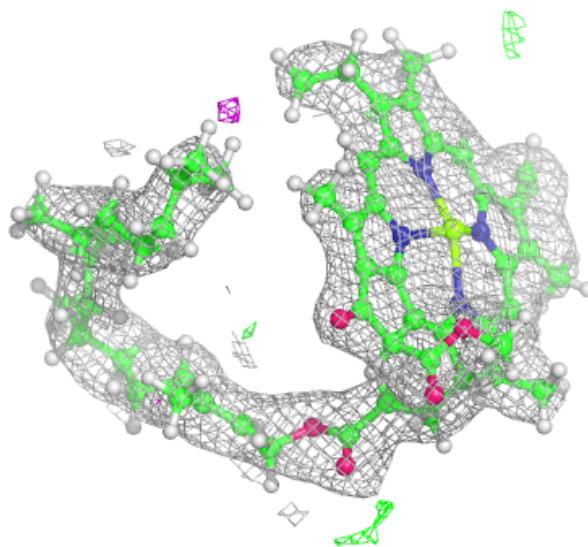
**Electron density around LHG b 623:**

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



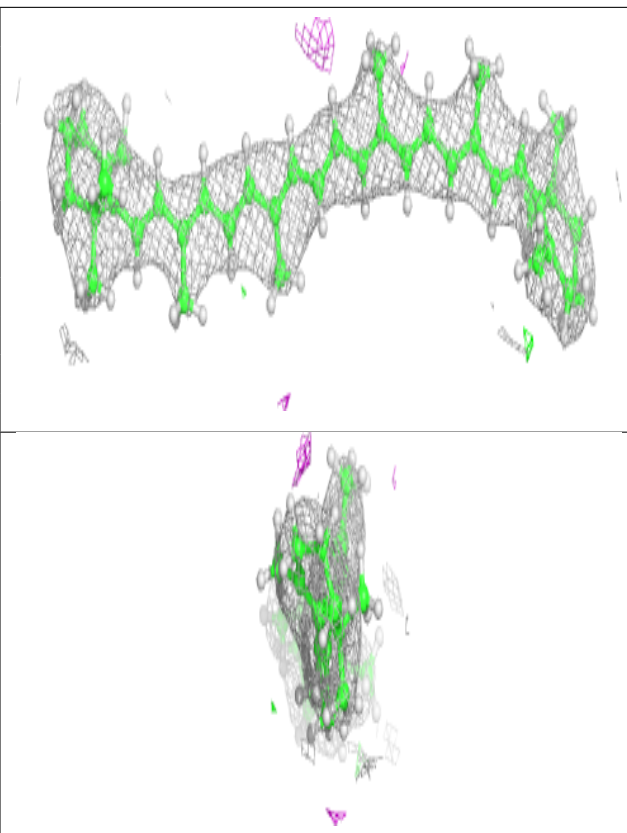
**Electron density around CLA C 503:**

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

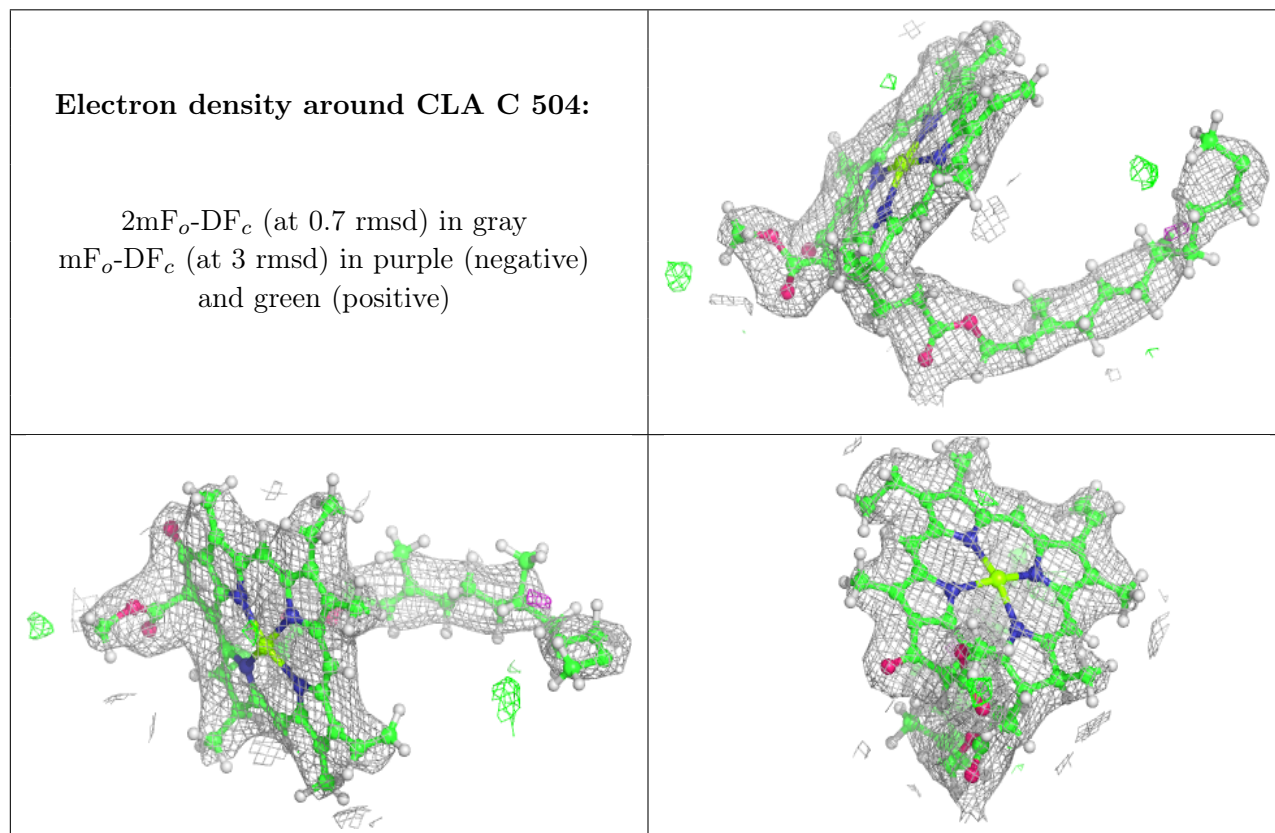


**Electron density around BCR c 514:**

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

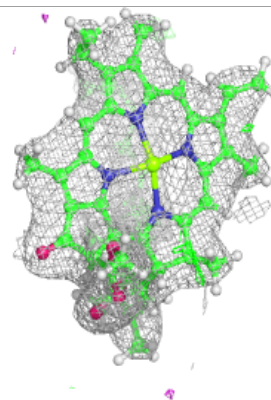
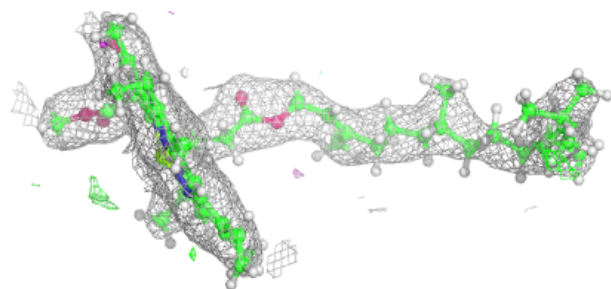
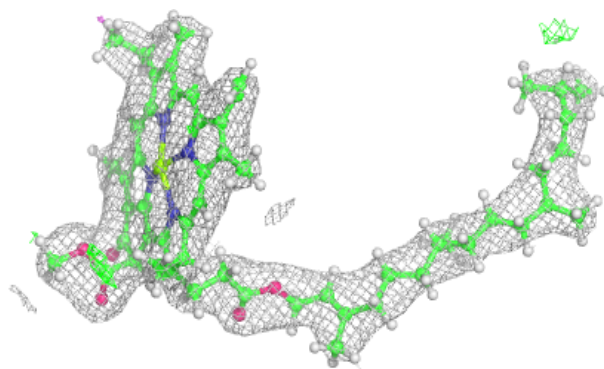
**Electron density around CLA C 504:**

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

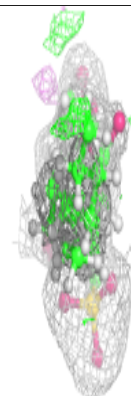
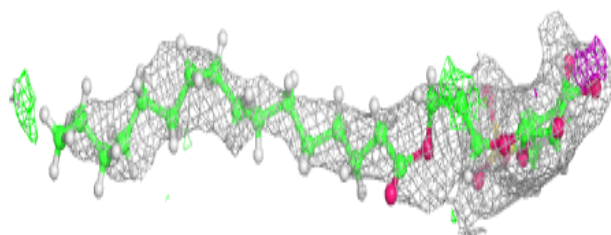
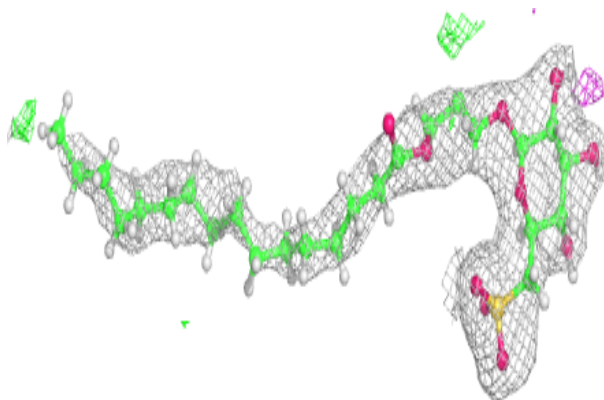


**Electron density around CLA B 609:**

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

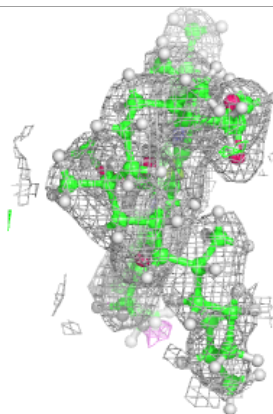
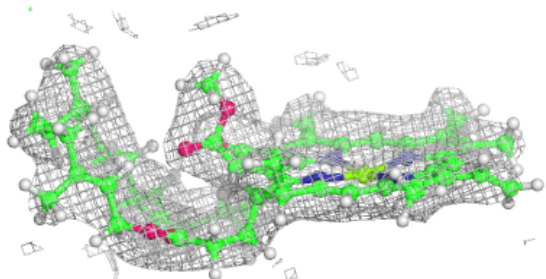
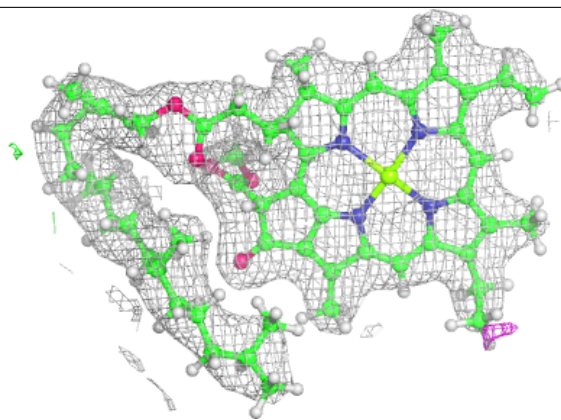
**Electron density around SQD F 102:**

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

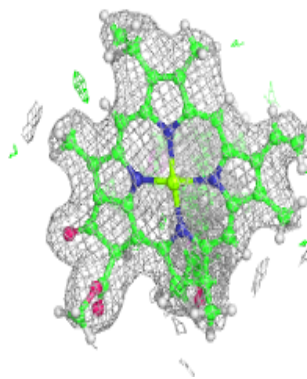
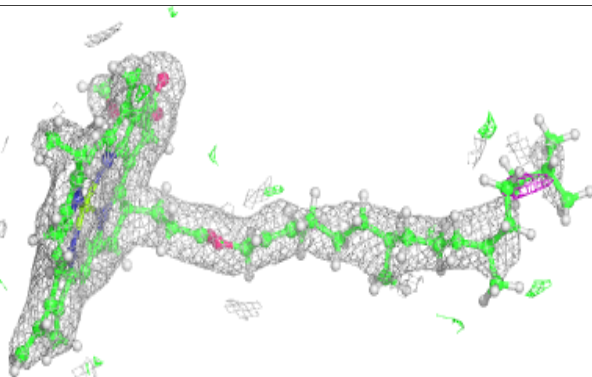
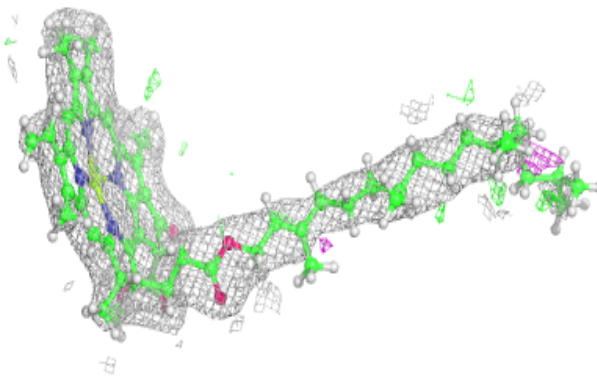


**Electron density around CLA B 610:**

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

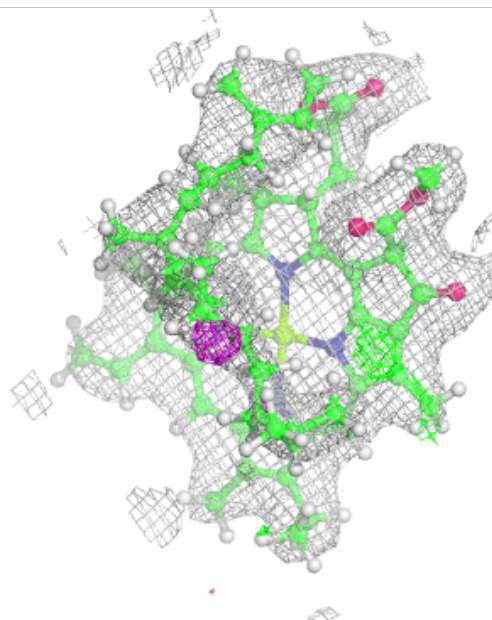
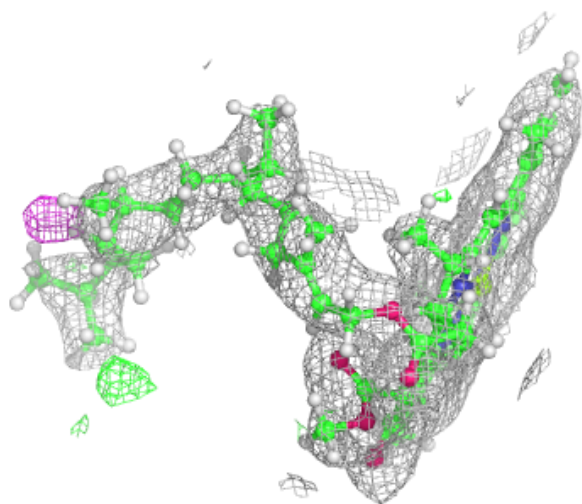
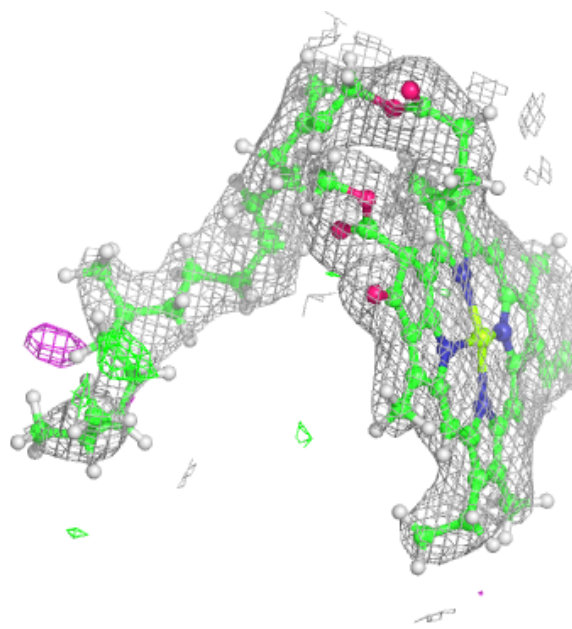
**Electron density around CLA b 604:**

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



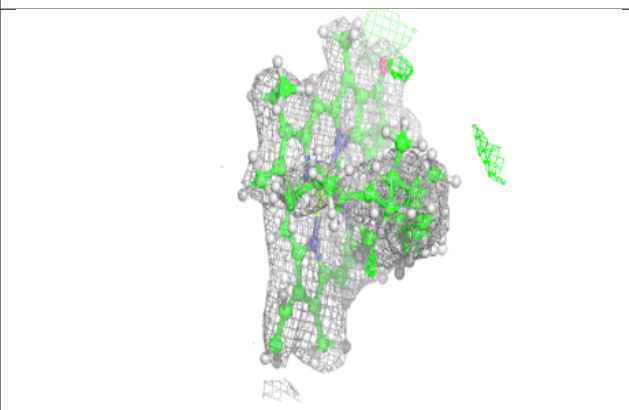
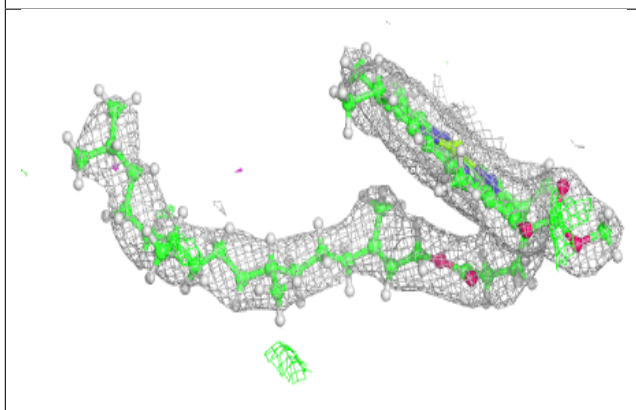
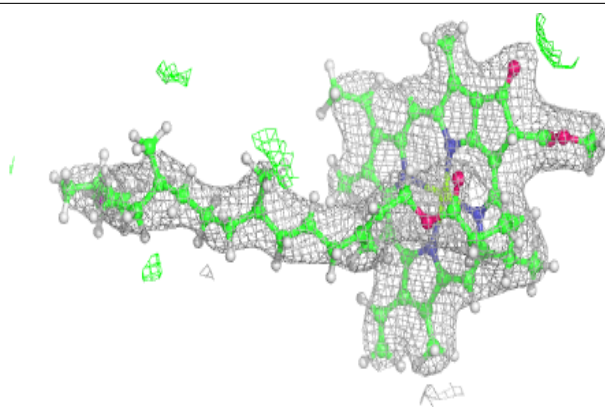
**Electron density around CLA B 613:**

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

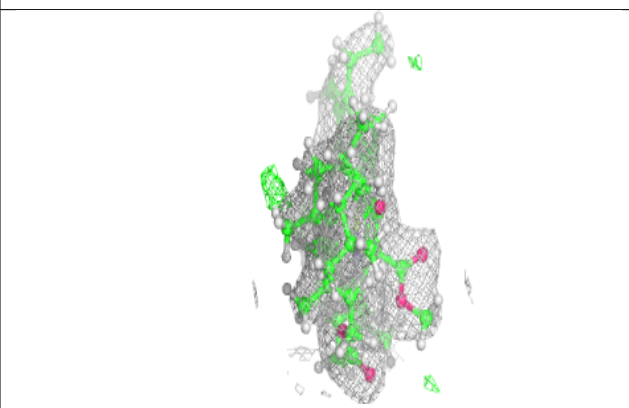
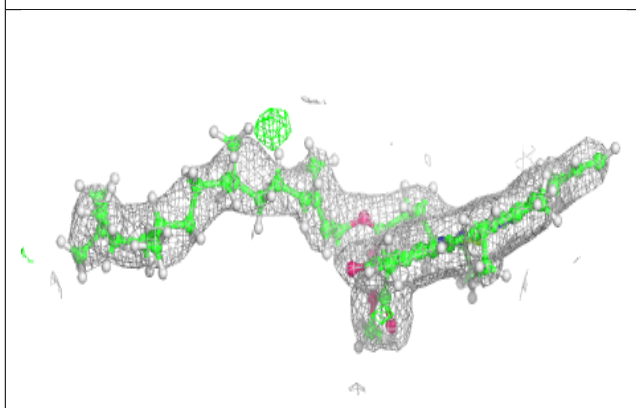
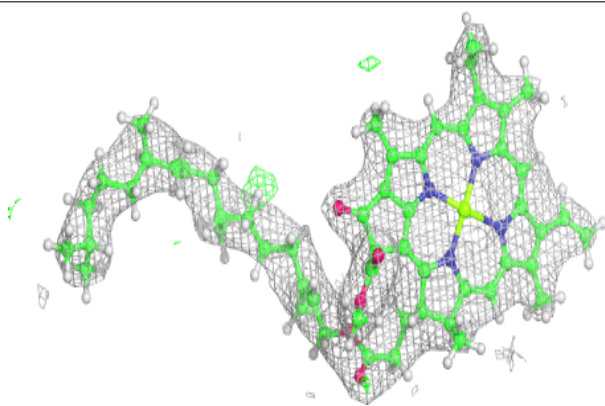


**Electron density around CLA b 608:**

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

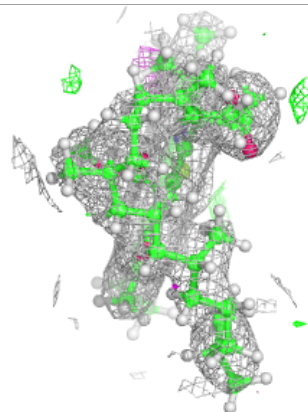
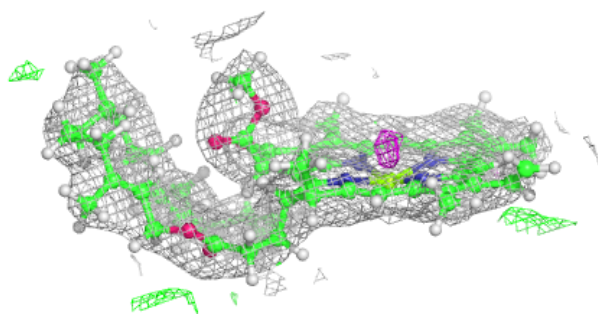
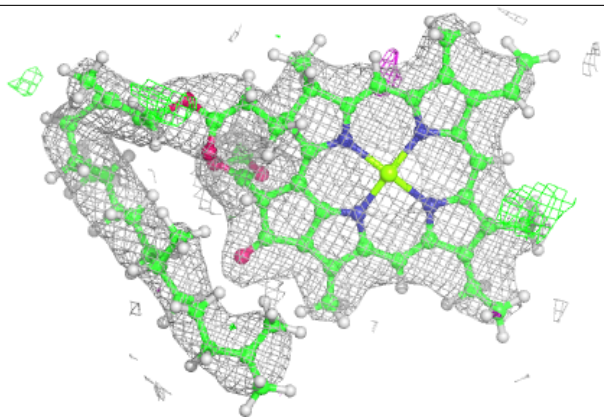
**Electron density around CLA B 602:**

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

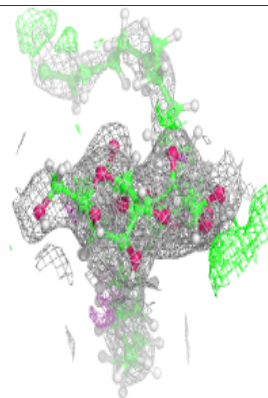
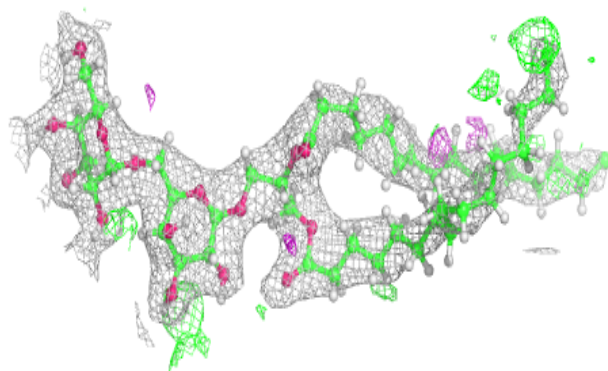
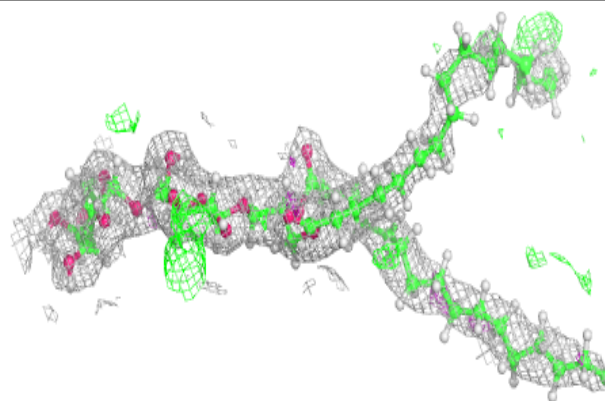


**Electron density around CLA b 610:**

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

**Electron density around DGD C 515:**

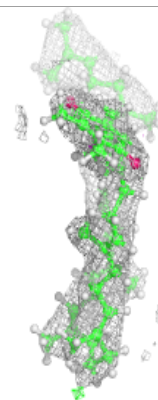
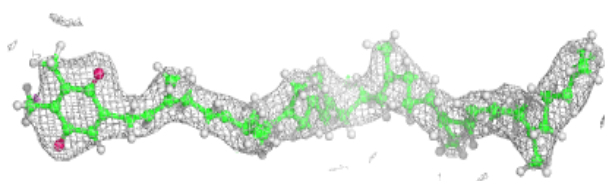
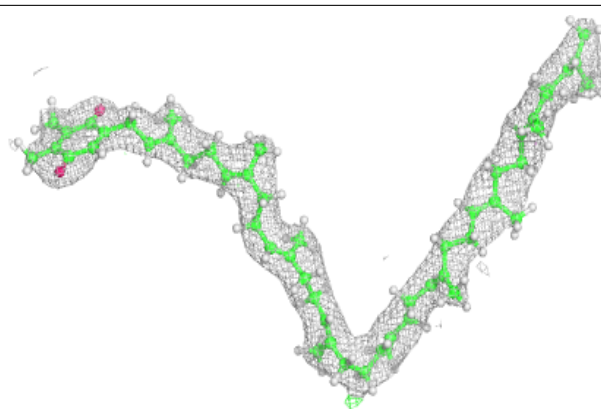
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



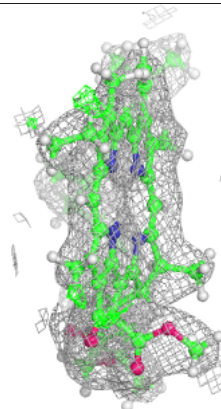
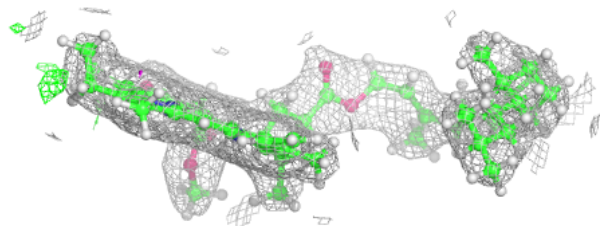
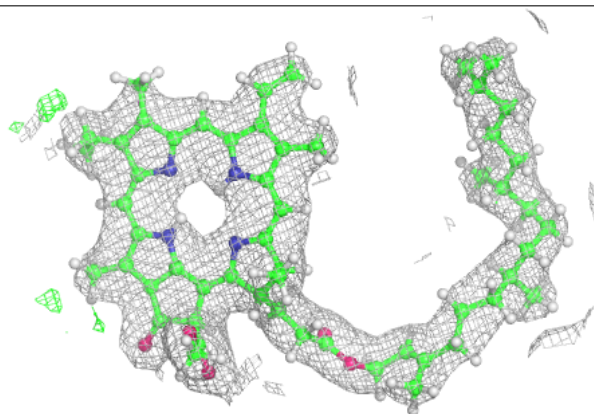


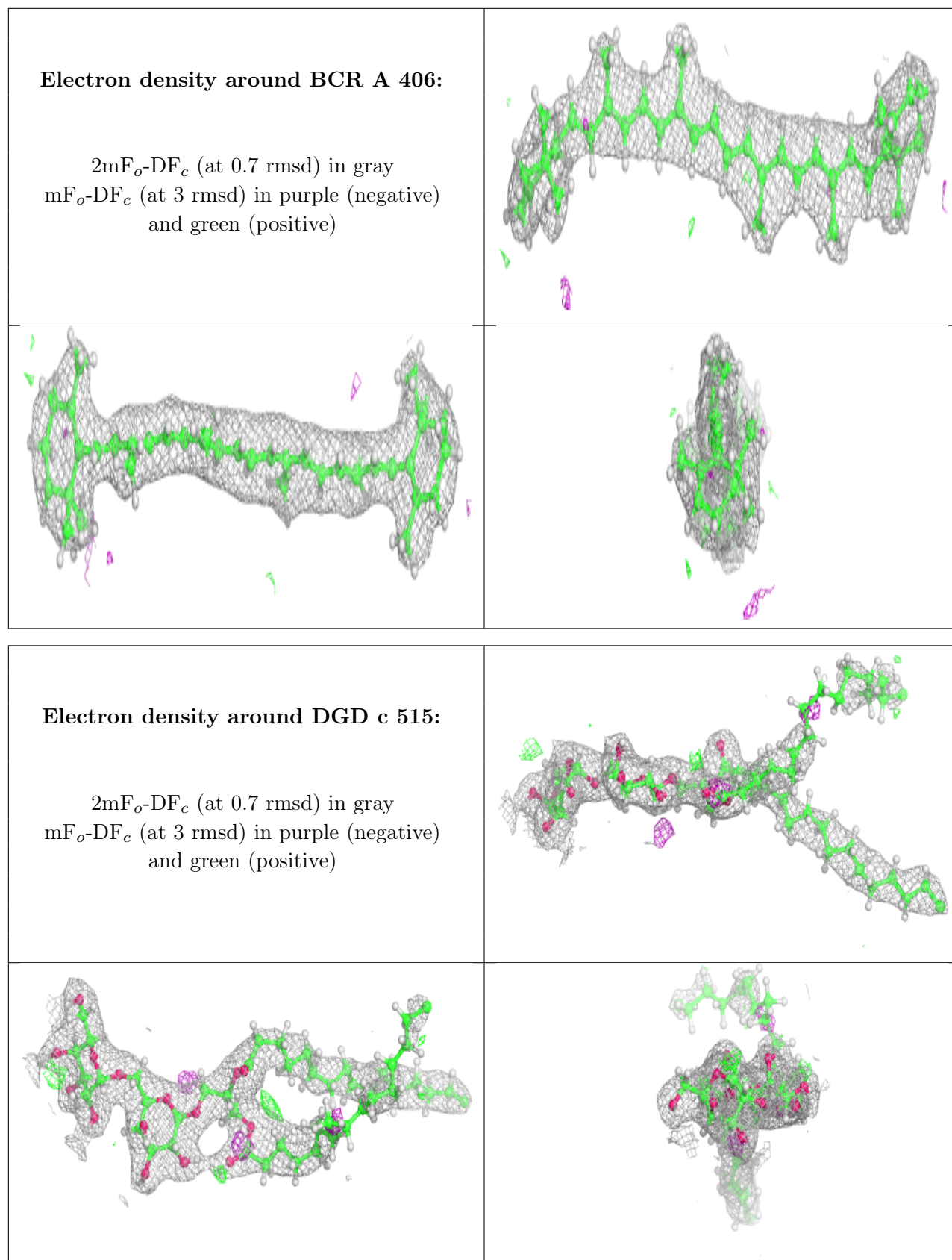
**Electron density around PL9 d 405:**

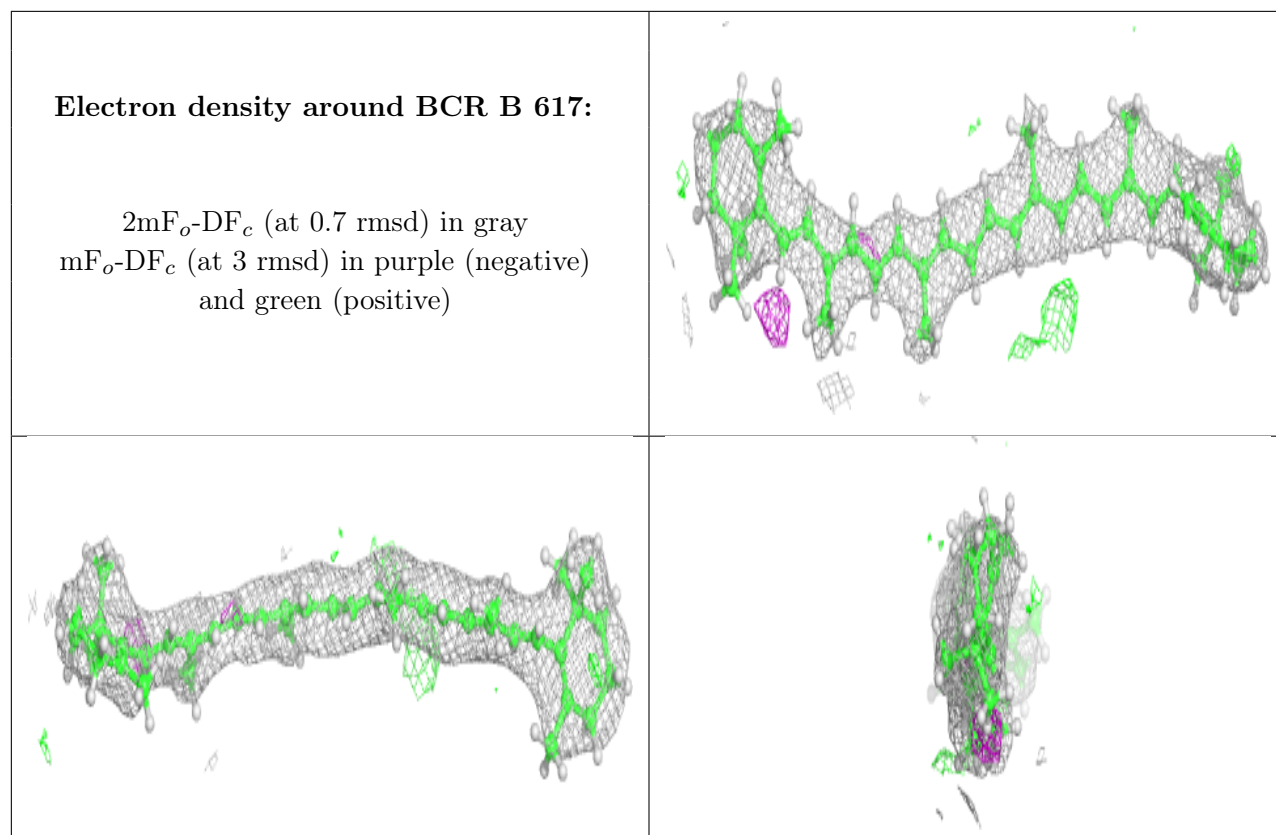
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around PHO a 404:**

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

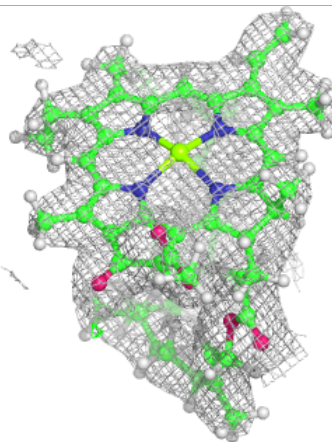
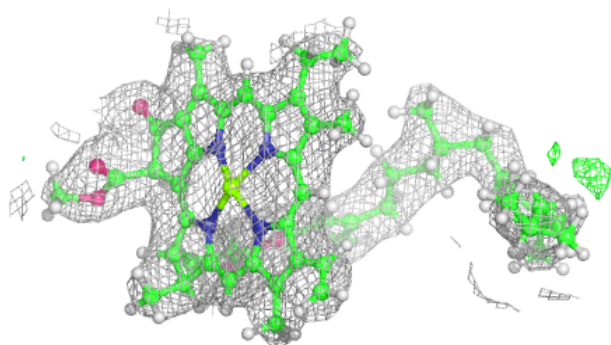
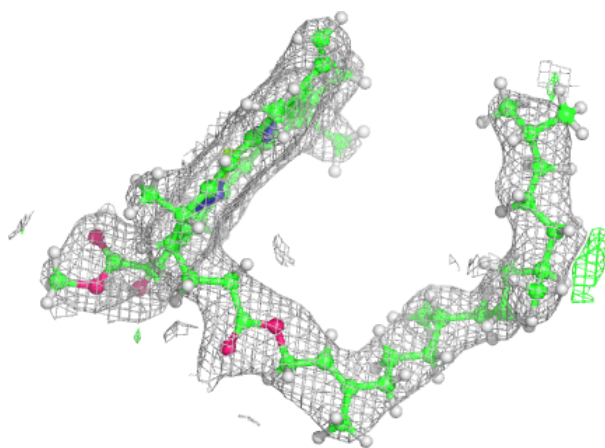






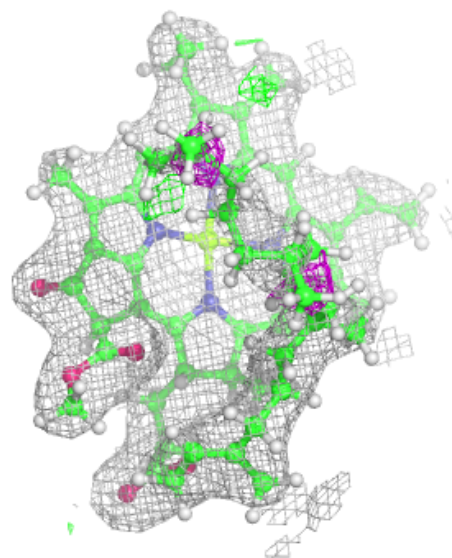
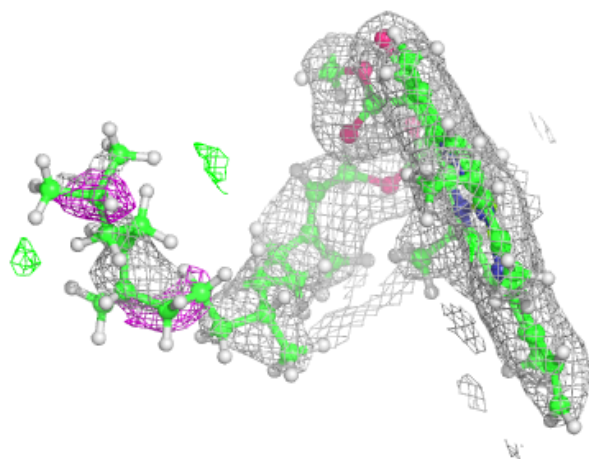
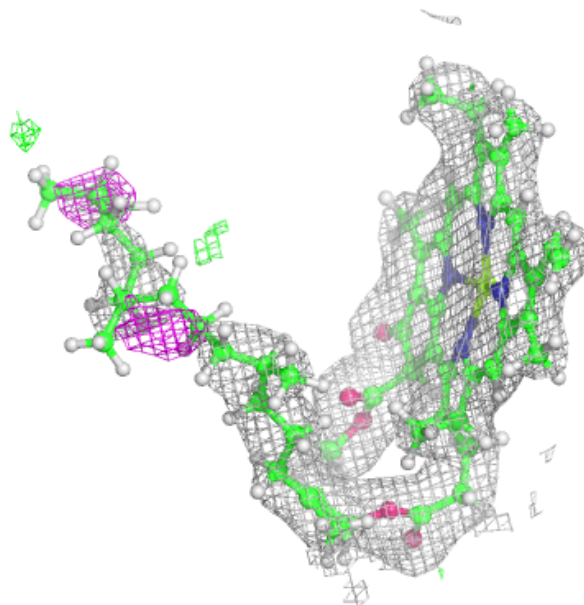
**Electron density around CLA b 611:**

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



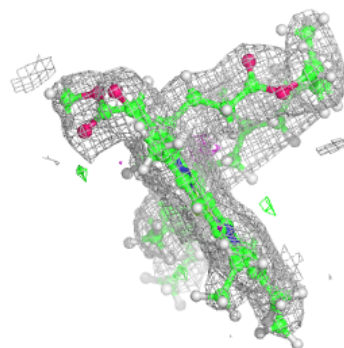
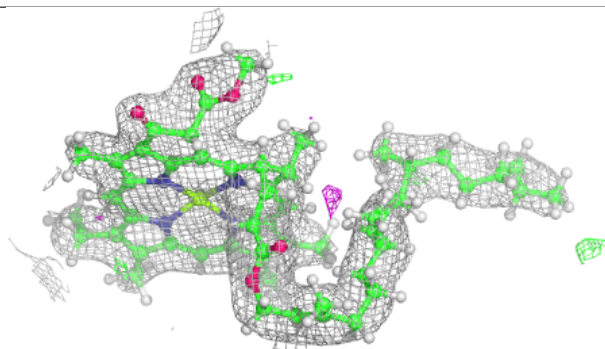
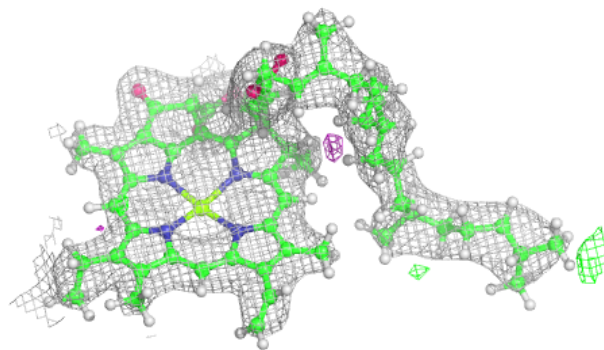
**Electron density around CLA b 613:**

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

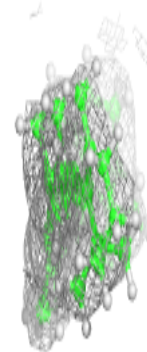
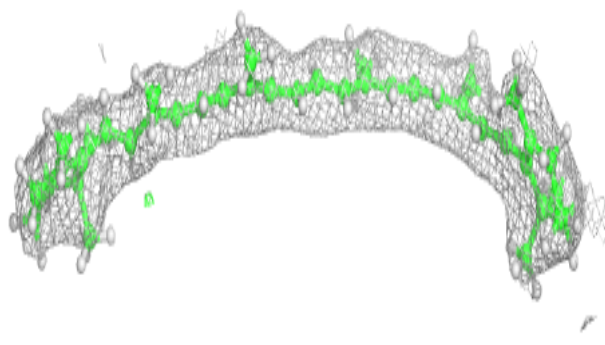
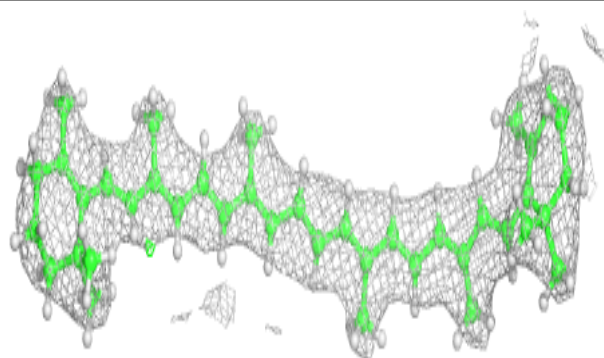


**Electron density around CLA a 411:**

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

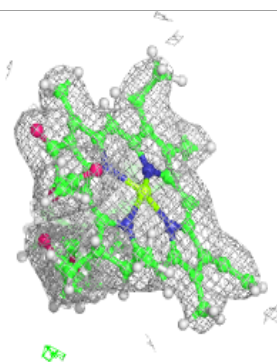
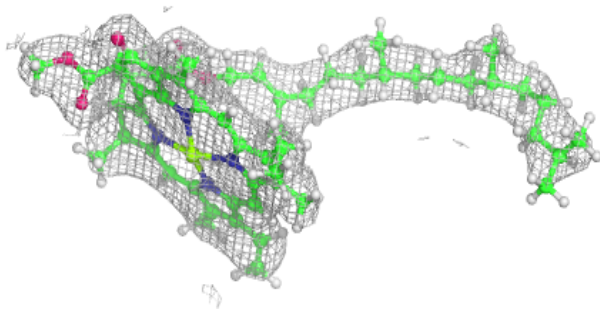
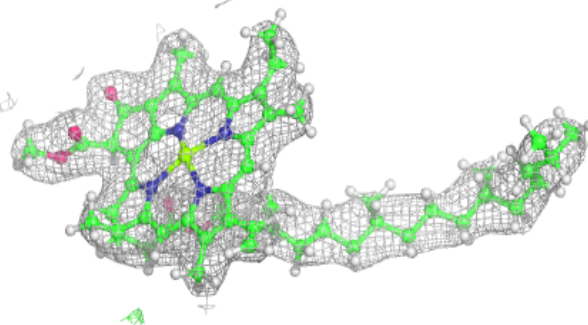
**Electron density around BCR t 101:**

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

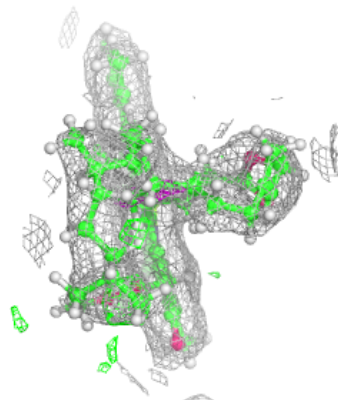
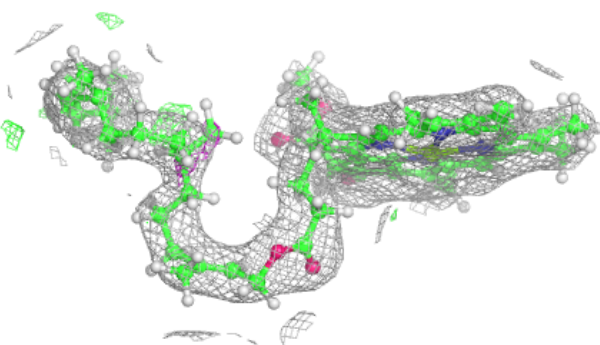
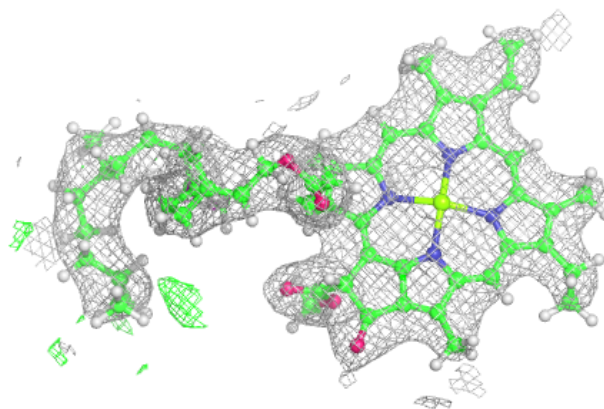


**Electron density around CLA B 608:**

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

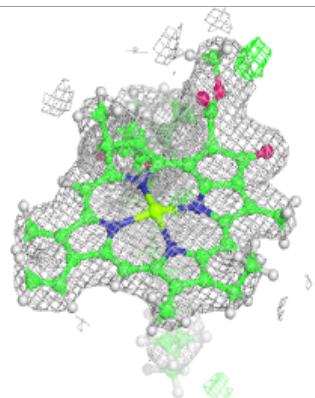
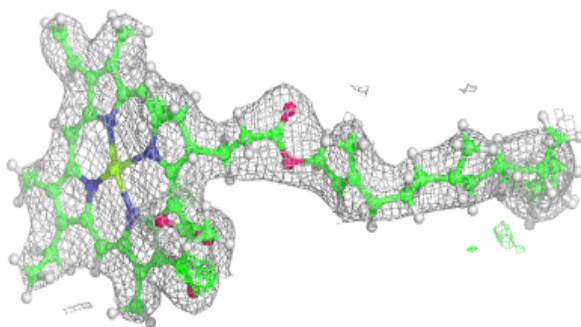
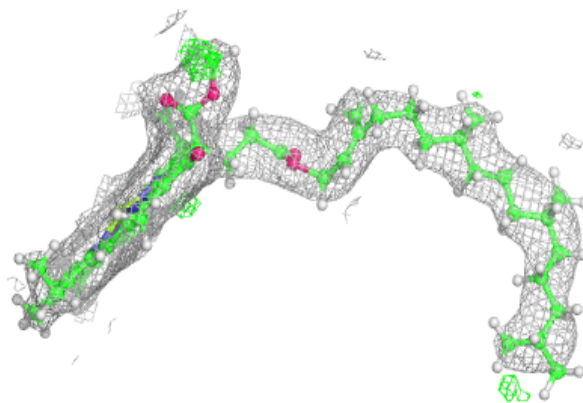
**Electron density around CLA b 612:**

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

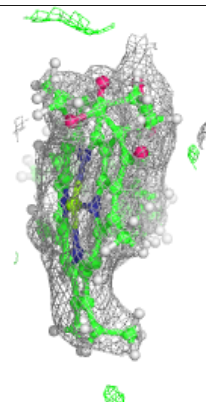
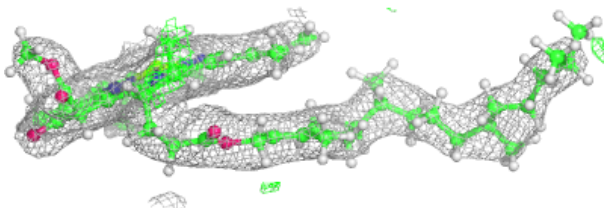
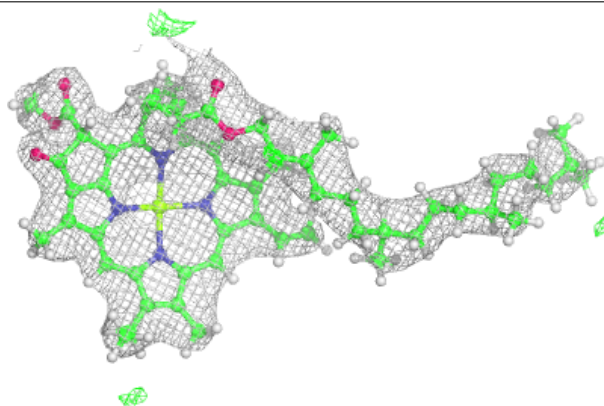


**Electron density around CLA D 403:**

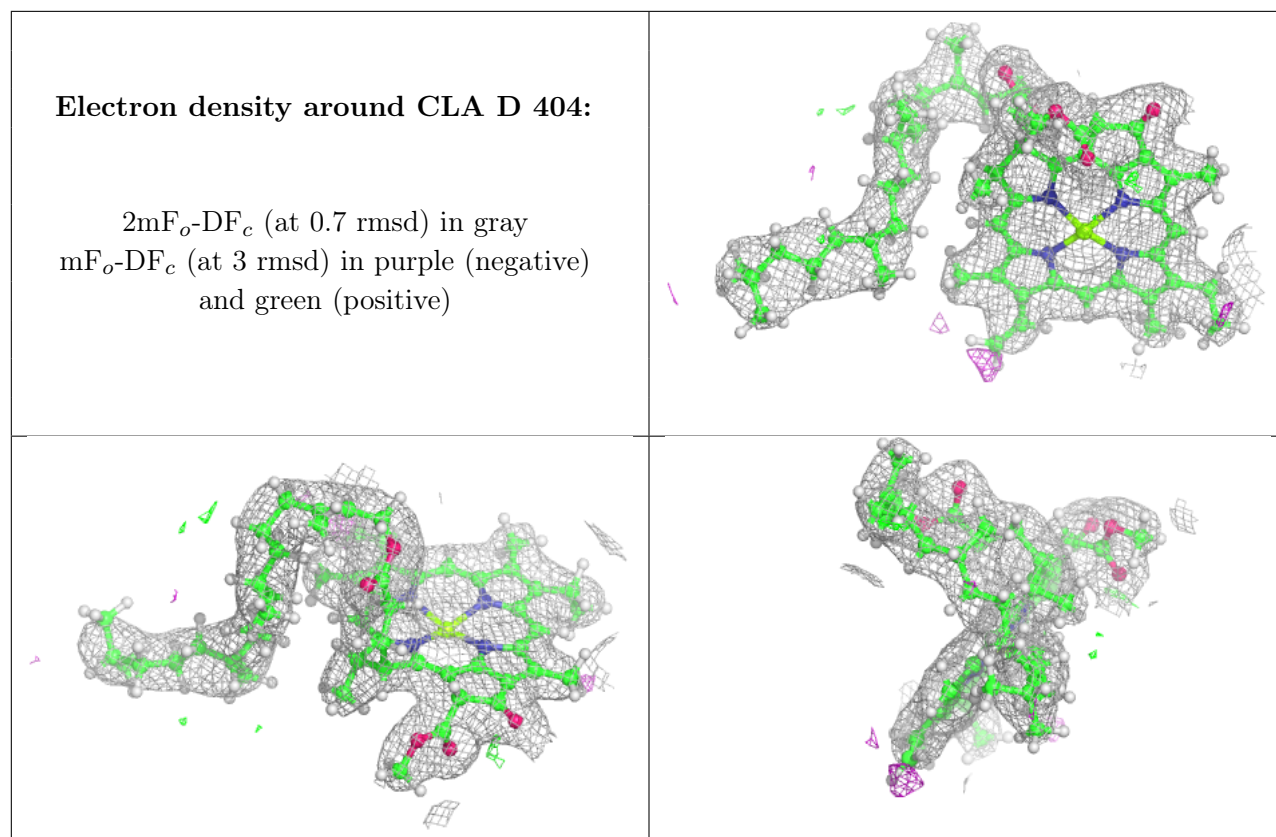
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around 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)

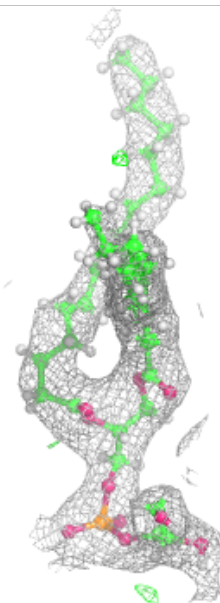
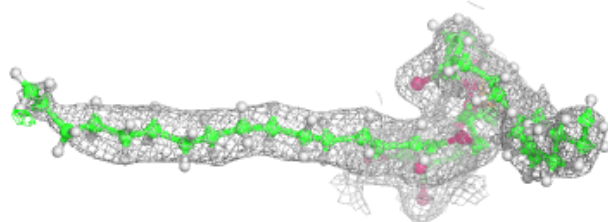
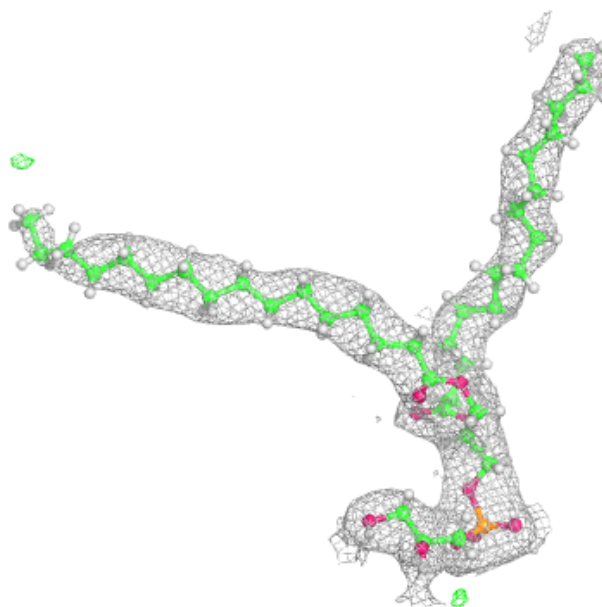






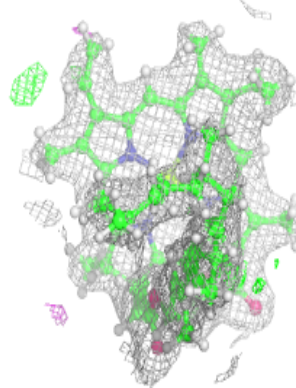
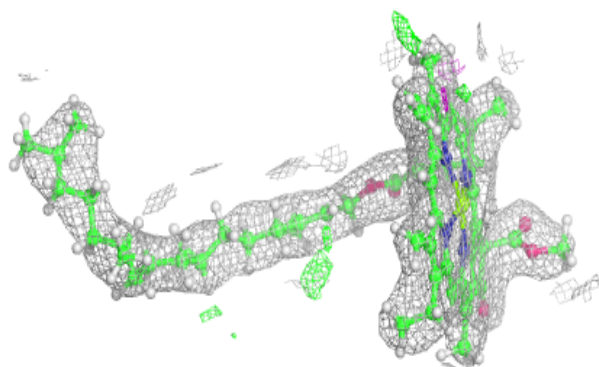
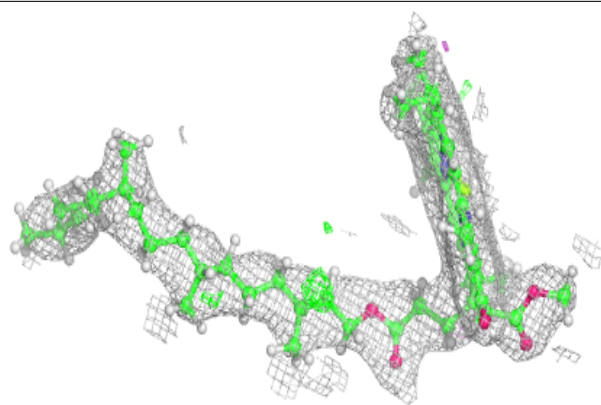
**Electron density around LHG 1 101:**

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

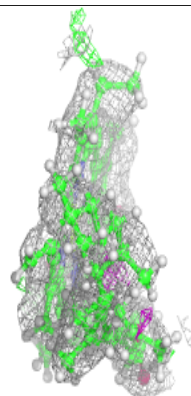
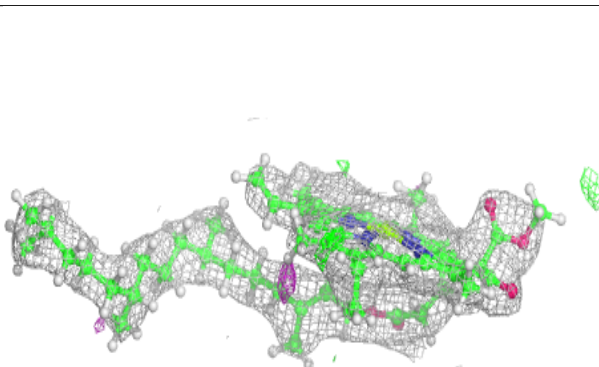
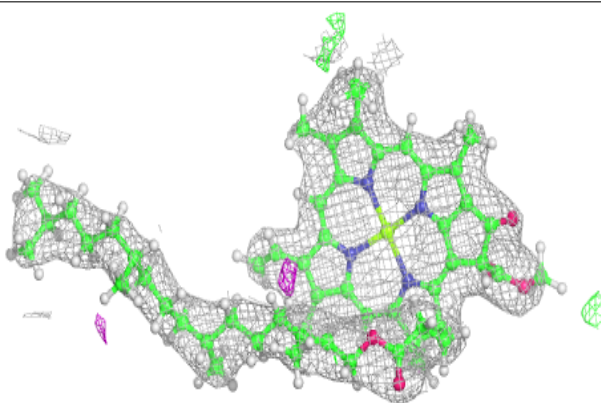


**Electron density around CLA b 605:**

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

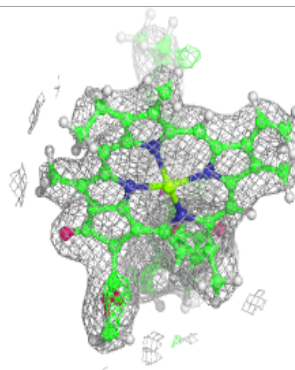
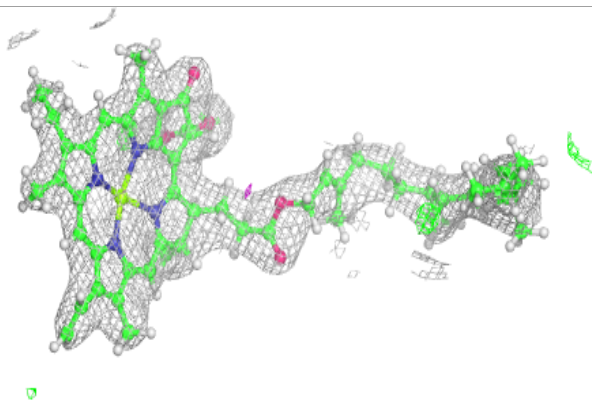
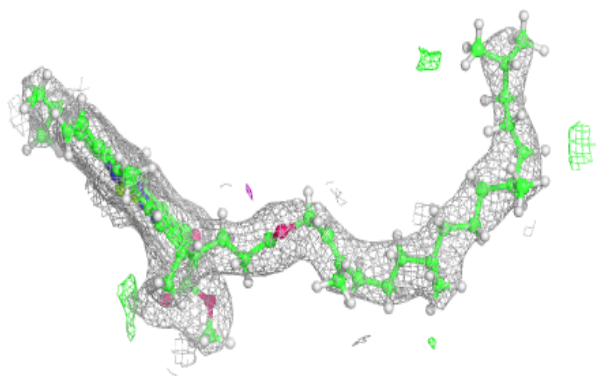
**Electron density around CLA c 501:**

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

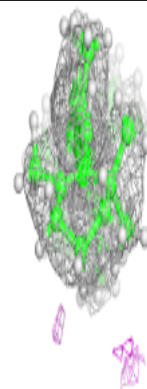
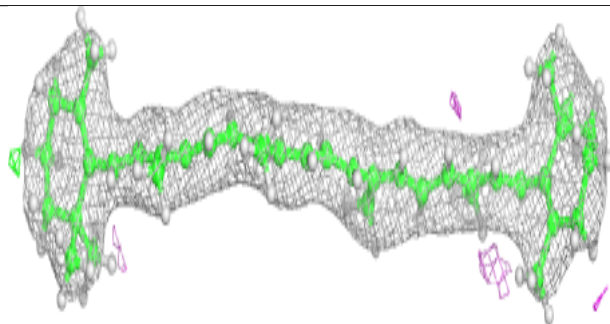
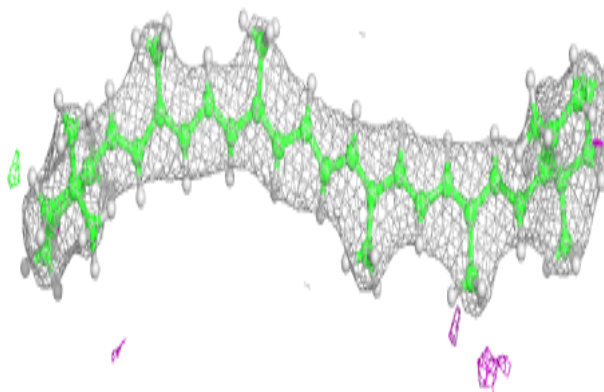


**Electron density around CLA d 402:**

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

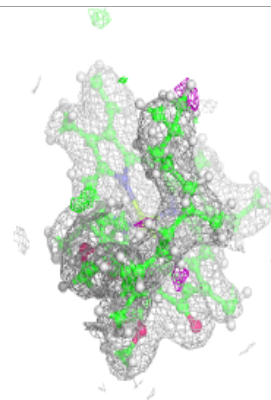
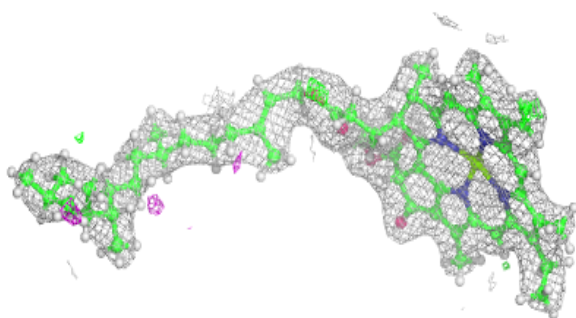
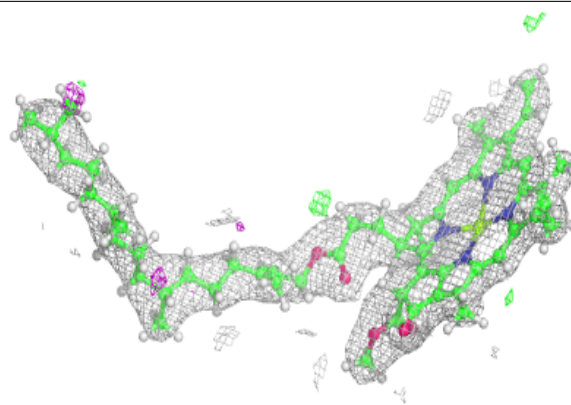
**Electron density around BCR a 406:**

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

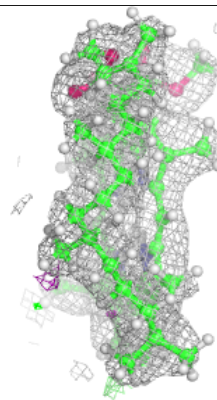
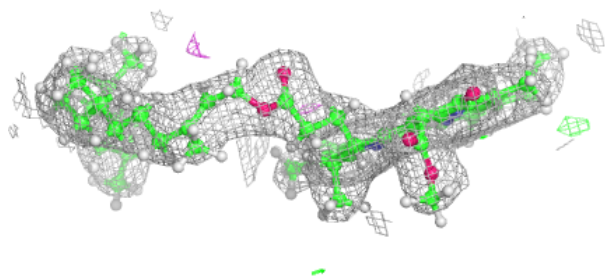
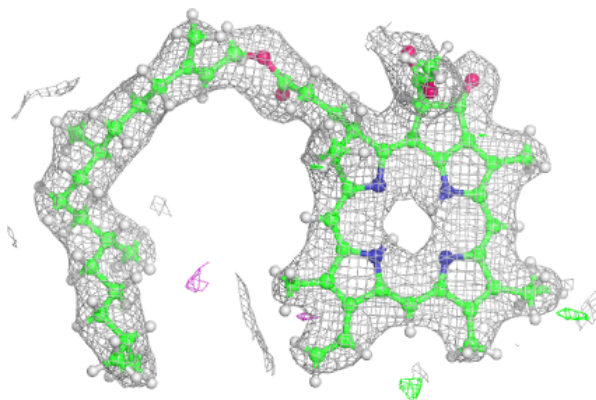


**Electron density around CLA A 402:**

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

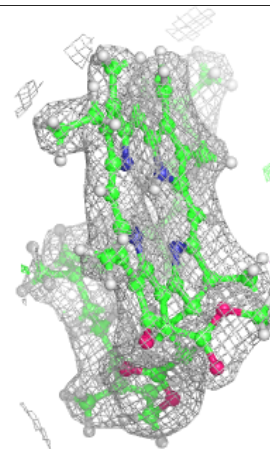
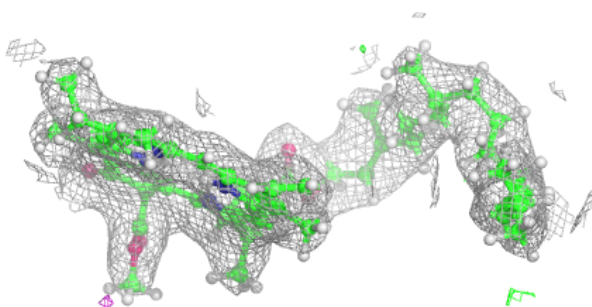
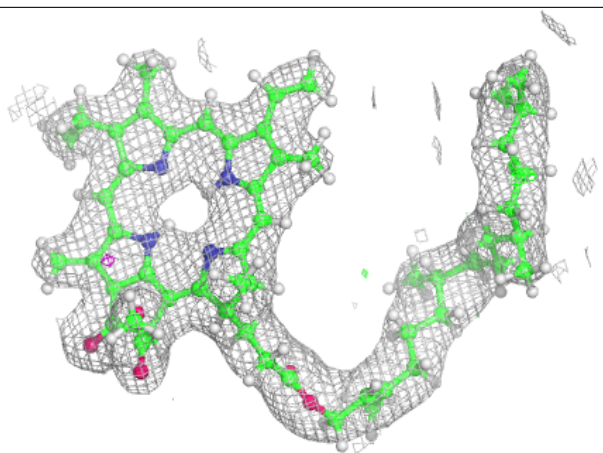
**Electron density around PHO A 404:**

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

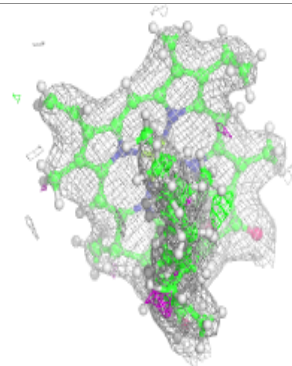
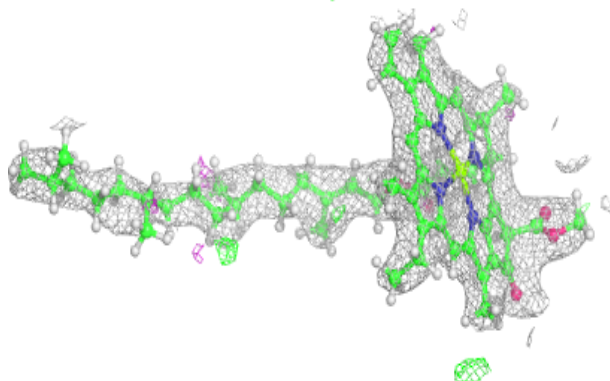
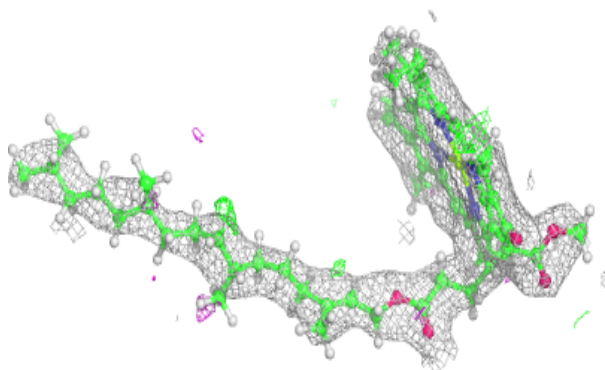


**Electron density around PHO D 401:**

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

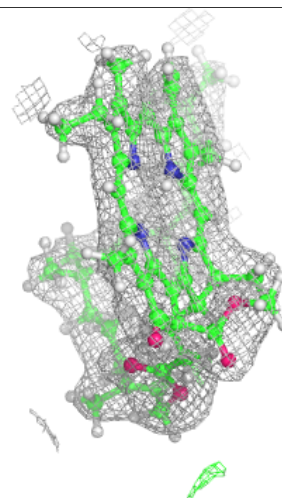
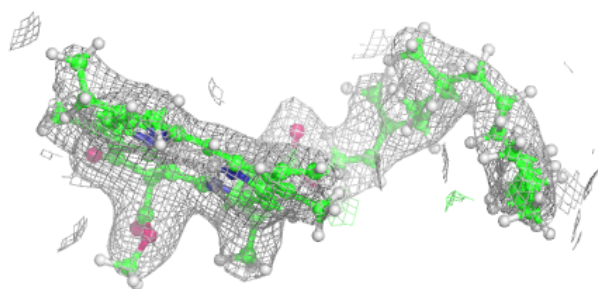
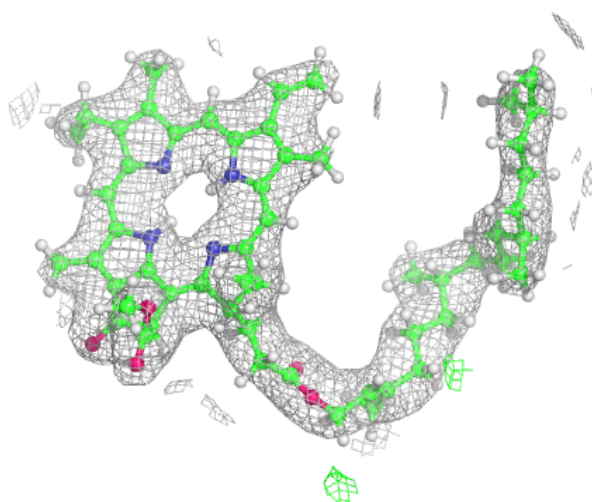
**Electron density around CLA b 607:**

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



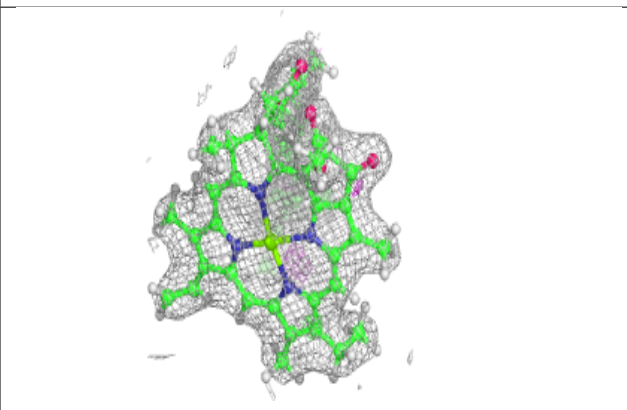
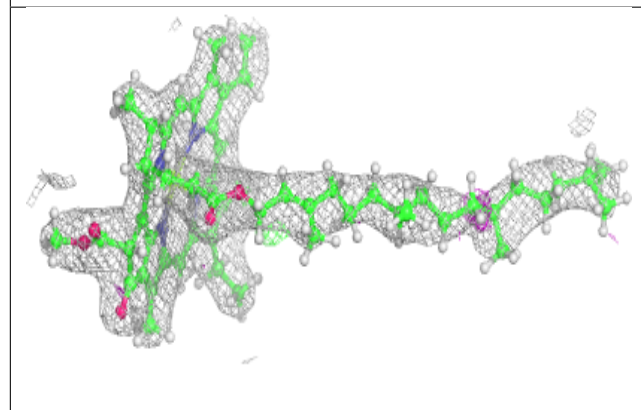
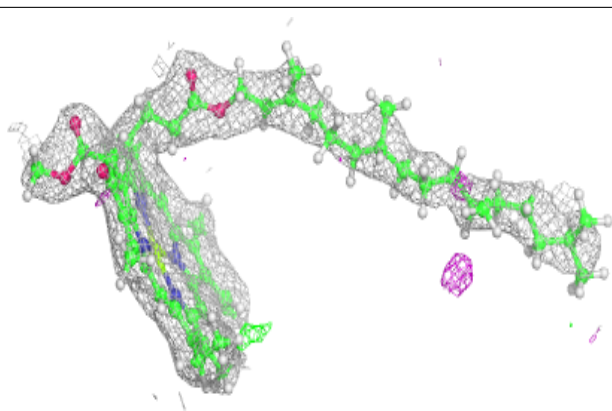
**Electron density around PHO d 401:**

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

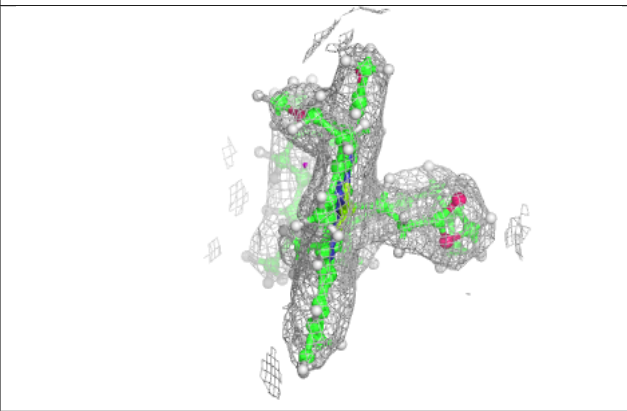
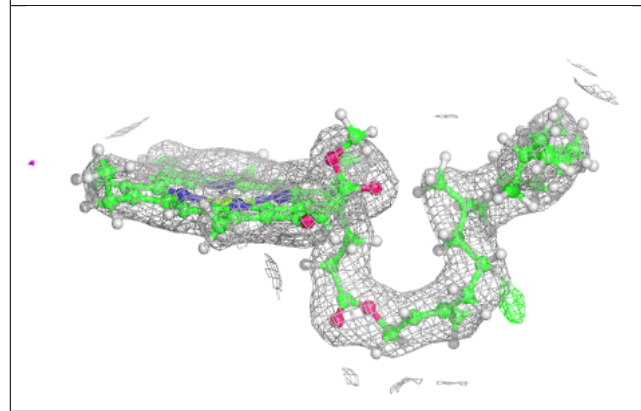
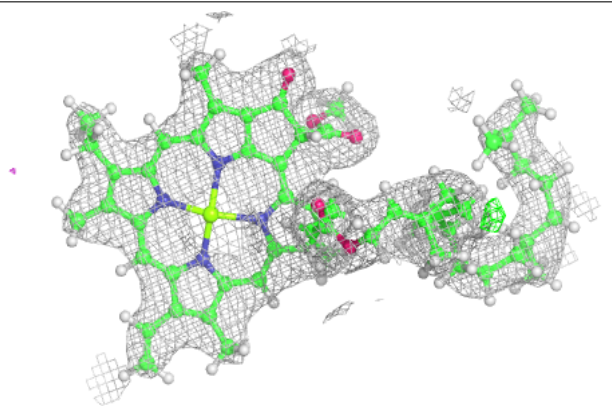


**Electron density around CLA B 607:**

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

**Electron density around CLA B 612:**

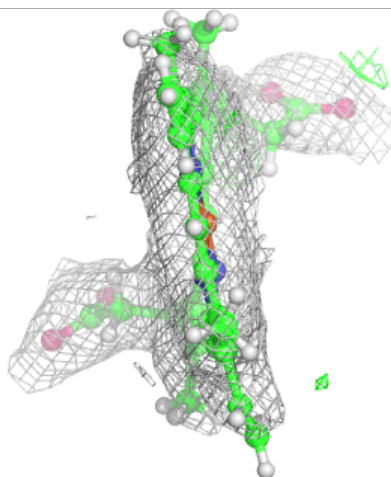
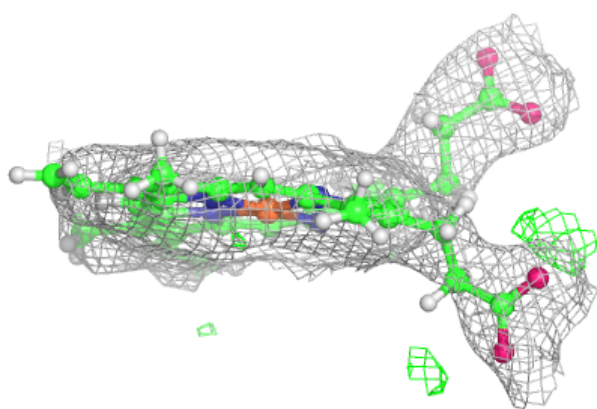
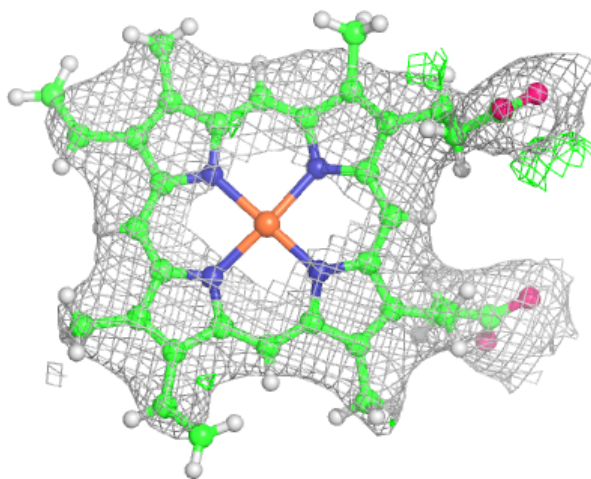
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





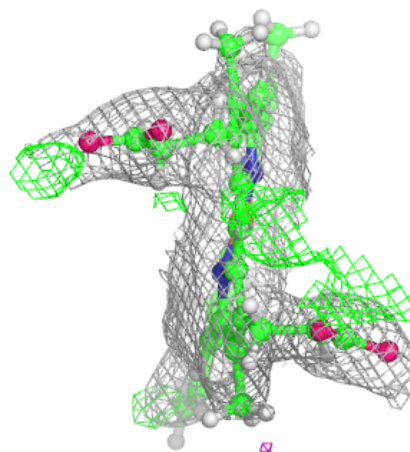
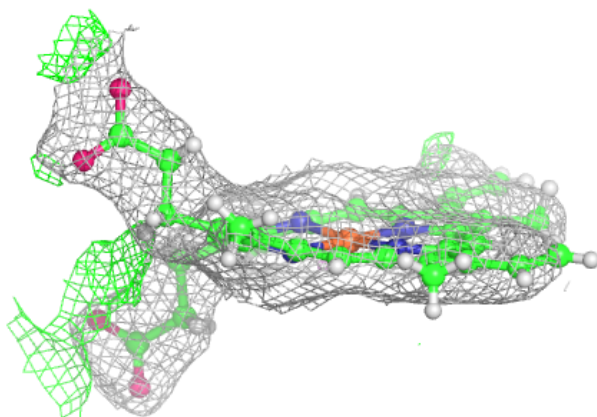
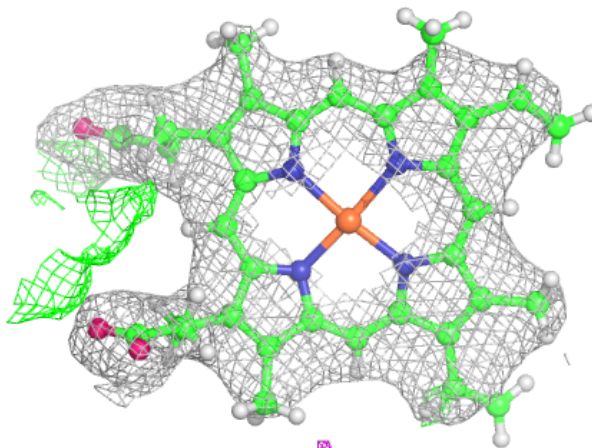
**Electron density around HEM F 101:**

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



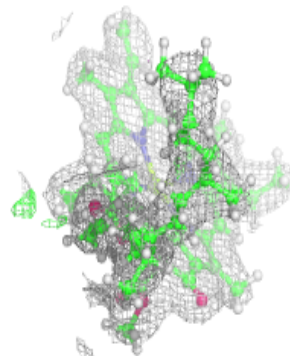
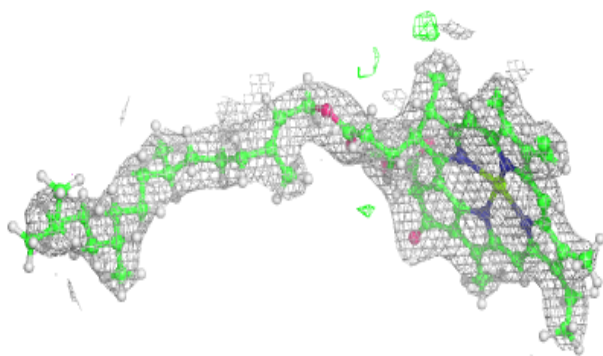
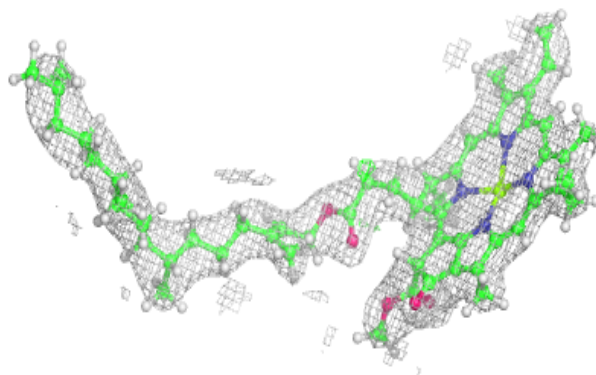
**Electron density around HEM e 101:**

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

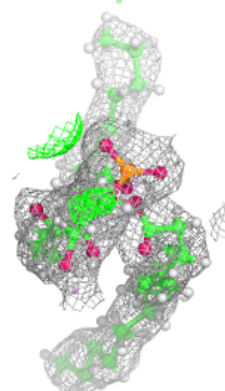
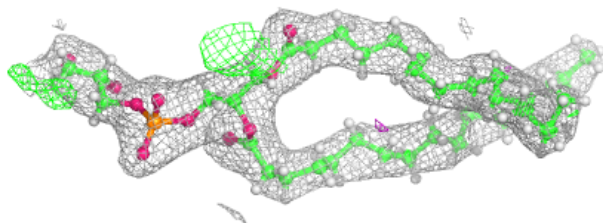
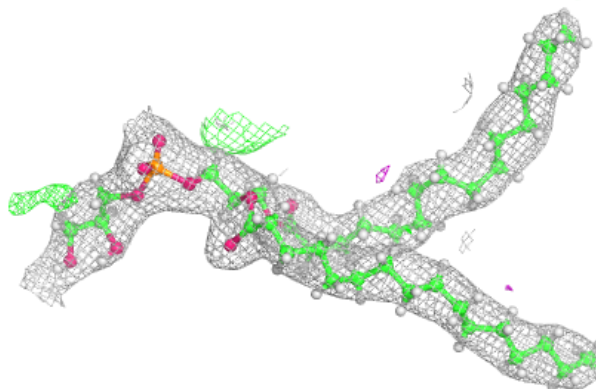


**Electron density around CLA a 402:**

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

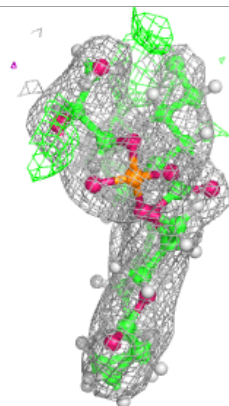
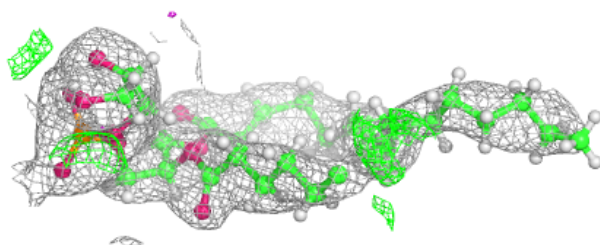
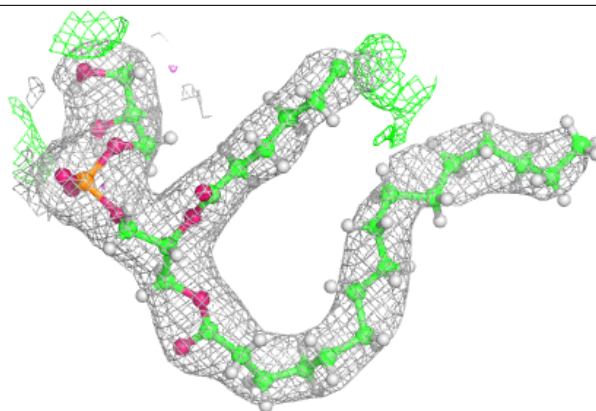
**Electron density around LHG d 406:**

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

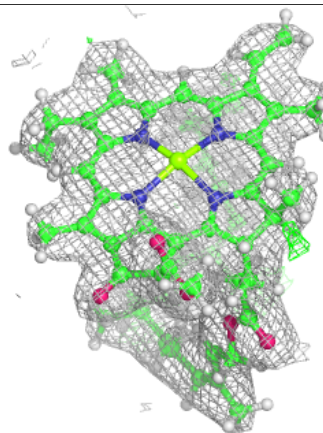
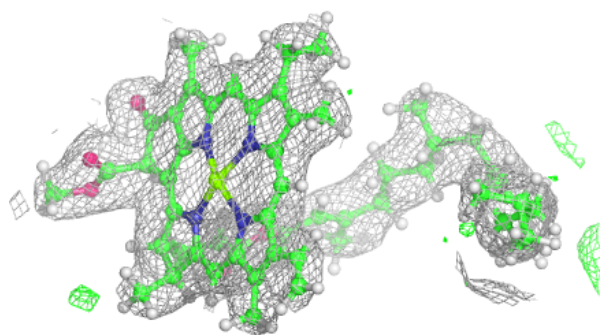
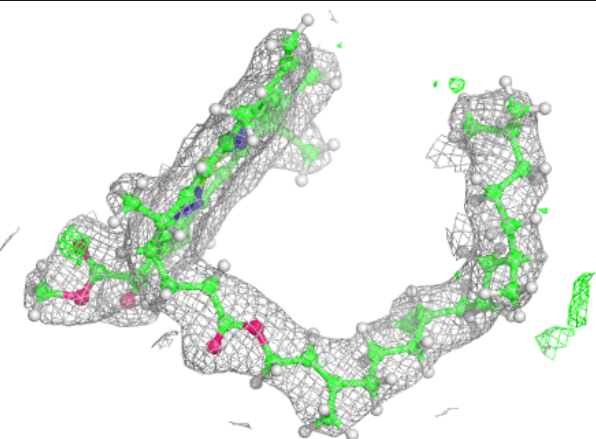


**Electron density around LHG d 407:**

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

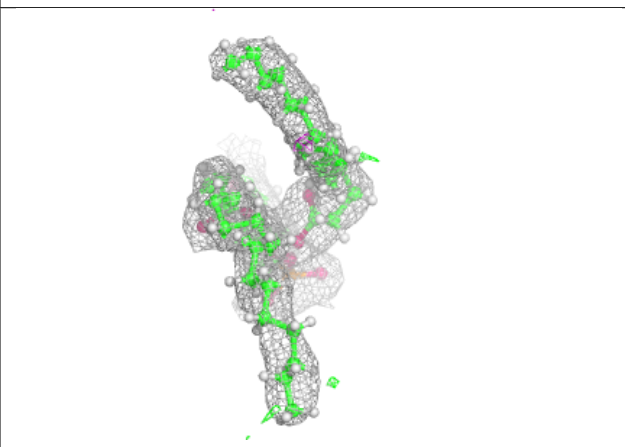
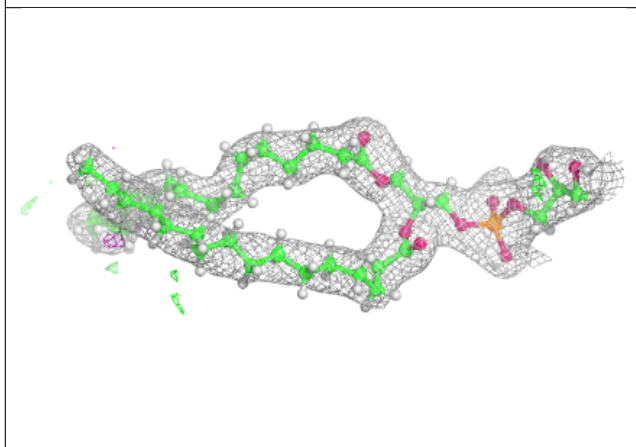
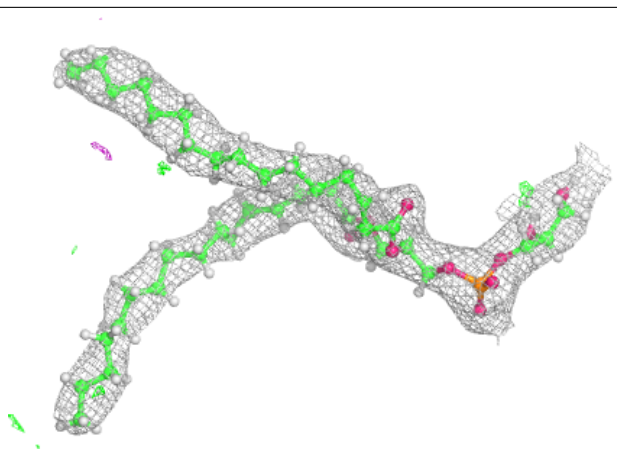
**Electron density around CLA B 611:**

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

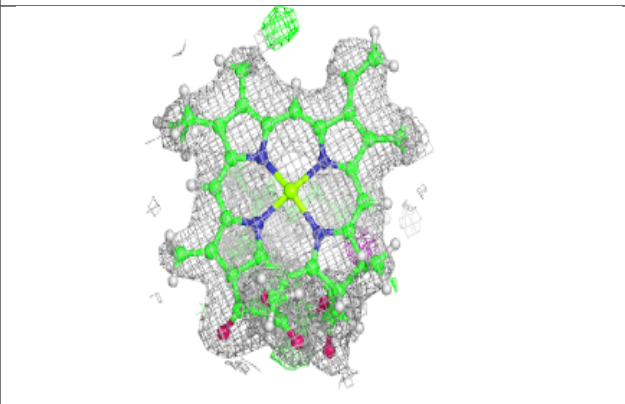
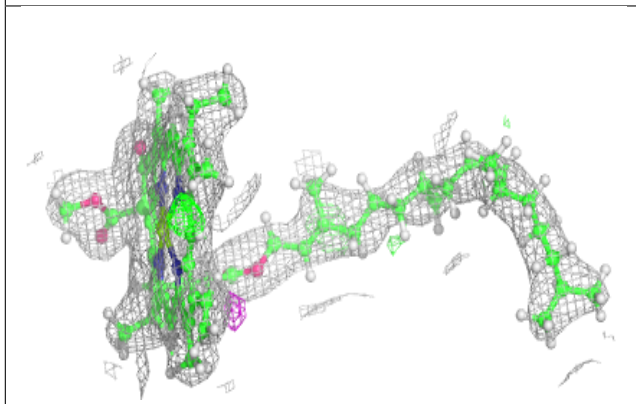
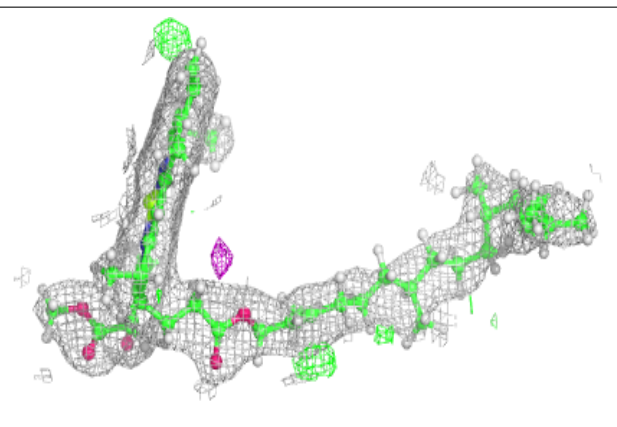


**Electron density around LHG D 409:**

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

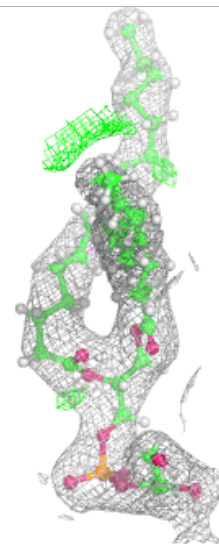
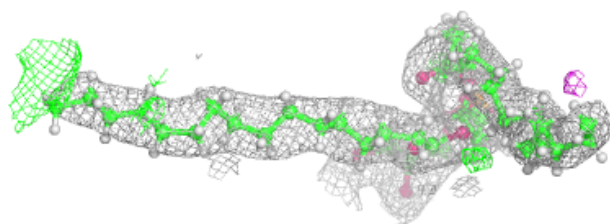
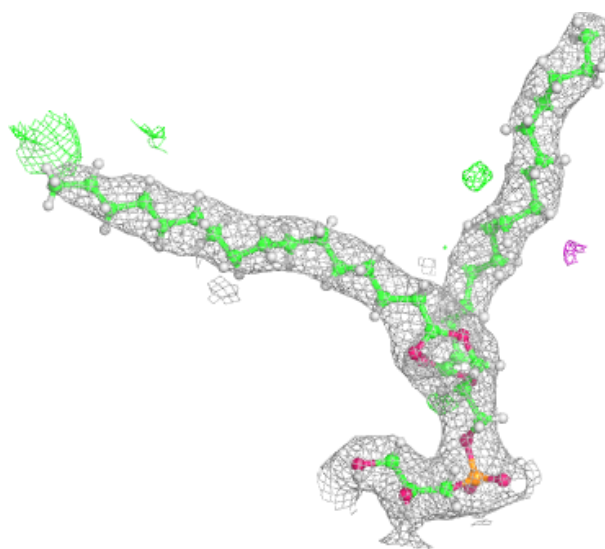
**Electron density around CLA B 605:**

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



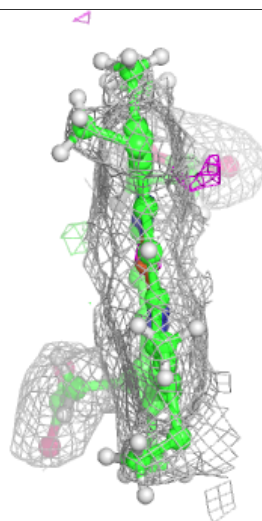
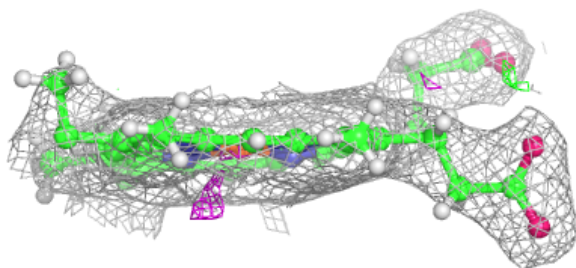
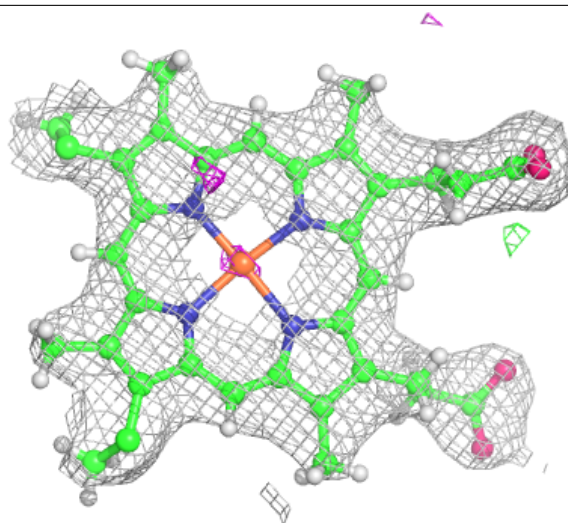
**Electron density around LHG L 102:**

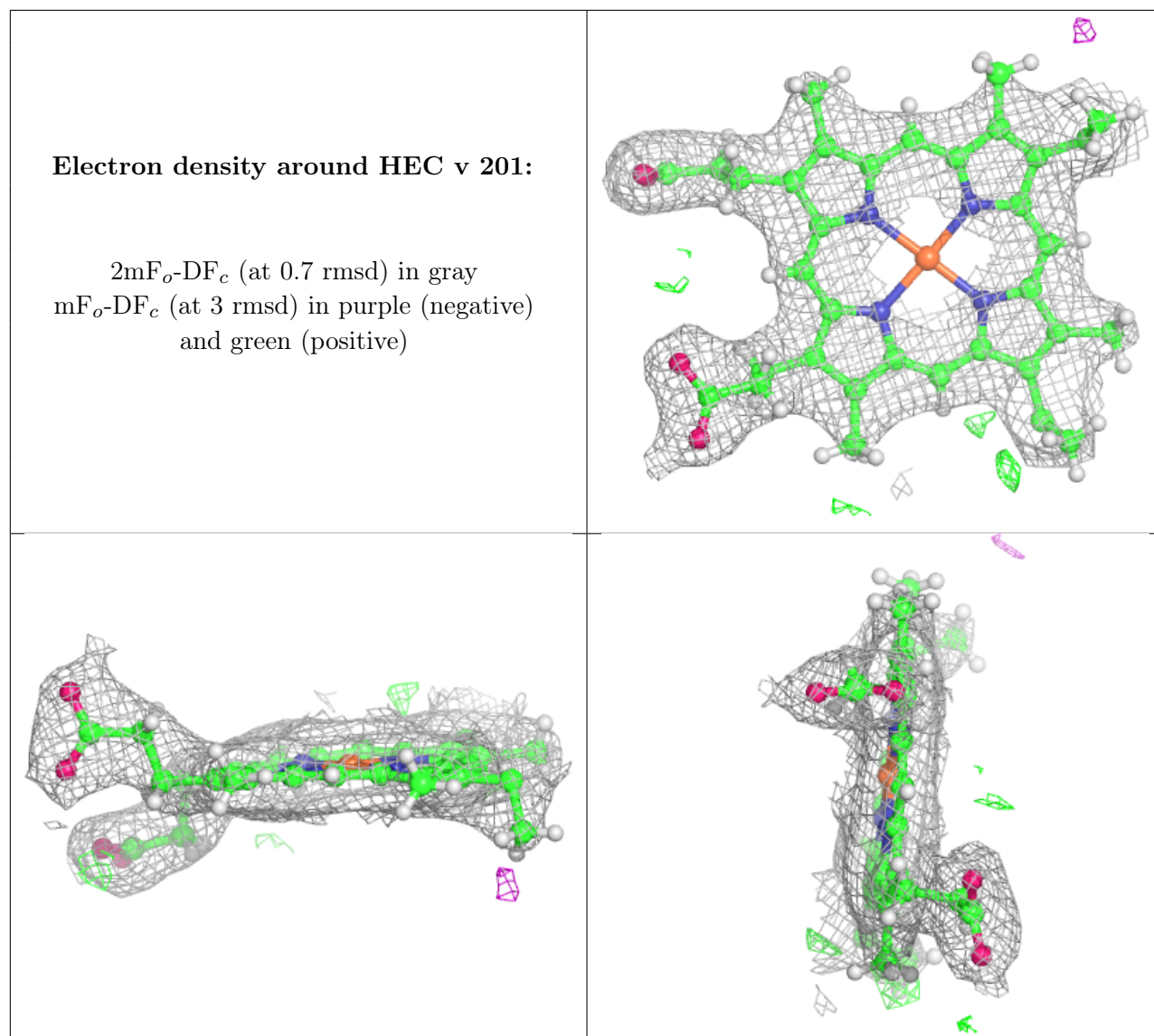
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**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)





## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.