



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 10:01 PM UTC

PDB ID : 8F4F / pdb_00008f4f
Title : RT XFEL structure of Photosystem II 500 microseconds after the third illumination at 2.03 Angstrom resolution
Authors : Bhowmick, A.; Hussein, R.; Bogacz, I.; Simon, P.S.; Ibrahim, M.; Chatterjee, R.; Doyle, M.D.; Cheah, M.H.; Fransson, T.; Chernev, P.; Kim, I.-S.; Makita, H.; Dasgupta, M.; Kaminsky, C.J.; Zhang, M.; Gatcke, J.; Haupt, S.; Nangca, I.I.; Keable, S.M.; Aydin, O.; Tono, K.; Owada, S.; Gee, L.B.; Fuller, F.D.; Batyuk, A.; Alonso-Mori, R.; Holton, J.M.; Paley, D.W.; Moriarty, N.W.; Mamedov, F.; Adams, P.D.; Brewster, A.S.; Dobbek, H.; Sauter, N.K.; Bergmann, U.; Zouni, A.; Messinger, J.; Kern, J.; Yano, J.; Yachandra, V.K.
Deposited on : 2022-11-10
Resolution : 2.03 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0

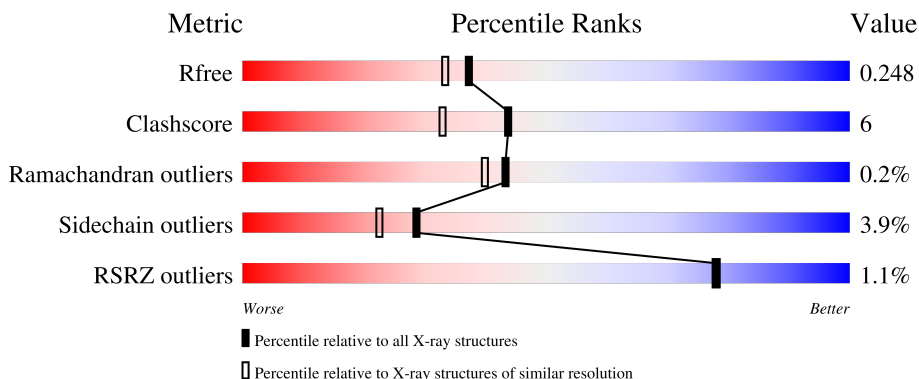
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

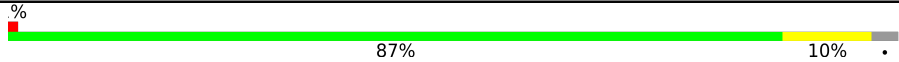
The reported resolution of this entry is 2.03 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (2.04-2.00)



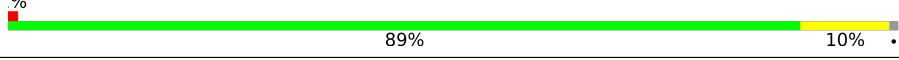
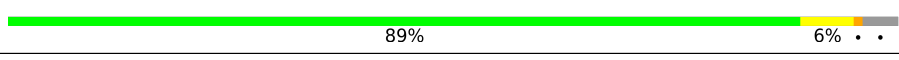

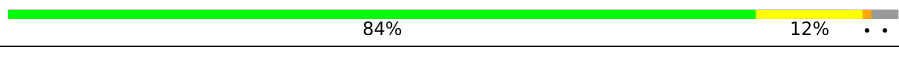

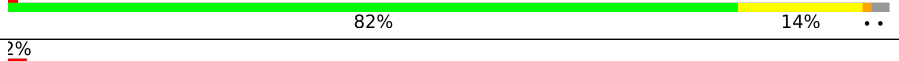

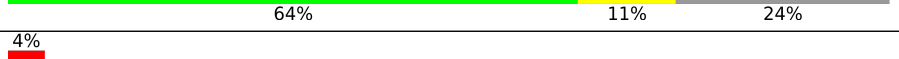
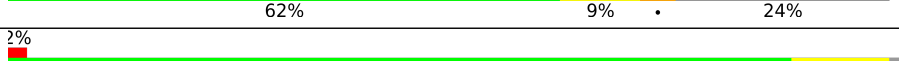
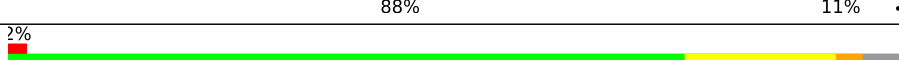
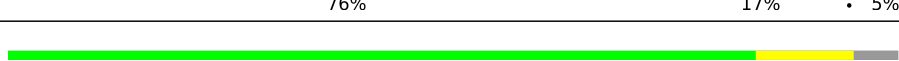
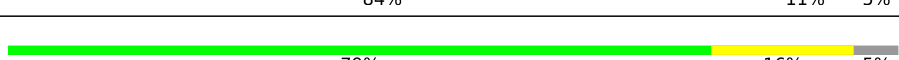
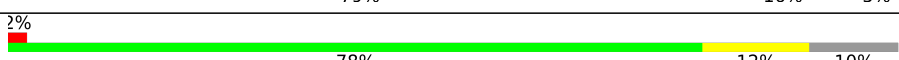
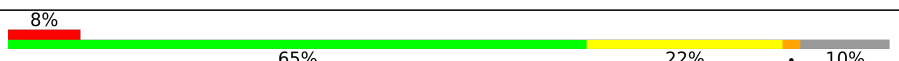
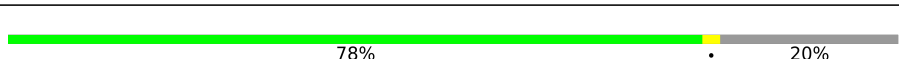
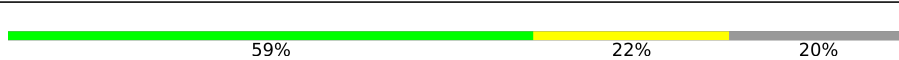



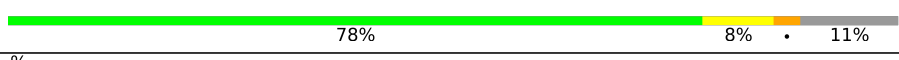
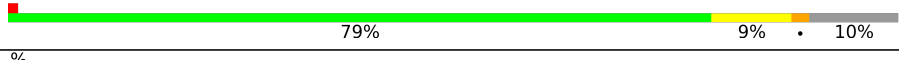
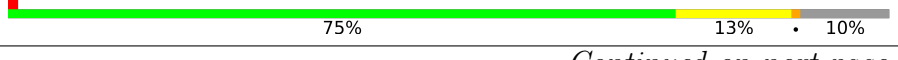

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively.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

Mol	Chain	Length	Quality of chain
1	A	344	

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Buster-report : wwPDB partial adaption of 1.1.7 (2018)
 Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
 CCP4 : 9.0.010 (Gargrove)
 Density-Fitness : 1.0.12
 Ideal geometry (proteins) : Engh & Huber (2001)
 Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
 Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
1	a	344	 83% 12% ..
2	B	510	 88% 10% .
2	b	510	 89% 10% .
3	C	461	 89% 6% ..
3	c	461	 84% 12% ..
4	D	352	 84% 12% ..
4	d	352	 83% 13% ..
5	E	84	 82% 14% ..
5	e	84	 75% 23% .
6	F	45	 64% 11% 24%
6	f	45	 62% 9% . 24%
7	H	66	 88% 11% .
7	h	66	 76% 17% . 5%
8	I	38	 84% 11% 5%
8	i	38	 79% 16% 5%
9	J	40	 78% 12% 10%
9	j	40	 65% 22% . 10%
10	K	46	 78% . 20%
10	k	46	 59% 22% 20%
11	L	37	 84% 16%
11	l	37	 84% 8% 5% .
12	M	36	 78% 14% 8%
12	m	36	 78% 8% . 11%
13	O	272	 79% 9% . 10%
13	o	272	 75% 13% . 10%

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

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
25	CLA	A	606	X	-	-	-
25	CLA	A	607	X	-	-	-
25	CLA	A	608	X	-	-	-
25	CLA	A	611	X	-	-	-
25	CLA	B	601	X	-	-	-
25	CLA	B	602	X	-	-	-
25	CLA	B	603	X	-	-	-
25	CLA	B	604	X	-	-	-
25	CLA	B	605	X	-	-	-
25	CLA	B	606	X	-	-	-
25	CLA	B	607	X	-	-	-
25	CLA	B	608	X	-	-	-
25	CLA	B	610	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	CLA	B	611	X	-	-	-
25	CLA	B	612	X	-	-	-
25	CLA	B	613	X	-	-	-
25	CLA	B	614	X	-	-	-
25	CLA	B	615	X	-	-	-
25	CLA	B	616	X	-	-	-
25	CLA	C	501	X	-	-	-
25	CLA	C	502	X	-	-	-
25	CLA	C	504	X	-	-	-
25	CLA	C	505	X	-	-	-
25	CLA	C	506	X	-	-	-
25	CLA	C	507	X	-	-	-
25	CLA	C	509	X	-	-	-
25	CLA	C	510	X	-	-	-
25	CLA	C	511	X	-	-	-
25	CLA	C	512	X	-	-	-
25	CLA	C	513	X	-	-	-
25	CLA	D	404	X	-	-	-
25	CLA	a	605	X	-	-	-
25	CLA	a	606	X	-	-	-
25	CLA	a	608	X	-	-	-
25	CLA	a	611	X	-	-	-
25	CLA	b	601	X	-	-	-
25	CLA	b	602	X	-	-	-
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25	CLA	b	604	X	-	-	-
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25	CLA	b	612	X	-	-	-
25	CLA	b	613	X	-	-	-
25	CLA	b	614	X	-	-	-
25	CLA	b	615	X	-	-	-
25	CLA	b	616	X	-	-	-
25	CLA	c	501	X	-	-	-
25	CLA	c	502	X	-	-	-
25	CLA	c	503	X	-	-	-
25	CLA	c	504	X	-	-	-
25	CLA	c	505	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	CLA	c	506	X	-	-	-
25	CLA	c	507	X	-	-	-
25	CLA	c	509	X	-	-	-
25	CLA	c	510	X	-	-	-
25	CLA	c	511	X	-	-	-
25	CLA	c	512	X	-	-	-
25	CLA	c	513	X	-	-	-
25	CLA	d	403	X	-	-	-
25	CLA	d	404	X	-	-	-

2 Entry composition [i](#)

There are 36 unique types of molecules in this entry. The entry contains 53209 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Photosystem II protein D1 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	334	3113	2030	513	551	19	0	64	0
1	a	334	3110	2027	513	551	19	0	64	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	505	4005	2631	666	695	13	0	4	0
2	b	505	3978	2610	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	N	O	S			
3	C	442	3509	2302	586	607	14	0	11	0
3	c	451	3583	2343	602	624	14	0	12	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	341	2731	1809	446	464	12	0	2	0
4	d	341	2737	1813	446	466	12	0	3	0

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	82	Total	C	N	O	0	1	0
			666	436	107	123			
5	e	82	Total	C	N	O	0	0	0
			664	434	108	122			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	34	Total	C	N	O	S	0	0	0
			275	187	45	42	1			
6	f	34	Total	C	N	O	S	0	0	0
			275	187	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	N	O	S	0	0	0
			510	341	82	85	2			
7	h	63	Total	C	N	O	S	0	0	0
			498	333	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	N	O	S	0	0	0
			296	200	46	49	1			
8	i	36	Total	C	N	O	S	0	0	0
			296	200	46	49	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	J	36	Total	C	N	O	S	0	0	0
			257	174	40	42	1			
9	j	36	Total	C	N	O	S	0	0	0
			257	174	40	42	1			

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

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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
10	k	37	293	204	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	N	O	S			
11	L	37	304	202	48	53	1	0	0	0
11	l	36	296	197	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	N	O	S			
12	M	33	256	171	37	47	1	0	0	0
12	m	32	251	168	36	46	1	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
13	O	244	1870	1168	313	385	4	0	1	0
13	o	244	1874	1170	317	383	4	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
14	T	30	258	181	36	39	2	0	0	0
14	t	30	256	180	36	38	2	0	0	0

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace	
			Total	C	N				O
15	U	97	774	491	129	154	0	0	0
15	u	97	774	491	129	154	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	V	137	Total	C	N	O	S	0	0	0
			1064	675	177	208	4			
16	v	137	Total	C	N	O	S	0	0	0
			1064	675	177	208	4			

- Molecule 17 is a protein called Photosystem II reaction center protein Ycf12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Y	27	Total	C	N	O	S	0	0	0
			196	128	35	30	3			
17	y	30	Total	C	N	O	S	0	0	0
			218	144	35	36	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	X	38	Total	C	N	O	S	0	0	0
			281	188	45	48				
18	x	39	Total	C	N	O	S	0	0	0
			286	191	46	49				

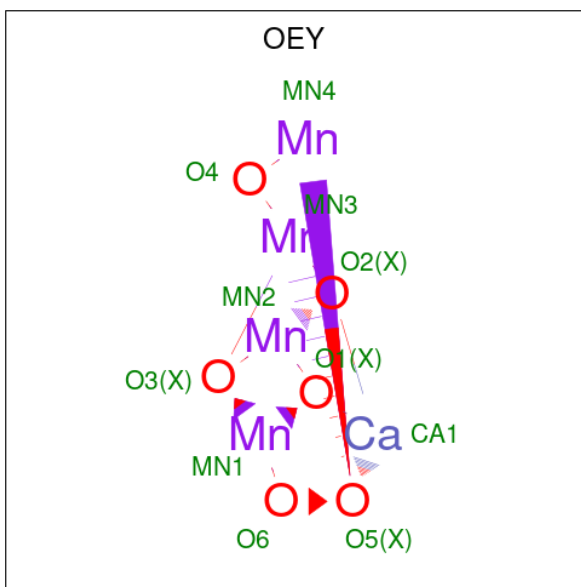
- Molecule 19 is a protein called Photosystem II reaction center protein Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	Z	62	Total	C	N	O	S	0	0	0
			479	328	72	77	2			
19	z	62	Total	C	N	O	S	0	0	0
			477	326	72	77	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	R	34	Total	C	N	O	S	0	0	0
			271	184	47	40				
20	r	31	Total	C	N	O	S	0	0	0
			246	166	43	37				

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	Ca	Mn	O		
21	A	1	22	2	8	12	0	1
21	a	1	22	2	8	12	0	1

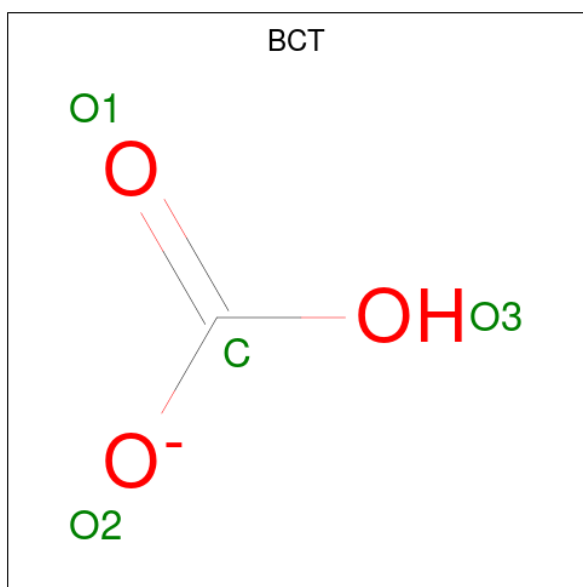
- Molecule 22 is FE (II) ION (CCD ID: FE2) (formula: Fe).

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

- Molecule 23 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

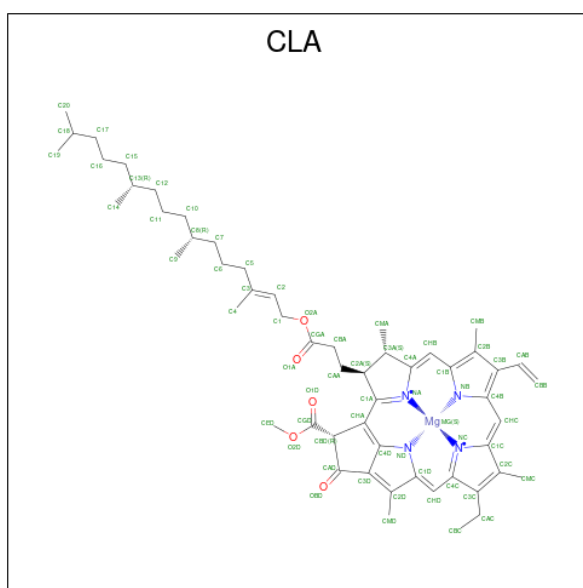
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
23	A	2	2	2	0	0
23	a	2	2	2	0	0

- Molecule 24 is BICARBONATE ION (CCD ID: BCT) (formula: CHO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
24	A	1	Total	C	O			
			4	1	3	0	0	
24	d	1	Total	C	O			
			4	1	3	0	0	

- Molecule 25 is CHLOROPHYLL A (CCD ID: CLA) (formula: $C_{55}H_{72}MgN_4O_5$).



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

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
25	A	1	Total	C	Mg	N	O	0	0
			54	44	1	4	5		
25	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	B	1	Total	C	Mg	N	O	0	0
			60	50	1	4	5		
25	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
25	C	1	Total	C	Mg	N	O	0	0
			59	49	1	4	5		
25	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	D	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	D	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	a	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	a	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	a	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	a	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

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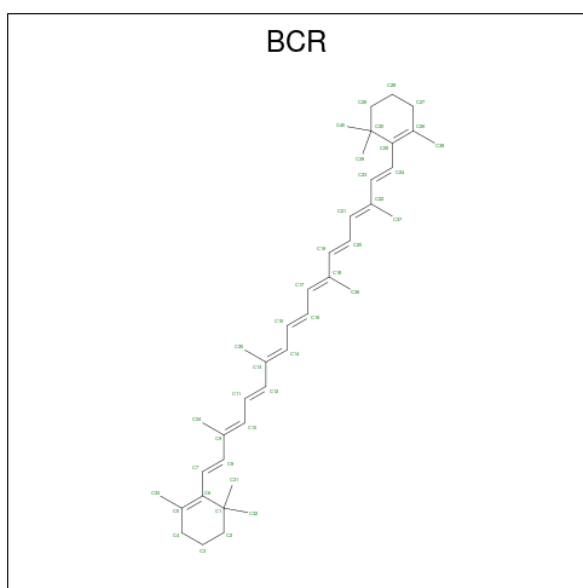
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	b	1	Total	C	Mg	N	O	0	0
			60	50	1	4	5		
25	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	c	1	Total	C	Mg	N	O	0	0
			64	54	1	4	5		
25	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
25	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	d	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
25	d	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

- Molecule 26 is BETA-CAROTENE (CCD ID: BCR) (formula: $C_{40}H_{56}$).



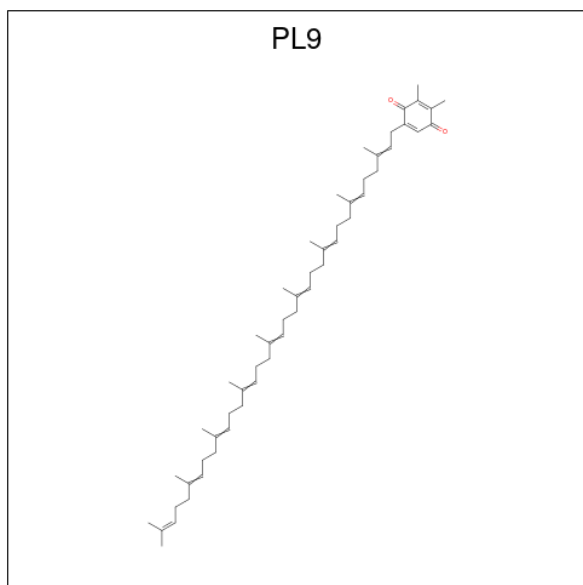
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	A	1	Total	C	0	0
			40	40		
26	B	1	Total	C	0	0
			40	40		
26	B	1	Total	C	0	0
			40	40		
26	B	1	Total	C	0	0
			40	40		
26	C	1	Total	C	0	0
			40	40		
26	D	1	Total	C	0	0
			40	40		

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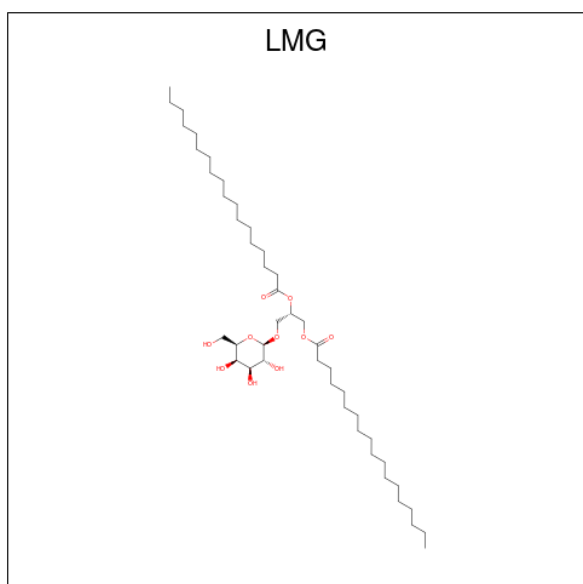
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	H	1	Total C 40 40	0	0
26	K	1	Total C 40 40	0	0
26	K	1	Total C 40 40	0	0
26	K	1	Total C 40 40	0	0
26	T	1	Total C 40 40	0	0
26	a	1	Total C 40 40	0	0
26	b	1	Total C 40 40	0	0
26	b	1	Total C 40 40	0	0
26	b	1	Total C 40 40	0	0
26	c	1	Total C 40 40	0	0
26	d	1	Total C 40 40	0	0
26	h	1	Total C 40 40	0	0
26	k	1	Total C 40 40	0	0
26	k	1	Total C 40 40	0	0
26	k	1	Total C 40 40	0	0
26	t	1	Total C 40 40	0	0

- Molecule 27 is 2,3-DIMETHYL-5-(3,7,11,15,19,23,27,31,35-NONAMETHYL-2,6,10,14,18,22,26,30,34-HEXATRIACONTANONAENYL-2,5-CYCLOHEXADIENE-1,4-DIONE-2,3-DIMETHYL-5-SOLANESYL-1,4-BENZOQUINONE (CCD ID: PL9) (formula: C₅₃H₈₀O₂).



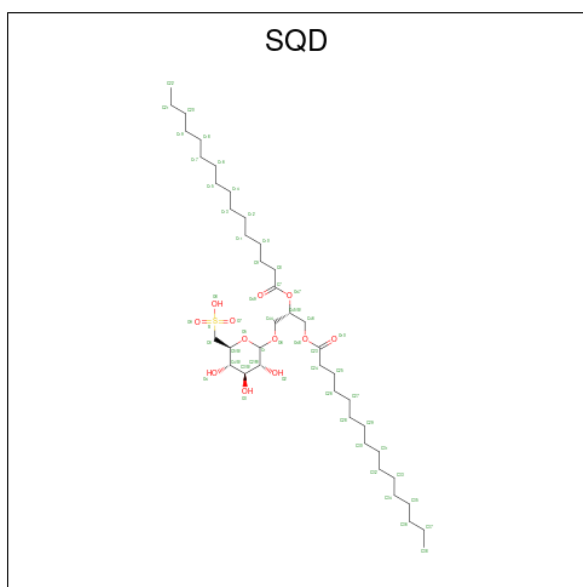
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
27	A	1	55	53	2	0	0
27	D	1	55	53	2	0	0
27	a	1	55	53	2	0	0
27	d	1	55	53	2	0	0

- Molecule 28 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (CCD ID: LMG) (formula: $C_{45}H_{86}O_{10}$).



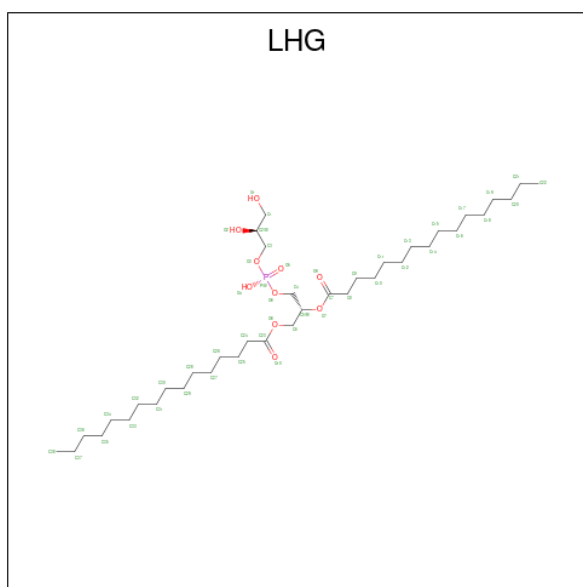
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
28	A	1	Total	C	O	0	0
			48	38	10		
28	B	1	Total	C	O	0	0
			51	41	10		
28	B	1	Total	C	O	0	0
			28	24	4		
28	C	1	Total	C	O	0	0
			48	38	10		
28	D	1	Total	C	O	0	0
			51	41	10		
28	D	1	Total	C	O	0	0
			33	27	6		
28	b	1	Total	C	O	0	0
			55	45	10		
28	c	1	Total	C	O	0	0
			37	27	10		
28	c	1	Total	C	O	0	0
			48	38	10		
28	c	1	Total	C	O	0	0
			49	39	10		
28	d	1	Total	C	O	0	0
			23	21	2		
28	d	1	Total	C	O	0	0
			44	34	10		
28	m	1	Total	C	O	0	0
			51	41	10		

- Molecule 29 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (CCD ID: SQD) (formula: C₄₁H₇₈O₁₂S).



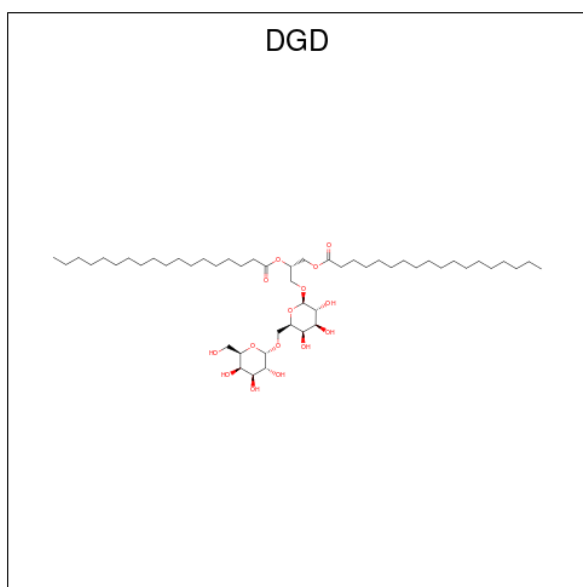
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
29	A	1	Total	C	O	S	0	0
			52	39	12	1		
29	A	1	Total	C	O		0	0
			39	35	4			
29	B	1	Total	C	O	S	0	0
			54	41	12	1		
29	D	1	Total	C	O	S	0	0
			36	25	10	1		
29	a	1	Total	C	O	S	0	0
			54	41	12	1		
29	a	1	Total	C	O		0	0
			36	31	5			
29	b	1	Total	C	O	S	0	0
			49	36	12	1		
29	f	1	Total	C	O	S	0	0
			41	28	12	1		

- Molecule 30 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: $C_{38}H_{75}O_{10}P$).



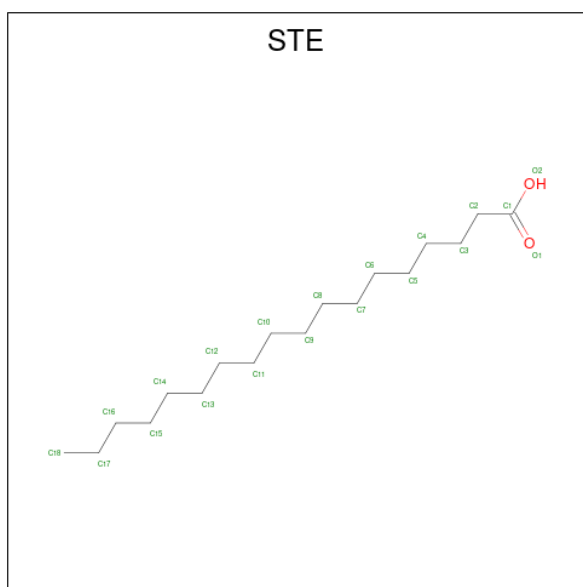
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
30	A	1	49	38	10	1	0	0
30	D	1	49	38	10	1	0	0
30	D	1	47	36	10	1	0	0
30	D	1	49	38	10	1	0	0
30	L	1	49	38	10	1	0	0
30	d	1	49	38	10	1	0	0
30	d	1	49	38	10	1	0	0
30	d	1	39	28	10	1	0	0
30	e	1	42	31	10	1	0	0
30	l	1	49	38	10	1	0	0

- Molecule 31 is DIGALACTOSYL DIACYL GLYCEROL (DGDG) (CCD ID: DGD) (formula: $C_{51}H_{96}O_{15}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
31	A	1	Total	C	O	0	0
			66	51	15		
31	C	1	Total	C	O	0	0
			62	47	15		
31	C	1	Total	C	O	0	0
			62	47	15		
31	H	1	Total	C	O	0	0
			62	47	15		
31	J	1	Total	C	O	0	0
			62	47	15		
31	a	1	Total	C	O	0	0
			44	39	5		
31	c	1	Total	C	O	0	0
			62	47	15		
31	c	1	Total	C	O	0	0
			62	47	15		
31	c	1	Total	C	O	0	0
			62	47	15		
31	h	1	Total	C	O	0	0
			62	47	15		

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



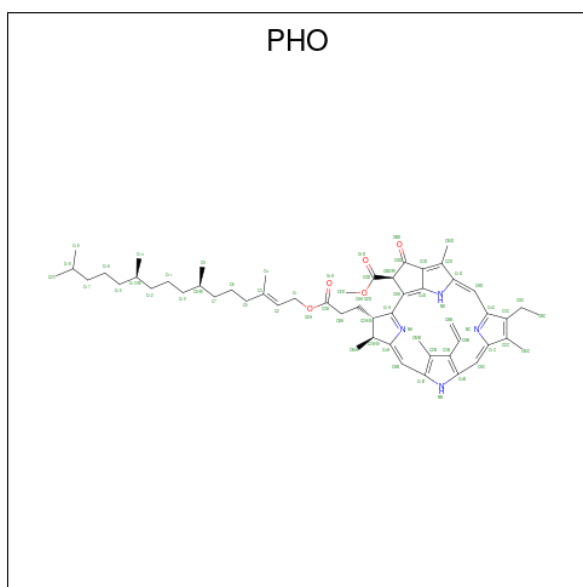
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
32	A	1	Total C O 20 18 2	0	0
32	B	1	Total C O 17 15 2	0	0
32	B	1	Total C O 12 10 2	0	0
32	B	1	Total C O 18 16 2	0	0
32	B	1	Total C O 12 10 2	0	0
32	B	1	Total C 16 16	0	0
32	C	1	Total C O 12 10 2	0	0
32	C	1	Total C O 12 10 2	0	0
32	C	1	Total C 16 16	0	0
32	D	1	Total C O 20 18 2	0	0
32	E	1	Total C O 12 10 2	0	0
32	H	1	Total C 18 18	0	0
32	I	1	Total C 15 15	0	0
32	J	1	Total C O 12 10 2	0	0

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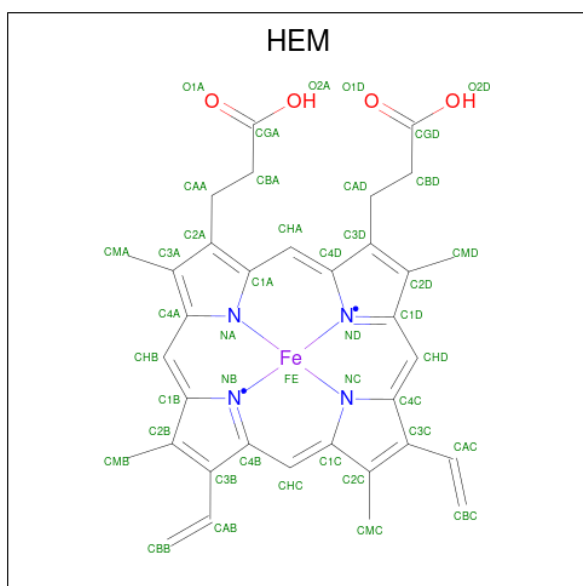
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
32	L	1	Total C O 12 10 2	0	0
32	M	1	Total C O 15 13 2	0	0
32	M	1	Total C 10 10	0	0
32	T	1	Total C 16 16	0	0
32	a	1	Total C O 12 10 2	0	0
32	b	1	Total C O 20 18 2	0	0
32	b	1	Total C O 16 14 2	0	0
32	b	1	Total C 15 15	0	0
32	b	1	Total C 10 10	0	0
32	c	1	Total C O 20 18 2	0	0
32	d	1	Total C O 17 15 2	0	0
32	d	1	Total C O 20 18 2	0	0
32	j	1	Total C O 12 10 2	0	0
32	k	1	Total C O 12 10 2	0	0
32	m	1	Total C 18 18	0	0
32	t	1	Total C O 14 12 2	0	0
32	t	1	Total C 10 10	0	0

- Molecule 33 is PHEOPHYTIN A (CCD ID: PHO) (formula: C₅₅H₇₄N₄O₅).



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

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



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	H	32	Total O 32 32	0	0
36	I	9	Total O 9 9	0	0
36	J	11	Total O 11 11	0	0
36	K	10	Total O 10 10	0	0
36	L	7	Total O 7 7	0	0
36	M	8	Total O 8 8	0	0
36	O	108	Total O 108 108	0	0
36	T	9	Total O 9 9	0	0
36	U	33	Total O 33 33	0	0
36	V	74	Total O 74 74	0	0
36	Y	10	Total O 10 10	0	0
36	X	11	Total O 11 11	0	0
36	Z	4	Total O 4 4	0	0
36	R	4	Total O 4 4	0	0
36	a	107	Total O 111 111	0	4
36	b	171	Total O 171 171	0	0
36	c	150	Total O 150 150	0	0
36	d	94	Total O 94 94	0	0
36	e	16	Total O 16 16	0	0
36	f	3	Total O 3 3	0	0
36	h	16	Total O 16 16	0	0

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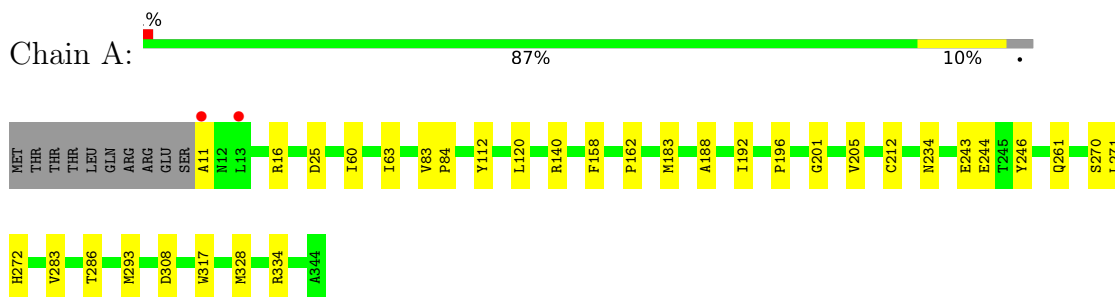
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	i	16	Total O 16 16	0	0
36	j	11	Total O 11 11	0	0
36	k	6	Total O 6 6	0	0
36	l	14	Total O 14 14	0	0
36	m	8	Total O 8 8	0	0
36	o	96	Total O 96 96	0	0
36	t	9	Total O 9 9	0	0
36	u	58	Total O 58 58	0	0
36	v	44	Total O 44 44	0	0
36	y	11	Total O 11 11	0	0
36	x	11	Total O 11 11	0	0
36	r	10	Total O 10 10	0	0

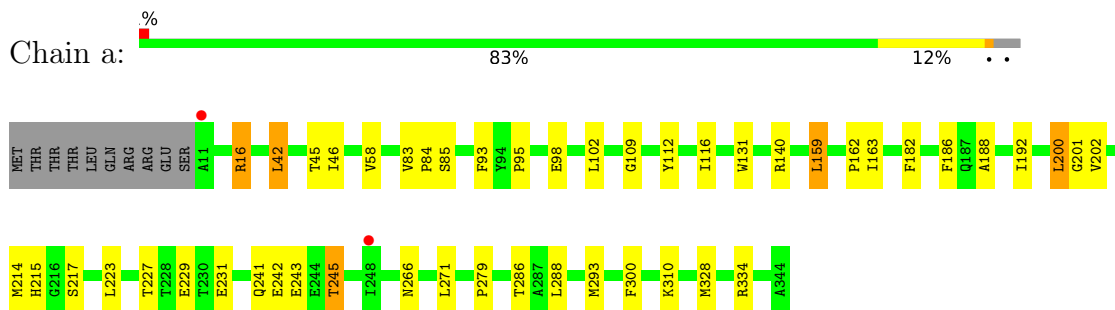
3 Residue-property plots [i](#)

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.

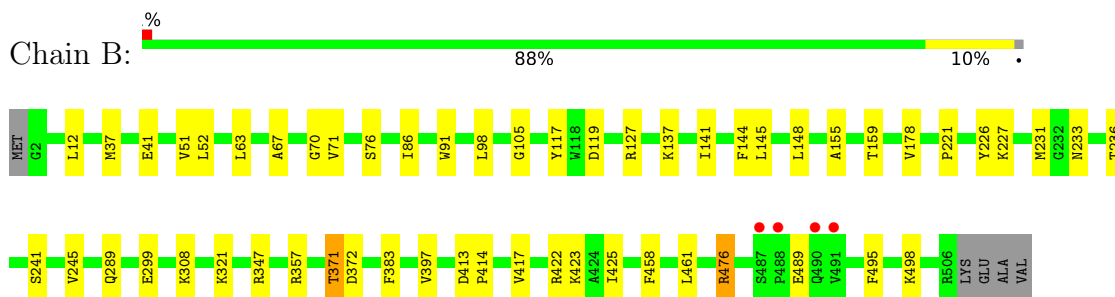
- Molecule 1: Photosystem II protein D1 1



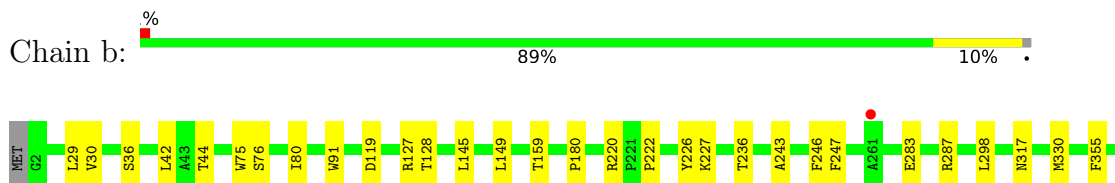
- Molecule 1: Photosystem II protein D1 1

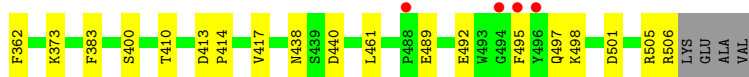


- Molecule 2: Photosystem II CP47 reaction center protein



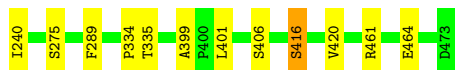
- Molecule 2: Photosystem II CP47 reaction center protein





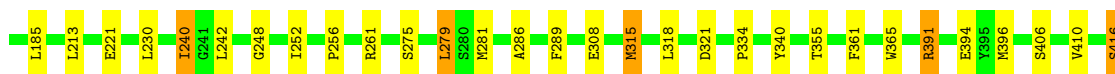
- Molecule 3: Photosystem II CP43 reaction center protein

Chain C: 89% 6% ..



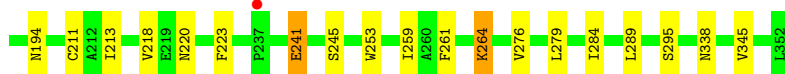
- Molecule 3: Photosystem II CP43 reaction center protein

Chain c: 84% 12% ..



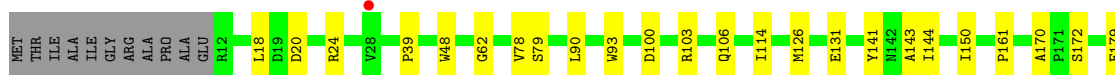
- Molecule 4: Photosystem II D2 protein

Chain D: 84% 12% ..

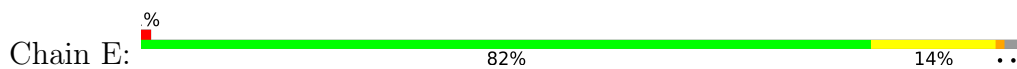


- Molecule 4: Photosystem II D2 protein

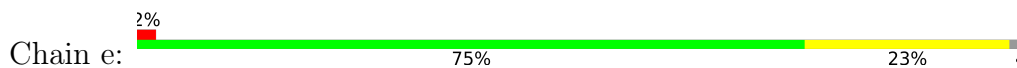
Chain d: 83% 13% ..



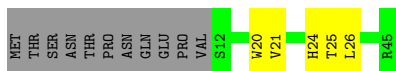
- Molecule 5: Cytochrome b559 subunit alpha



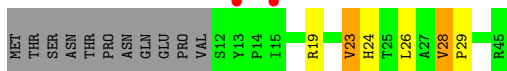
- Molecule 5: Cytochrome b559 subunit alpha



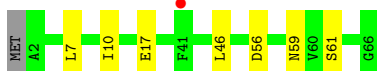
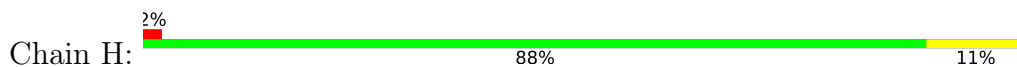
- Molecule 6: Cytochrome b559 subunit beta



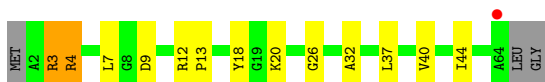
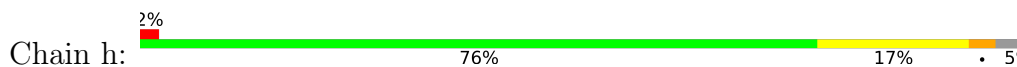
- Molecule 6: Cytochrome b559 subunit beta



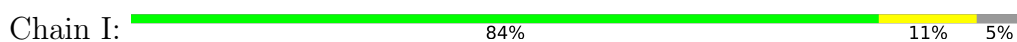
- Molecule 7: Photosystem II reaction center protein H




- Molecule 7: Photosystem II reaction center protein H



- Molecule 8: Photosystem II reaction center protein I




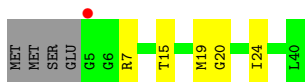
- Molecule 8: Photosystem II reaction center protein I

Chain i:  79% 16% 5%



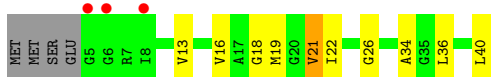
- Molecule 9: Photosystem II reaction center protein J

Chain J:  2% 78% 12% 10%




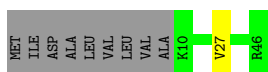
- Molecule 9: Photosystem II reaction center protein J

Chain j:  8% 65% 22% 10%



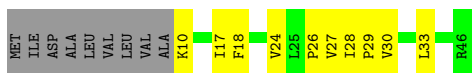
- Molecule 10: Photosystem II reaction center protein K

Chain K:  78% 20%




- Molecule 10: Photosystem II reaction center protein K

Chain k:  59% 22% 20%




- Molecule 11: Photosystem II reaction center protein L

Chain L:  84% 16%




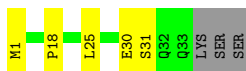
- Molecule 11: Photosystem II reaction center protein L

Chain l:  84% 8% 5% 5%




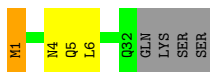
- Molecule 12: Photosystem II reaction center protein M

Chain M:  78% 14% 8%




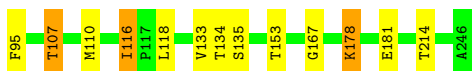
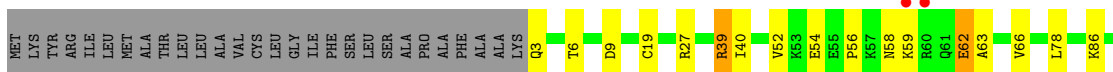
- Molecule 12: Photosystem II reaction center protein M

Chain m:  78% 8% 11%




- Molecule 13: Photosystem II manganese-stabilizing polypeptide

Chain O:  79% 9% 10%




- Molecule 13: Photosystem II manganese-stabilizing polypeptide

Chain o:  75% 13% 10%




- Molecule 14: Photosystem II reaction center protein T

Chain T:  81% 3% 6% 6% 6%




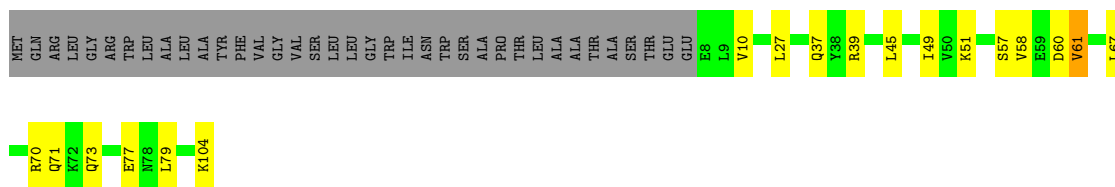
- Molecule 14: Photosystem II reaction center protein T

Chain t:  88% 6% 6%



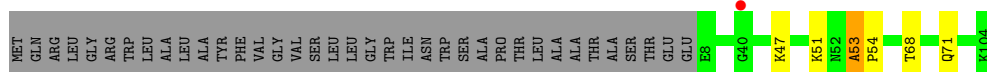
- Molecule 15: Photosystem II 12 kDa extrinsic protein

Chain U:  59% 13% 28%




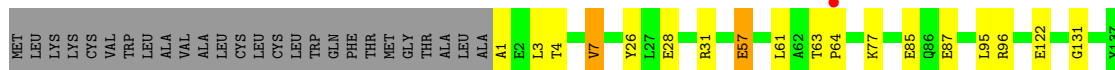
- Molecule 15: Photosystem II 12 kDa extrinsic protein

Chain u:  68% 28%



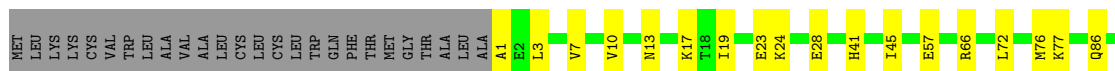
- Molecule 16: Cytochrome c-550

Chain V:  73% 10% 16%



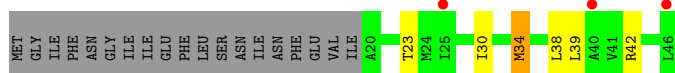
- Molecule 16: Cytochrome c-550

Chain v:  67% 17% 16%



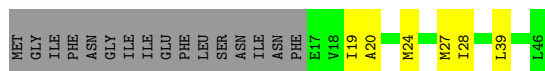
- Molecule 17: Photosystem II reaction center protein Ycf12

Chain Y:  7% 46% 11% 41%

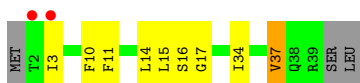


- Molecule 17: Photosystem II reaction center protein Ycf12

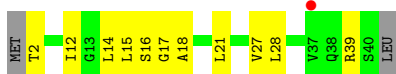
Chain y:  52% 13% 35%



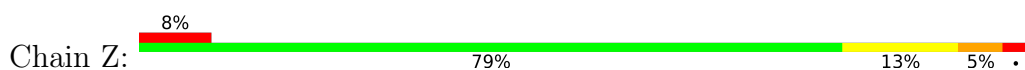
- Molecule 18: Photosystem II reaction center X protein



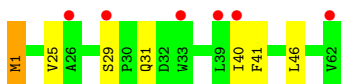
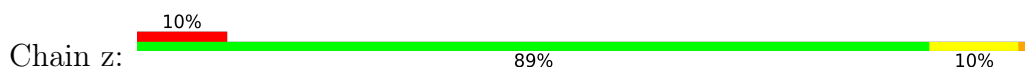
- Molecule 18: Photosystem II reaction center X protein



- Molecule 19: Photosystem II reaction center protein Z



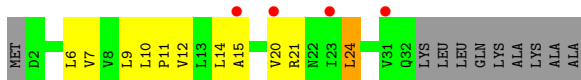
- Molecule 19: Photosystem II reaction center protein Z



- Molecule 20: Photosystem II protein Y



- Molecule 20: Photosystem II protein Y



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	117.53Å 222.83Å 309.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.23 – 2.03 31.23 – 2.03	Depositor EDS
% Data completeness (in resolution range)	98.9 (31.23-2.03) 85.2 (31.23-2.03)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.33 (at 2.03Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.199 , 0.248 0.200 , 0.248	Depositor DCC
R_{free} test set	4617 reflections (0.74%)	wwPDB-VP
Wilson B-factor (Å ²)	27.5	Xtrriage
Anisotropy	0.276	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 56.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	53209	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.62% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.32	0/3212	0.49	0/4376
1	a	0.31	0/3209	0.48	0/4372
2	B	0.33	0/4155	0.48	0/5661
2	b	0.31	0/4118	0.46	0/5611
3	C	0.31	0/3625	0.47	0/4935
3	c	0.29	0/3705	0.45	0/5042
4	D	0.35	0/2825	0.50	0/3847
4	d	0.34	0/2834	0.51	0/3859
5	E	0.25	0/688	0.41	0/940
5	e	0.22	0/683	0.42	0/932
6	F	0.27	0/284	0.42	0/387
6	f	0.27	0/284	0.49	0/387
7	H	0.31	0/523	0.47	0/713
7	h	0.28	0/511	0.44	0/697
8	I	0.31	0/293	0.46	0/396
8	i	0.32	0/293	0.46	0/396
9	J	0.26	0/263	0.38	0/356
9	j	0.25	0/263	0.40	0/356
10	K	0.26	0/303	0.43	0/416
10	k	0.25	0/303	0.41	0/416
11	L	0.34	0/311	0.44	0/422
11	l	0.33	0/303	0.49	0/412
12	M	0.33	0/249	0.45	0/341
12	m	0.34	0/244	0.47	0/334
13	O	0.30	0/1904	0.52	0/2585
13	o	0.31	0/1905	0.50	0/2583
14	T	0.32	0/257	0.48	0/349
14	t	0.30	0/255	0.44	0/346
15	U	0.27	0/785	0.45	0/1064
15	u	0.31	0/785	0.49	0/1064
16	V	0.30	0/1085	0.50	0/1473
16	v	0.26	0/1085	0.43	0/1473

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	Y	0.25	0/197	0.38	0/264
17	y	0.19	0/219	0.40	0/294
18	X	0.25	0/284	0.39	0/384
18	x	0.22	0/289	0.28	0/391
19	Z	0.20	0/490	0.41	0/669
19	z	0.18	0/488	0.30	0/666
20	R	0.25	0/277	0.40	0/380
20	r	0.21	0/252	0.36	0/347
All	All	0.31	0/44038	0.47	0/59936

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
16	V	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
16	V	63	THR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3113	0	2981	29	0
1	a	3110	0	2972	36	0
2	B	4005	0	3871	36	0
2	b	3978	0	3836	38	0
3	C	3509	0	3426	22	0
3	c	3583	0	3499	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	2731	0	2637	35	0
4	d	2737	0	2643	31	0
5	E	666	0	651	11	0
5	e	664	0	648	12	0
6	F	275	0	282	3	0
6	f	275	0	282	4	0
7	H	510	0	532	4	0
7	h	498	0	518	11	0
8	I	296	0	311	1	0
8	i	296	0	311	6	0
9	J	257	0	268	3	0
9	j	257	0	268	7	0
10	K	293	0	305	0	0
10	k	293	0	305	4	0
11	L	304	0	316	8	0
11	l	296	0	304	3	0
12	M	256	0	269	5	0
12	m	251	0	267	4	0
13	O	1870	0	1830	20	0
13	o	1874	0	1846	21	0
14	T	258	0	261	4	0
14	t	256	0	256	1	0
15	U	774	0	773	8	0
15	u	774	0	773	5	0
16	V	1064	0	1073	13	0
16	v	1064	0	1073	15	0
17	Y	196	0	217	4	0
17	y	218	0	241	4	0
18	X	281	0	312	6	0
18	x	286	0	314	9	0
19	Z	479	0	516	10	0
19	z	477	0	509	4	0
20	R	271	0	298	4	0
20	r	246	0	263	4	0
21	A	22	0	0	2	0
21	a	22	0	0	1	0
22	A	1	0	0	0	0
22	a	1	0	0	0	0
23	A	2	0	0	0	0
23	a	2	0	0	0	0
24	A	4	0	1	1	0
24	d	4	0	1	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	A	249	0	264	6	0
25	B	1035	0	1139	30	0
25	C	839	0	922	30	0
25	D	130	0	144	6	0
25	a	260	0	288	8	0
25	b	1035	0	1139	37	0
25	c	839	0	919	36	0
25	d	130	0	144	3	0
26	A	40	0	56	0	0
26	B	120	0	168	5	0
26	C	40	0	56	2	0
26	D	40	0	56	1	0
26	H	40	0	56	5	0
26	K	120	0	168	4	0
26	T	40	0	56	3	0
26	a	40	0	56	0	0
26	b	120	0	168	6	0
26	c	40	0	56	4	0
26	d	40	0	56	1	0
26	h	40	0	56	5	0
26	k	120	0	168	4	0
26	t	40	0	56	4	0
27	A	55	0	80	6	0
27	D	55	0	80	2	0
27	a	55	0	80	5	0
27	d	55	0	80	3	0
28	A	48	0	66	0	0
28	B	79	0	112	7	0
28	C	48	0	66	1	0
28	D	84	0	116	4	0
28	b	55	0	86	1	0
28	c	134	0	181	6	0
28	d	67	0	92	1	0
28	m	51	0	72	4	0
29	A	91	0	136	2	0
29	B	54	0	78	5	0
29	D	36	0	46	1	0
29	a	90	0	134	4	0
29	b	49	0	65	5	0
29	f	41	0	49	3	0
30	A	49	0	74	1	0
30	D	145	0	215	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	L	49	0	74	1	0
30	d	137	0	199	6	0
30	e	42	0	57	5	0
30	l	49	0	74	5	0
31	A	66	0	96	4	0
31	C	124	0	164	2	0
31	H	62	0	82	2	0
31	J	62	0	82	5	0
31	a	44	0	75	3	0
31	c	186	0	246	12	0
31	h	62	0	82	0	0
32	A	20	0	35	0	0
32	B	75	0	117	5	0
32	C	40	0	63	1	0
32	D	20	0	35	6	0
32	E	12	0	16	0	0
32	H	18	0	35	2	0
32	I	15	0	26	2	0
32	J	12	0	16	0	0
32	L	12	0	16	1	0
32	M	25	0	38	0	0
32	T	16	0	31	2	0
32	a	12	0	16	0	0
32	b	61	0	104	4	0
32	c	20	0	35	1	0
32	d	37	0	61	7	0
32	j	12	0	16	1	0
32	k	12	0	16	0	0
32	m	18	0	35	2	0
32	t	24	0	36	0	0
33	D	128	0	148	1	0
33	a	64	0	74	1	0
33	d	64	0	74	3	0
34	E	43	0	30	2	0
34	f	43	0	30	3	0
35	V	43	0	30	0	0
35	v	43	0	30	1	0
36	A	128	0	0	6	0
36	B	185	0	0	2	0
36	C	160	0	0	1	0
36	D	123	0	0	2	0
36	E	17	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	F	2	0	0	0	0
36	H	32	0	0	0	0
36	I	9	0	0	0	0
36	J	11	0	0	0	0
36	K	10	0	0	0	0
36	L	7	0	0	0	0
36	M	8	0	0	1	0
36	O	108	0	0	5	0
36	R	4	0	0	0	0
36	T	9	0	0	0	0
36	U	33	0	0	1	0
36	V	74	0	0	2	0
36	X	11	0	0	0	0
36	Y	10	0	0	1	0
36	Z	4	0	0	0	0
36	a	111	0	0	3	0
36	b	171	0	0	3	0
36	c	150	0	0	2	0
36	d	94	0	0	0	0
36	e	16	0	0	0	0
36	f	3	0	0	0	0
36	h	16	0	0	0	0
36	i	16	0	0	3	0
36	j	11	0	0	2	0
36	k	6	0	0	0	0
36	l	14	0	0	1	0
36	m	8	0	0	1	0
36	o	96	0	0	3	0
36	r	10	0	0	1	0
36	t	9	0	0	0	0
36	u	58	0	0	2	0
36	v	44	0	0	1	0
36	x	11	0	0	0	0
36	y	11	0	0	0	0
All	All	53209	0	52752	630	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 630 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:A:601[B]:OEY:O5	21:A:601[B]:OEY:O6	1.93	0.85
32:D:413:STE:H142	18:X:17:GLY:HA2	1.60	0.83
25:C:513:CLA:HBB1	26:K:101:BCR:H24C	1.58	0.83
15:u:53:ALA:O	36:u:201:HOH:O	1.95	0.82
2:B:357:ARG:NH1	36:D:501:HOH:O	2.15	0.79

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	395/344 (115%)	391 (99%)	4 (1%)	0	100	100
1	a	395/344 (115%)	390 (99%)	5 (1%)	0	100	100
2	B	507/510 (99%)	502 (99%)	5 (1%)	0	100	100
2	b	503/510 (99%)	495 (98%)	8 (2%)	0	100	100
3	C	451/461 (98%)	439 (97%)	11 (2%)	1 (0%)	43	40
3	c	461/461 (100%)	448 (97%)	12 (3%)	1 (0%)	43	40
4	D	340/352 (97%)	331 (97%)	9 (3%)	0	100	100
4	d	341/352 (97%)	331 (97%)	10 (3%)	0	100	100
5	E	81/84 (96%)	81 (100%)	0	0	100	100
5	e	80/84 (95%)	79 (99%)	1 (1%)	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%)	59 (94%)	4 (6%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	35 (100%)	0	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%)	28 (93%)	2 (7%)	0	100	100
13	O	243/272 (89%)	230 (95%)	10 (4%)	3 (1%)	10	4
13	o	242/272 (89%)	234 (97%)	8 (3%)	0	100	100
14	T	28/32 (88%)	28 (100%)	0	0	100	100
14	t	28/32 (88%)	27 (96%)	1 (4%)	0	100	100
15	U	95/134 (71%)	93 (98%)	2 (2%)	0	100	100
15	u	95/134 (71%)	91 (96%)	3 (3%)	1 (1%)	11	5
16	V	135/163 (83%)	128 (95%)	6 (4%)	1 (1%)	18	10
16	v	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
17	Y	25/46 (54%)	22 (88%)	3 (12%)	0	100	100
17	y	28/46 (61%)	28 (100%)	0	0	100	100
18	X	36/41 (88%)	34 (94%)	2 (6%)	0	100	100
18	x	37/41 (90%)	36 (97%)	1 (3%)	0	100	100
19	Z	60/62 (97%)	57 (95%)	1 (2%)	2 (3%)	3	1
19	z	60/62 (97%)	60 (100%)	0	0	100	100
20	R	32/41 (78%)	32 (100%)	0	0	100	100
20	r	29/41 (71%)	28 (97%)	1 (3%)	0	100	100
All	All	5386/5700 (94%)	5252 (98%)	125 (2%)	9 (0%)	43	40

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	416	SER
16	V	64	PRO
19	Z	31	GLN
3	c	416	SER
13	O	59	LYS

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	322/280 (115%)	319 (99%)	3 (1%)	70	73
1	a	321/280 (115%)	309 (96%)	12 (4%)	30	24
2	B	407/407 (100%)	399 (98%)	8 (2%)	48	48
2	b	402/407 (99%)	393 (98%)	9 (2%)	45	45
3	C	353/362 (98%)	347 (98%)	6 (2%)	53	53
3	c	362/362 (100%)	345 (95%)	17 (5%)	23	16
4	D	277/283 (98%)	271 (98%)	6 (2%)	45	45
4	d	278/283 (98%)	266 (96%)	12 (4%)	26	19
5	E	72/73 (99%)	69 (96%)	3 (4%)	26	20
5	e	71/73 (97%)	67 (94%)	4 (6%)	19	12
6	F	28/39 (72%)	27 (96%)	1 (4%)	31	26
6	f	28/39 (72%)	26 (93%)	2 (7%)	13	7
7	H	54/55 (98%)	52 (96%)	2 (4%)	30	24
7	h	53/55 (96%)	50 (94%)	3 (6%)	18	11
8	I	32/34 (94%)	30 (94%)	2 (6%)	16	9
8	i	32/34 (94%)	32 (100%)	0	100	100
9	J	24/28 (86%)	24 (100%)	0	100	100
9	j	24/28 (86%)	22 (92%)	2 (8%)	10	5
10	K	30/37 (81%)	29 (97%)	1 (3%)	33	29
10	k	30/37 (81%)	26 (87%)	4 (13%)	4	1
11	L	35/35 (100%)	34 (97%)	1 (3%)	37	34
11	l	34/35 (97%)	30 (88%)	4 (12%)	5	1
12	M	28/32 (88%)	27 (96%)	1 (4%)	31	26
12	m	28/32 (88%)	28 (100%)	0	100	100
13	O	206/228 (90%)	198 (96%)	8 (4%)	28	22
13	o	207/228 (91%)	195 (94%)	12 (6%)	18	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	T	26/28 (93%)	25 (96%)	1 (4%)	29	23
14	t	25/28 (89%)	24 (96%)	1 (4%)	28	22
15	U	84/112 (75%)	77 (92%)	7 (8%)	10	5
15	u	84/112 (75%)	84 (100%)	0	100	100
16	V	117/138 (85%)	115 (98%)	2 (2%)	53	53
16	v	117/138 (85%)	113 (97%)	4 (3%)	32	28
17	Y	19/37 (51%)	16 (84%)	3 (16%)	2	0
17	y	22/37 (60%)	20 (91%)	2 (9%)	9	4
18	X	31/34 (91%)	28 (90%)	3 (10%)	8	2
18	x	31/34 (91%)	28 (90%)	3 (10%)	8	2
19	Z	52/52 (100%)	43 (83%)	9 (17%)	2	0
19	z	51/52 (98%)	49 (96%)	2 (4%)	28	22
20	R	28/33 (85%)	23 (82%)	5 (18%)	2	0
20	r	25/33 (76%)	18 (72%)	7 (28%)	0	0
All	All	4450/4654 (96%)	4278 (96%)	172 (4%)	28	22

5 of 172 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	d	233	ARG
13	o	53	LYS
4	d	291	LEU
7	h	7	LEU
13	o	130	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
2	b	338	GLN
3	c	25	ASN
13	o	219	GLN
2	b	497	GLN
3	c	311	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
14	FME	T	1	14	8,9,10	1.28	1 (12%)	8,9,11	1.10	1 (12%)
12	FME	m	1	12	8,9,10	1.04	1 (12%)	8,9,11	0.90	0
12	FME	M	1	12	8,9,10	0.99	0	8,9,11	1.01	0
8	FME	I	1	8	8,9,10	1.06	1 (12%)	8,9,11	0.69	0
14	FME	t	1	14	8,9,10	1.10	0	8,9,11	0.80	0
8	FME	i	1	8	8,9,10	1.00	0	8,9,11	1.04	1 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
14	FME	T	1	14	-	1/7/9/11	-
12	FME	m	1	12	-	3/7/9/11	-
12	FME	M	1	12	-	1/7/9/11	-
8	FME	I	1	8	-	0/7/9/11	-
14	FME	t	1	14	-	3/7/9/11	-
8	FME	i	1	8	-	0/7/9/11	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	T	1	FME	CA-N	-2.87	1.42	1.46
8	I	1	FME	CA-N	-2.10	1.43	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	m	1	FME	CA-N	-2.04	1.43	1.46

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	T	1	FME	C-CA-N	2.58	114.48	109.50
8	i	1	FME	CA-N-CN	-2.01	119.73	122.82

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	m	1	FME	O-C-CA-CB
14	t	1	FME	C-CA-CB-CG
14	t	1	FME	N-CA-CB-CG
14	T	1	FME	CB-CG-SD-CE
14	t	1	FME	CB-CG-SD-CE

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	T	1	FME	1	0
12	m	1	FME	1	0
12	M	1	FME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 188 ligands modelled in this entry, 6 are monoatomic - leaving 182 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
25	CLA	B	608	-	69,73,73	1.22	10 (14%)	82,113,113	1.35	7 (8%)
25	CLA	C	501	-	69,73,73	1.49	10 (14%)	82,113,113	1.48	7 (8%)
35	HEC	v	201	16	46,50,50	1.90	4 (8%)	58,82,82	1.80	5 (8%)
26	BCR	k	103	-	41,41,41	1.02	2 (4%)	56,56,56	1.09	2 (3%)
31	DGD	c	515	-	63,63,67	0.99	4 (6%)	77,77,81	1.40	11 (14%)
32	STE	b	625	-	9,9,19	0.40	0	8,8,19	0.63	0
32	STE	L	102	-	11,11,19	0.67	0	11,11,19	1.19	1 (9%)
25	CLA	C	507	36	69,73,73	1.27	7 (10%)	82,113,113	1.48	9 (10%)
25	CLA	a	605	-	69,73,73	1.44	10 (14%)	82,113,113	1.46	8 (9%)
26	BCR	d	405	-	41,41,41	1.05	3 (7%)	56,56,56	1.17	5 (8%)
25	CLA	B	605	-	69,73,73	1.21	7 (10%)	82,113,113	1.32	9 (10%)
25	CLA	B	613	-	69,73,73	1.34	7 (10%)	82,113,113	1.41	6 (7%)
32	STE	H	103	-	17,17,19	0.36	0	16,16,19	0.80	0
25	CLA	C	506	-	69,73,73	1.23	7 (10%)	82,113,113	1.35	7 (8%)
32	STE	b	621	-	19,19,19	0.59	0	19,19,19	1.14	0
27	PL9	D	406	-	55,55,55	0.98	4 (7%)	68,69,69	1.48	15 (22%)
25	CLA	b	616	-	64,68,73	1.30	8 (12%)	76,107,113	1.56	7 (9%)
25	CLA	C	509	-	69,73,73	1.20	8 (11%)	82,113,113	1.28	8 (9%)
32	STE	B	627	-	15,15,19	0.33	0	14,14,19	0.87	0
32	STE	M	101	-	14,14,19	0.67	0	14,14,19	1.25	1 (7%)
35	HEC	V	201	16	46,50,50	1.83	6 (13%)	58,82,82	1.96	8 (13%)
29	SQD	a	612	-	52,54,54	1.60	7 (13%)	62,65,65	1.77	9 (14%)
31	DGD	C	516	-	63,63,67	1.04	5 (7%)	77,77,81	1.36	10 (12%)
32	STE	d	413	-	19,19,19	0.56	0	19,19,19	1.19	1 (5%)
29	SQD	B	623	-	52,54,54	1.57	8 (15%)	62,65,65	1.56	8 (12%)
28	LMG	c	521	-	49,49,55	0.89	3 (6%)	57,57,63	1.26	7 (12%)
25	CLA	c	502	-	69,73,73	1.25	6 (8%)	82,113,113	1.31	7 (8%)
32	STE	C	520	-	15,15,19	0.38	0	14,14,19	0.80	0
32	STE	t	102	-	13,13,19	0.70	0	13,13,19	1.16	2 (15%)
28	LMG	C	517	-	48,48,55	0.82	1 (2%)	56,56,63	1.33	6 (10%)
32	STE	B	626	-	11,11,19	0.66	0	11,11,19	1.55	2 (18%)
25	CLA	b	603	-	69,73,73	1.29	9 (13%)	82,113,113	1.33	10 (12%)
25	CLA	c	511	3	69,73,73	1.44	6 (8%)	82,113,113	1.46	7 (8%)
31	DGD	c	517	-	63,63,67	0.92	3 (4%)	77,77,81	1.39	10 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
21	OEY	a	601[B]	3,36,1	0,16,16	-	-	-	-	-
26	BCR	H	101	-	41,41,41	0.97	2 (4%)	56,56,56	1.22	6 (10%)
31	DGD	J	101	-	63,63,67	0.84	3 (4%)	77,77,81	1.41	11 (14%)
21	OEY	a	601[A]	3,36,1	0,16,16	-	-	-	-	-
25	CLA	c	512	-	69,73,73	1.33	12 (17%)	82,113,113	1.35	7 (8%)
29	SQD	A	613	-	50,52,54	1.58	7 (14%)	60,63,65	1.95	12 (20%)
25	CLA	b	610	36	69,73,73	1.26	6 (8%)	82,113,113	1.21	8 (9%)
25	CLA	c	510	-	69,73,73	1.35	7 (10%)	82,113,113	1.26	8 (9%)
25	CLA	B	604	-	69,73,73	1.45	7 (10%)	82,113,113	1.58	9 (10%)
25	CLA	d	404	-	69,73,73	1.22	9 (13%)	82,113,113	1.29	8 (9%)
25	CLA	b	607	36	69,73,73	1.10	5 (7%)	82,113,113	1.26	10 (12%)
25	CLA	c	506	-	69,73,73	1.33	8 (11%)	82,113,113	1.27	6 (7%)
25	CLA	B	616	-	64,68,73	1.27	7 (10%)	76,107,113	1.36	6 (7%)
25	CLA	b	602	-	69,73,73	1.20	7 (10%)	82,113,113	1.34	8 (9%)
31	DGD	a	614	-	43,43,67	0.69	2 (4%)	45,45,81	1.40	6 (13%)
31	DGD	h	102	-	63,63,67	0.96	4 (6%)	77,77,81	1.45	12 (15%)
25	CLA	c	509	-	69,73,73	1.17	8 (11%)	82,113,113	1.47	7 (8%)
33	PHO	a	607	-	58,69,69	2.03	10 (17%)	55,99,99	1.39	6 (10%)
25	CLA	b	606	-	69,73,73	1.29	7 (10%)	82,113,113	1.45	7 (8%)
25	CLA	d	403	-	69,73,73	1.20	8 (11%)	82,113,113	1.26	6 (7%)
31	DGD	c	516	-	63,63,67	1.03	7 (11%)	77,77,81	1.45	15 (19%)
33	PHO	D	401	-	58,69,69	1.91	10 (17%)	55,99,99	1.39	4 (7%)
25	CLA	a	611	36	69,73,73	1.39	7 (10%)	82,113,113	1.41	11 (13%)
30	LHG	D	410	-	46,46,48	0.82	3 (6%)	49,52,54	1.28	6 (12%)
24	BCT	d	401	22	3,3,3	1.16	0	2,3,3	2.97	1 (50%)
25	CLA	B	603	-	69,73,73	1.35	6 (8%)	82,113,113	1.37	9 (10%)
25	CLA	b	604	-	69,73,73	1.32	8 (11%)	82,113,113	1.49	11 (13%)
28	LMG	d	410	-	21,21,55	0.52	0	20,20,63	1.19	2 (10%)
26	BCR	K	103	-	41,41,41	1.07	2 (4%)	56,56,56	1.16	2 (3%)
32	STE	b	624	-	14,14,19	0.30	0	13,13,19	0.97	0
25	CLA	D	404	-	69,73,73	1.26	8 (11%)	82,113,113	1.20	4 (4%)
26	BCR	t	101	-	41,41,41	0.98	2 (4%)	56,56,56	1.28	6 (10%)
33	PHO	d	402	-	58,69,69	2.07	10 (17%)	55,99,99	1.54	8 (14%)
28	LMG	c	518	-	37,37,55	0.95	2 (5%)	45,45,63	1.31	5 (11%)
26	BCR	b	619	-	41,41,41	0.97	2 (4%)	56,56,56	1.16	3 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	BCR	b	617	-	41,41,41	1.07	3 (7%)	56,56,56	1.34	7 (12%)
30	LHG	e	101	-	41,41,48	0.78	1 (2%)	44,47,54	1.31	6 (13%)
27	PL9	d	406	-	55,55,55	0.90	1 (1%)	68,69,69	1.58	14 (20%)
26	BCR	K	101	-	41,41,41	1.05	2 (4%)	56,56,56	1.32	8 (14%)
33	PHO	D	402	-	58,69,69	2.14	9 (15%)	55,99,99	1.48	6 (10%)
25	CLA	B	607	36	69,73,73	1.14	6 (8%)	82,113,113	1.26	6 (7%)
34	HEM	f	101	5,6	50,50,50	1.58	11 (22%)	67,82,82	1.34	8 (11%)
25	CLA	c	503	-	69,73,73	1.26	8 (11%)	82,113,113	1.49	7 (8%)
25	CLA	A	611	36	69,73,73	1.19	6 (8%)	82,113,113	1.41	7 (8%)
32	STE	I	101	-	14,14,19	0.35	0	13,13,19	0.88	0
27	PL9	A	610	-	55,55,55	0.71	0	68,69,69	1.50	10 (14%)
25	CLA	c	507	36	69,73,73	1.24	9 (13%)	82,113,113	1.37	7 (8%)
29	SQD	a	613	-	35,35,54	1.73	5 (14%)	37,37,65	1.37	3 (8%)
28	LMG	m	101	-	51,51,55	0.91	3 (5%)	59,59,63	1.39	7 (11%)
26	BCR	b	618	-	41,41,41	1.09	2 (4%)	56,56,56	1.26	6 (10%)
32	STE	m	102	-	17,17,19	0.36	0	16,16,19	0.90	0
25	CLA	B	615	-	69,73,73	1.29	6 (8%)	82,113,113	1.41	7 (8%)
32	STE	B	624	-	11,11,19	0.75	0	11,11,19	1.40	2 (18%)
34	HEM	E	101	5,6	50,50,50	1.54	6 (12%)	67,82,82	1.15	5 (7%)
31	DGD	H	102	-	63,63,67	1.10	7 (11%)	77,77,81	1.44	9 (11%)
25	CLA	b	601	36	69,73,73	1.40	7 (10%)	82,113,113	1.40	9 (10%)
32	STE	b	623	-	15,15,19	0.67	0	15,15,19	1.12	0
25	CLA	b	609	-	69,73,73	1.27	7 (10%)	82,113,113	1.38	9 (10%)
28	LMG	D	411	-	31,31,55	0.69	1 (3%)	33,33,63	1.24	3 (9%)
28	LMG	c	520	-	48,48,55	0.82	1 (2%)	56,56,63	1.39	9 (16%)
25	CLA	b	605	-	69,73,73	1.21	6 (8%)	82,113,113	1.35	10 (12%)
26	BCR	c	514	-	41,41,41	1.09	3 (7%)	56,56,56	1.17	5 (8%)
25	CLA	B	609	-	69,73,73	1.24	8 (11%)	82,113,113	1.36	6 (7%)
28	LMG	D	407	-	51,51,55	0.94	3 (5%)	59,59,63	1.36	8 (13%)
32	STE	J	102	-	11,11,19	0.72	0	11,11,19	1.16	0
25	CLA	b	611	-	69,73,73	1.33	6 (8%)	82,113,113	1.35	9 (10%)
25	CLA	c	505	-	69,73,73	1.29	8 (11%)	82,113,113	1.37	8 (9%)
32	STE	t	103	-	9,9,19	0.32	0	8,8,19	0.84	0
30	LHG	d	408	-	48,48,48	0.69	0	51,54,54	1.26	6 (11%)
32	STE	B	625	-	17,17,19	0.68	0	17,17,19	1.00	0
26	BCR	T	101	-	41,41,41	1.01	2 (4%)	56,56,56	1.27	6 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	CLA	B	602	-	69,73,73	1.21	5 (7%)	82,113,113	1.36	8 (9%)
29	SQD	A	615	-	38,38,54	1.74	5 (13%)	40,40,65	1.13	2 (5%)
32	STE	E	102	-	11,11,19	0.77	0	11,11,19	1.13	1 (9%)
25	CLA	C	505	-	69,73,73	1.20	7 (10%)	82,113,113	1.21	7 (8%)
26	BCR	k	102	-	41,41,41	1.06	3 (7%)	56,56,56	1.09	2 (3%)
25	CLA	B	610	36	69,73,73	1.18	7 (10%)	82,113,113	1.39	10 (12%)
25	CLA	A	607	36	69,73,73	1.44	8 (11%)	82,113,113	1.41	14 (17%)
25	CLA	B	612	-	69,73,73	1.24	8 (11%)	82,113,113	1.36	9 (10%)
25	CLA	B	606	-	69,73,73	1.36	7 (10%)	82,113,113	1.51	8 (9%)
30	LHG	L	101	-	48,48,48	0.64	1 (2%)	51,54,54	1.27	4 (7%)
26	BCR	D	405	-	41,41,41	0.99	2 (4%)	56,56,56	1.24	4 (7%)
25	CLA	C	508	-	69,73,73	1.30	9 (13%)	82,113,113	1.51	11 (13%)
29	SQD	f	102	-	39,41,54	1.65	7 (17%)	49,52,65	1.70	10 (20%)
25	CLA	C	511	3	69,73,73	1.34	8 (11%)	82,113,113	1.44	5 (6%)
25	CLA	C	513	-	69,73,73	1.39	9 (13%)	82,113,113	1.30	8 (9%)
28	LMG	b	622	-	55,55,55	0.87	4 (7%)	63,63,63	1.43	11 (17%)
25	CLA	C	504	36	63,67,73	1.50	10 (15%)	74,105,113	1.36	10 (13%)
32	STE	M	102	-	9,9,19	0.37	0	8,8,19	0.83	0
25	CLA	B	611	-	69,73,73	1.16	7 (10%)	82,113,113	1.40	9 (10%)
32	STE	a	615	-	11,11,19	0.80	0	11,11,19	1.01	0
25	CLA	A	608	-	58,62,73	1.27	8 (13%)	68,99,113	1.40	12 (17%)
25	CLA	a	606	36	69,73,73	1.26	6 (8%)	82,113,113	1.37	9 (10%)
25	CLA	c	508	-	68,72,73	1.35	9 (13%)	80,111,113	1.30	7 (8%)
32	STE	D	413	-	19,19,19	0.59	0	19,19,19	1.14	0
32	STE	C	519	-	11,11,19	0.72	0	11,11,19	1.10	0
27	PL9	a	610	-	55,55,55	0.75	0	68,69,69	1.47	11 (16%)
32	STE	k	104	-	11,11,19	0.76	0	11,11,19	1.07	0
28	LMG	B	620	-	51,51,55	0.83	2 (3%)	59,59,63	1.36	5 (8%)
25	CLA	B	601	36	69,73,73	1.34	7 (10%)	82,113,113	1.53	8 (9%)
26	BCR	h	101	-	41,41,41	0.99	2 (4%)	56,56,56	1.26	6 (10%)
25	CLA	B	614	-	69,73,73	1.38	9 (13%)	82,113,113	1.27	10 (12%)
32	STE	j	101	-	11,11,19	0.74	0	11,11,19	1.19	1 (9%)
25	CLA	b	613	-	69,73,73	1.24	7 (10%)	82,113,113	1.34	10 (12%)
25	CLA	c	504	36	64,68,73	1.32	7 (10%)	76,107,113	1.31	8 (10%)
28	LMG	B	622	-	26,26,55	0.76	2 (7%)	26,26,63	1.21	1 (3%)
30	LHG	A	614	-	48,48,48	0.79	2 (4%)	51,54,54	1.20	5 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	STE	B	621	-	16,16,19	0.70	0	16,16,19	1.04	0
26	BCR	a	609	-	41,41,41	0.96	2 (4%)	56,56,56	1.17	4 (7%)
24	BCT	A	605	22	3,3,3	1.15	0	2,3,3	2.84	1 (50%)
25	CLA	C	503	-	69,73,73	1.39	9 (13%)	82,113,113	1.54	10 (12%)
28	LMG	d	411	-	44,44,55	0.90	2 (4%)	52,52,63	1.33	6 (11%)
26	BCR	B	619	-	41,41,41	1.00	2 (4%)	56,56,56	1.37	9 (16%)
32	STE	c	519	-	19,19,19	0.64	0	19,19,19	0.89	0
25	CLA	c	513	-	69,73,73	1.20	7 (10%)	82,113,113	1.24	6 (7%)
32	STE	T	102	-	15,15,19	0.38	0	14,14,19	0.75	0
31	DGD	C	515	-	63,63,67	1.02	5 (7%)	77,77,81	1.30	10 (12%)
29	SQD	b	620	-	47,49,54	1.65	9 (19%)	57,60,65	1.88	11 (19%)
30	LHG	l	101	-	48,48,48	0.82	2 (4%)	51,54,54	1.23	4 (7%)
25	CLA	D	403	-	69,73,73	1.20	7 (10%)	82,113,113	1.36	10 (12%)
25	CLA	b	608	-	69,73,73	1.26	9 (13%)	82,113,113	1.32	8 (9%)
29	SQD	D	408	-	34,36,54	1.50	6 (17%)	42,45,65	1.84	11 (26%)
25	CLA	b	612	-	69,73,73	1.14	5 (7%)	82,113,113	1.37	11 (13%)
31	DGD	A	616	-	67,67,67	1.09	9 (13%)	81,81,81	1.33	10 (12%)
21	OEY	A	601[B]	3,36,1	0,16,16	-	-	-	-	-
25	CLA	C	502	-	69,73,73	1.12	6 (8%)	82,113,113	1.23	5 (6%)
25	CLA	C	510	-	69,73,73	1.29	10 (14%)	82,113,113	1.48	7 (8%)
32	STE	d	412	-	16,16,19	0.65	0	16,16,19	1.10	0
21	OEY	A	601[A]	3,36,1	0,16,16	-	-	-	-	-
28	LMG	A	612	-	48,48,55	0.70	0	56,56,63	1.36	6 (10%)
26	BCR	K	102	-	41,41,41	1.09	2 (4%)	56,56,56	1.17	3 (5%)
25	CLA	b	614	-	69,73,73	1.38	7 (10%)	82,113,113	1.29	10 (12%)
26	BCR	k	101	-	41,41,41	1.09	2 (4%)	56,56,56	1.23	7 (12%)
25	CLA	C	512	-	69,73,73	1.36	9 (13%)	82,113,113	1.38	10 (12%)
30	LHG	d	407	-	48,48,48	0.82	3 (6%)	51,54,54	1.30	5 (9%)
26	BCR	C	514	-	41,41,41	1.04	2 (4%)	56,56,56	1.21	6 (10%)
30	LHG	D	412	-	48,48,48	0.82	1 (2%)	51,54,54	1.38	7 (13%)
26	BCR	A	609	-	41,41,41	0.92	1 (2%)	56,56,56	1.23	5 (8%)
26	BCR	B	618	-	41,41,41	1.09	2 (4%)	56,56,56	1.22	5 (8%)
25	CLA	c	501	-	69,73,73	1.31	9 (13%)	82,113,113	1.38	6 (7%)
26	BCR	B	617	-	41,41,41	1.00	3 (7%)	56,56,56	1.24	3 (5%)
32	STE	C	518	-	11,11,19	0.71	0	11,11,19	1.38	1 (9%)
25	CLA	b	615	-	69,73,73	1.40	7 (10%)	82,113,113	1.29	5 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
30	LHG	d	409	-	38,38,48	0.71	1 (2%)	41,44,54	1.14	3 (7%)
25	CLA	a	608	-	69,73,73	1.23	6 (8%)	82,113,113	1.17	4 (4%)
32	STE	A	617	-	19,19,19	0.62	0	19,19,19	0.95	0
25	CLA	A	606	-	69,73,73	1.35	8 (11%)	82,113,113	1.34	7 (8%)
30	LHG	D	409	-	48,48,48	0.74	3 (6%)	51,54,54	1.25	7 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	CLA	B	608	-	1/1/15/20	1/39/115/115	-
25	CLA	C	501	-	1/1/15/20	5/39/115/115	-
35	HEC	v	201	16	-	6/14/54/54	-
26	BCR	k	103	-	-	5/29/63/63	0/2/2/2
31	DGD	c	515	-	-	27/51/91/95	0/2/2/2
32	STE	b	625	-	-	4/7/7/17	-
32	STE	L	102	-	-	4/9/9/17	-
25	CLA	C	507	36	1/1/15/20	9/39/115/115	-
25	CLA	a	605	-	1/1/15/20	1/39/115/115	-
26	BCR	d	405	-	-	7/29/63/63	0/2/2/2
25	CLA	B	605	-	1/1/15/20	10/39/115/115	-
25	CLA	B	613	-	1/1/15/20	13/39/115/115	-
32	STE	H	103	-	-	11/15/15/17	-
25	CLA	C	506	-	1/1/15/20	12/39/115/115	-
32	STE	b	621	-	-	11/17/17/17	-
27	PL9	D	406	-	-	10/53/73/73	0/1/1/1
25	CLA	b	616	-	1/1/14/20	4/33/109/115	-
25	CLA	C	509	-	1/1/15/20	13/39/115/115	-
32	STE	B	627	-	-	7/13/13/17	-
32	STE	M	101	-	-	3/12/12/17	-
35	HEC	V	201	16	-	6/14/54/54	-
29	SQD	a	612	-	-	29/49/69/69	0/1/1/1
31	DGD	C	516	-	-	17/51/91/95	0/2/2/2
32	STE	d	413	-	-	10/17/17/17	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
29	SQD	B	623	-	-	25/49/69/69	0/1/1/1
28	LMG	c	521	-	-	27/44/64/70	0/1/1/1
25	CLA	c	502	-	1/1/15/20	10/39/115/115	-
32	STE	C	520	-	-	5/13/13/17	-
32	STE	t	102	-	-	7/11/11/17	-
28	LMG	C	517	-	-	18/43/63/70	0/1/1/1
32	STE	B	626	-	-	3/9/9/17	-
25	CLA	b	603	-	1/1/15/20	6/39/115/115	-
25	CLA	c	511	3	1/1/15/20	5/39/115/115	-
31	DGD	c	517	-	-	22/51/91/95	0/2/2/2
26	BCR	H	101	-	-	3/29/63/63	0/2/2/2
31	DGD	J	101	-	-	15/51/91/95	0/2/2/2
25	CLA	c	512	-	1/1/15/20	16/39/115/115	-
29	SQD	A	613	-	-	19/47/67/69	0/1/1/1
25	CLA	b	610	36	1/1/15/20	9/39/115/115	-
25	CLA	c	510	-	1/1/15/20	11/39/115/115	-
25	CLA	B	604	-	1/1/15/20	13/39/115/115	-
25	CLA	d	404	-	1/1/15/20	7/39/115/115	-
25	CLA	b	607	36	1/1/15/20	11/39/115/115	-
25	CLA	c	506	-	1/1/15/20	11/39/115/115	-
25	CLA	B	616	-	1/1/14/20	12/33/109/115	-
25	CLA	b	602	-	1/1/15/20	9/39/115/115	-
31	DGD	a	614	-	-	26/45/45/95	-
31	DGD	h	102	-	-	16/51/91/95	0/2/2/2
25	CLA	c	509	-	1/1/15/20	13/39/115/115	-
33	PHO	a	607	-	-	4/37/103/103	0/5/6/6
25	CLA	b	606	-	1/1/15/20	12/39/115/115	-
25	CLA	d	403	-	1/1/15/20	10/39/115/115	-
31	DGD	c	516	-	-	23/51/91/95	0/2/2/2
33	PHO	D	401	-	-	3/37/103/103	0/5/6/6
25	CLA	a	611	36	1/1/15/20	3/39/115/115	-
30	LHG	D	410	-	-	21/51/51/53	-
25	CLA	B	603	-	1/1/15/20	10/39/115/115	-
25	CLA	b	604	-	1/1/15/20	8/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	LMG	d	410	-	-	11/17/17/70	-
26	BCR	K	103	-	-	7/29/63/63	0/2/2/2
32	STE	b	624	-	-	10/12/12/17	-
25	CLA	D	404	-	1/1/15/20	9/39/115/115	-
26	BCR	t	101	-	-	4/29/63/63	0/2/2/2
33	PHO	d	402	-	-	11/37/103/103	0/5/6/6
28	LMG	c	518	-	-	13/31/51/70	0/1/1/1
26	BCR	b	619	-	-	4/29/63/63	0/2/2/2
26	BCR	b	617	-	-	4/29/63/63	0/2/2/2
30	LHG	e	101	-	-	22/46/46/53	-
27	PL9	d	406	-	-	13/53/73/73	0/1/1/1
26	BCR	K	101	-	-	11/29/63/63	0/2/2/2
33	PHO	D	402	-	-	1/37/103/103	0/5/6/6
25	CLA	B	607	36	1/1/15/20	9/39/115/115	-
34	HEM	f	101	5,6	-	2/14/54/54	-
25	CLA	c	503	-	1/1/15/20	13/39/115/115	-
25	CLA	A	611	36	1/1/15/20	4/39/115/115	-
32	STE	I	101	-	-	4/12/12/17	-
27	PL9	A	610	-	-	20/53/73/73	0/1/1/1
25	CLA	c	507	36	1/1/15/20	10/39/115/115	-
29	SQD	a	613	-	-	22/37/37/69	-
28	LMG	m	101	-	-	24/46/66/70	0/1/1/1
26	BCR	b	618	-	-	5/29/63/63	0/2/2/2
32	STE	m	102	-	-	8/15/15/17	-
25	CLA	B	615	-	1/1/15/20	7/39/115/115	-
32	STE	B	624	-	-	5/9/9/17	-
34	HEM	E	101	5,6	-	2/14/54/54	-
31	DGD	H	102	-	-	17/51/91/95	0/2/2/2
25	CLA	b	601	36	1/1/15/20	17/39/115/115	-
32	STE	b	623	-	-	9/13/13/17	-
25	CLA	b	609	-	-	12/39/115/115	-
28	LMG	D	411	-	-	13/33/33/70	-
28	LMG	c	520	-	-	20/43/63/70	0/1/1/1
25	CLA	b	605	-	1/1/15/20	8/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	BCR	c	514	-	-	2/29/63/63	0/2/2/2
25	CLA	B	609	-	-	7/39/115/115	-
28	LMG	D	407	-	-	19/46/66/70	0/1/1/1
32	STE	J	102	-	-	3/9/9/17	-
25	CLA	b	611	-	1/1/15/20	11/39/115/115	-
25	CLA	c	505	-	1/1/15/20	9/39/115/115	-
32	STE	t	103	-	-	5/7/7/17	-
30	LHG	d	408	-	-	19/53/53/53	-
32	STE	B	625	-	-	5/15/15/17	-
26	BCR	T	101	-	-	8/29/63/63	0/2/2/2
25	CLA	B	602	-	1/1/15/20	10/39/115/115	-
29	SQD	A	615	-	-	15/39/39/69	-
32	STE	E	102	-	-	5/9/9/17	-
25	CLA	C	505	-	1/1/15/20	6/39/115/115	-
26	BCR	k	102	-	-	7/29/63/63	0/2/2/2
25	CLA	B	610	36	1/1/15/20	7/39/115/115	-
25	CLA	B	612	-	1/1/15/20	10/39/115/115	-
25	CLA	A	607	36	1/1/15/20	7/39/115/115	-
25	CLA	B	606	-	1/1/15/20	14/39/115/115	-
30	LHG	L	101	-	-	15/53/53/53	-
26	BCR	D	405	-	-	5/29/63/63	0/2/2/2
25	CLA	C	508	-	-	6/39/115/115	-
29	SQD	f	102	-	-	14/36/56/69	0/1/1/1
25	CLA	C	511	3	1/1/15/20	6/39/115/115	-
25	CLA	C	513	-	1/1/15/20	13/39/115/115	-
28	LMG	b	622	-	-	27/50/70/70	0/1/1/1
25	CLA	C	504	36	1/1/13/20	8/32/108/115	-
32	STE	M	102	-	-	2/7/7/17	-
25	CLA	B	611	-	1/1/15/20	2/39/115/115	-
32	STE	a	615	-	-	5/9/9/17	-
25	CLA	A	608	-	1/1/12/20	5/26/102/115	-
25	CLA	a	606	36	1/1/15/20	8/39/115/115	-
25	CLA	c	508	-	-	8/38/114/115	-
32	STE	D	413	-	-	12/17/17/17	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	STE	C	519	-	-	5/9/9/17	-
27	PL9	a	610	-	-	16/53/73/73	0/1/1/1
32	STE	k	104	-	-	4/9/9/17	-
28	LMG	B	620	-	-	14/46/66/70	0/1/1/1
25	CLA	B	601	36	1/1/15/20	18/39/115/115	-
26	BCR	h	101	-	-	7/29/63/63	0/2/2/2
25	CLA	B	614	-	1/1/15/20	16/39/115/115	-
32	STE	j	101	-	-	5/9/9/17	-
25	CLA	b	613	-	1/1/15/20	8/39/115/115	-
25	CLA	c	504	36	1/1/14/20	7/33/109/115	-
28	LMG	B	622	-	-	12/22/22/70	-
30	LHG	A	614	-	-	24/53/53/53	-
32	STE	B	621	-	-	6/14/14/17	-
26	BCR	a	609	-	-	0/29/63/63	0/2/2/2
25	CLA	C	503	-	-	7/39/115/115	-
28	LMG	d	411	-	-	15/39/59/70	0/1/1/1
26	BCR	B	619	-	-	3/29/63/63	0/2/2/2
32	STE	c	519	-	-	11/17/17/17	-
25	CLA	c	513	-	1/1/15/20	12/39/115/115	-
32	STE	T	102	-	-	8/13/13/17	-
31	DGD	C	515	-	-	17/51/91/95	0/2/2/2
29	SQD	b	620	-	-	22/44/64/69	0/1/1/1
30	LHG	l	101	-	-	15/53/53/53	-
25	CLA	D	403	-	-	7/39/115/115	-
25	CLA	b	608	-	1/1/15/20	5/39/115/115	-
29	SQD	D	408	-	-	15/28/48/69	0/1/1/1
25	CLA	b	612	-	1/1/15/20	12/39/115/115	-
31	DGD	A	616	-	-	28/55/95/95	0/2/2/2
25	CLA	C	502	-	1/1/15/20	6/39/115/115	-
25	CLA	C	510	-	1/1/15/20	7/39/115/115	-
32	STE	d	412	-	-	8/14/14/17	-
28	LMG	A	612	-	-	20/43/63/70	0/1/1/1
26	BCR	K	102	-	-	7/29/63/63	0/2/2/2
25	CLA	b	614	-	1/1/15/20	13/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	BCR	k	101	-	-	7/29/63/63	0/2/2/2
25	CLA	C	512	-	1/1/15/20	10/39/115/115	-
30	LHG	d	407	-	-	15/53/53/53	-
26	BCR	C	514	-	-	2/29/63/63	0/2/2/2
30	LHG	D	412	-	-	14/53/53/53	-
26	BCR	A	609	-	-	4/29/63/63	0/2/2/2
26	BCR	B	618	-	-	3/29/63/63	0/2/2/2
25	CLA	c	501	-	1/1/15/20	4/39/115/115	-
26	BCR	B	617	-	-	4/29/63/63	0/2/2/2
32	STE	C	518	-	-	5/9/9/17	-
25	CLA	b	615	-	1/1/15/20	9/39/115/115	-
30	LHG	d	409	-	-	13/43/43/53	-
25	CLA	a	608	-	1/1/15/20	8/39/115/115	-
32	STE	A	617	-	-	10/17/17/17	-
25	CLA	A	606	-	1/1/15/20	3/39/115/115	-
30	LHG	D	409	-	-	22/53/53/53	-

The worst 5 of 792 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	D	402	PHO	C1B-C2B	9.21	1.49	1.39
33	d	402	PHO	C1B-C2B	9.12	1.49	1.39
33	D	402	PHO	C3B-C4B	8.87	1.50	1.41
33	a	607	PHO	C1B-C2B	8.76	1.49	1.39
33	d	402	PHO	C3B-C4B	8.22	1.49	1.41

The worst 5 of 1087 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	V	201	HEC	CBB-CAB-C3B	-10.47	106.50	127.43
25	B	604	CLA	C4A-NA-C1A	9.64	111.08	106.68
25	b	616	CLA	C4A-NA-C1A	9.10	110.83	106.68
25	B	601	CLA	C4A-NA-C1A	9.04	110.80	106.68
25	c	511	CLA	C4A-NA-C1A	8.69	110.64	106.68

5 of 64 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
25	A	606	CLA	ND
25	A	607	CLA	ND
25	A	608	CLA	ND
25	A	611	CLA	ND
25	B	601	CLA	ND

5 of 1807 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	B	603	CLA	C4-C3-C5-C6
25	B	614	CLA	CAD-CBD-CGD-O1D
25	B	614	CLA	CAD-CBD-CGD-O2D
25	C	507	CLA	CHA-CBD-CGD-O1D
25	C	507	CLA	CHA-CBD-CGD-O2D

There are no ring outliers.

149 monomers are involved in 312 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	C	501	CLA	1	0
35	v	201	HEC	1	0
26	k	103	BCR	1	0
31	c	515	DGD	3	0
32	L	102	STE	1	0
25	C	507	CLA	2	0
25	a	605	CLA	4	0
26	d	405	BCR	1	0
25	B	605	CLA	1	0
25	B	613	CLA	3	0
32	H	103	STE	2	0
25	C	506	CLA	4	0
32	b	621	STE	4	0
27	D	406	PL9	2	0
25	b	616	CLA	3	0
25	C	509	CLA	2	0
31	C	516	DGD	2	0
32	d	413	STE	6	0
29	B	623	SQD	5	0
28	c	521	LMG	3	0
25	c	502	CLA	3	0
28	C	517	LMG	1	0
25	b	603	CLA	3	0
25	c	511	CLA	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
31	c	517	DGD	6	0
21	a	601[B]	OEY	1	0
26	H	101	BCR	5	0
31	J	101	DGD	5	0
25	c	512	CLA	5	0
29	A	613	SQD	1	0
25	b	610	CLA	1	0
25	c	510	CLA	4	0
25	B	604	CLA	1	0
25	d	404	CLA	2	0
25	b	607	CLA	1	0
25	c	506	CLA	3	0
25	B	616	CLA	1	0
25	b	602	CLA	3	0
31	a	614	DGD	3	0
25	c	509	CLA	5	0
33	a	607	PHO	1	0
25	b	606	CLA	3	0
25	d	403	CLA	1	0
31	c	516	DGD	4	0
25	a	611	CLA	3	0
25	B	603	CLA	1	0
25	b	604	CLA	2	0
28	d	410	LMG	1	0
26	K	103	BCR	1	0
25	D	404	CLA	3	0
26	t	101	BCR	4	0
33	d	402	PHO	3	0
28	c	518	LMG	2	0
26	b	619	BCR	3	0
26	b	617	BCR	1	0
30	e	101	LHG	5	0
27	d	406	PL9	3	0
26	K	101	BCR	2	0
33	D	402	PHO	1	0
25	B	607	CLA	3	0
34	f	101	HEM	3	0
25	c	503	CLA	5	0
32	I	101	STE	2	0
27	A	610	PL9	6	0
25	c	507	CLA	3	0
29	a	613	SQD	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	m	101	LMG	4	0
26	b	618	BCR	2	0
32	m	102	STE	2	0
25	B	615	CLA	2	0
32	B	624	STE	1	0
34	E	101	HEM	2	0
31	H	102	DGD	2	0
25	b	601	CLA	4	0
25	b	609	CLA	3	0
28	D	411	LMG	2	0
28	c	520	LMG	1	0
25	b	605	CLA	4	0
26	c	514	BCR	4	0
25	B	609	CLA	2	0
28	D	407	LMG	2	0
25	b	611	CLA	2	0
25	c	505	CLA	3	0
30	d	408	LHG	2	0
32	B	625	STE	2	0
26	T	101	BCR	3	0
25	B	602	CLA	2	0
29	A	615	SQD	1	0
25	C	505	CLA	2	0
26	k	102	BCR	1	0
25	A	607	CLA	2	0
25	B	612	CLA	2	0
25	B	606	CLA	1	0
30	L	101	LHG	1	0
26	D	405	BCR	1	0
25	C	508	CLA	5	0
29	f	102	SQD	3	0
25	C	511	CLA	4	0
25	C	513	CLA	4	0
28	b	622	LMG	1	0
25	C	504	CLA	3	0
25	B	611	CLA	1	0
25	A	608	CLA	1	0
25	a	606	CLA	2	0
25	c	508	CLA	3	0
32	D	413	STE	6	0
27	a	610	PL9	5	0
28	B	620	LMG	5	0

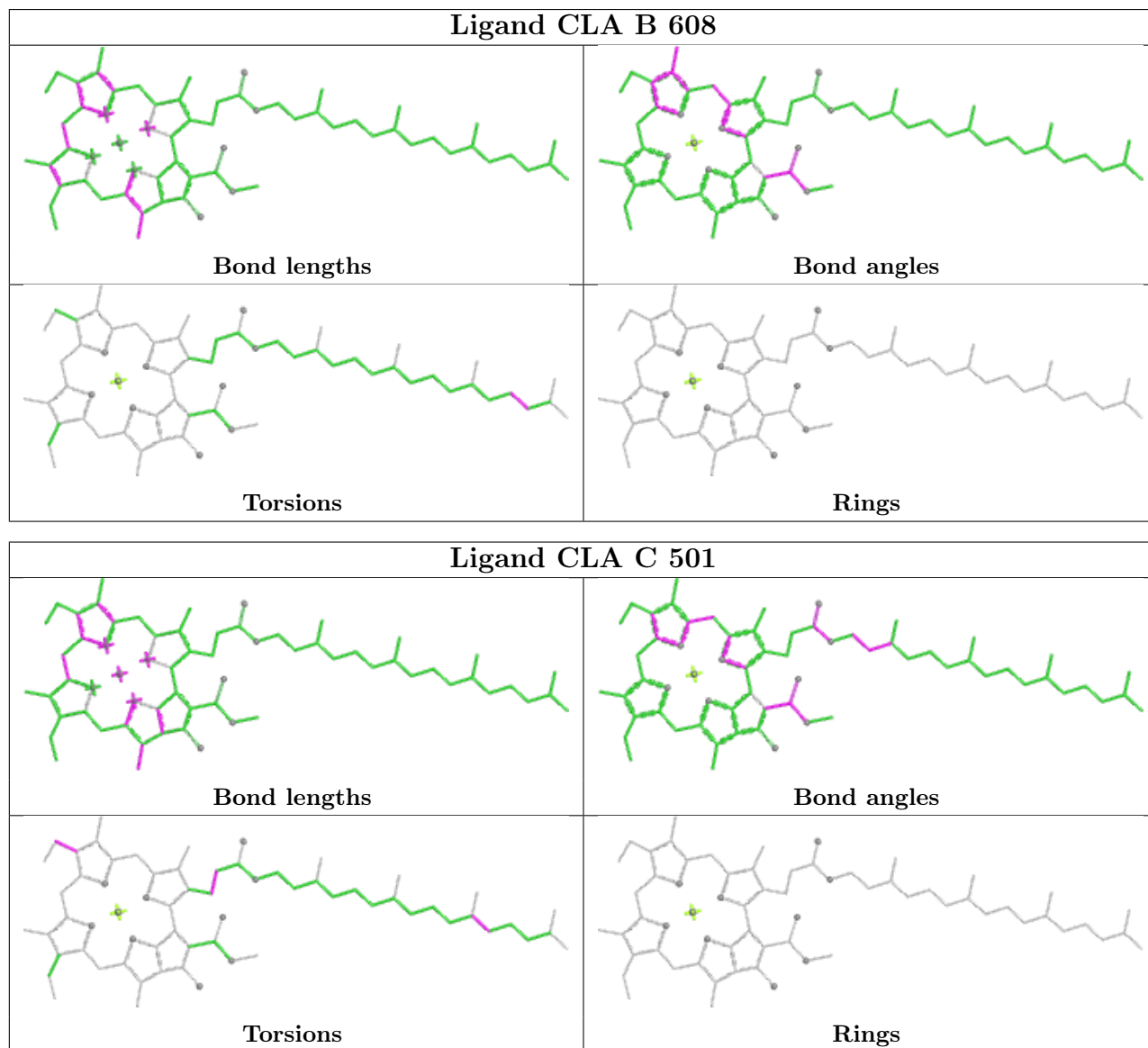
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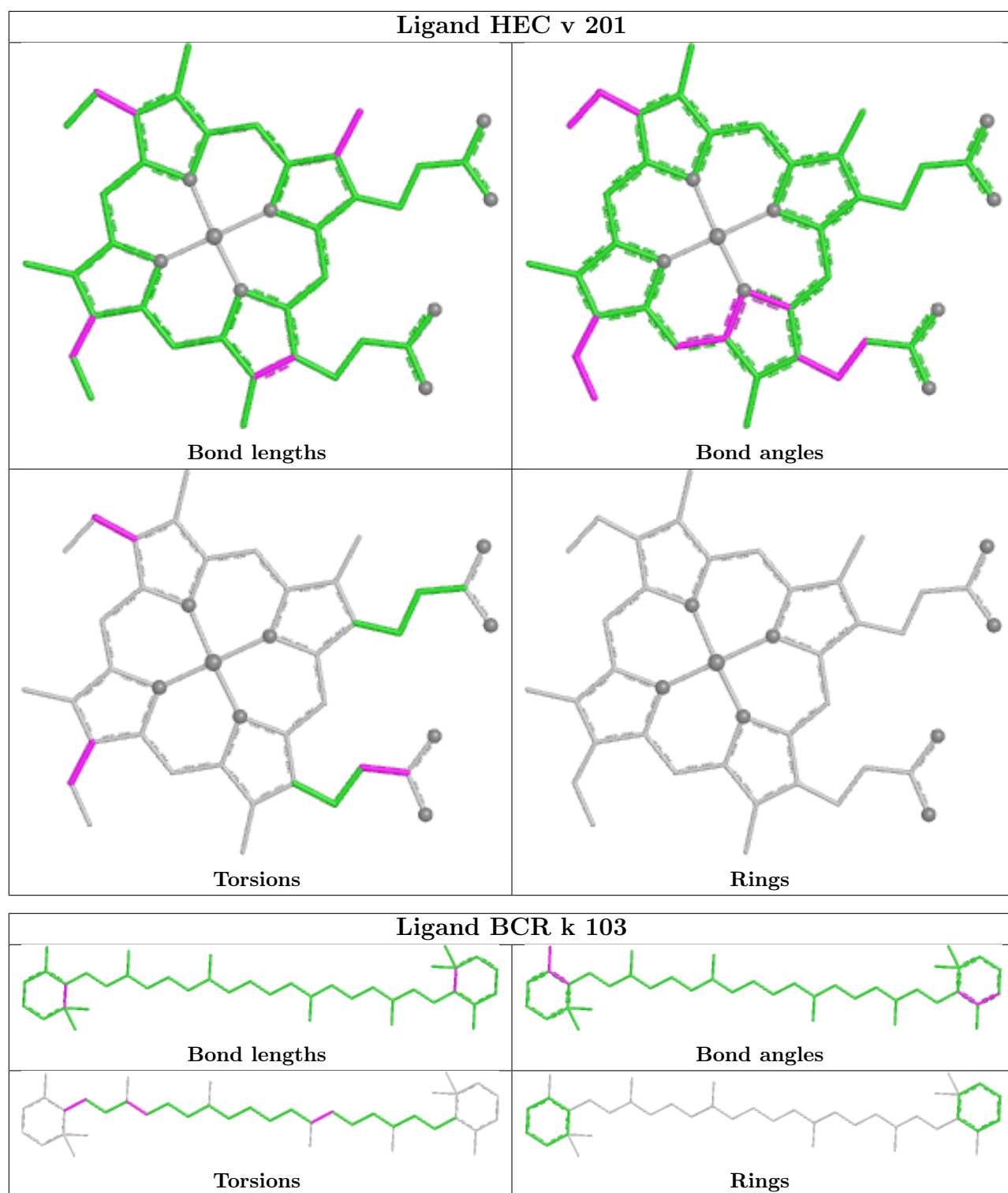
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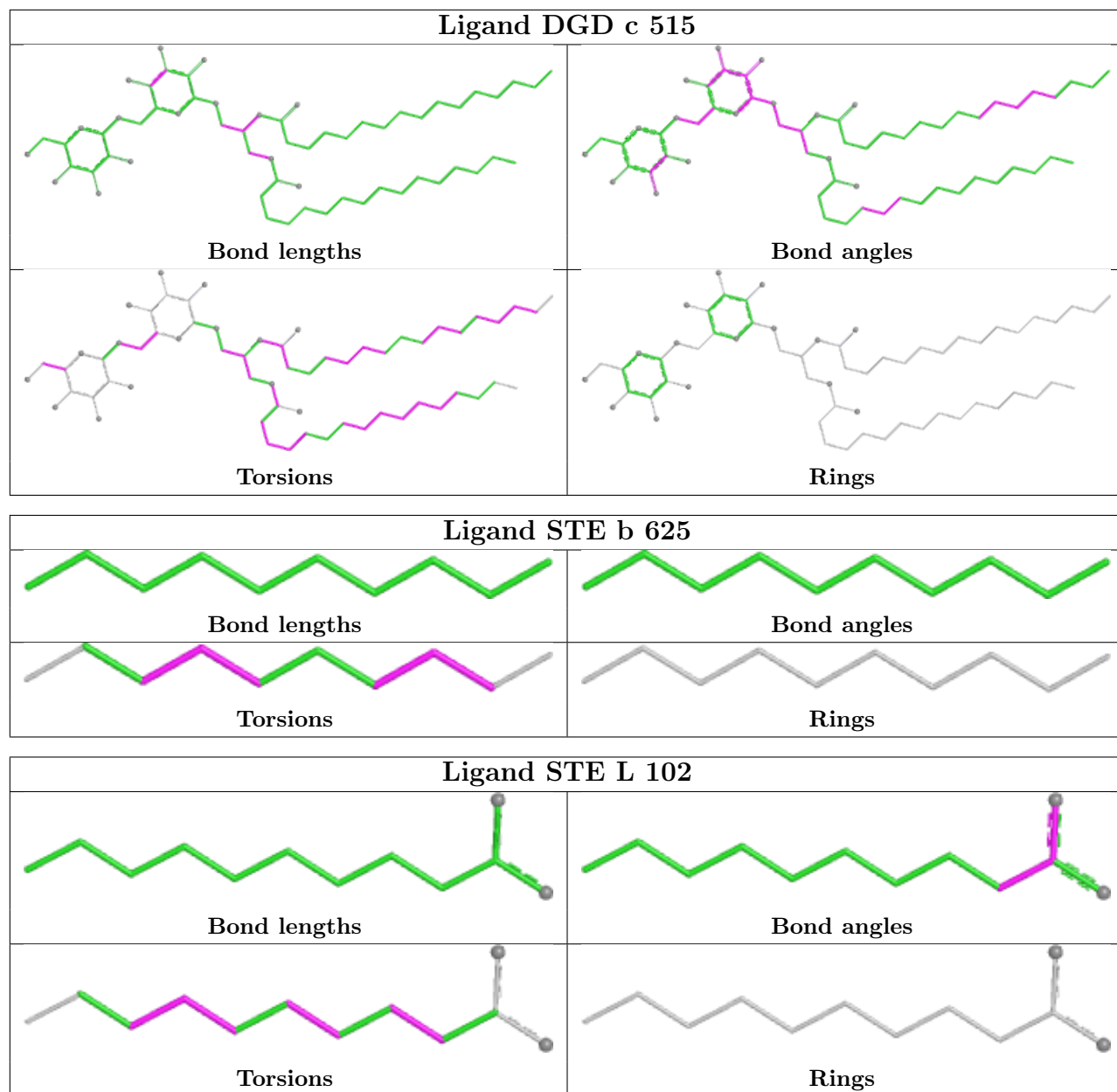
Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	B	601	CLA	6	0
26	h	101	BCR	5	0
25	B	614	CLA	7	0
32	j	101	STE	1	0
25	b	613	CLA	1	0
25	c	504	CLA	2	0
28	B	622	LMG	2	0
30	A	614	LHG	1	0
32	B	621	STE	2	0
24	A	605	BCT	1	0
26	B	619	BCR	2	0
32	c	519	STE	1	0
25	c	513	CLA	3	0
32	T	102	STE	2	0
29	b	620	SQD	5	0
30	l	101	LHG	5	0
25	D	403	CLA	3	0
25	b	608	CLA	3	0
29	D	408	SQD	1	0
25	b	612	CLA	3	0
31	A	616	DGD	4	0
21	A	601[B]	OEY	1	0
25	C	502	CLA	4	0
25	C	510	CLA	2	0
32	d	412	STE	1	0
21	A	601[A]	OEY	1	0
26	K	102	BCR	1	0
25	b	614	CLA	5	0
26	k	101	BCR	2	0
25	C	512	CLA	3	0
30	d	407	LHG	4	0
26	C	514	BCR	2	0
30	D	412	LHG	5	0
26	B	618	BCR	2	0
25	c	501	CLA	3	0
26	B	617	BCR	1	0
32	C	518	STE	1	0
25	b	615	CLA	4	0
25	a	608	CLA	1	0
25	A	606	CLA	3	0
30	D	409	LHG	2	0

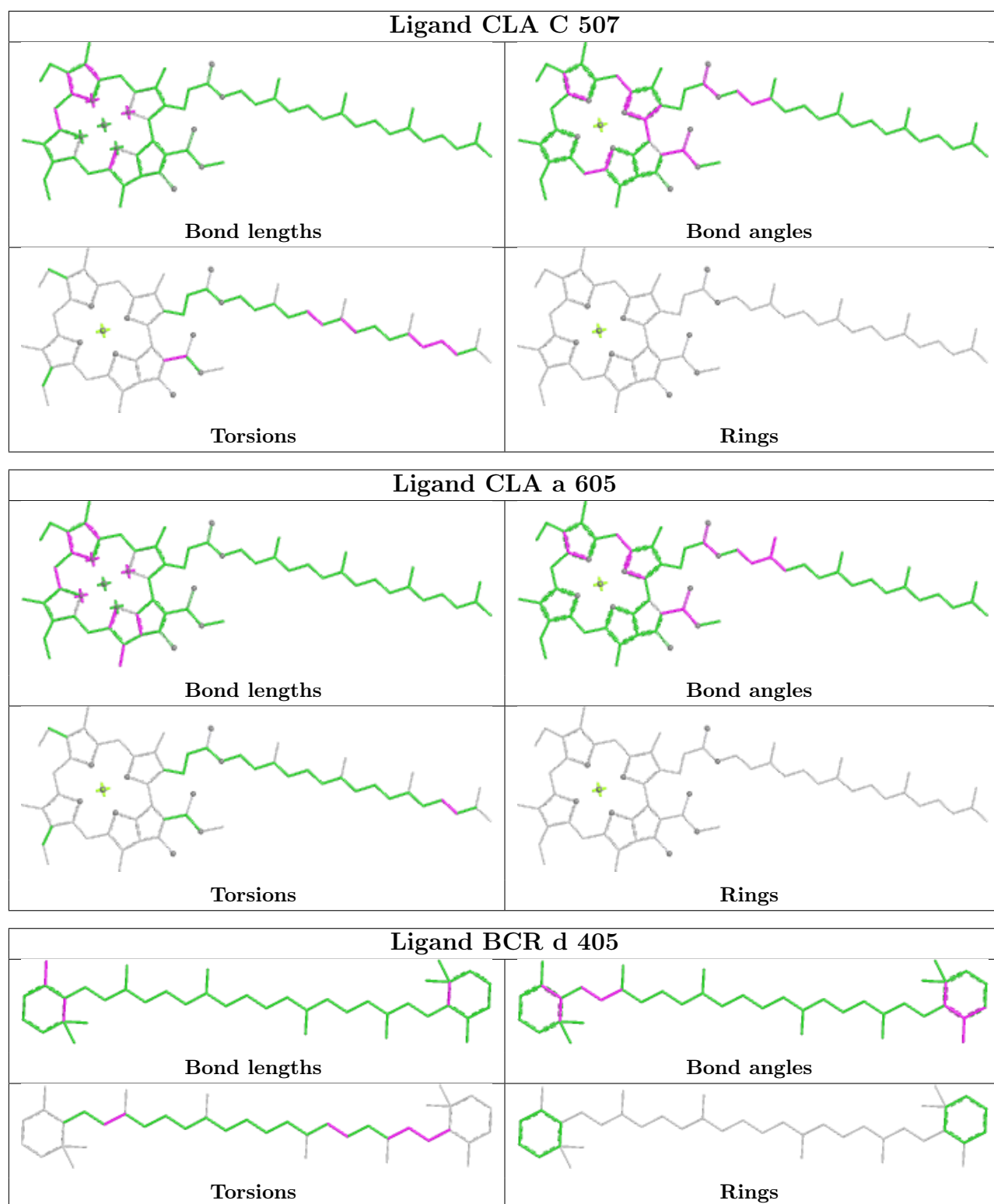
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

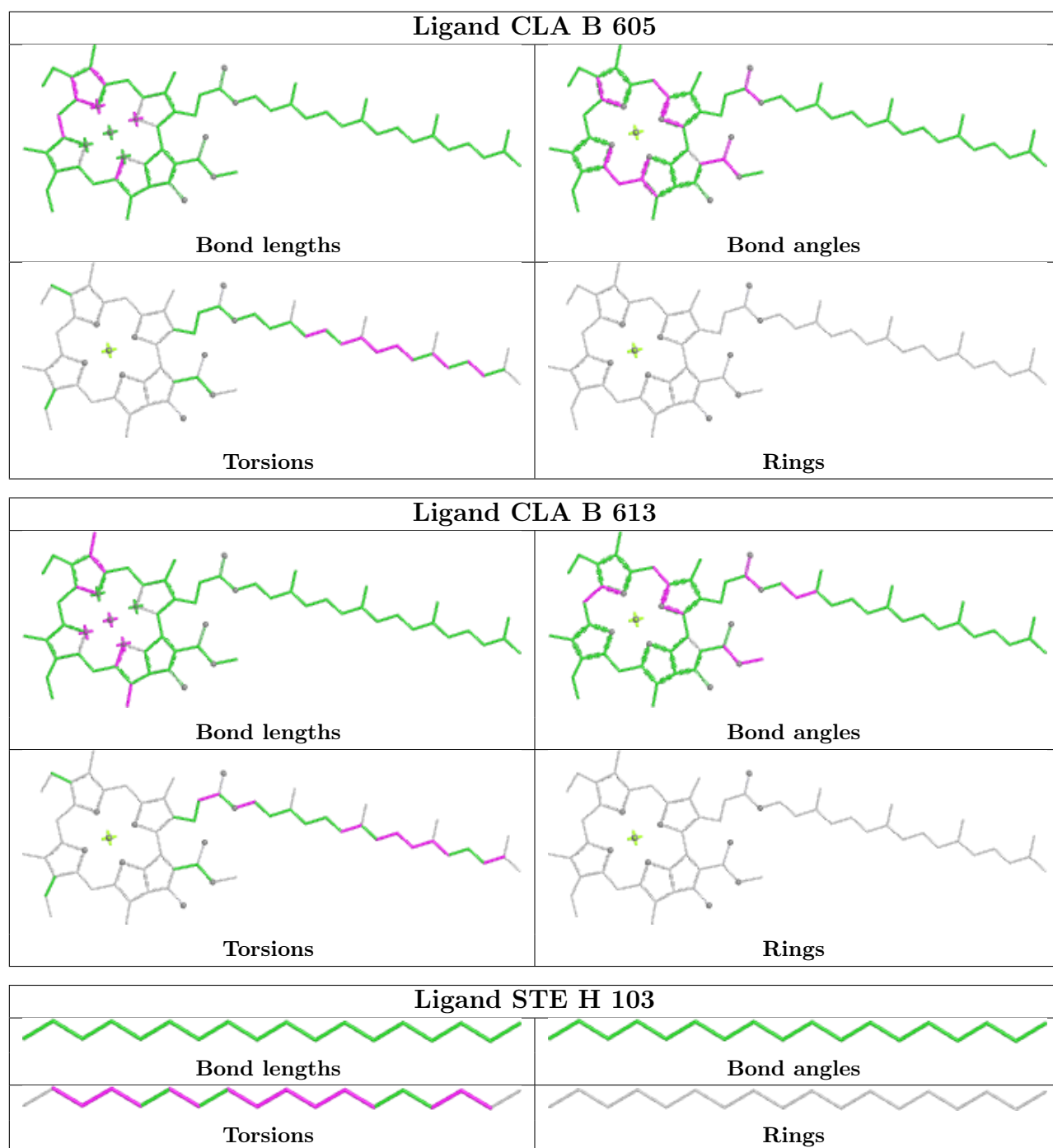
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within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

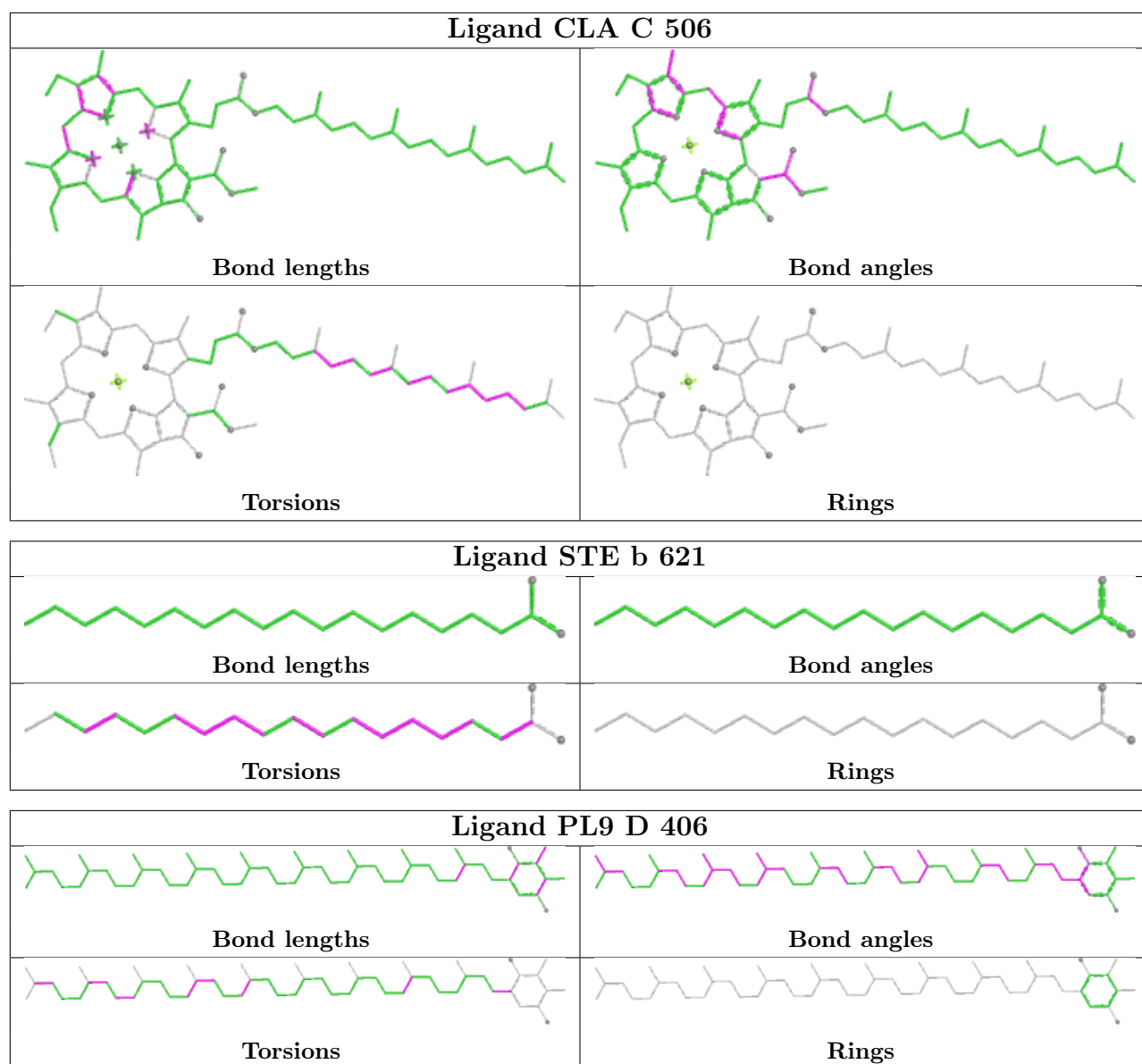


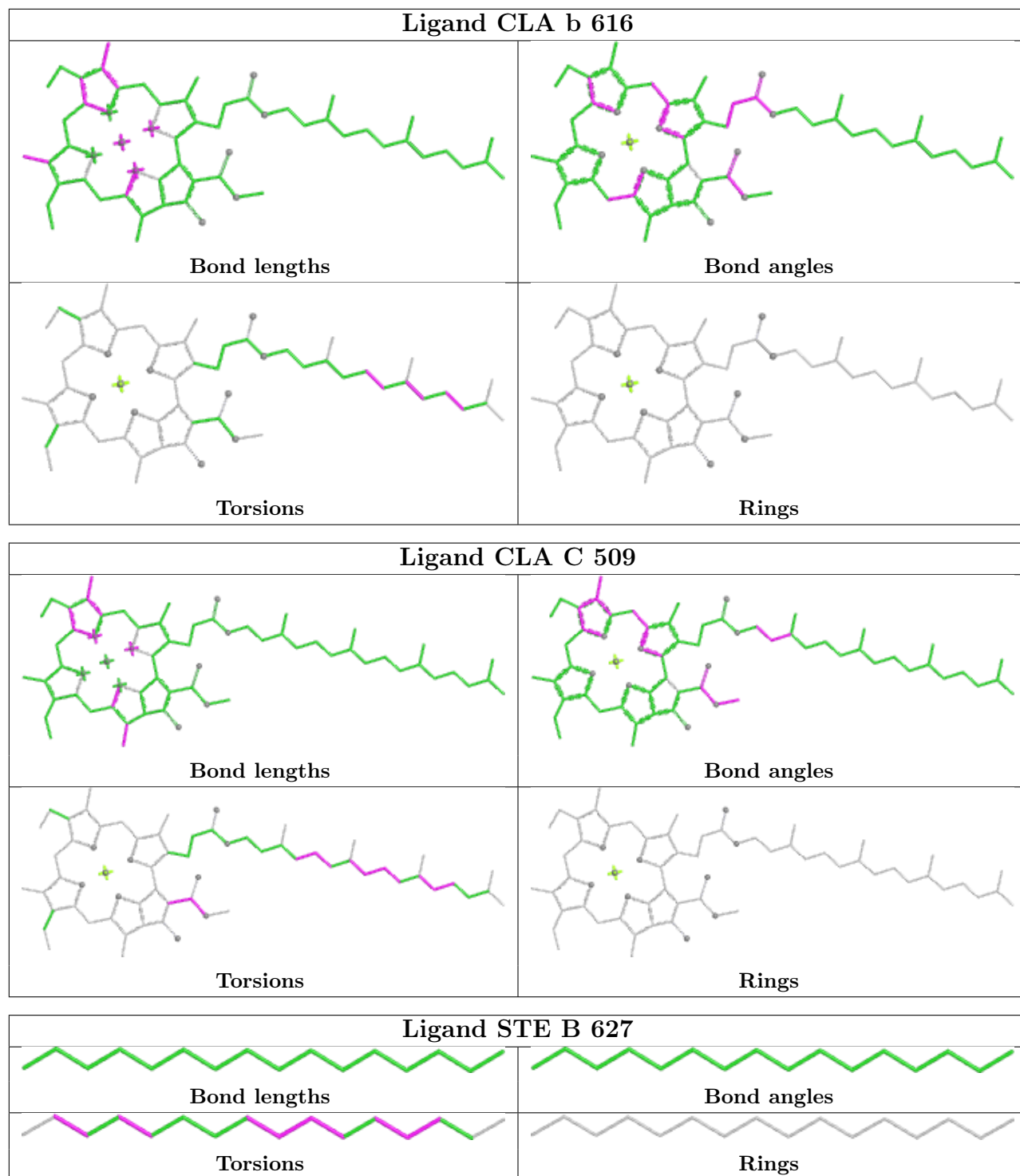


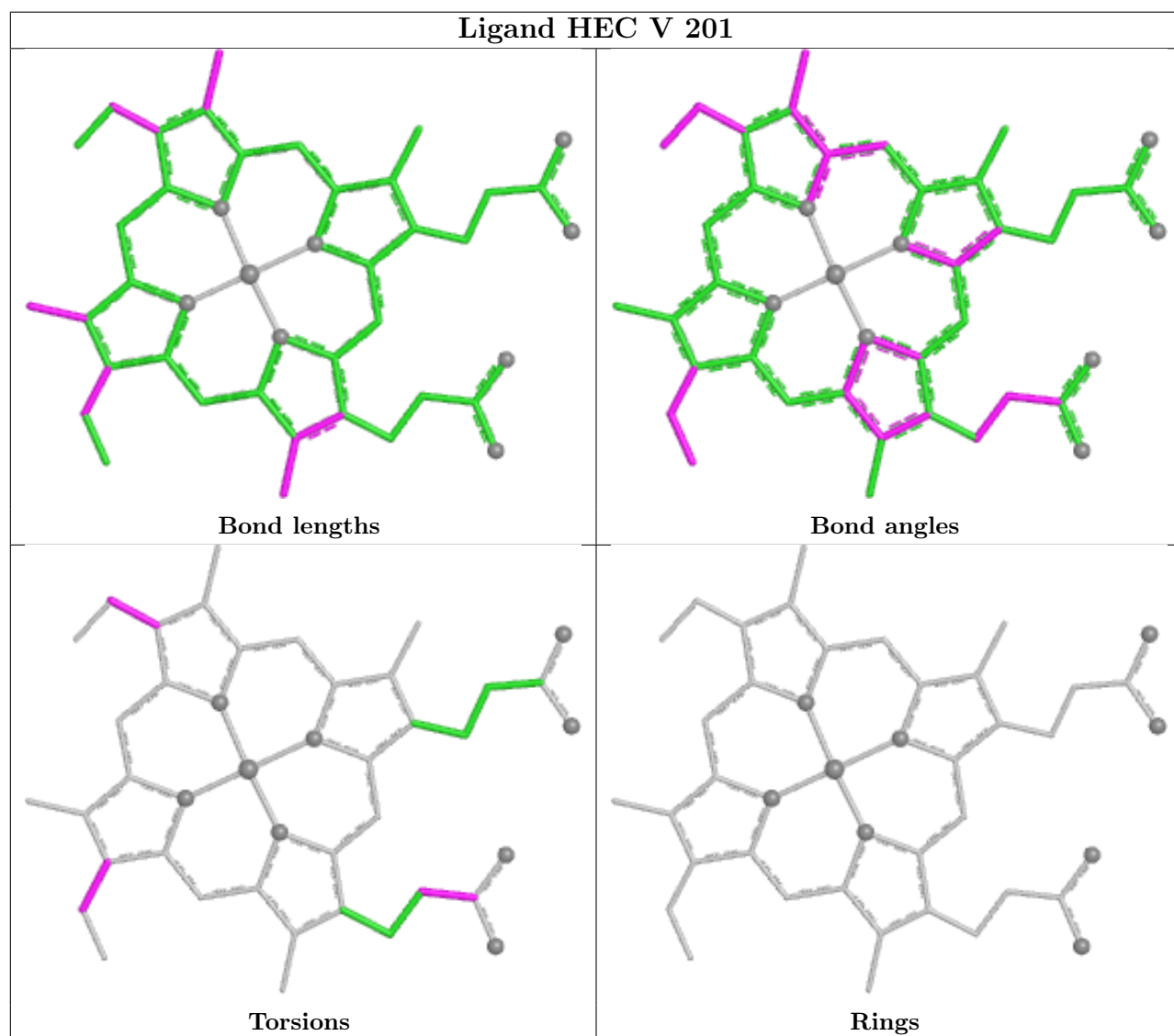
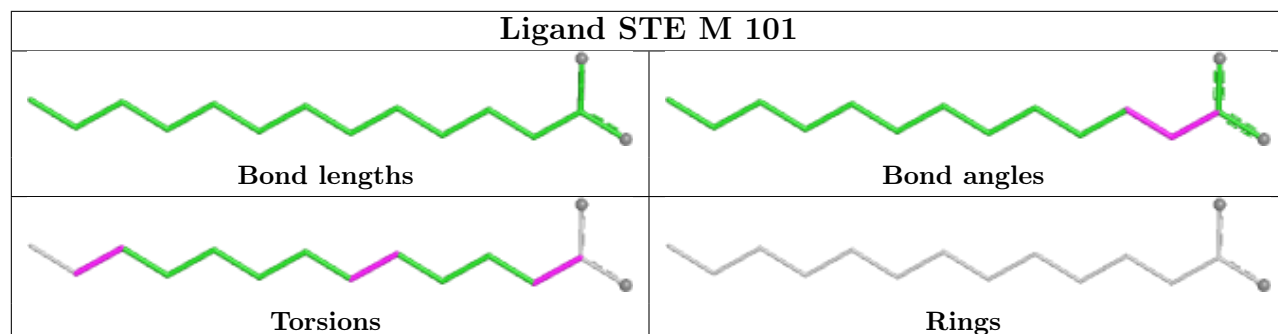


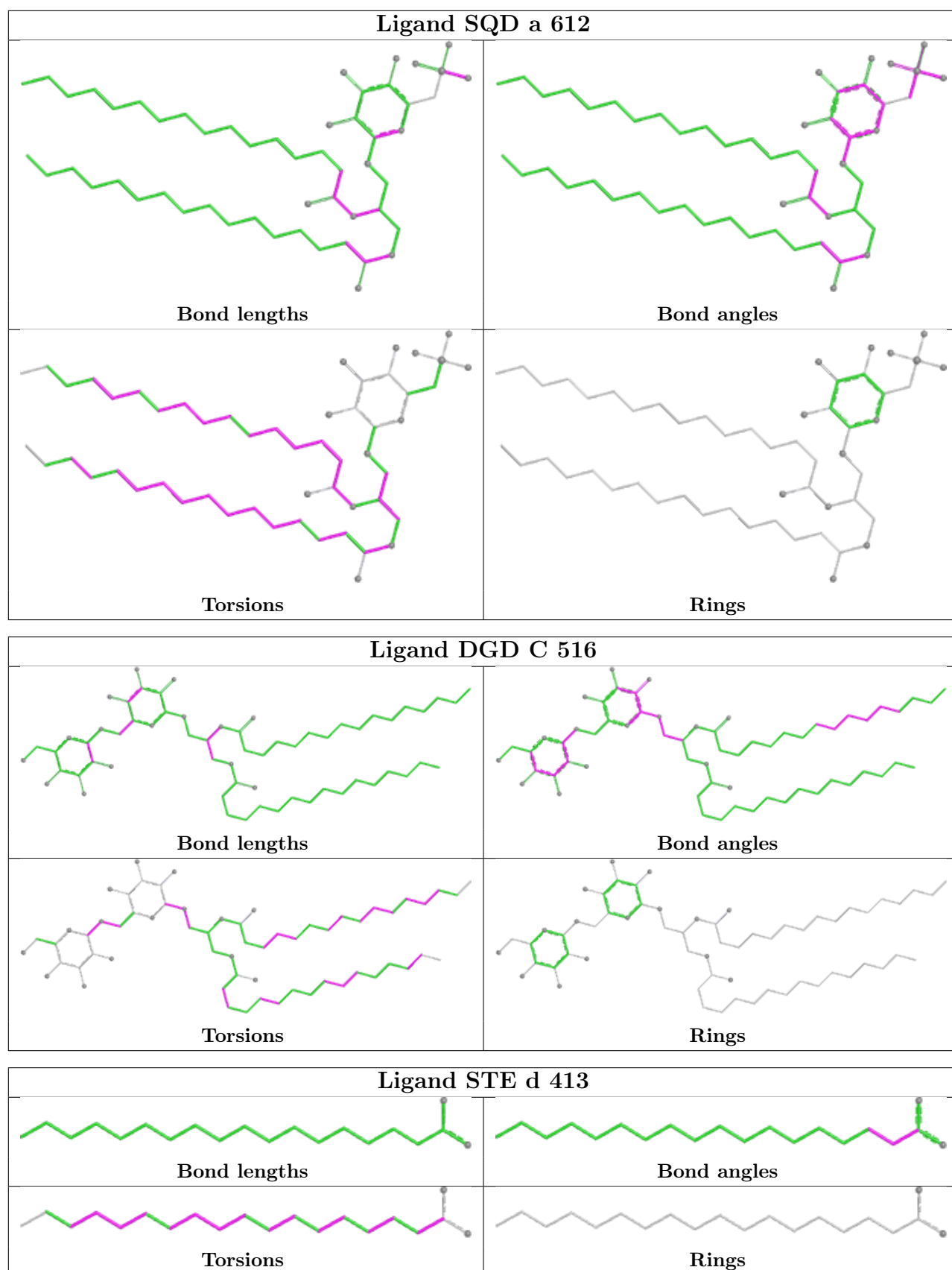


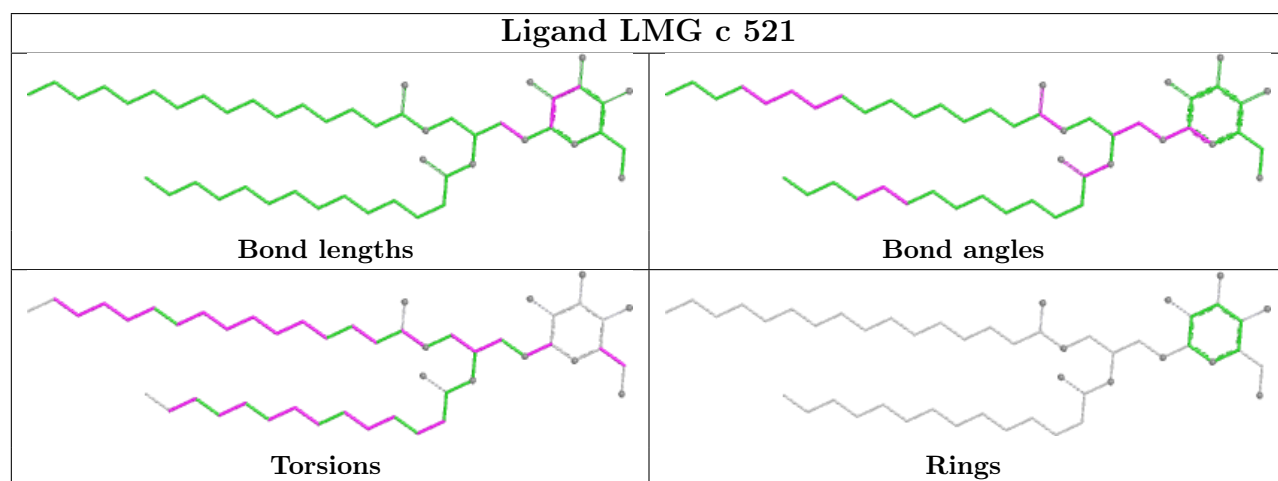
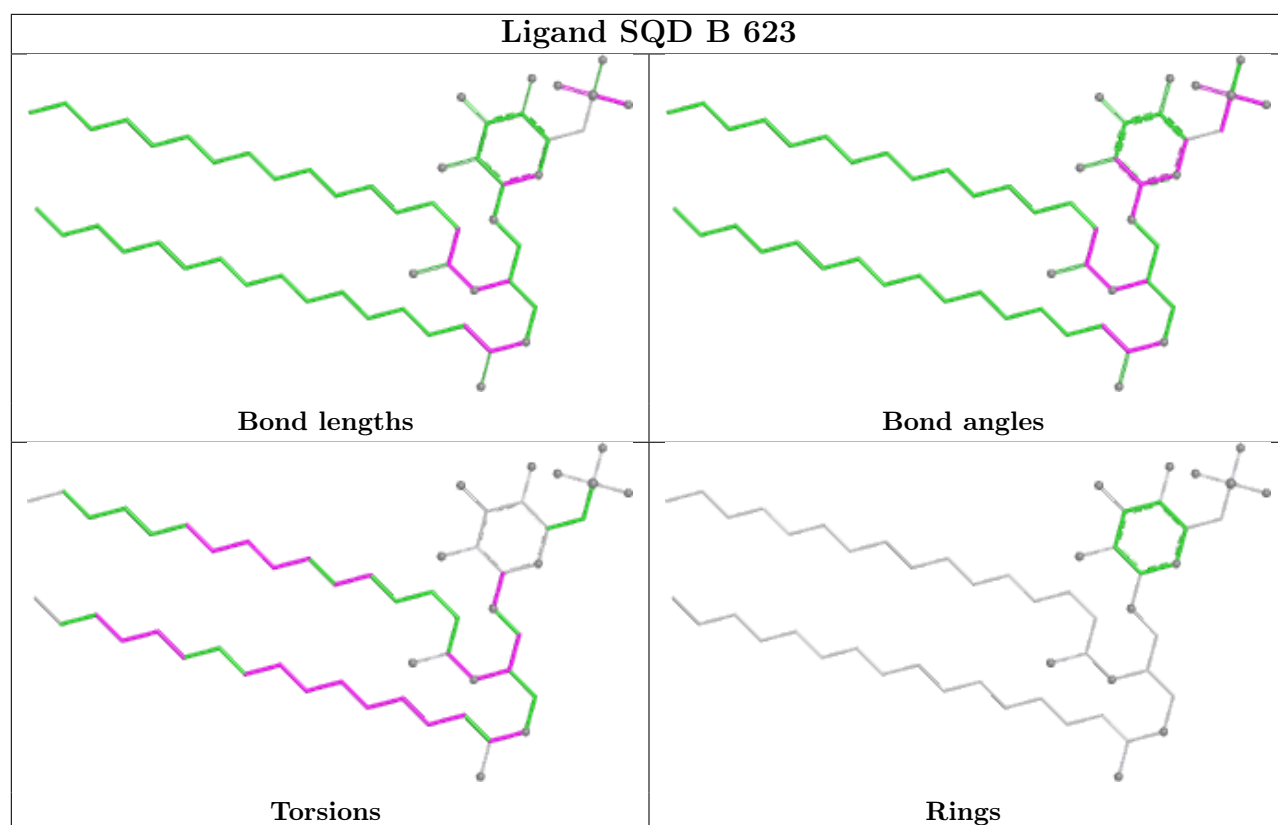


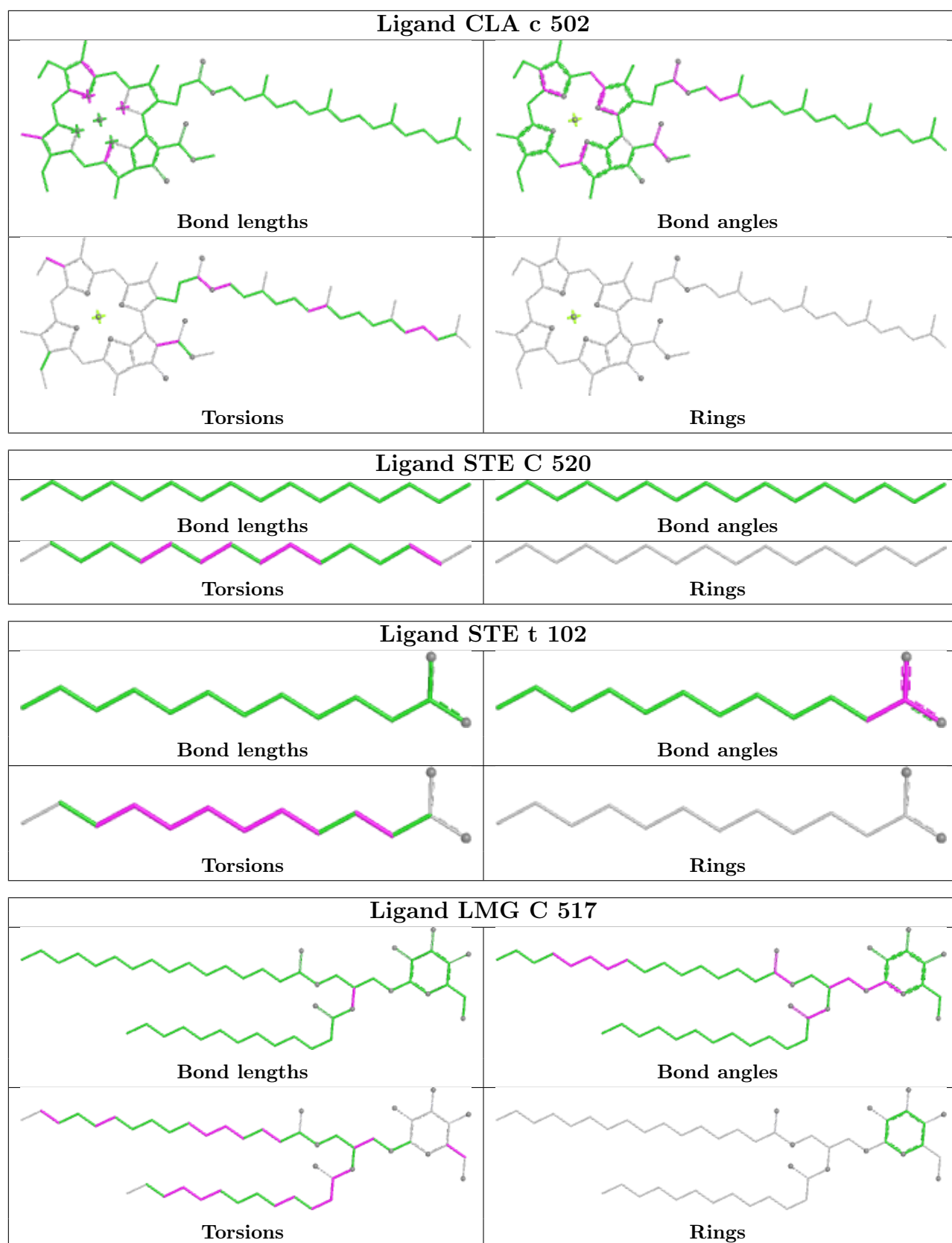


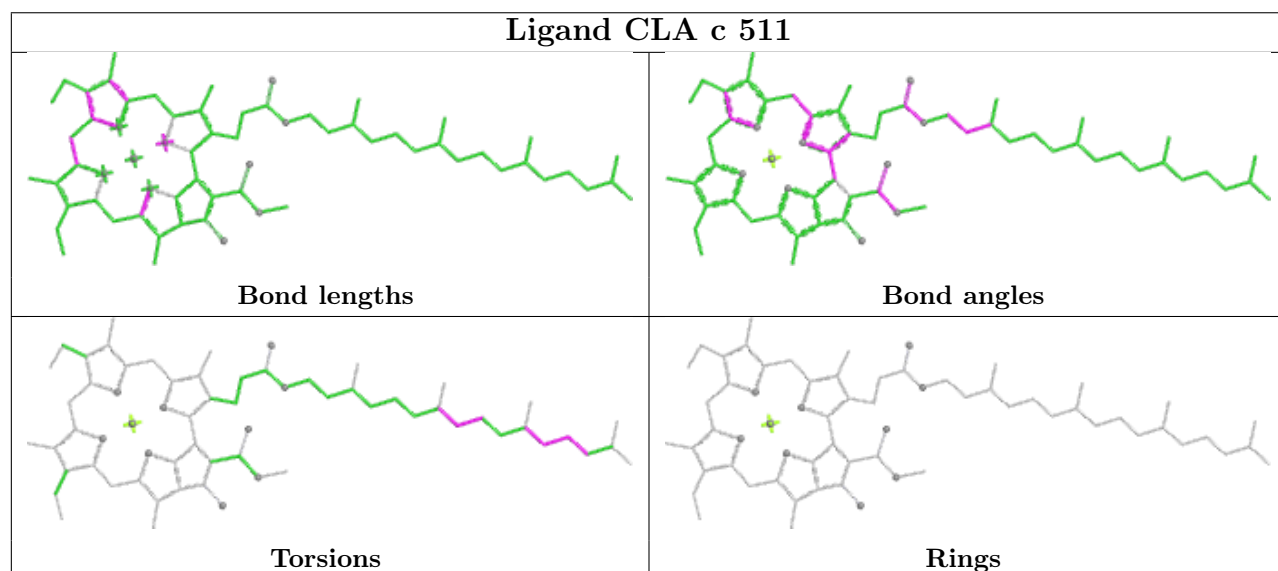
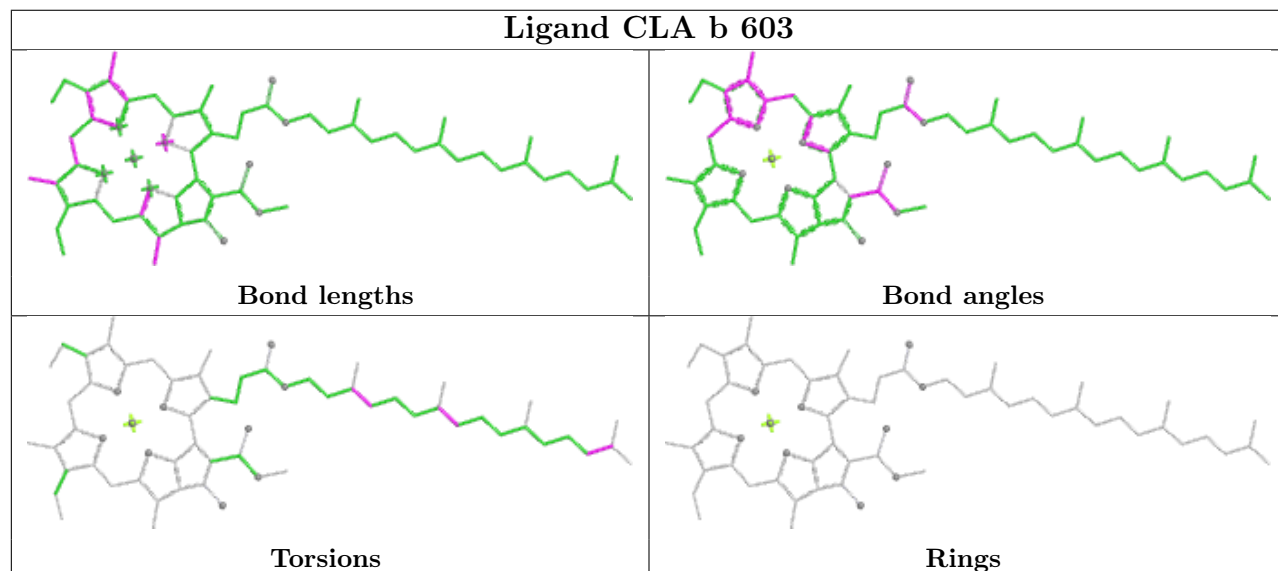
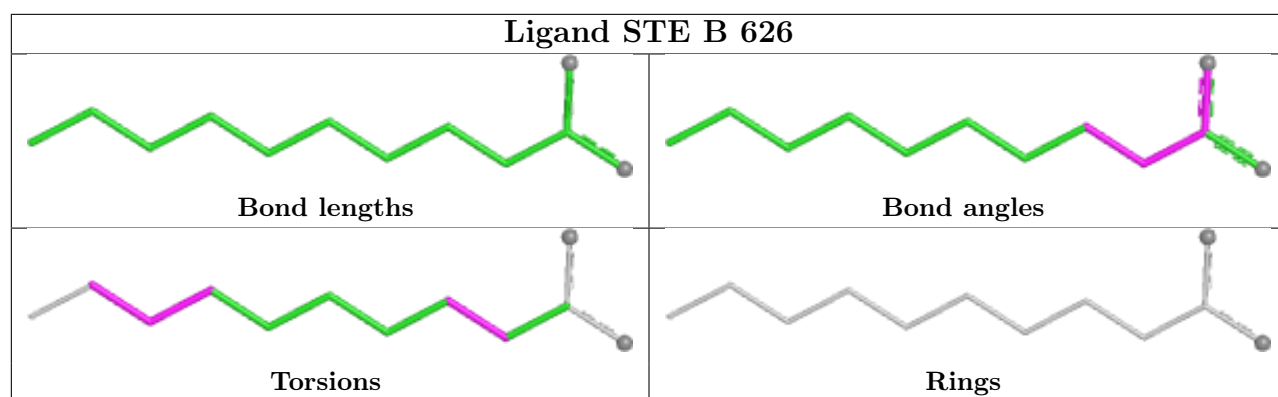


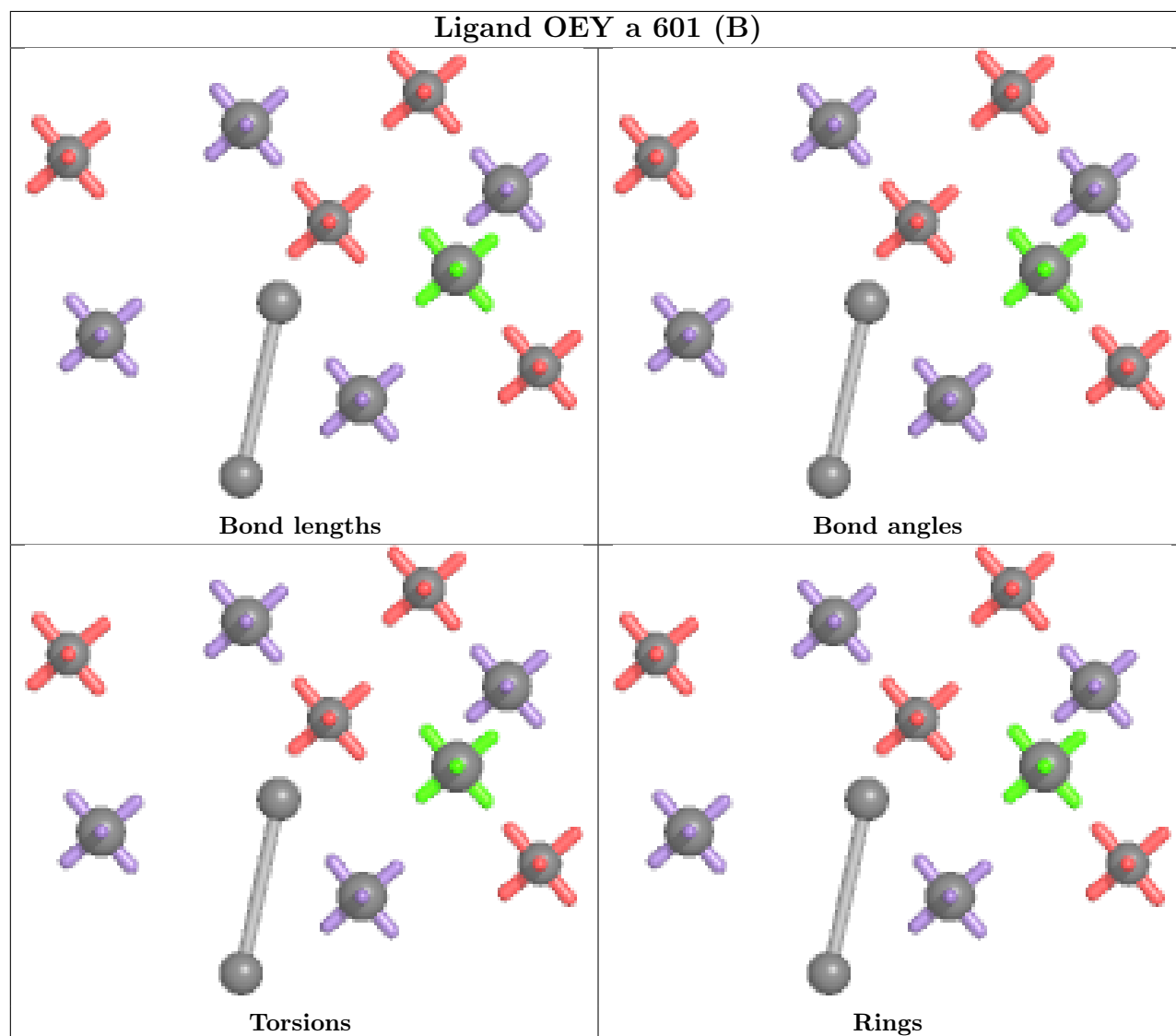
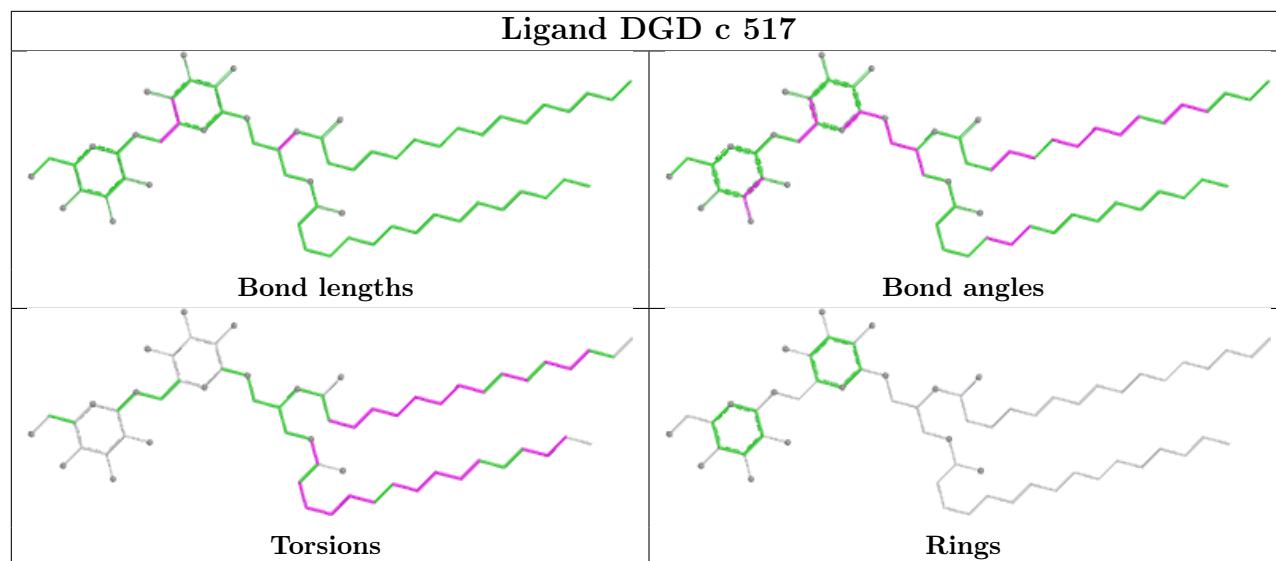


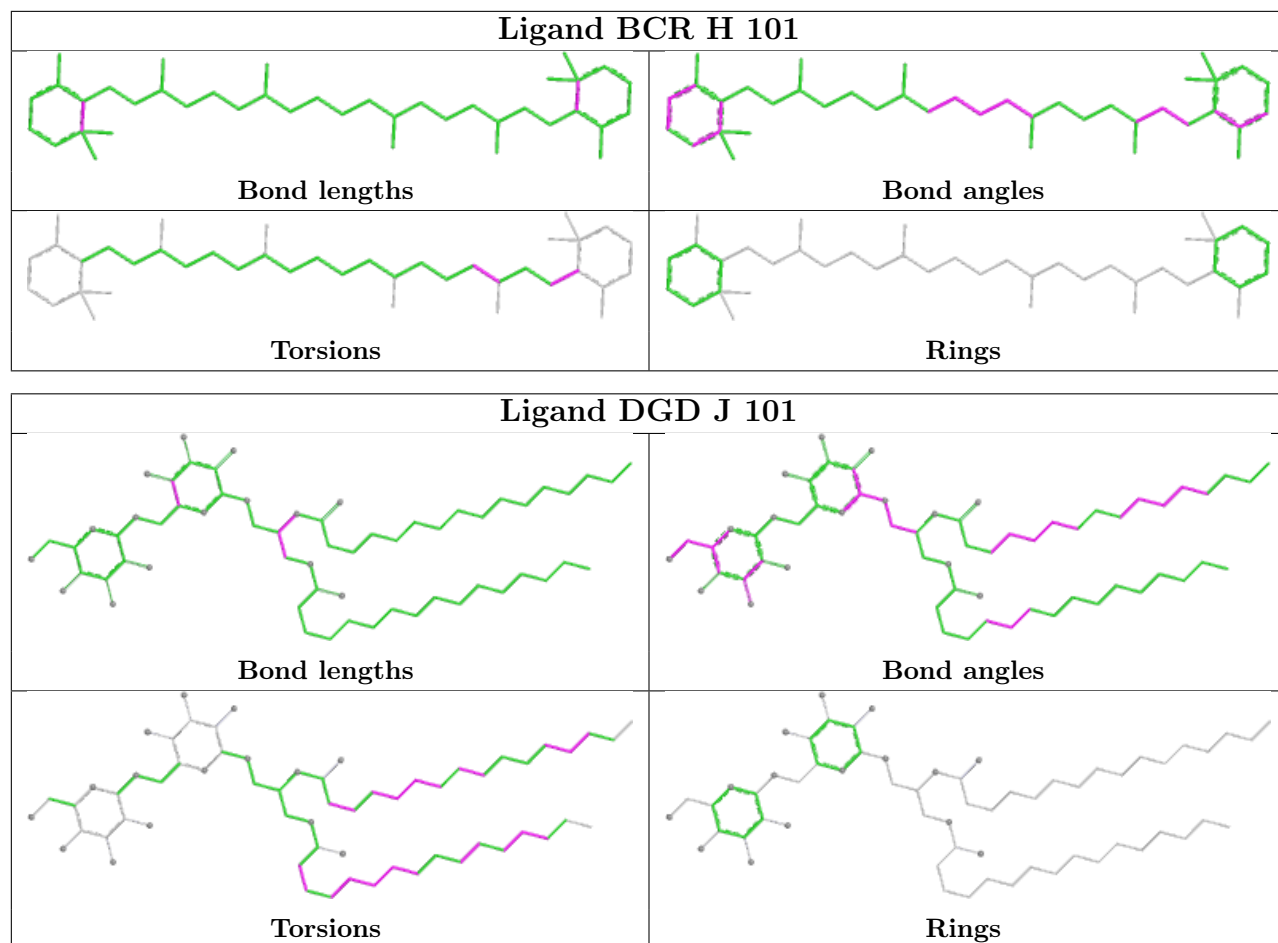


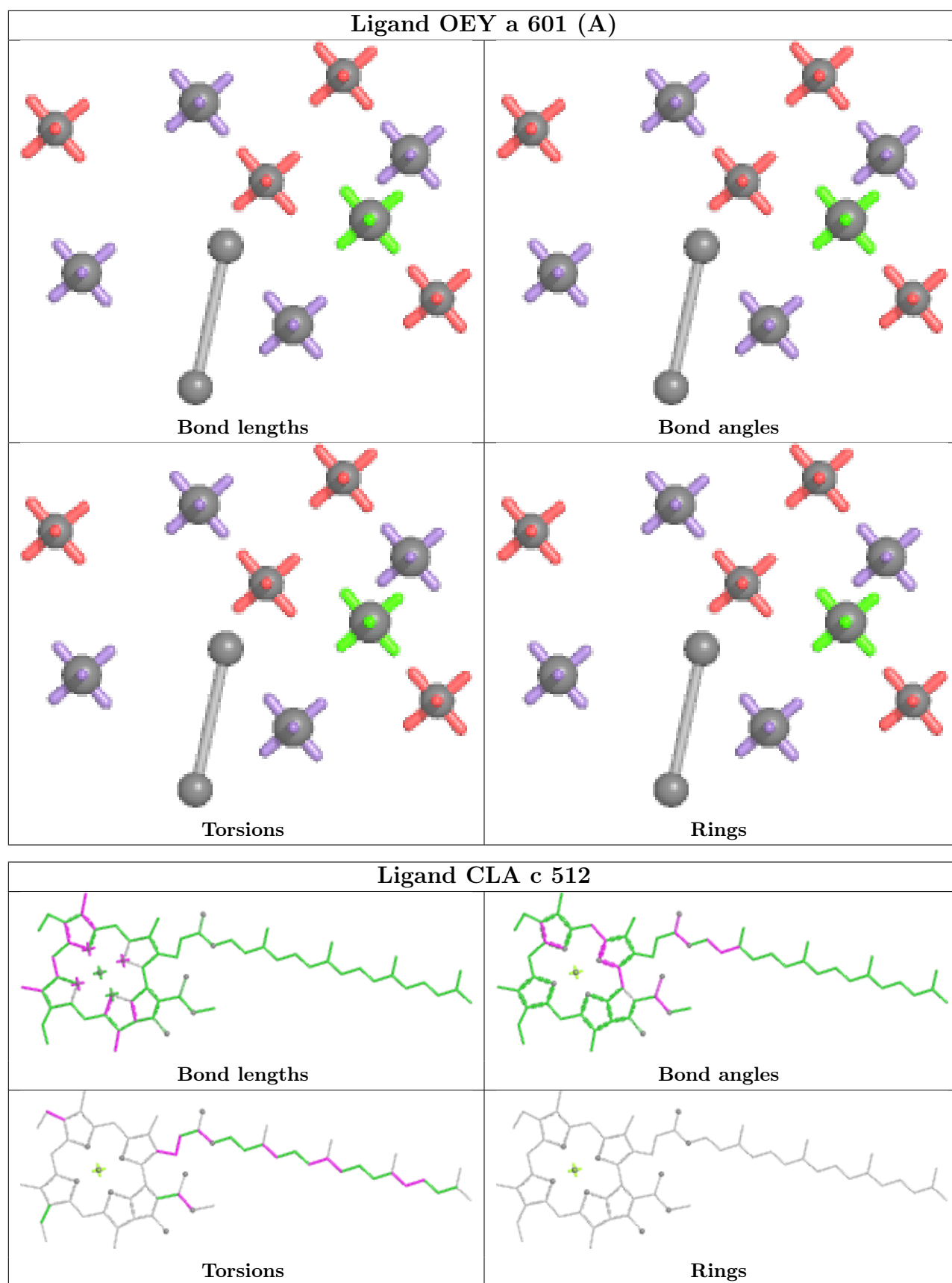


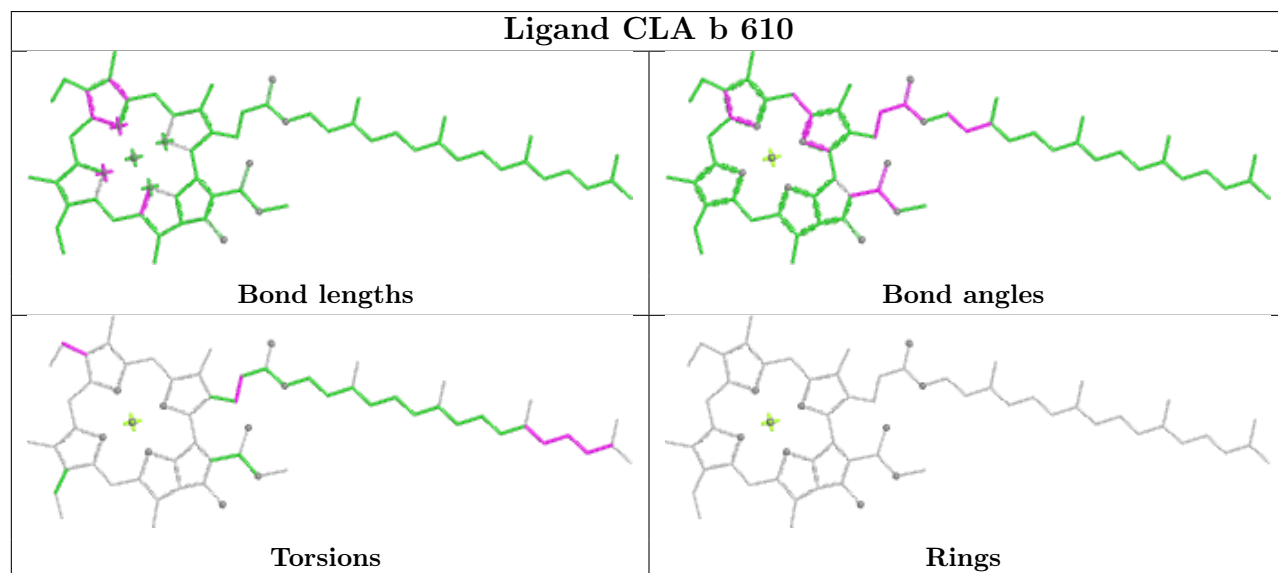
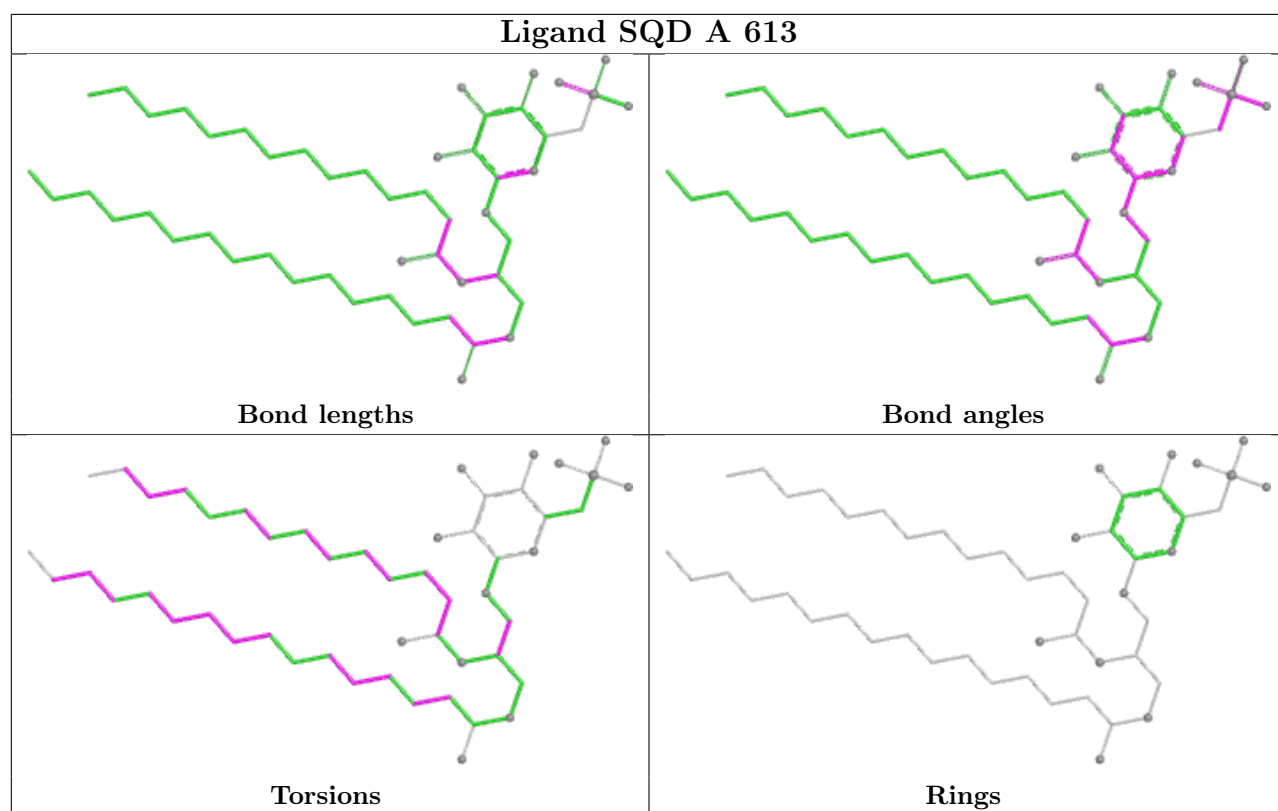


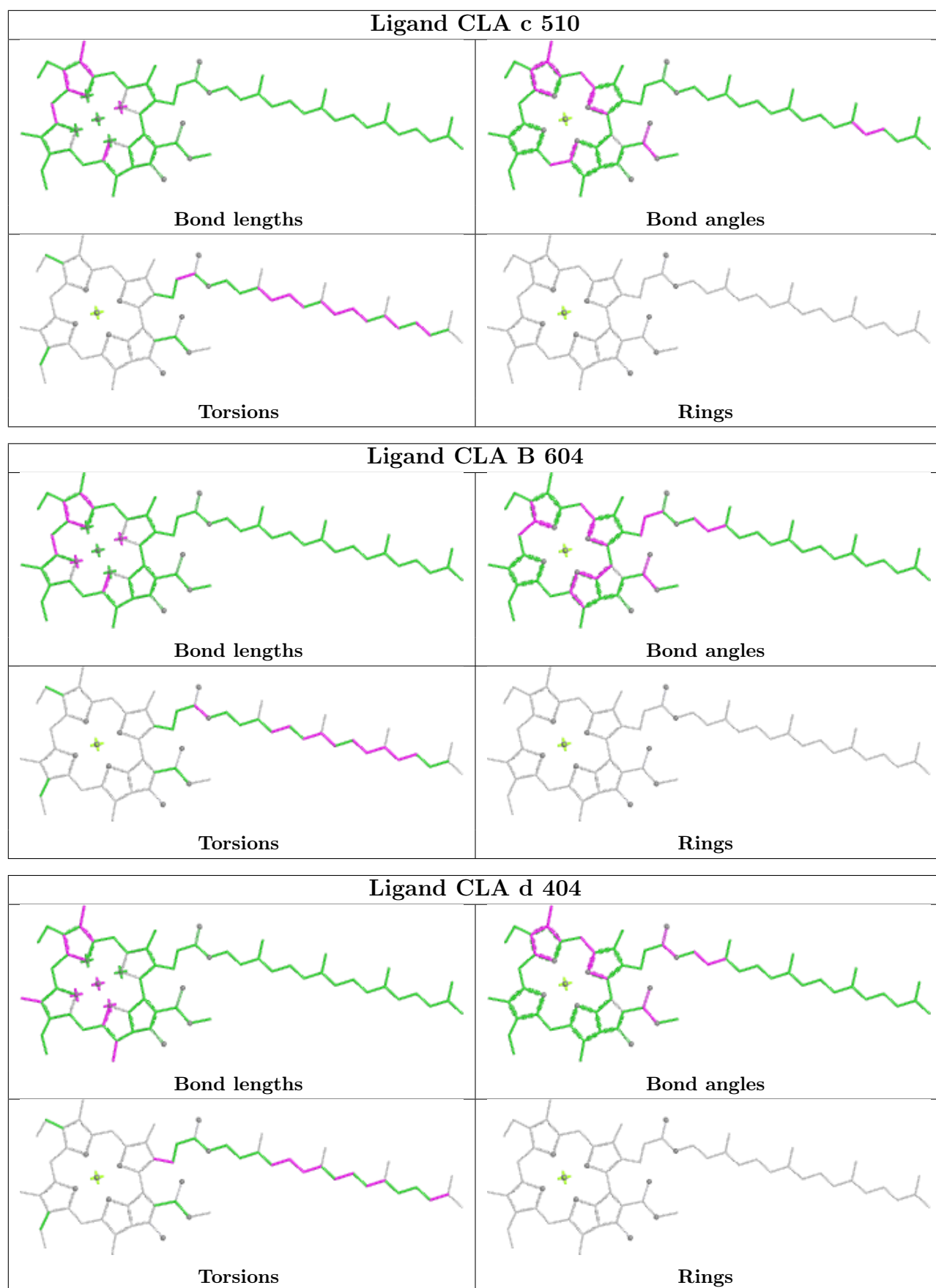


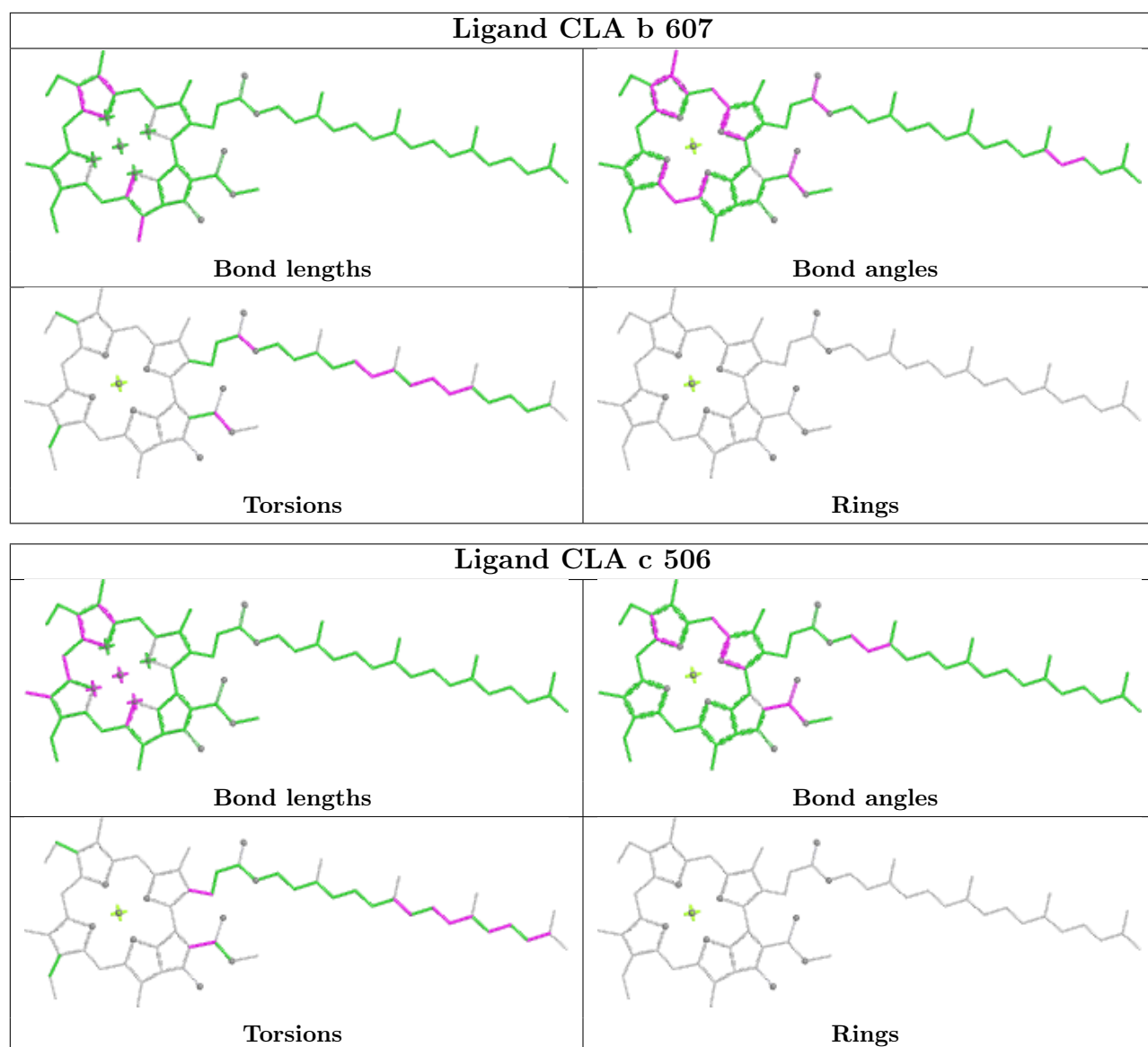


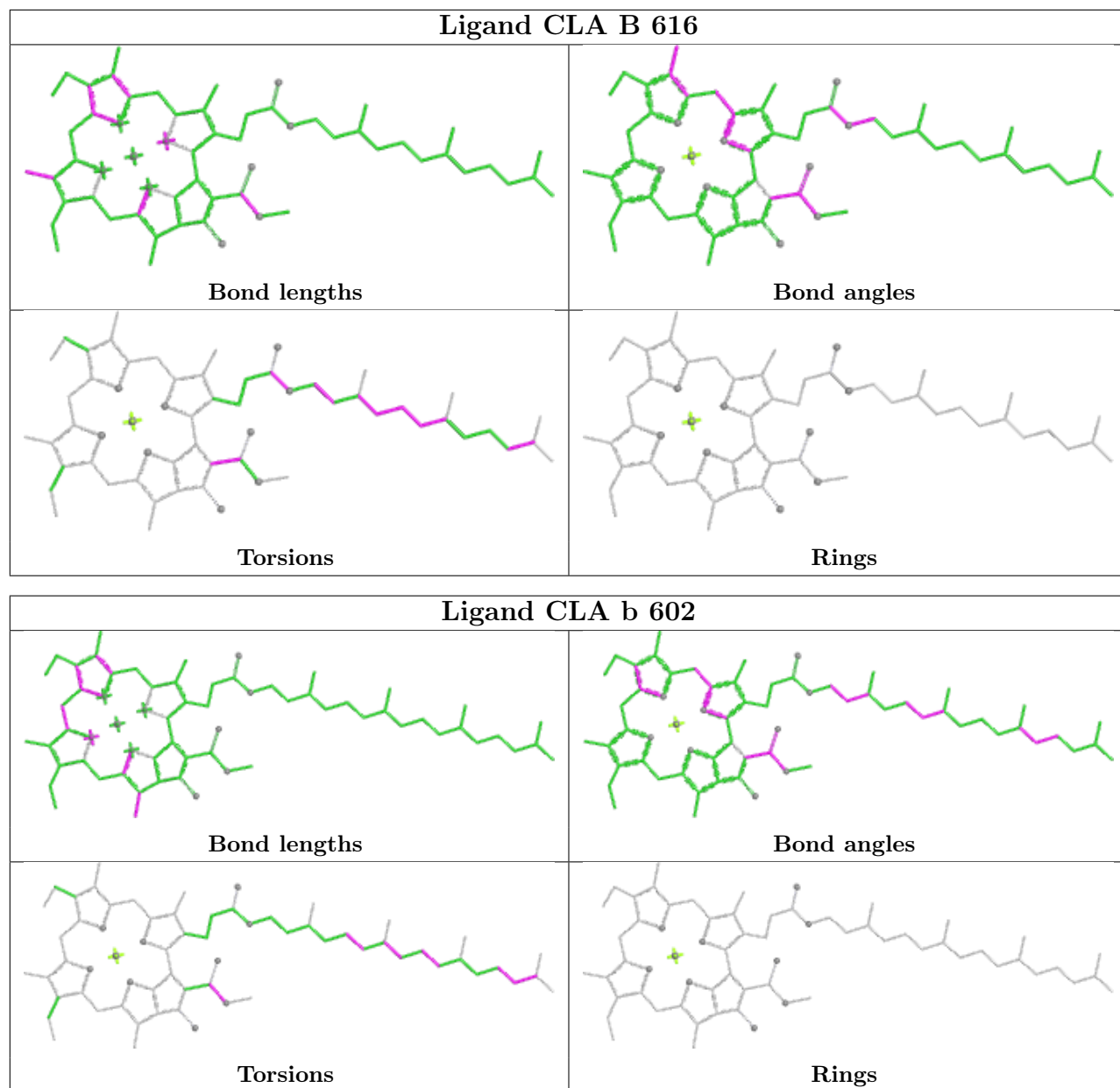


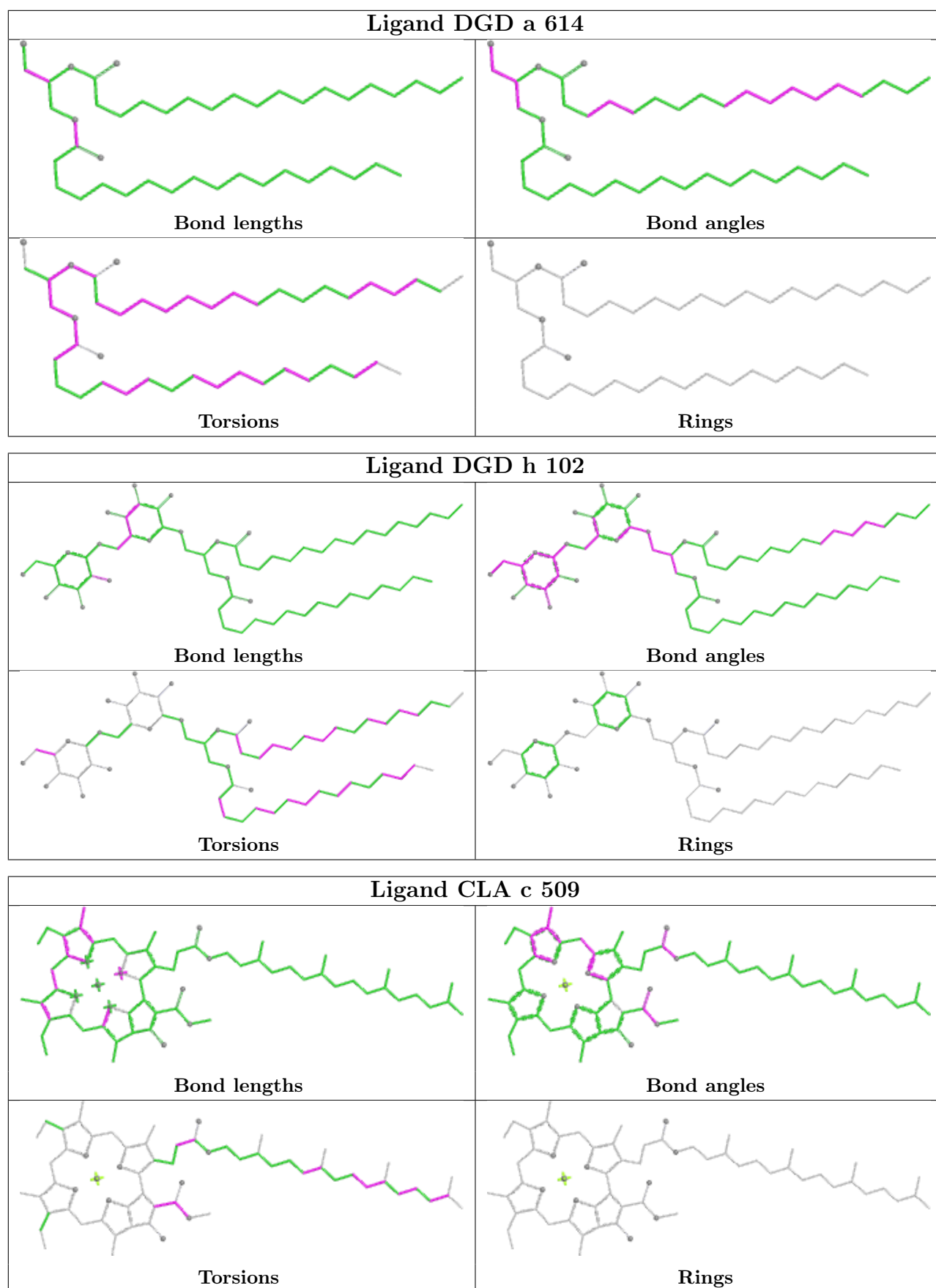


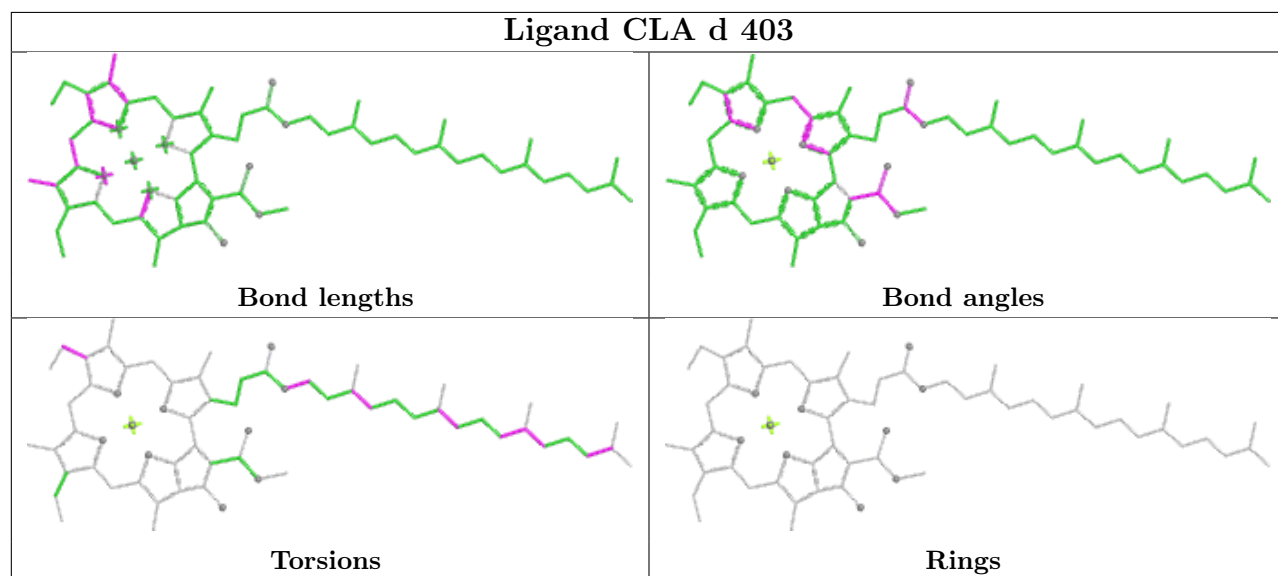
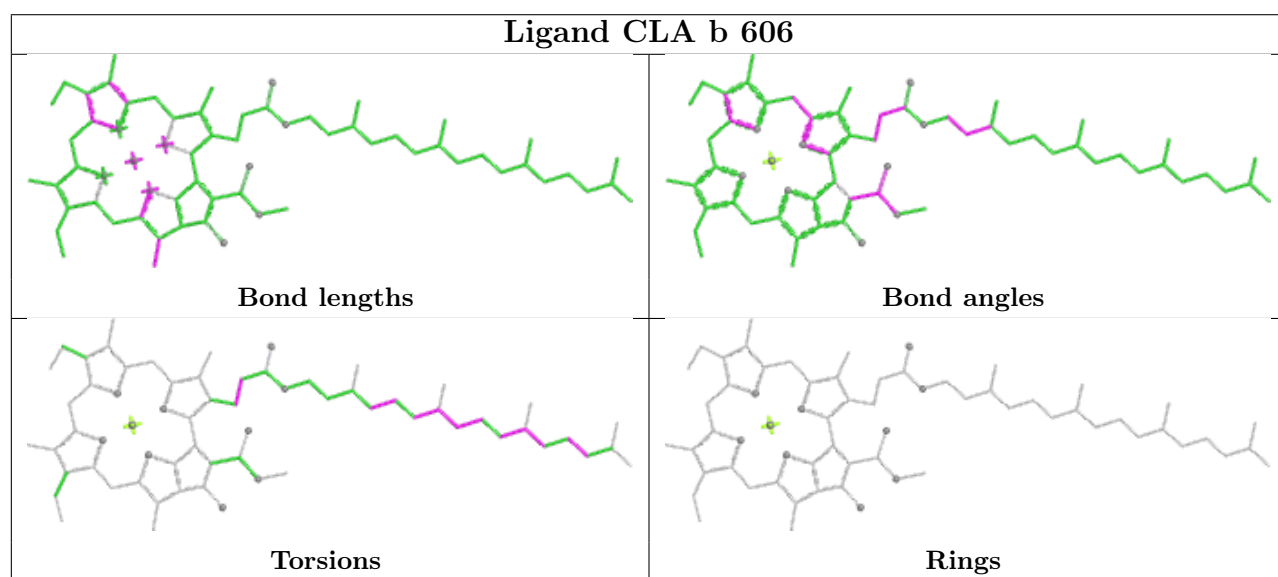
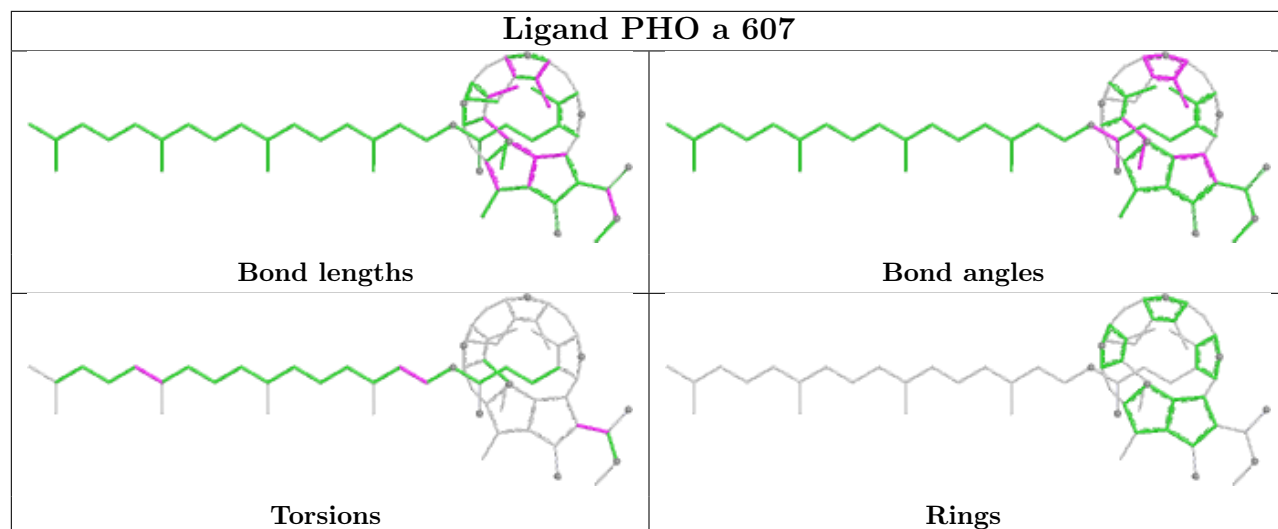


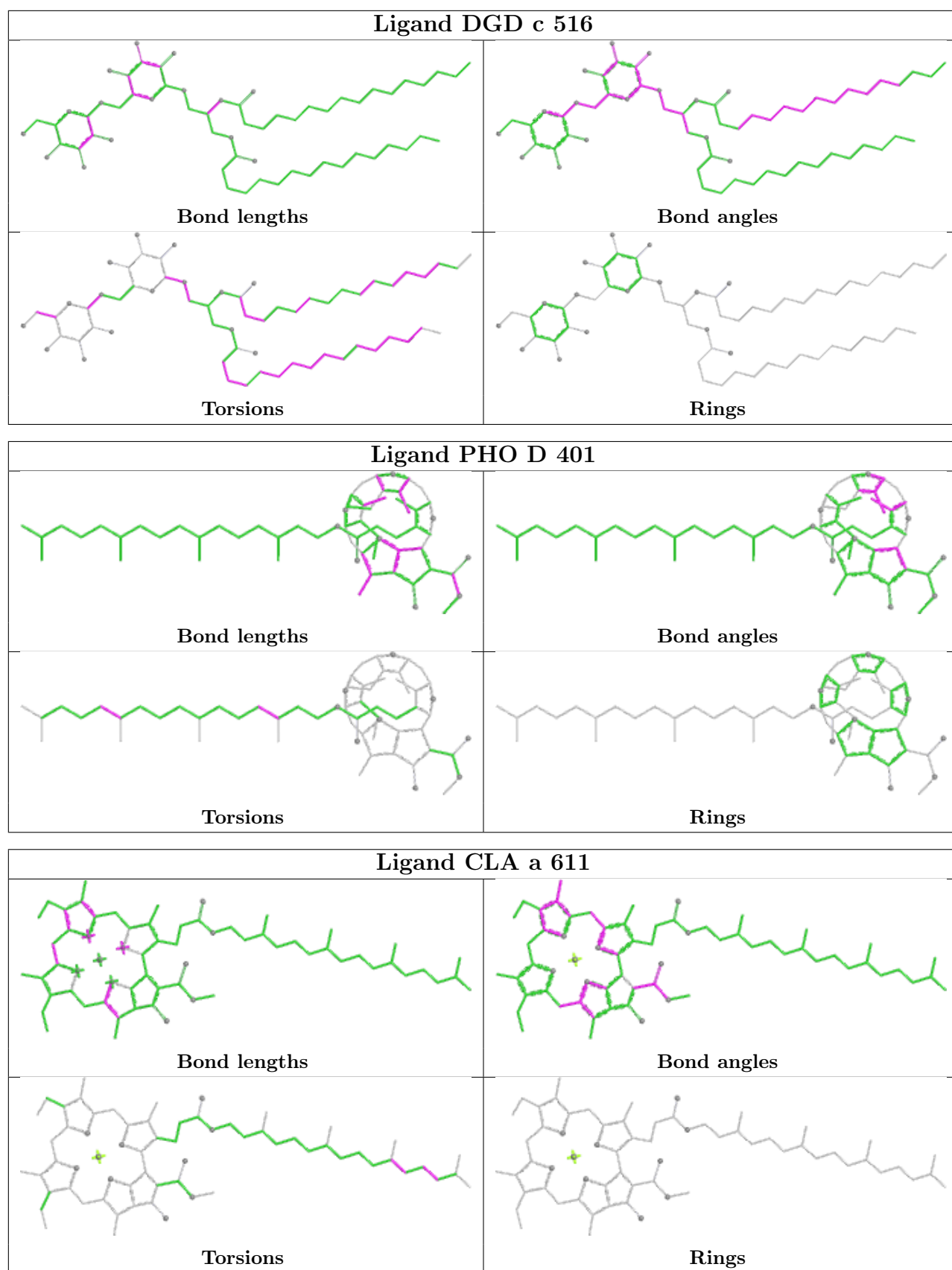


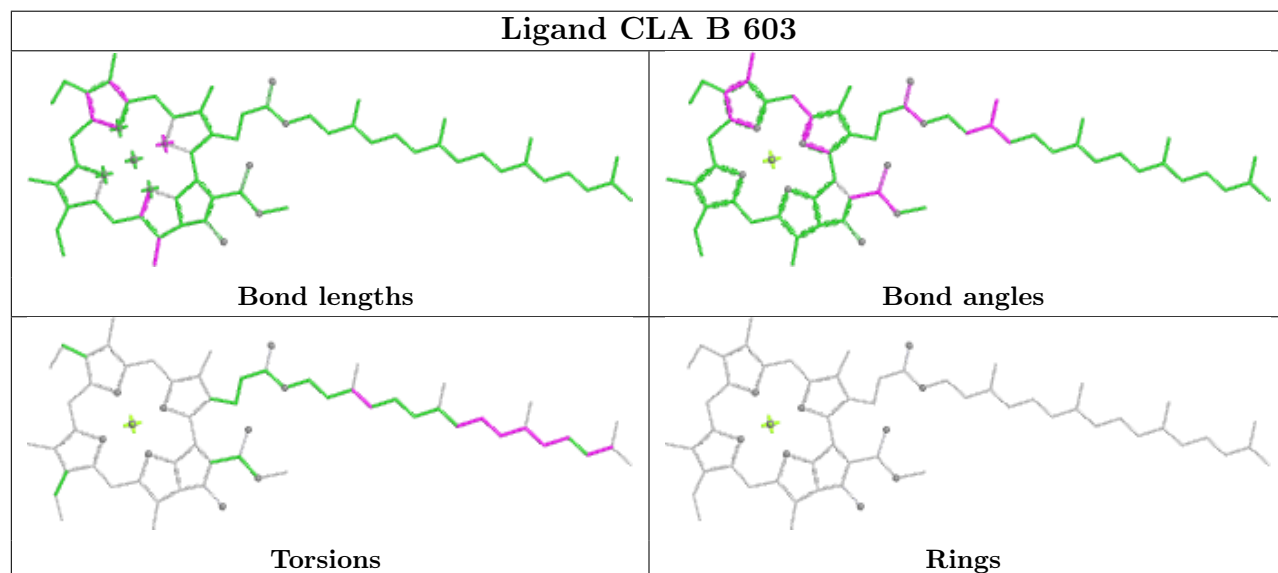
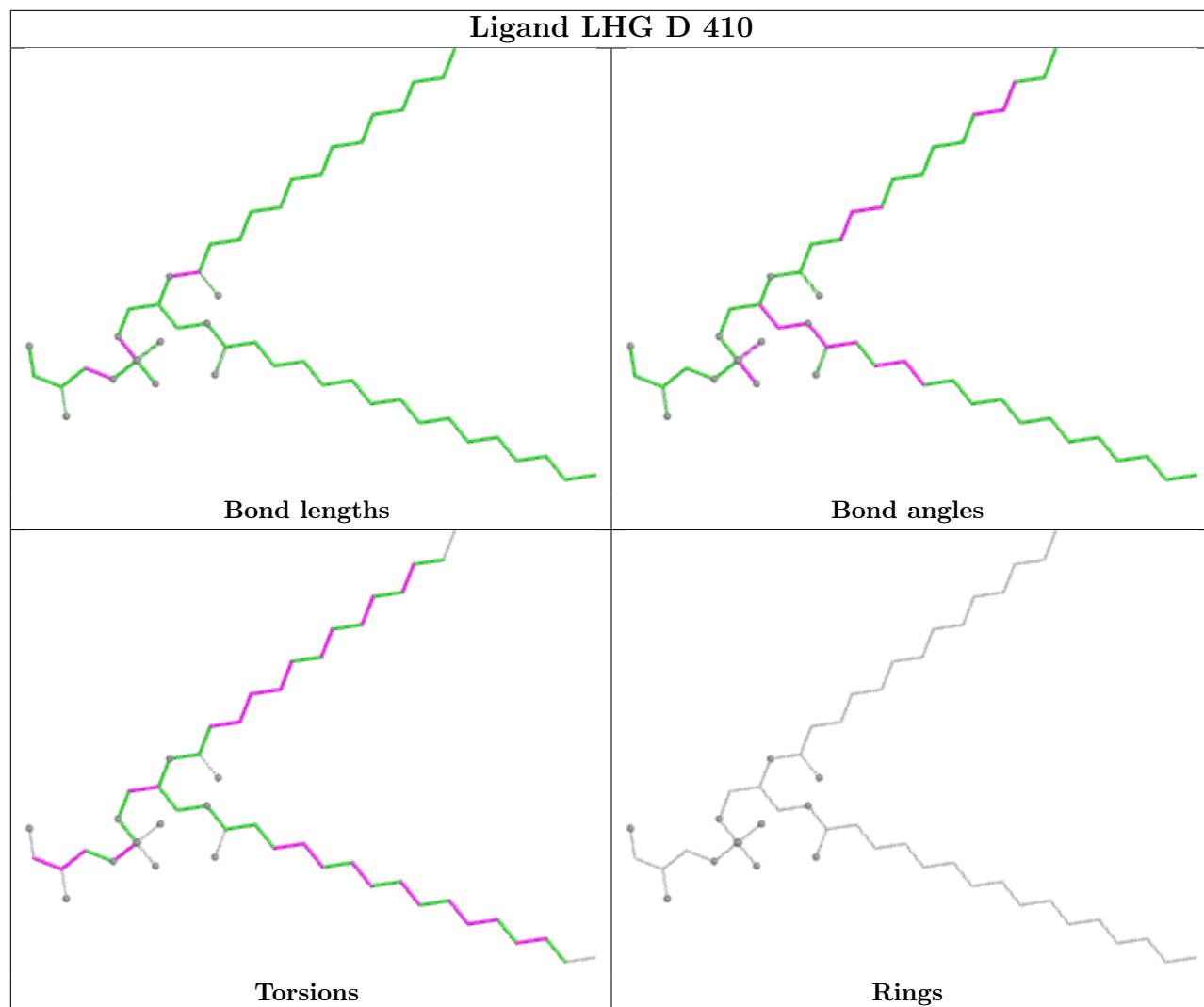


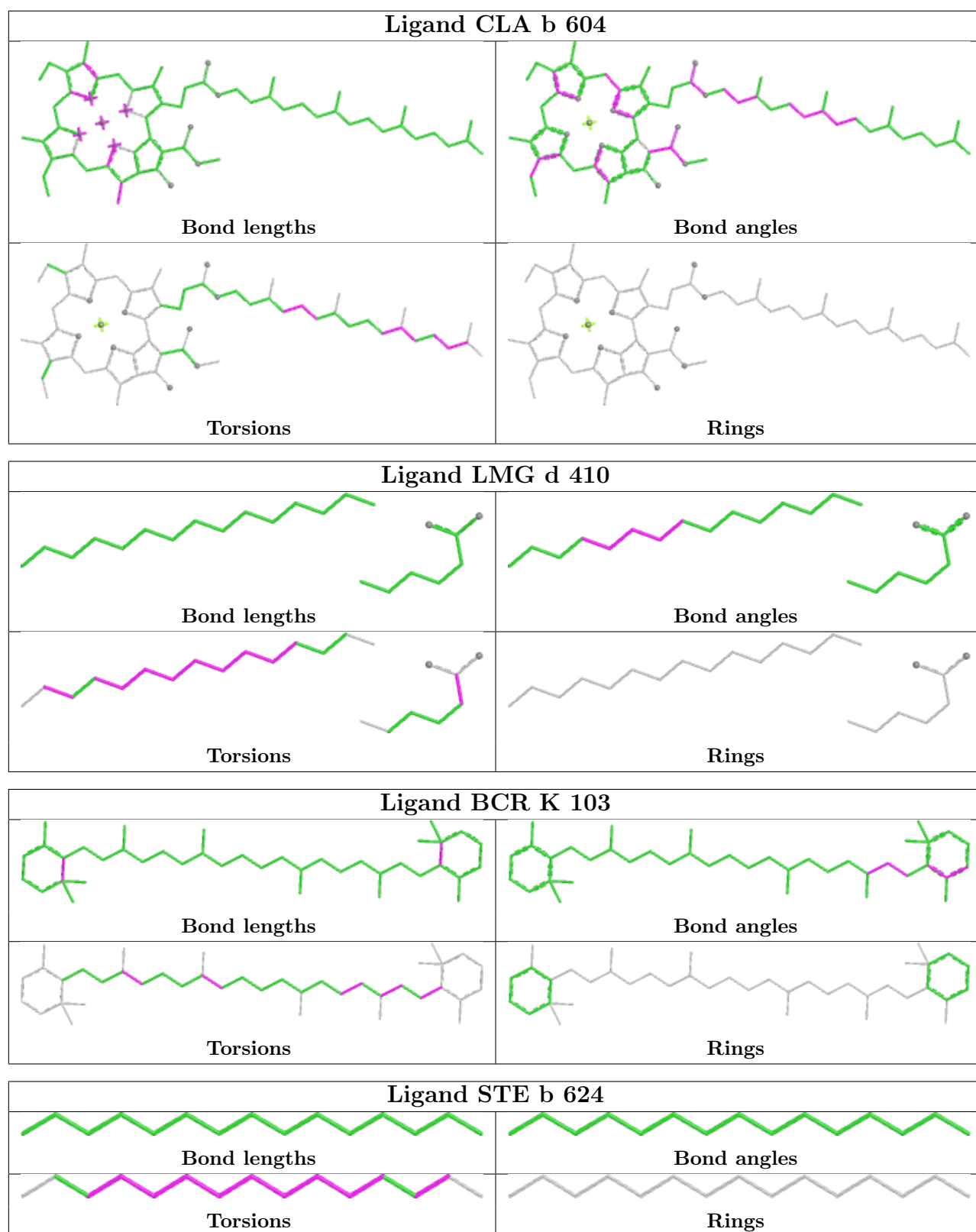


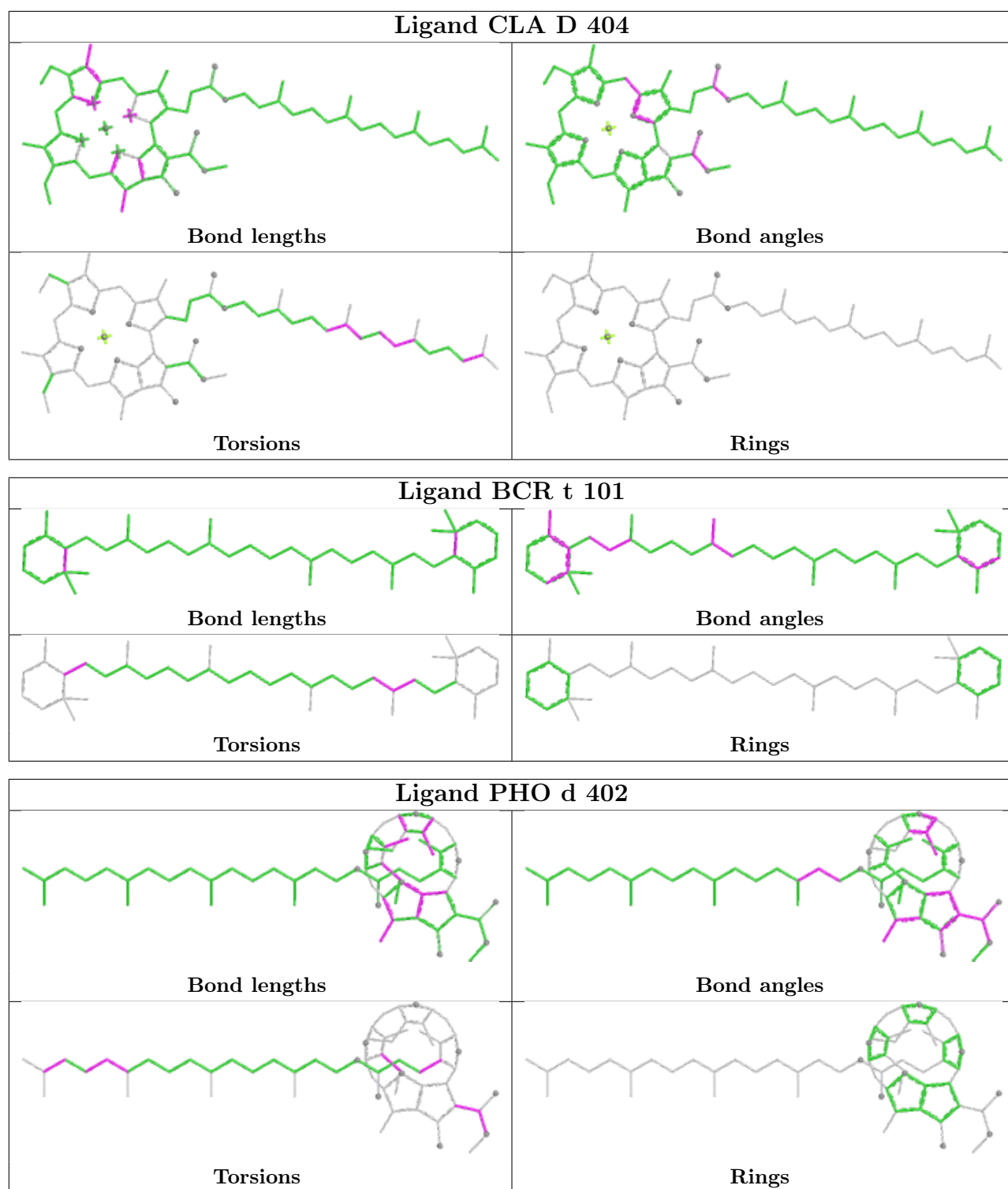


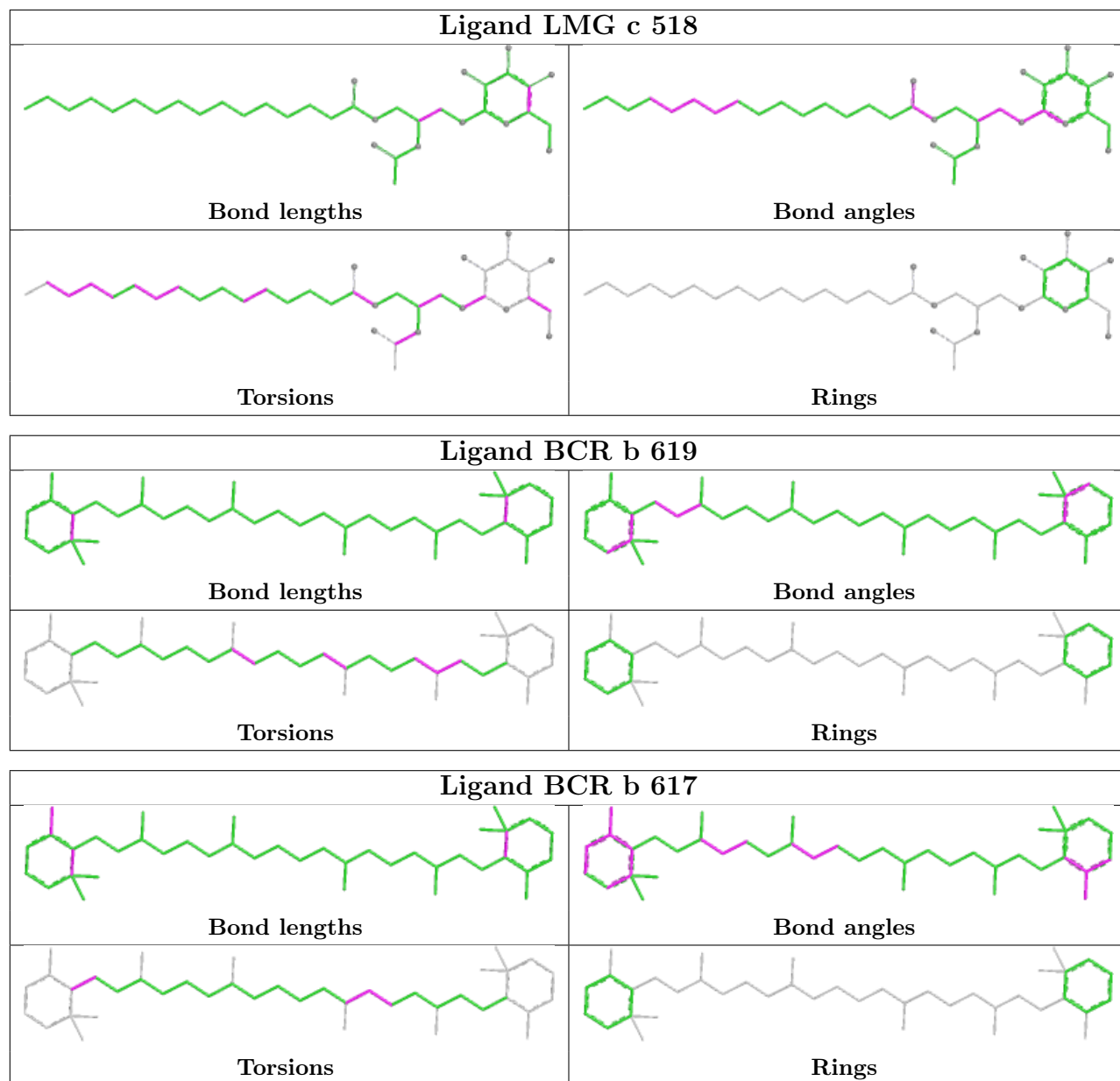


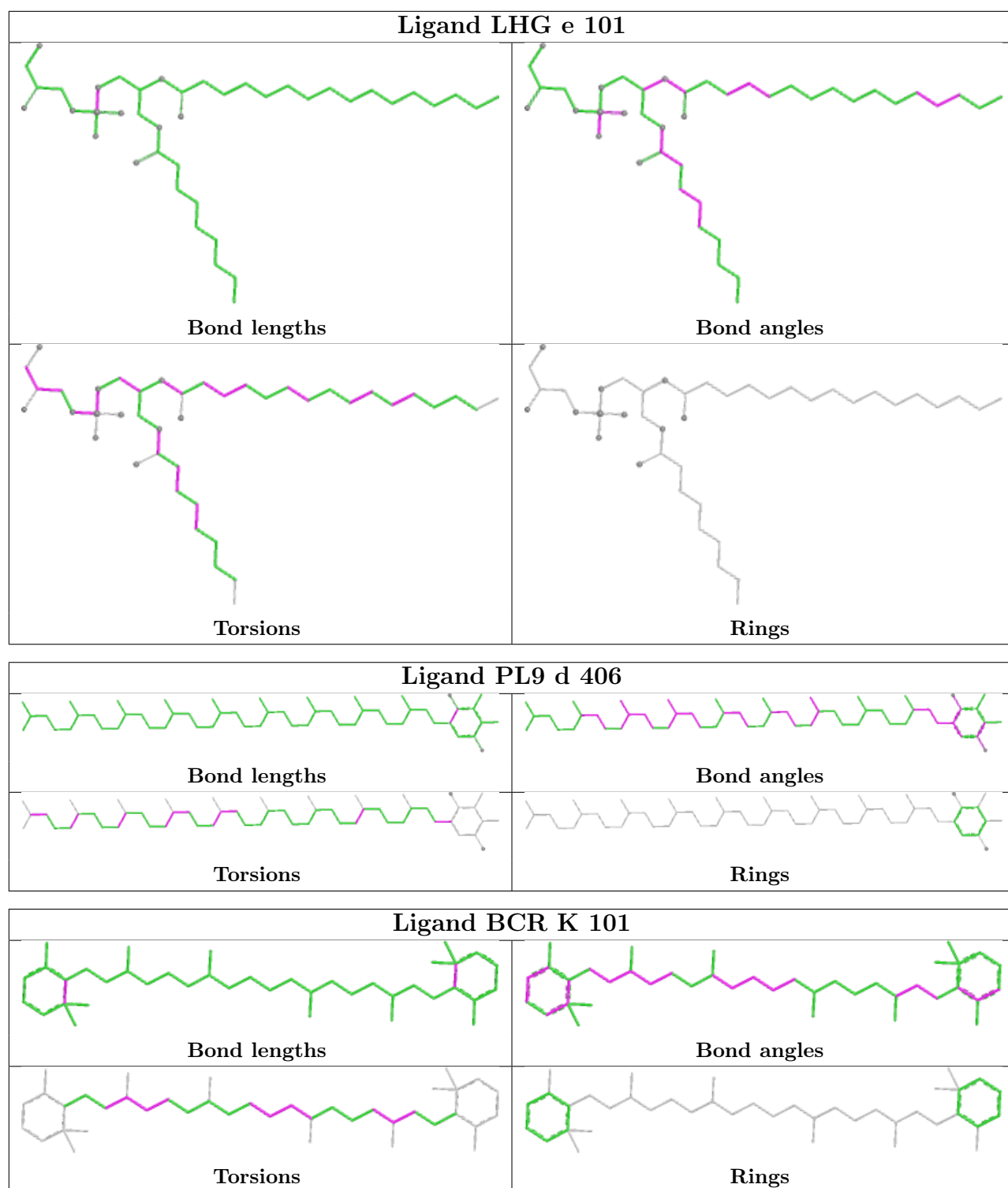


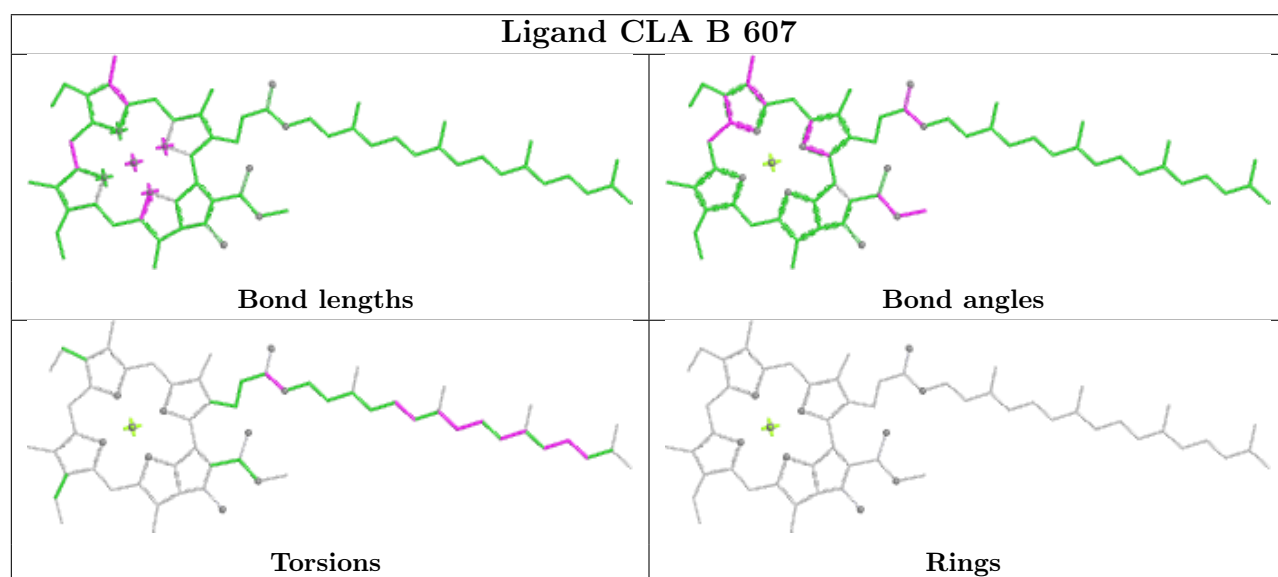
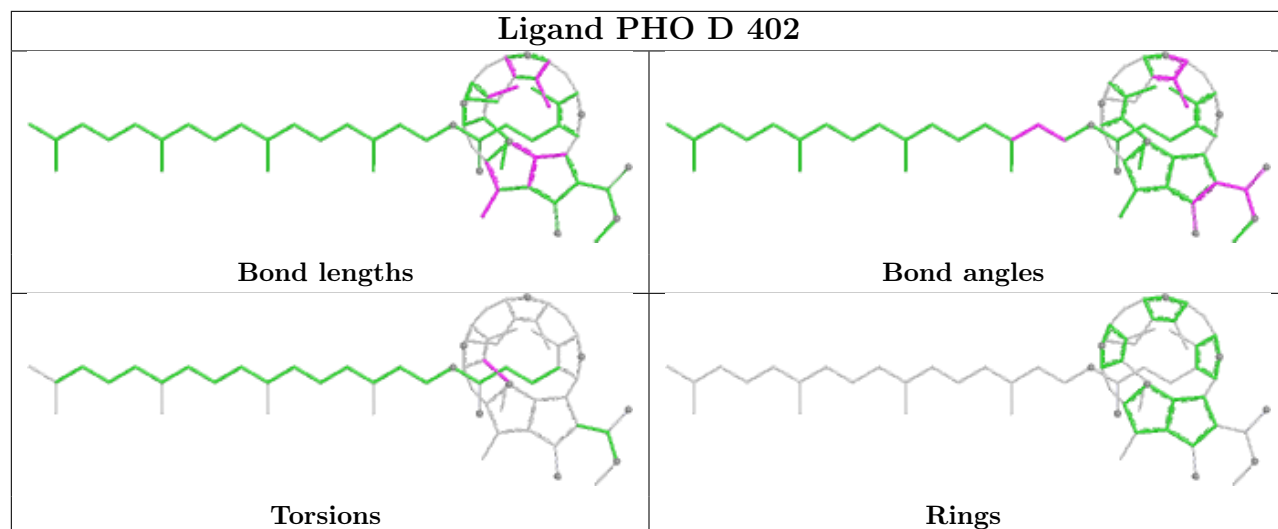


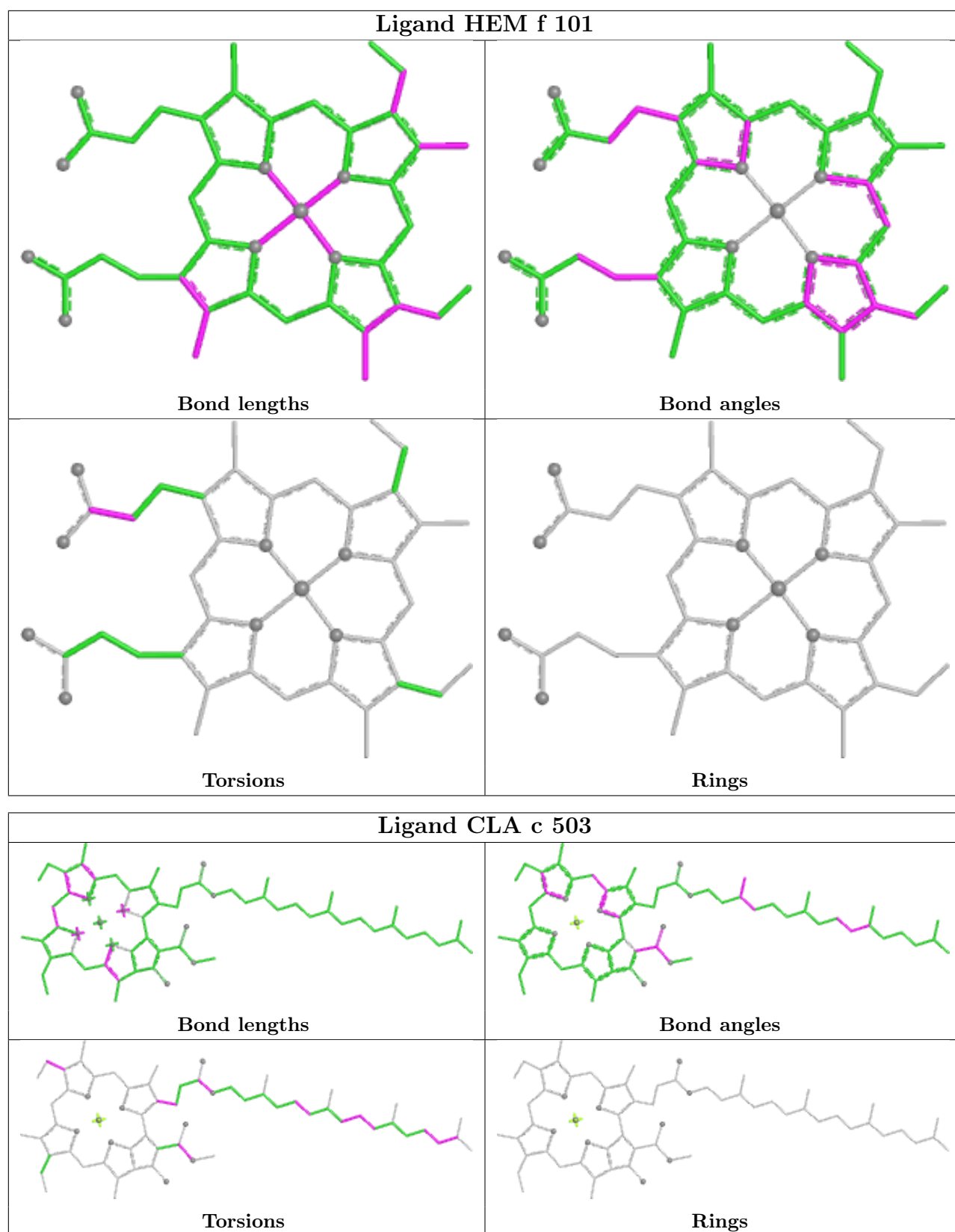


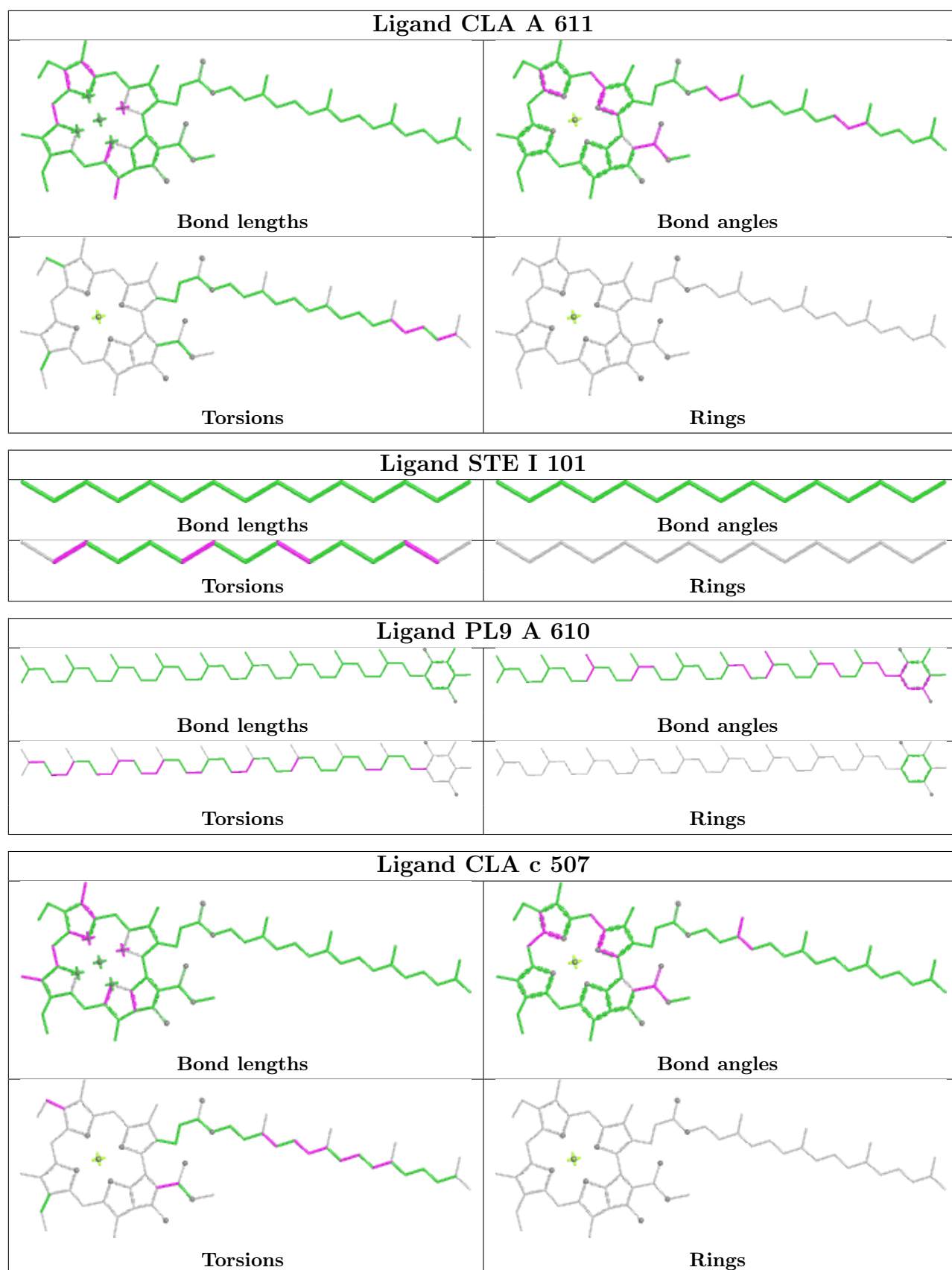


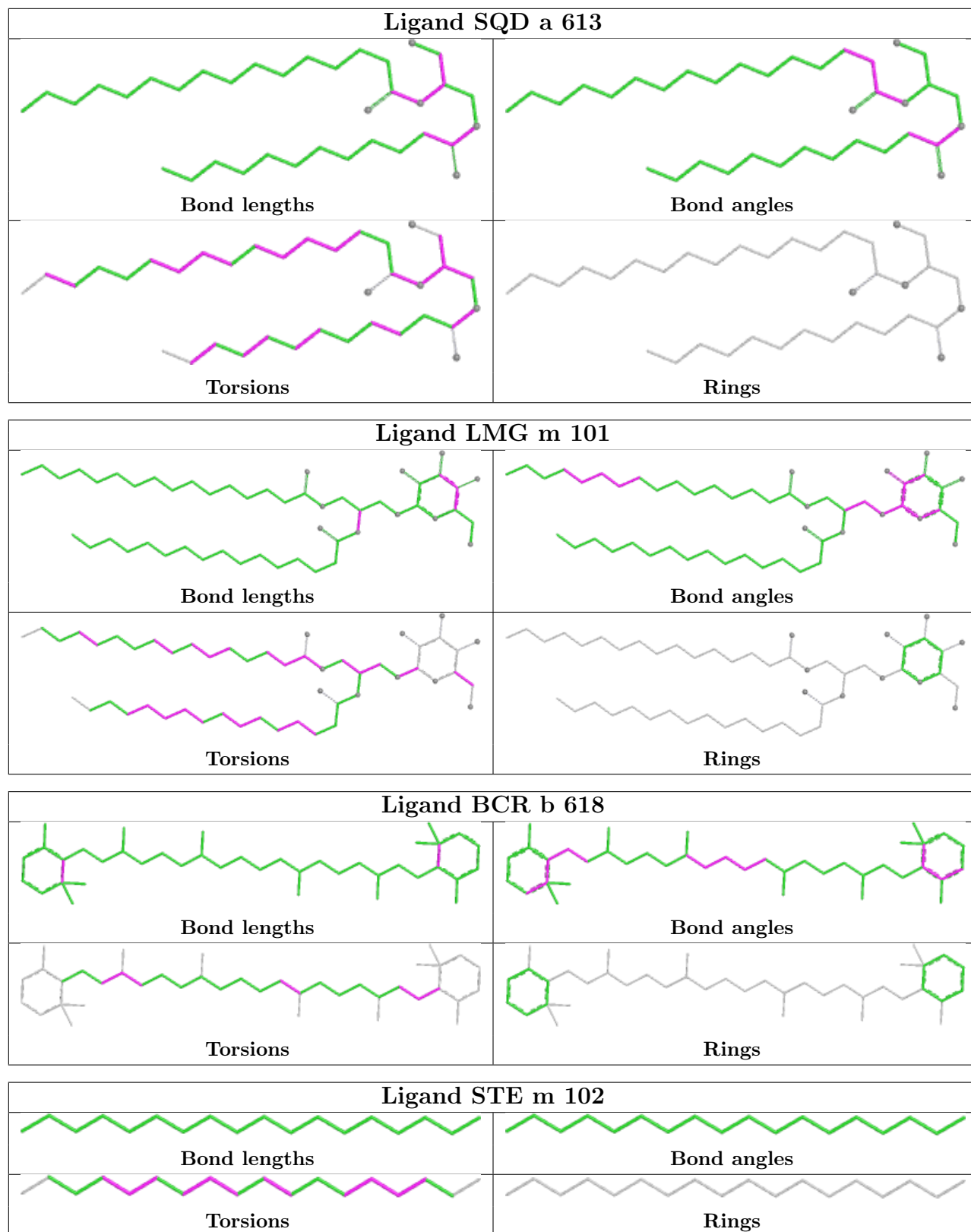


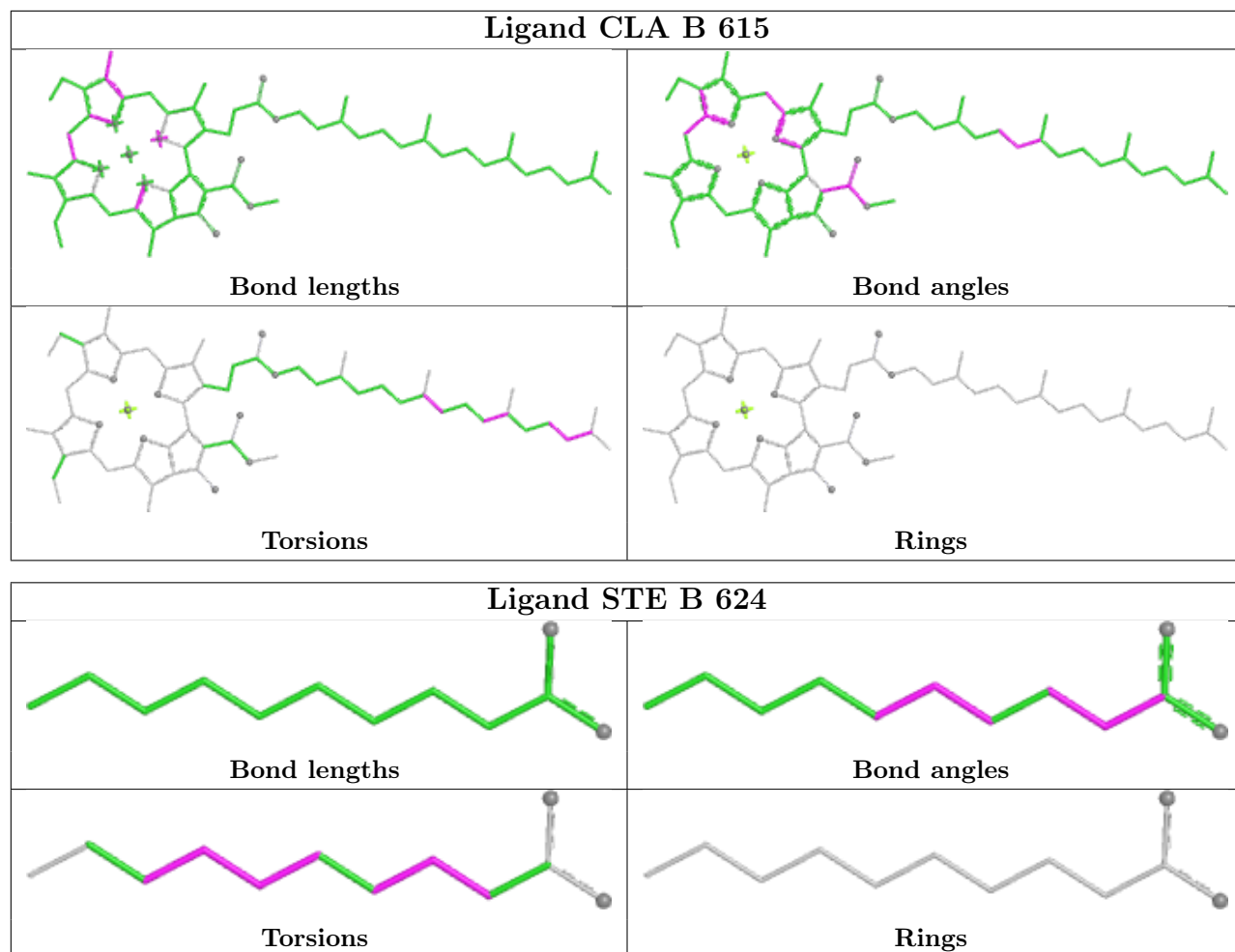


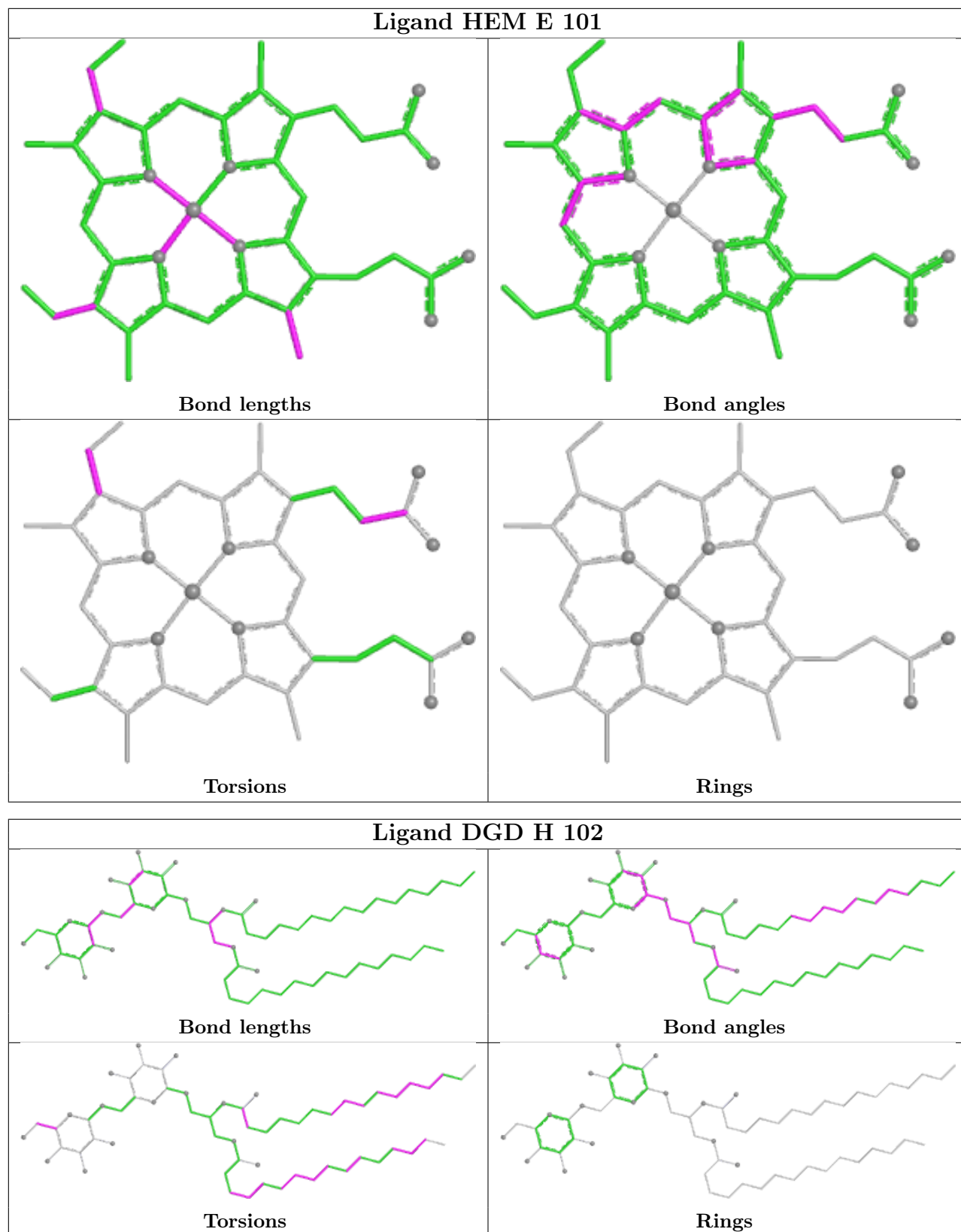


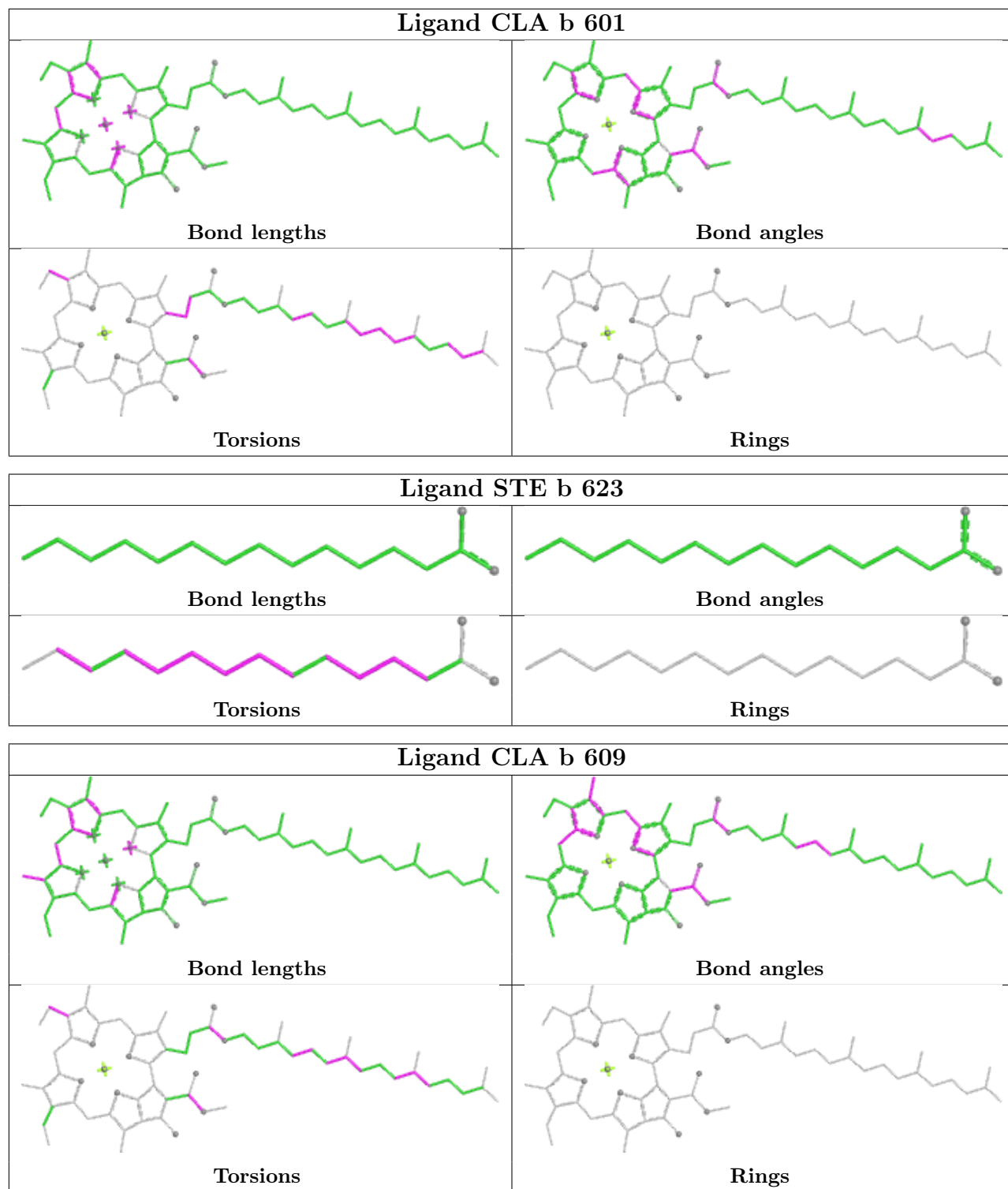


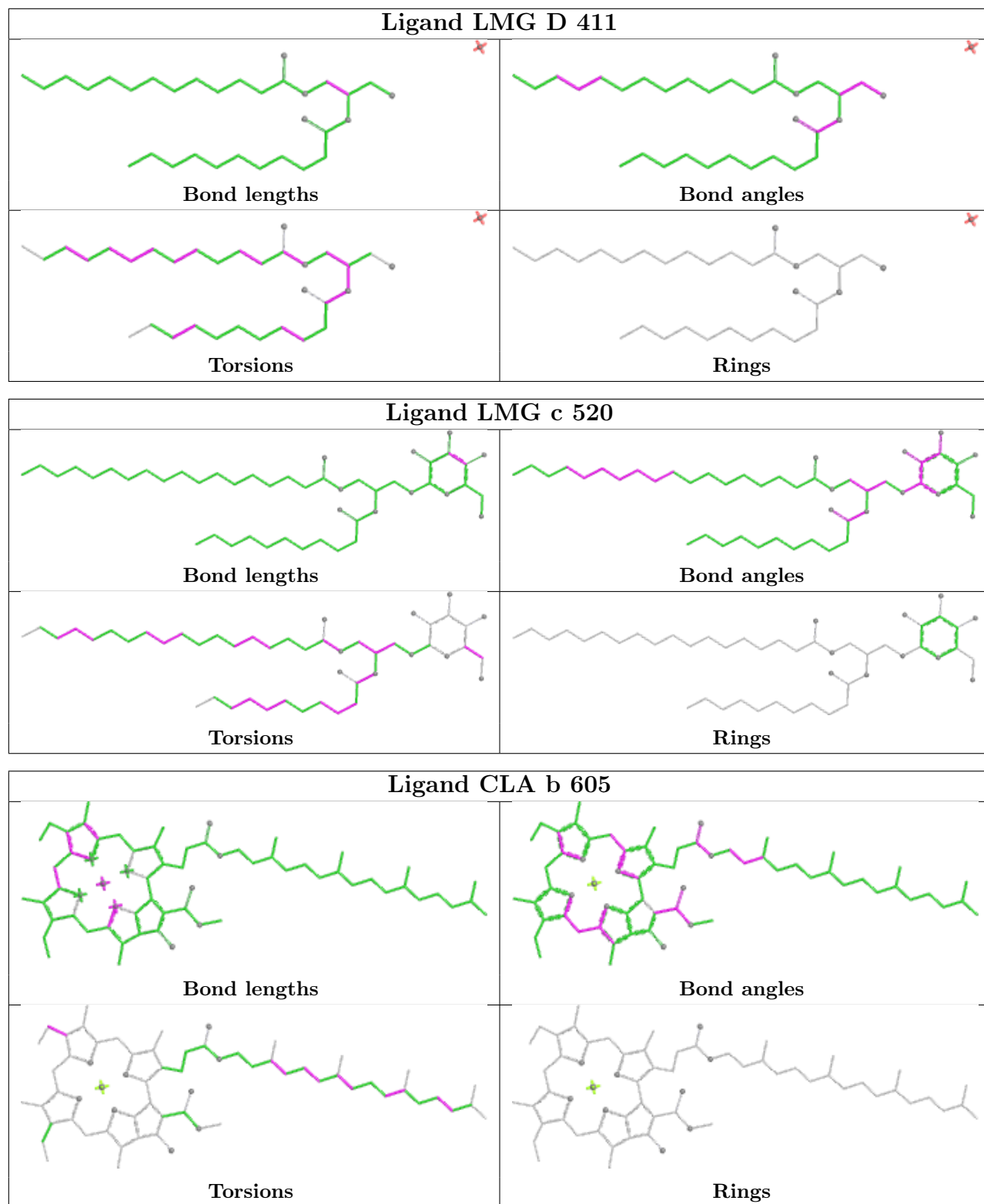


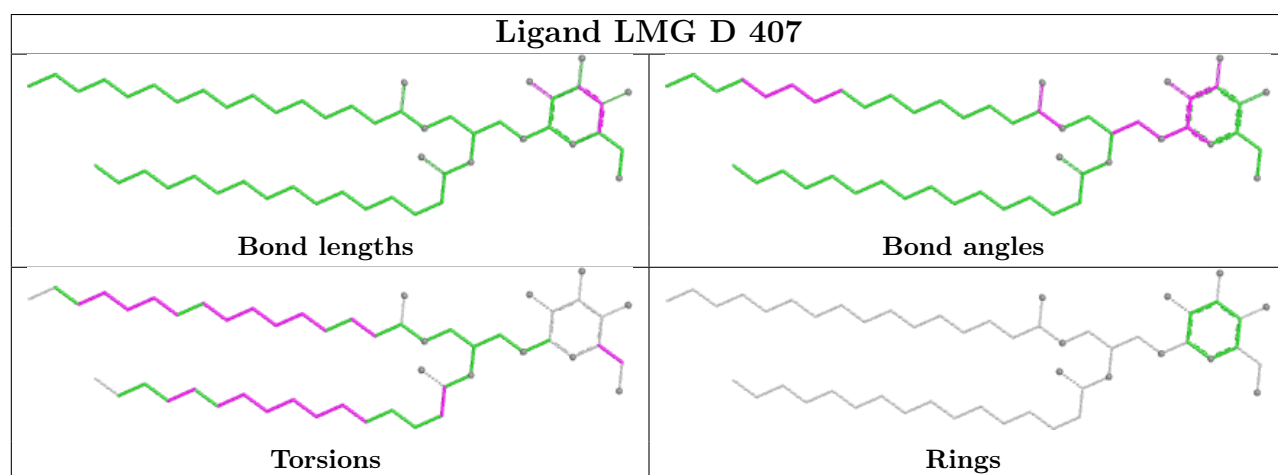
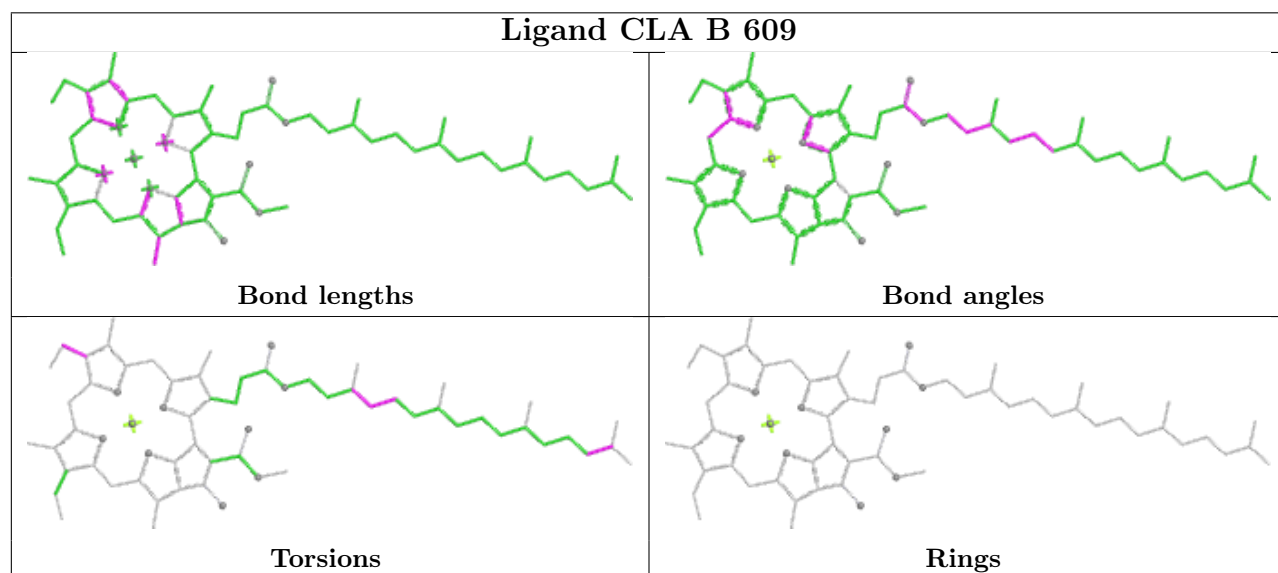
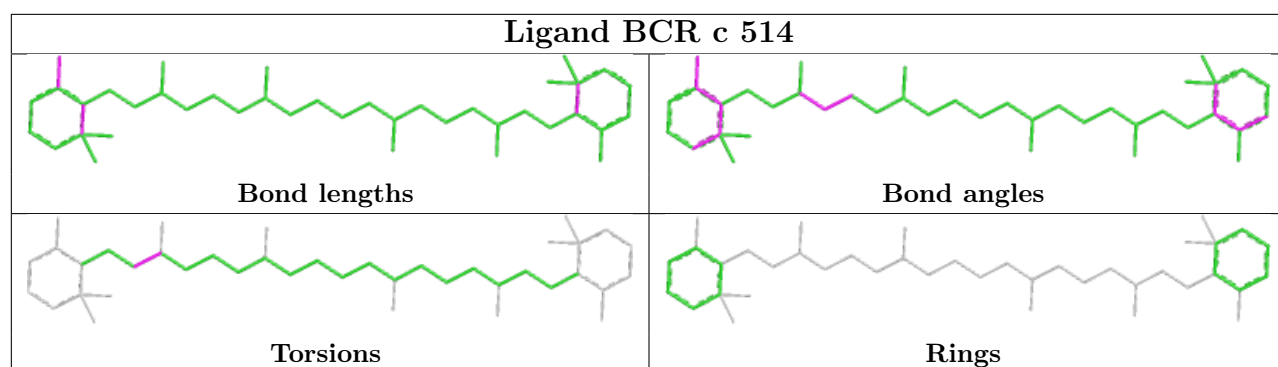


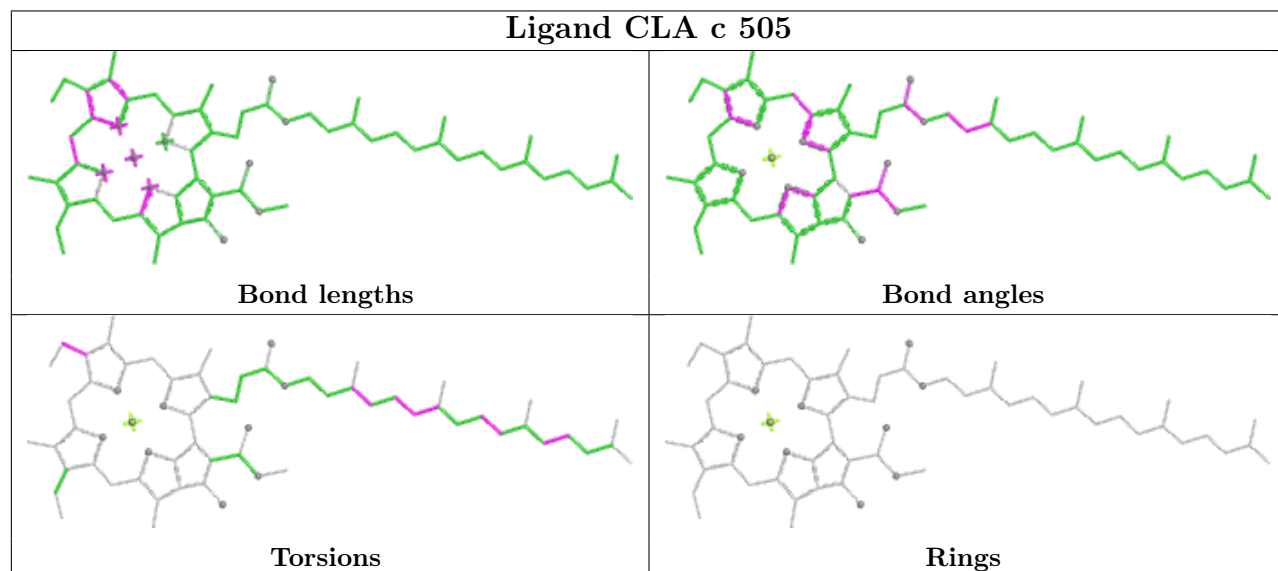
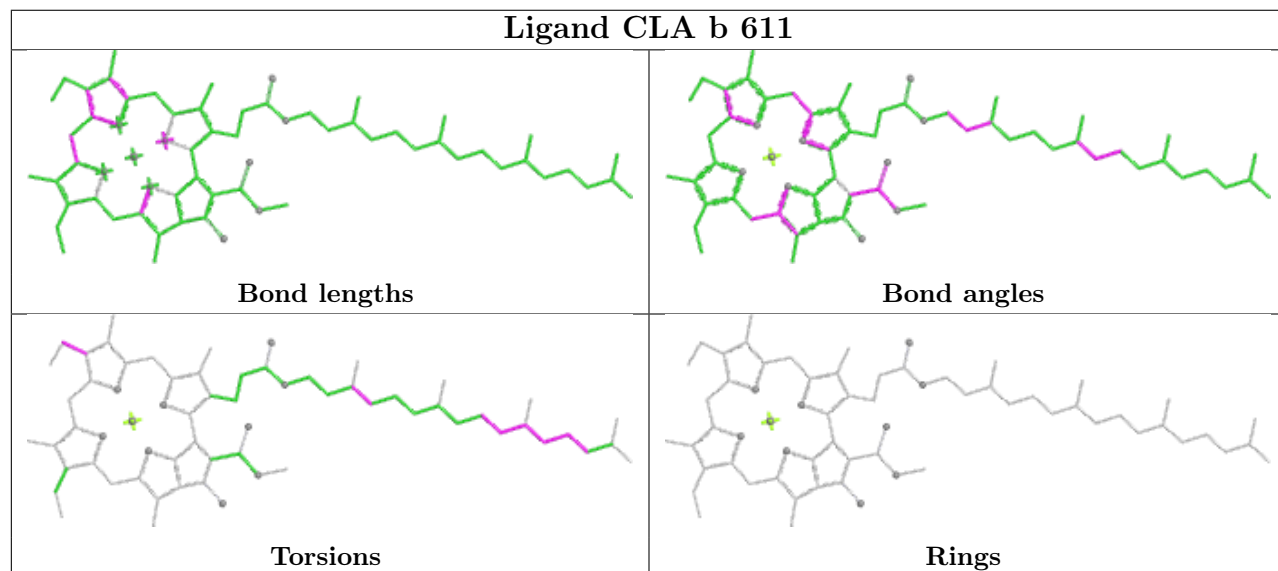
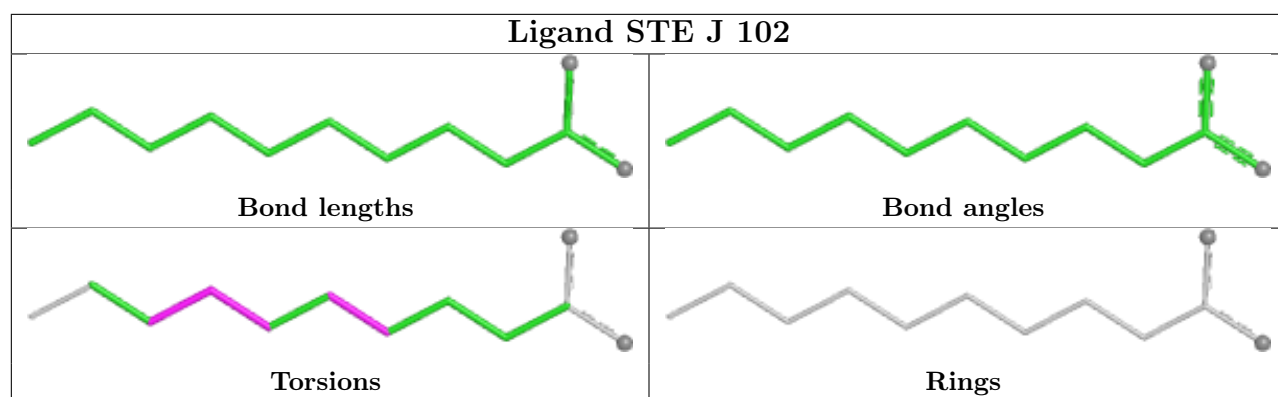


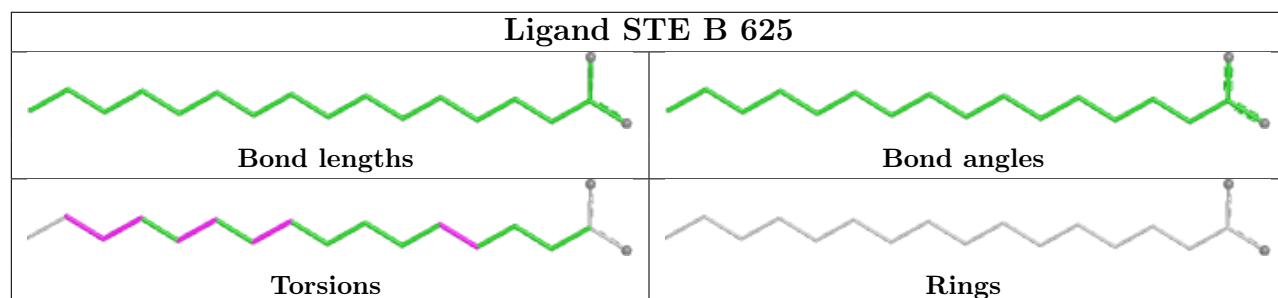
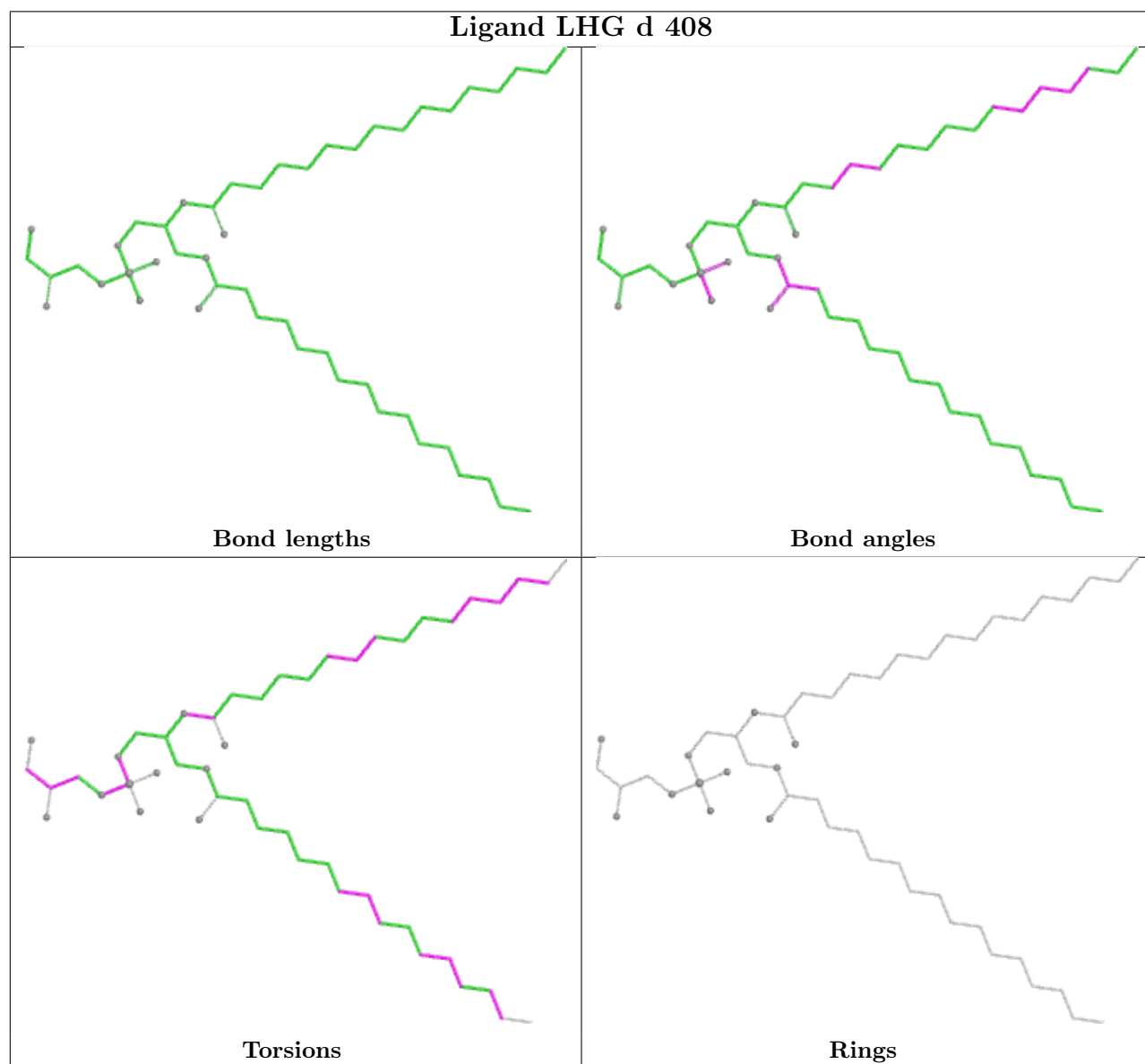
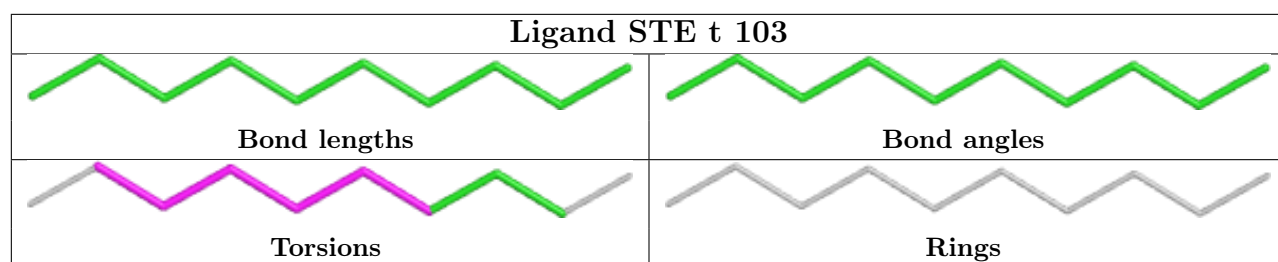


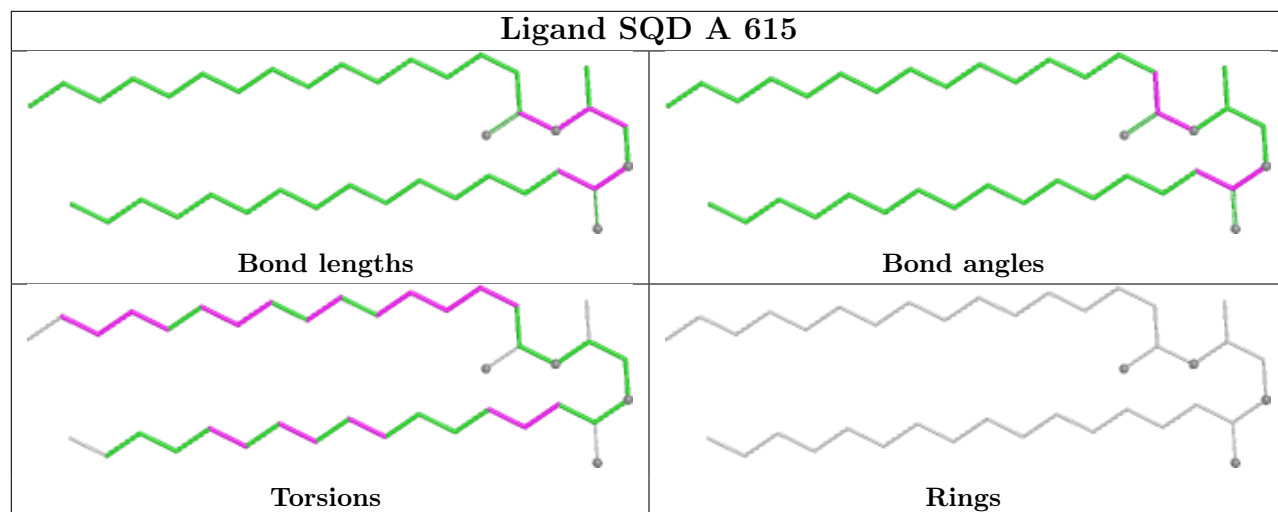
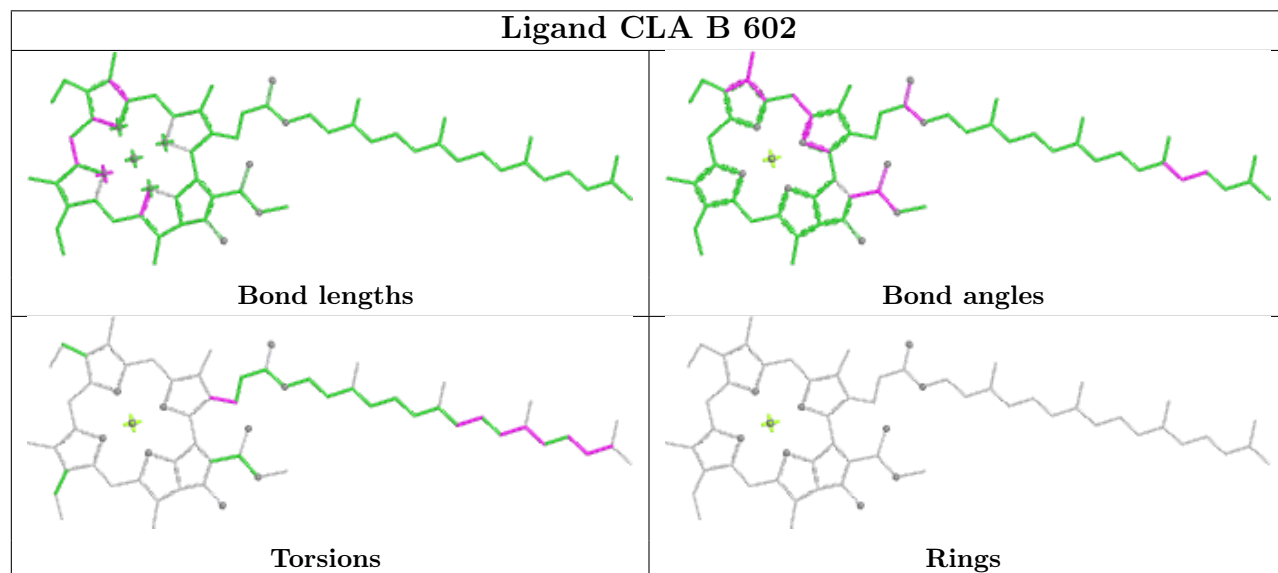
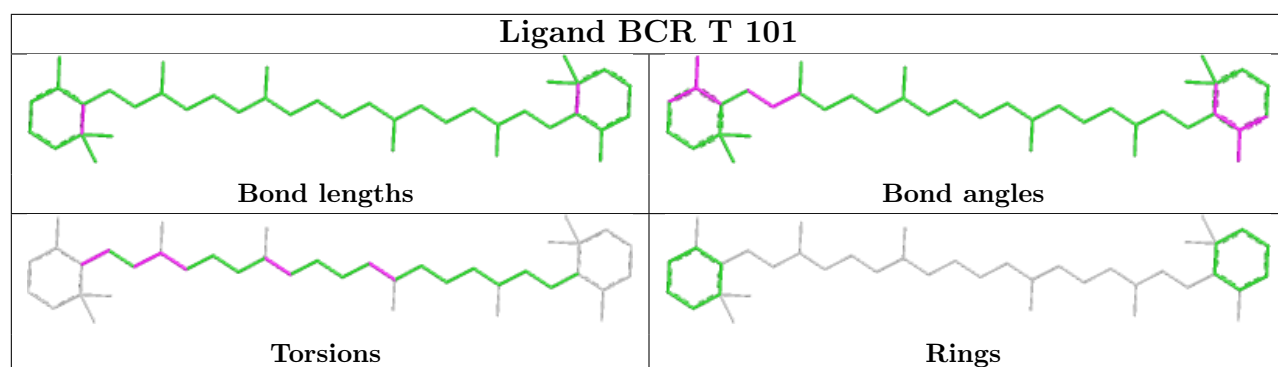


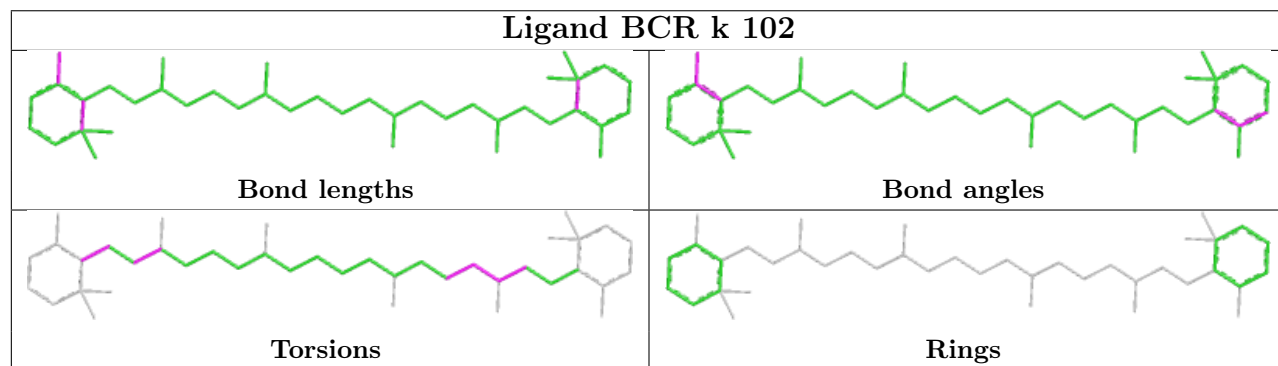
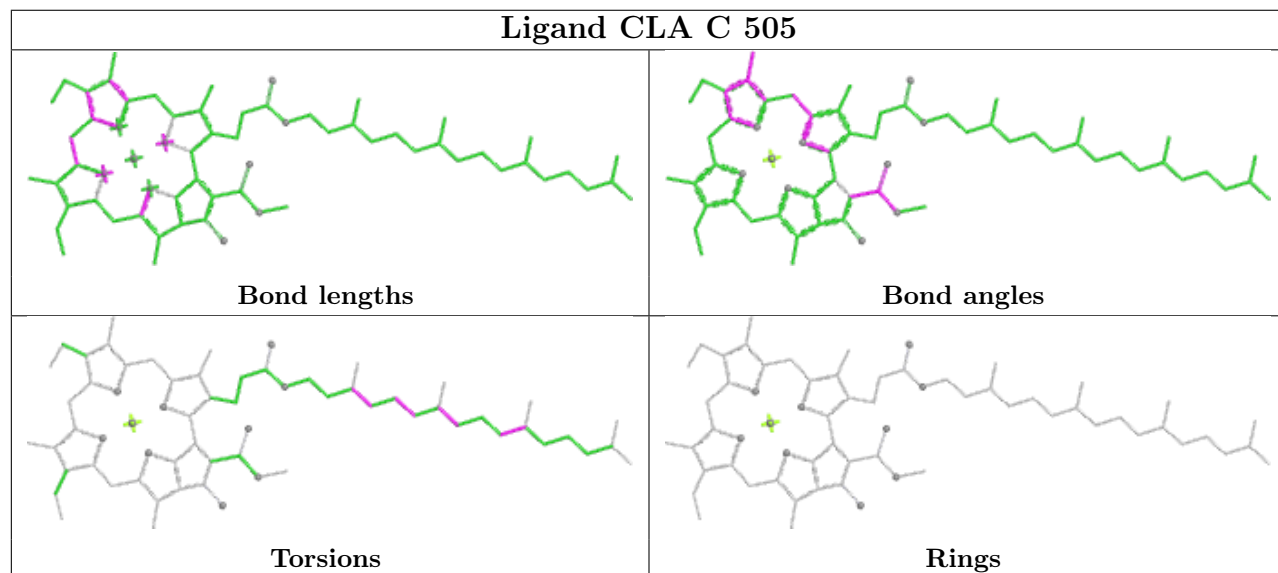
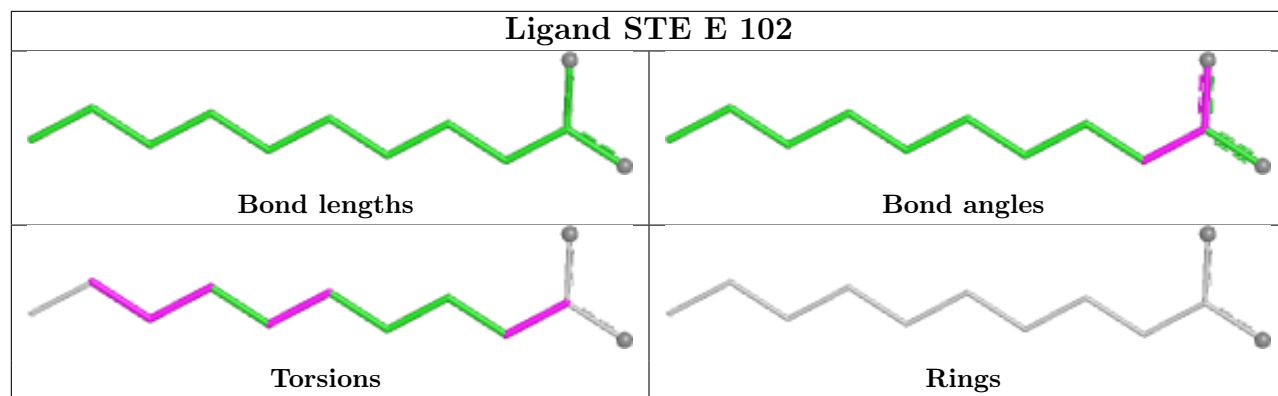


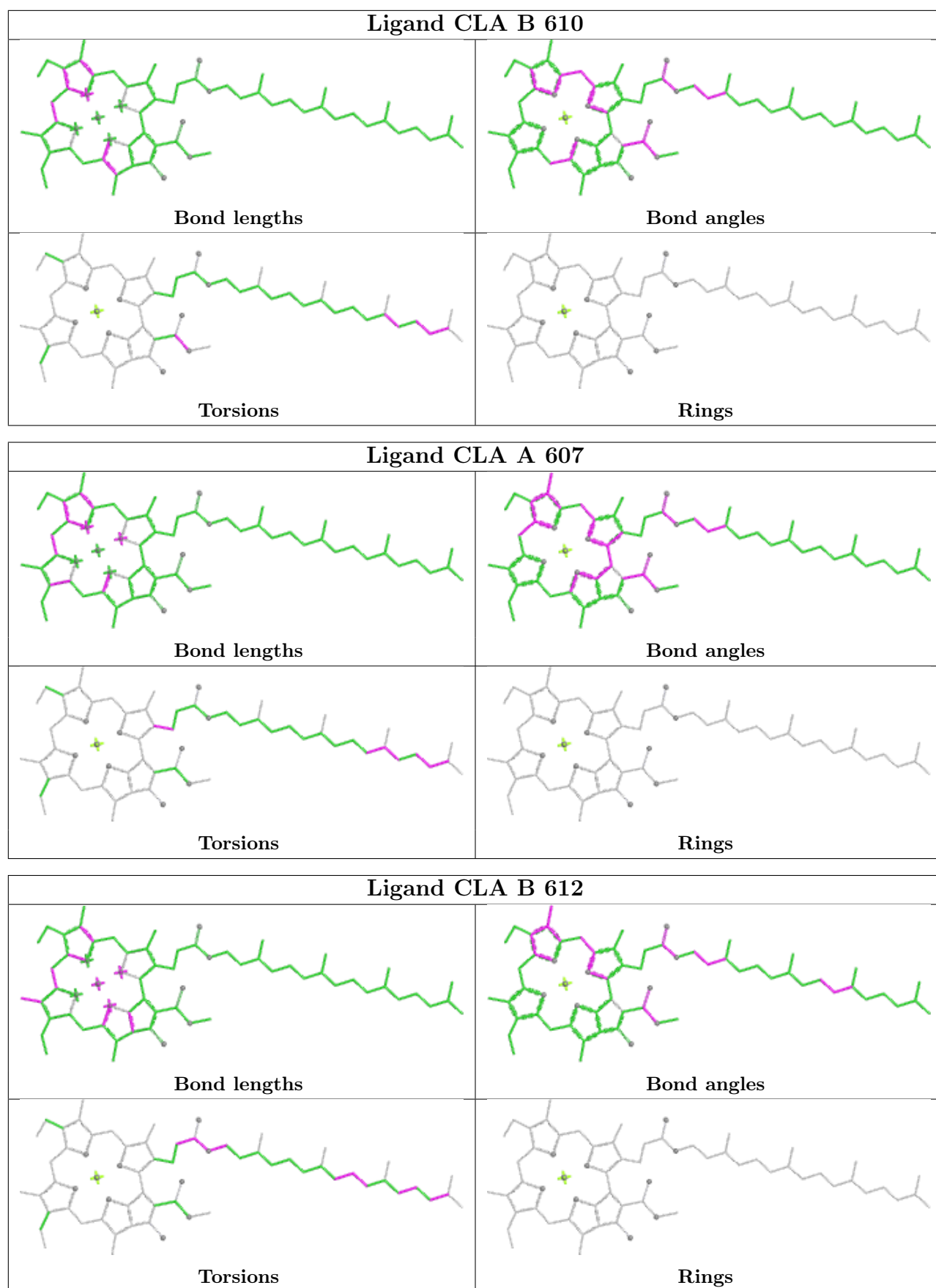


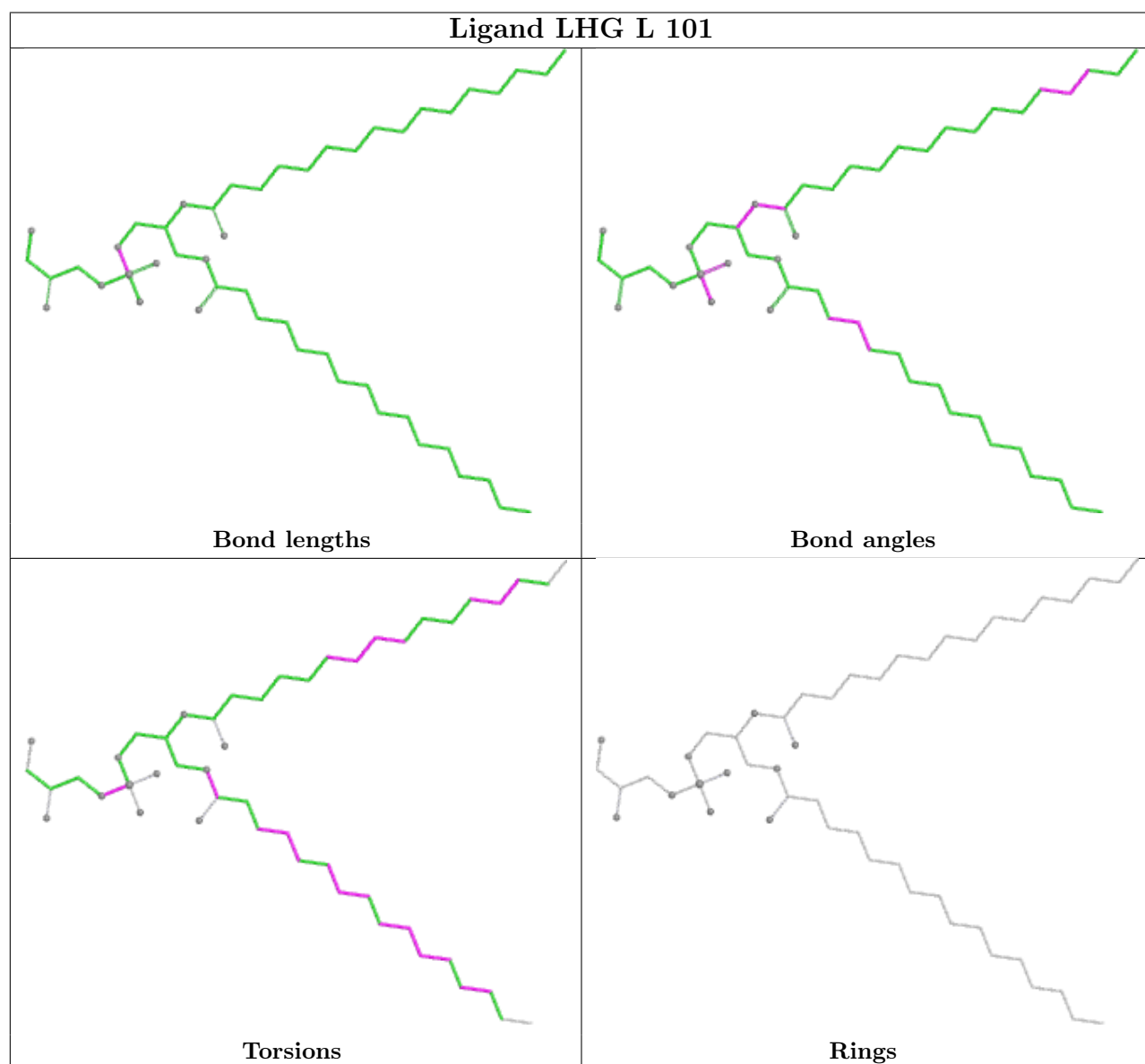
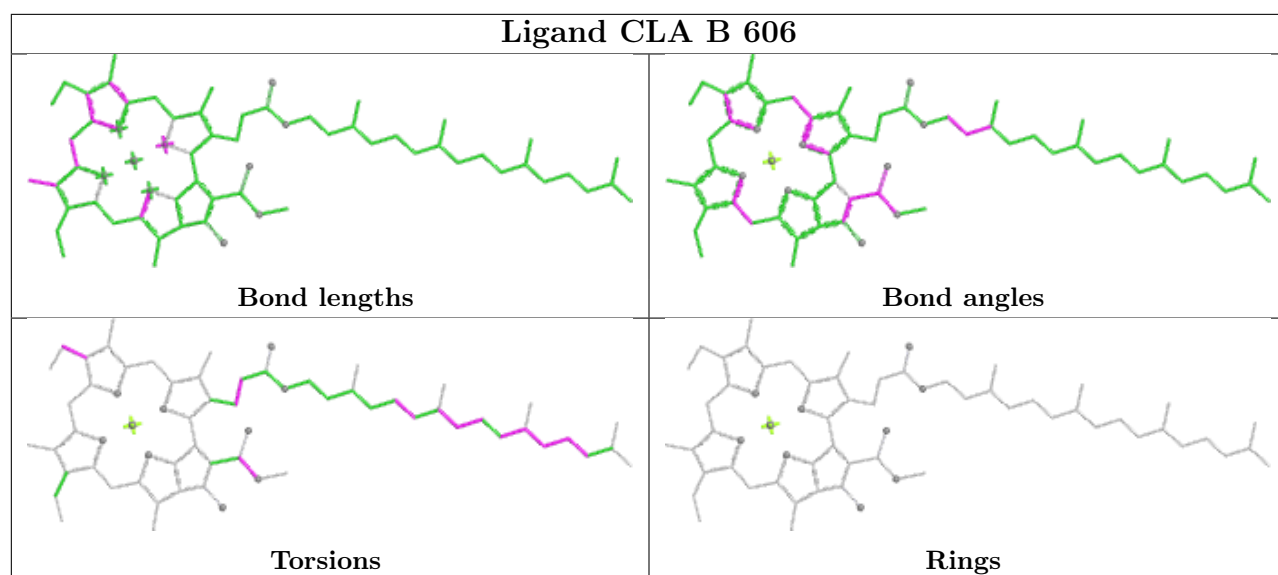


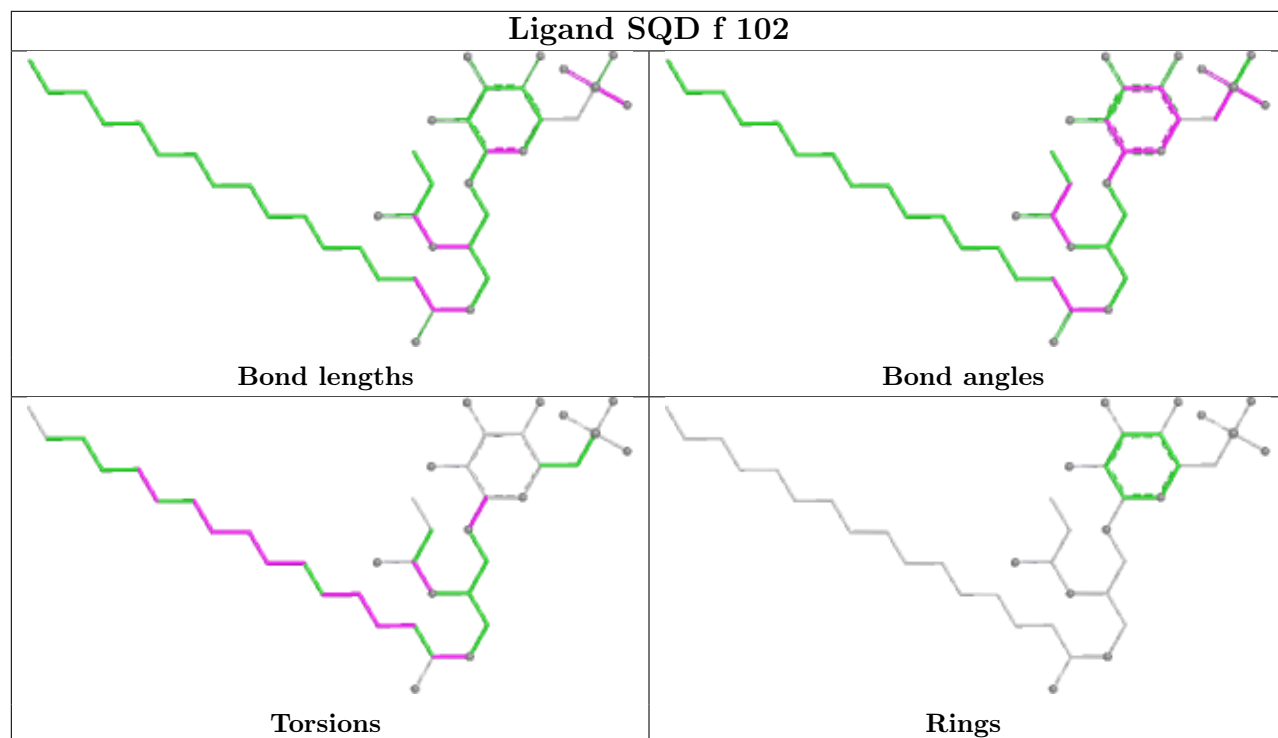
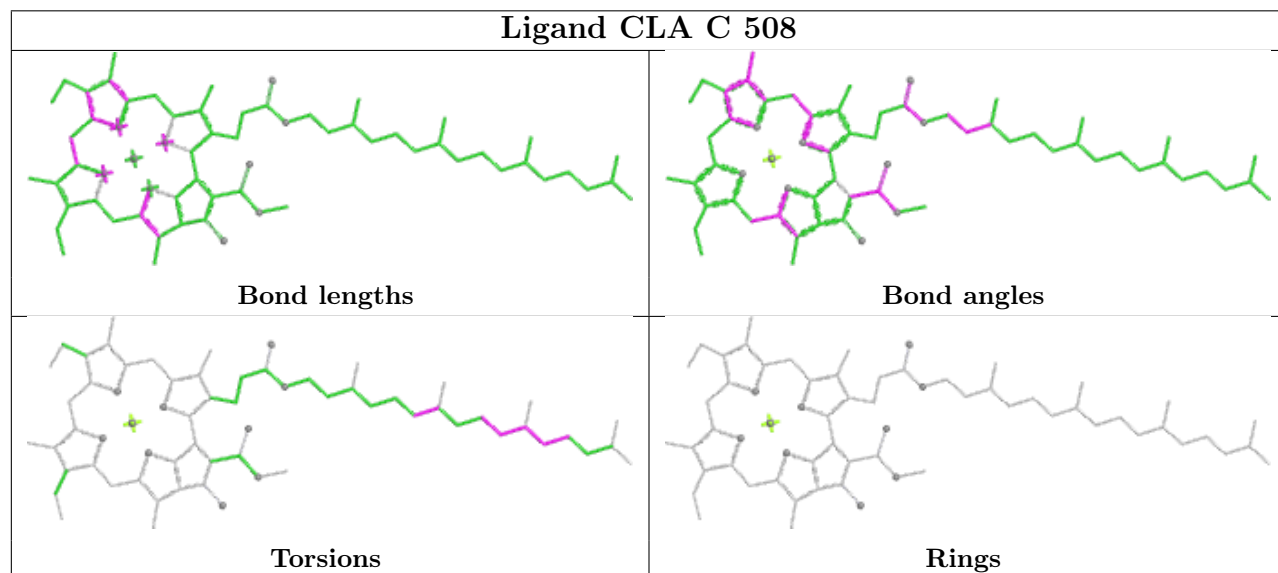
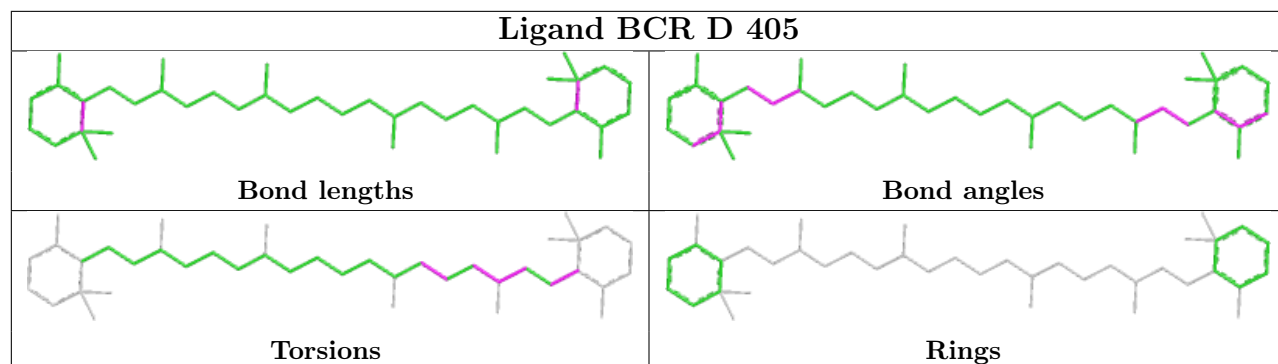


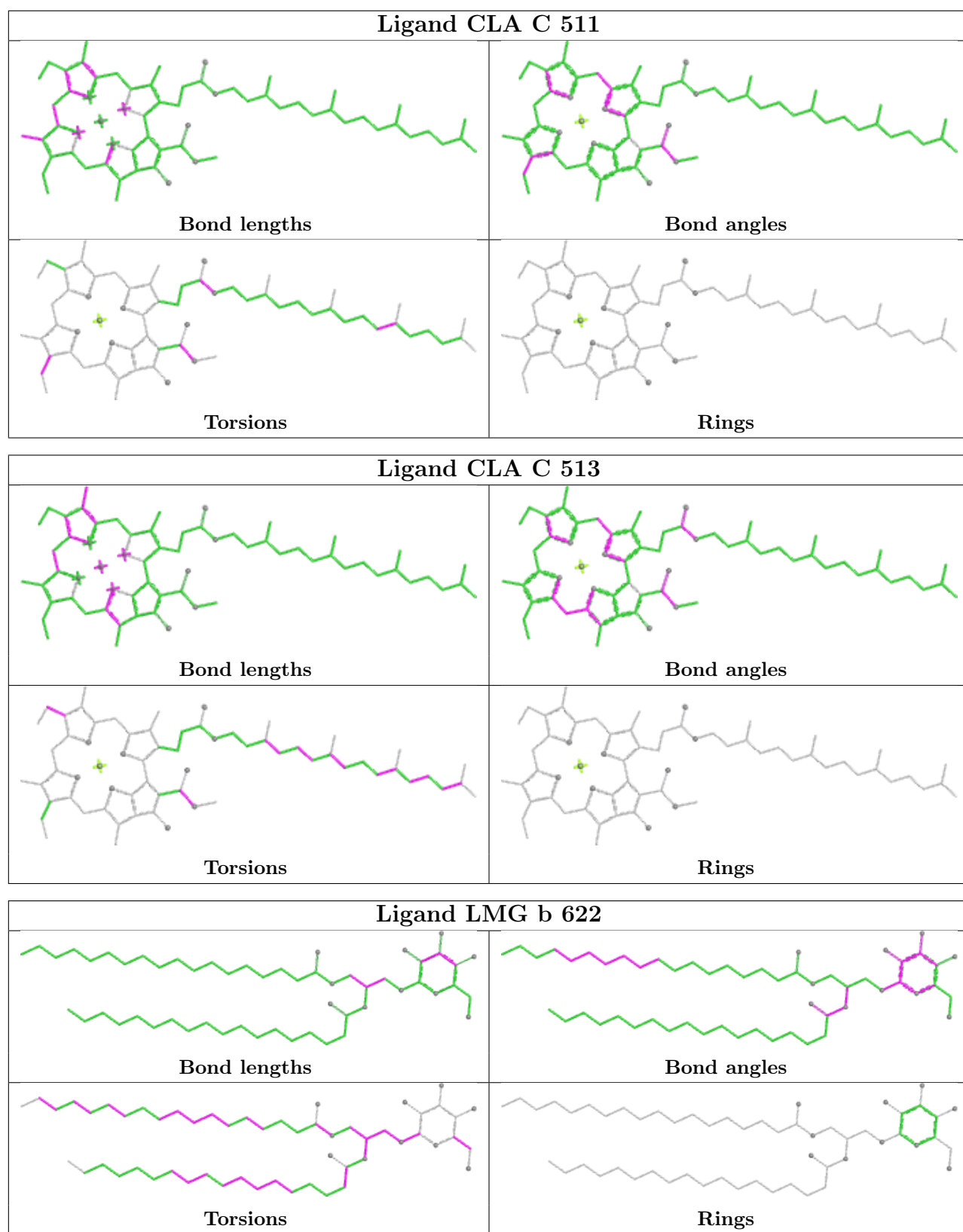


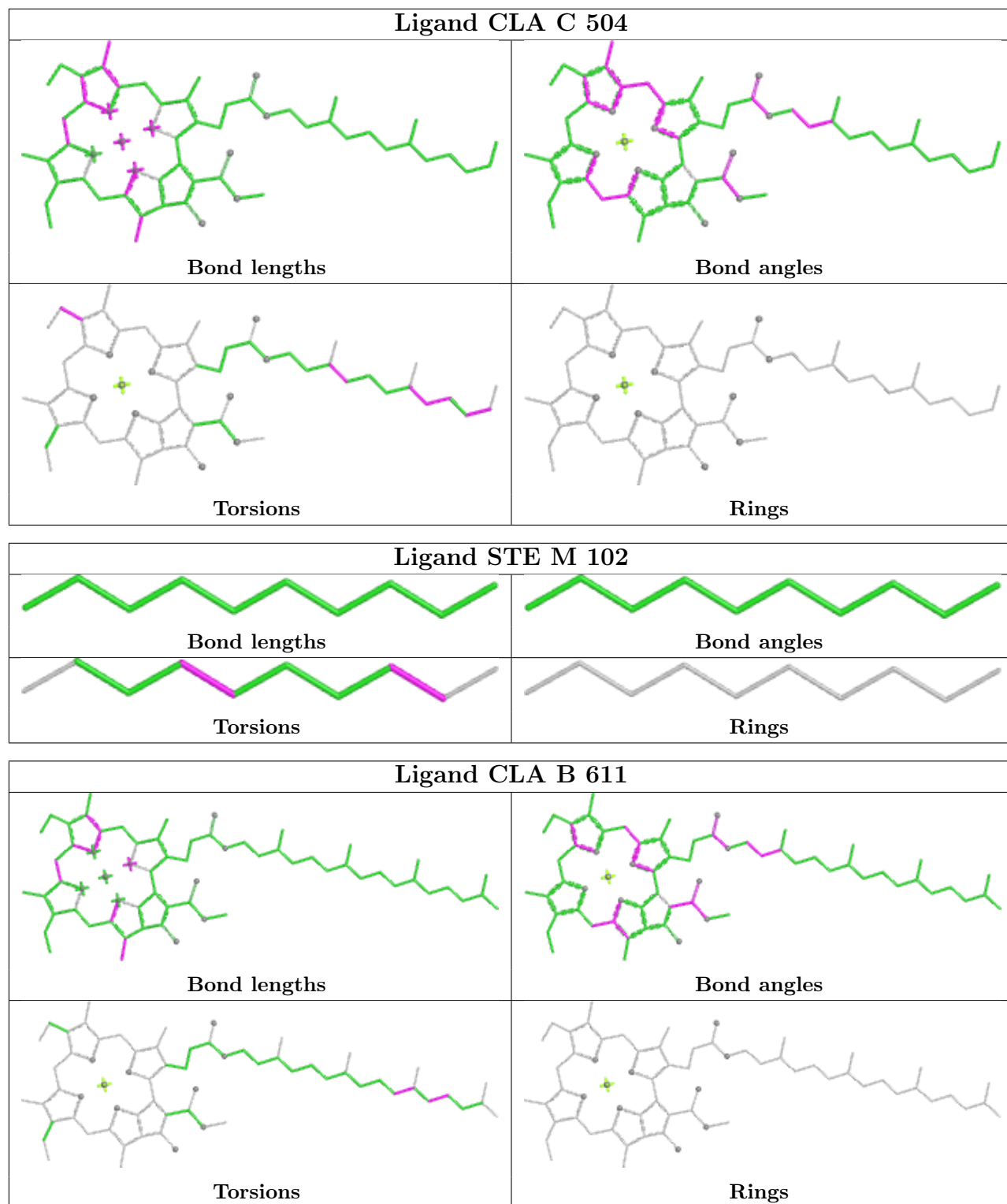


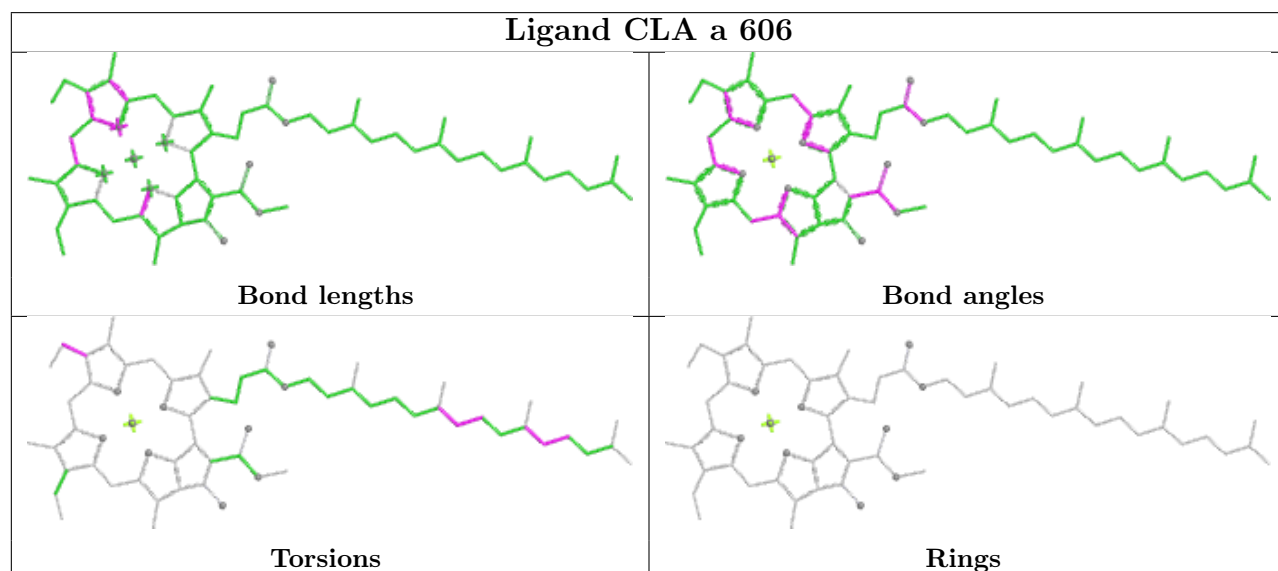
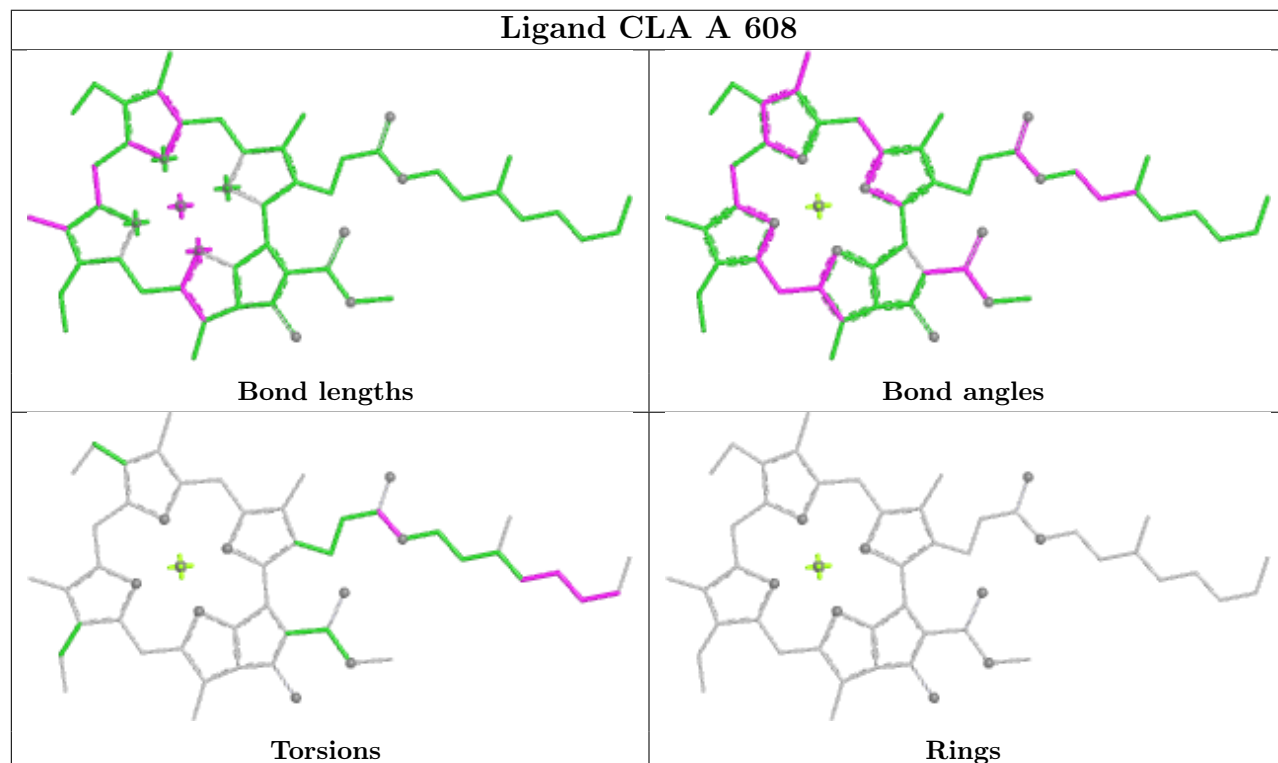
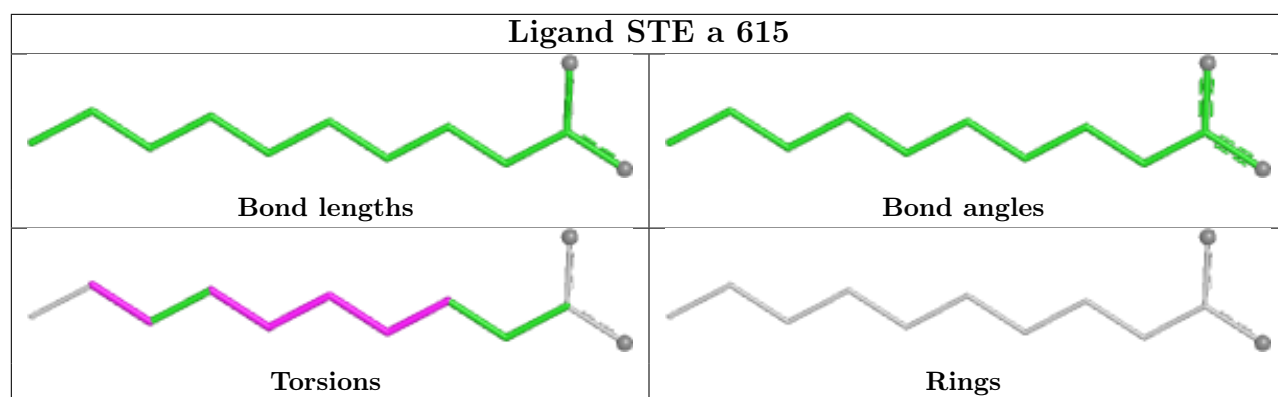


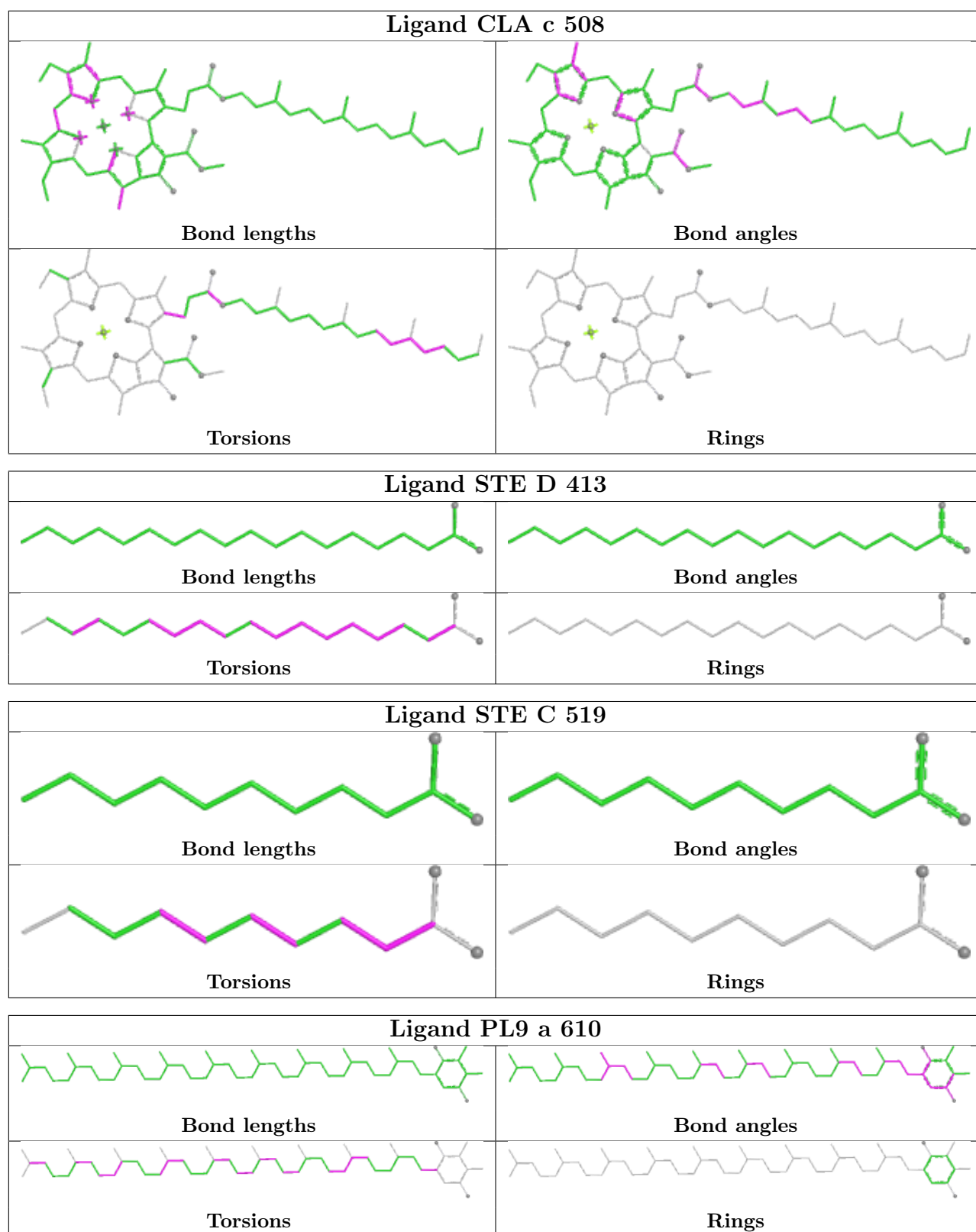


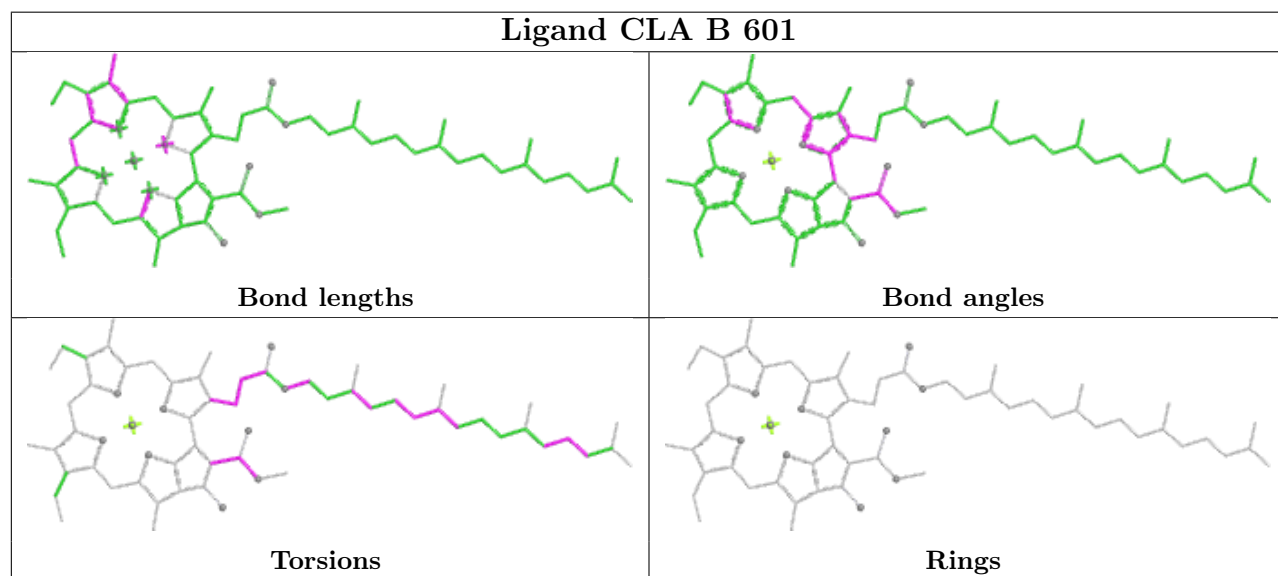
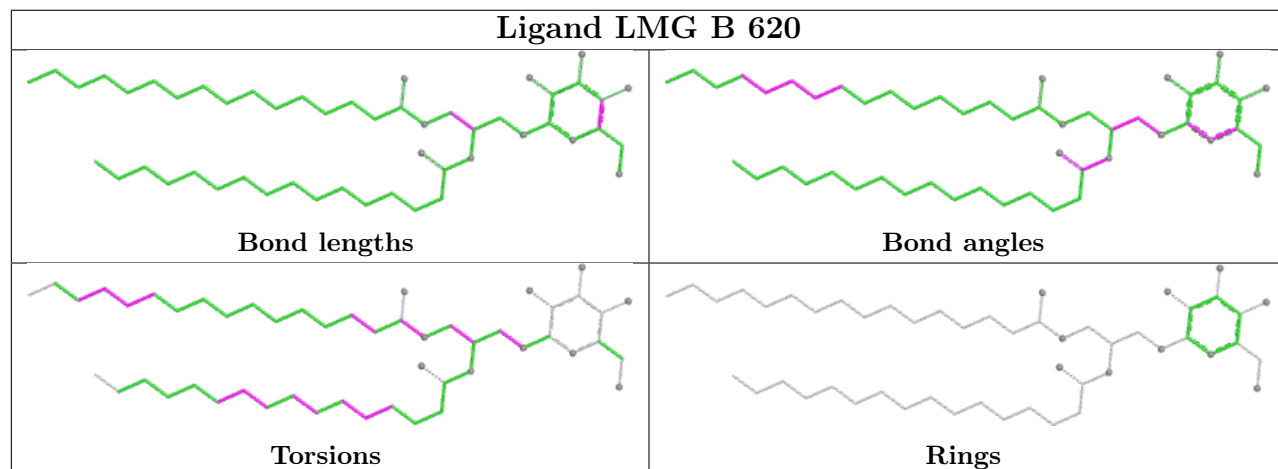
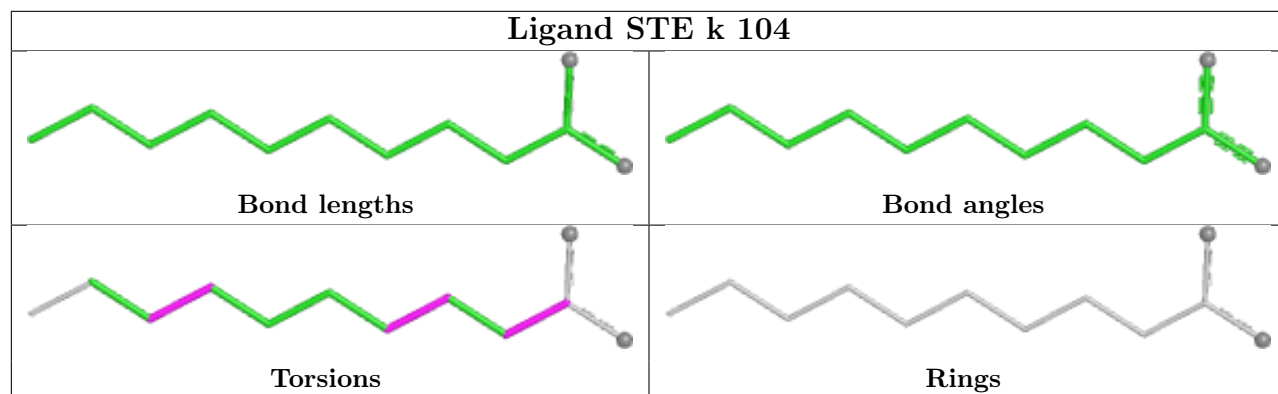


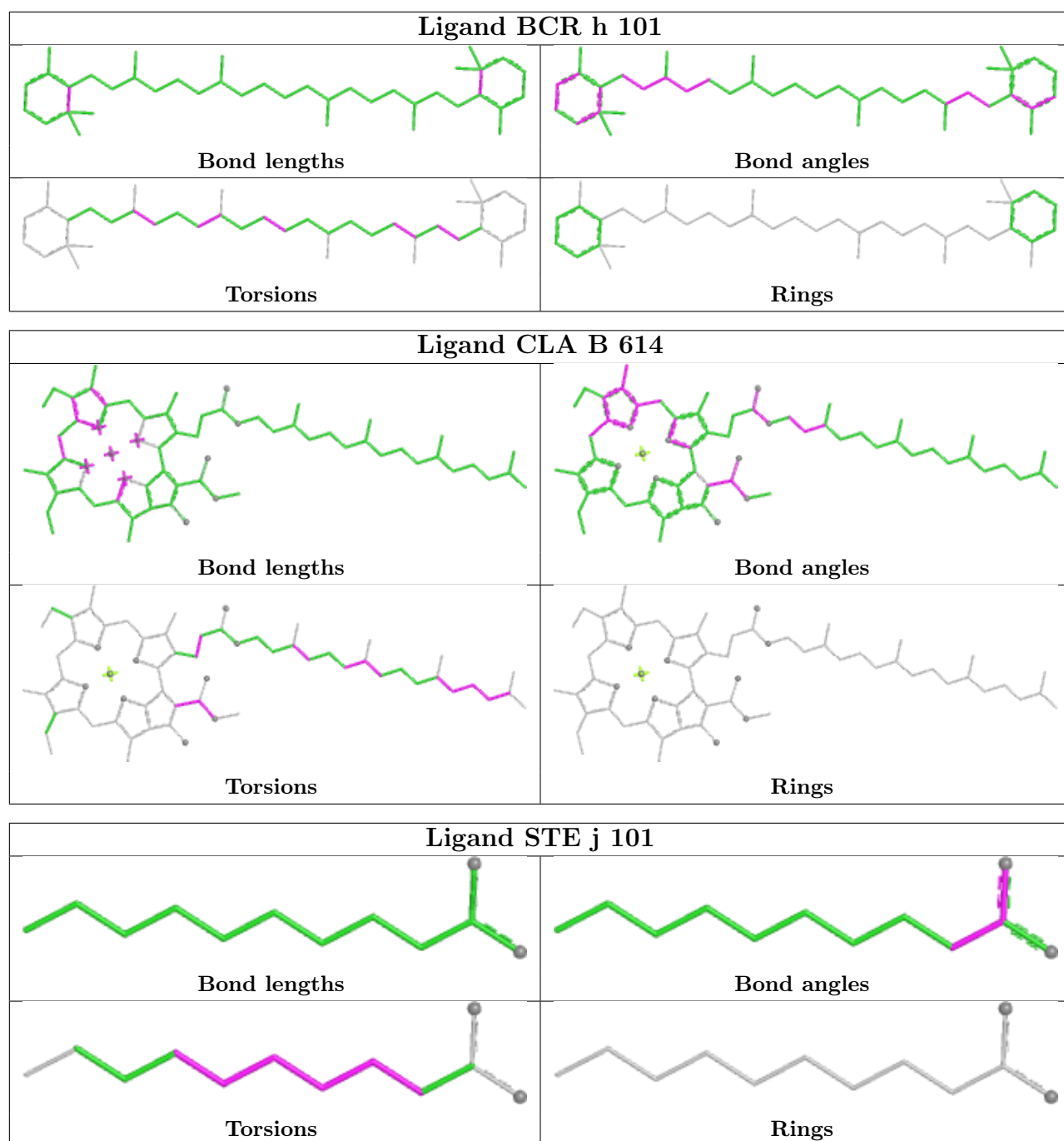


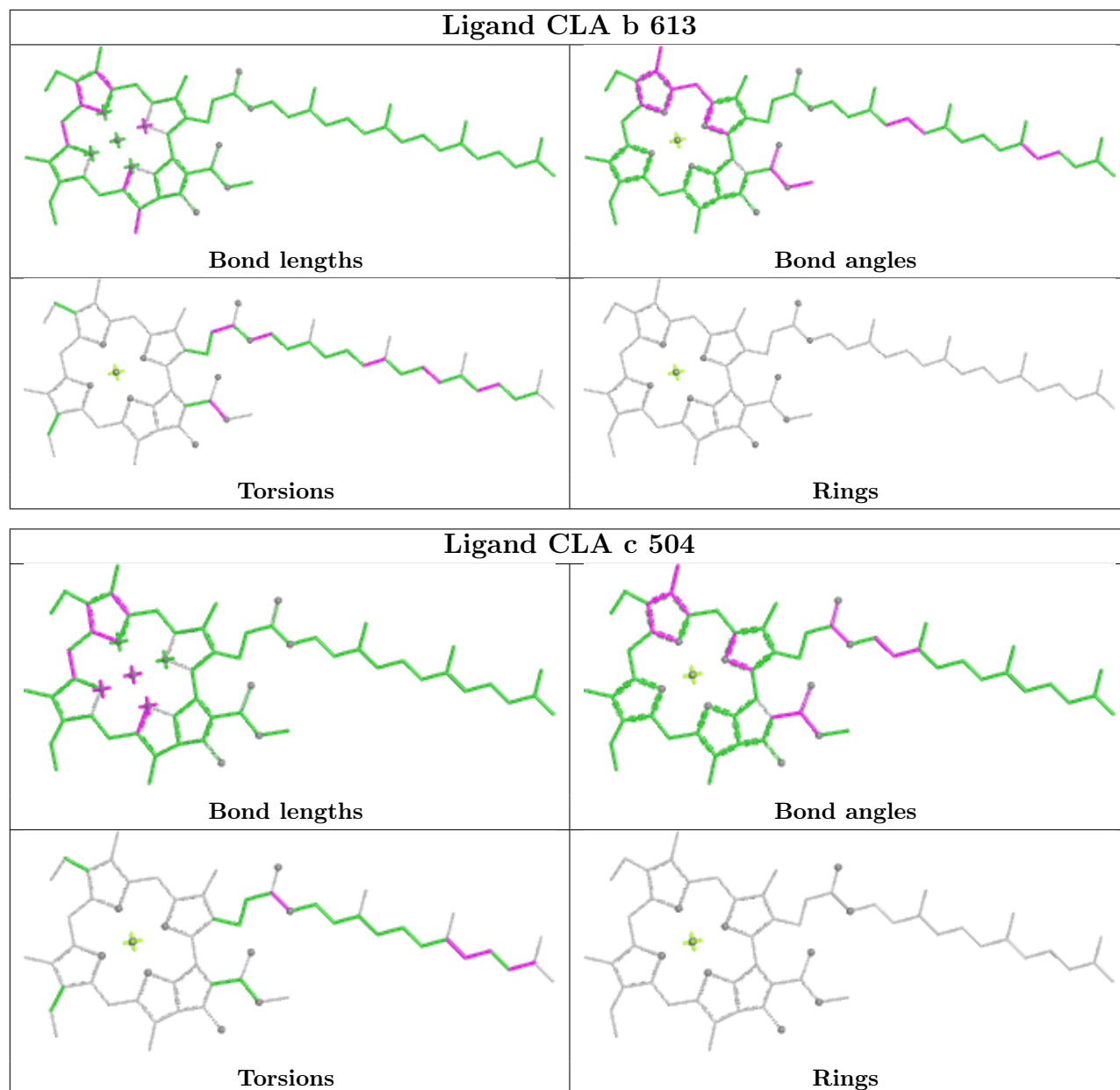


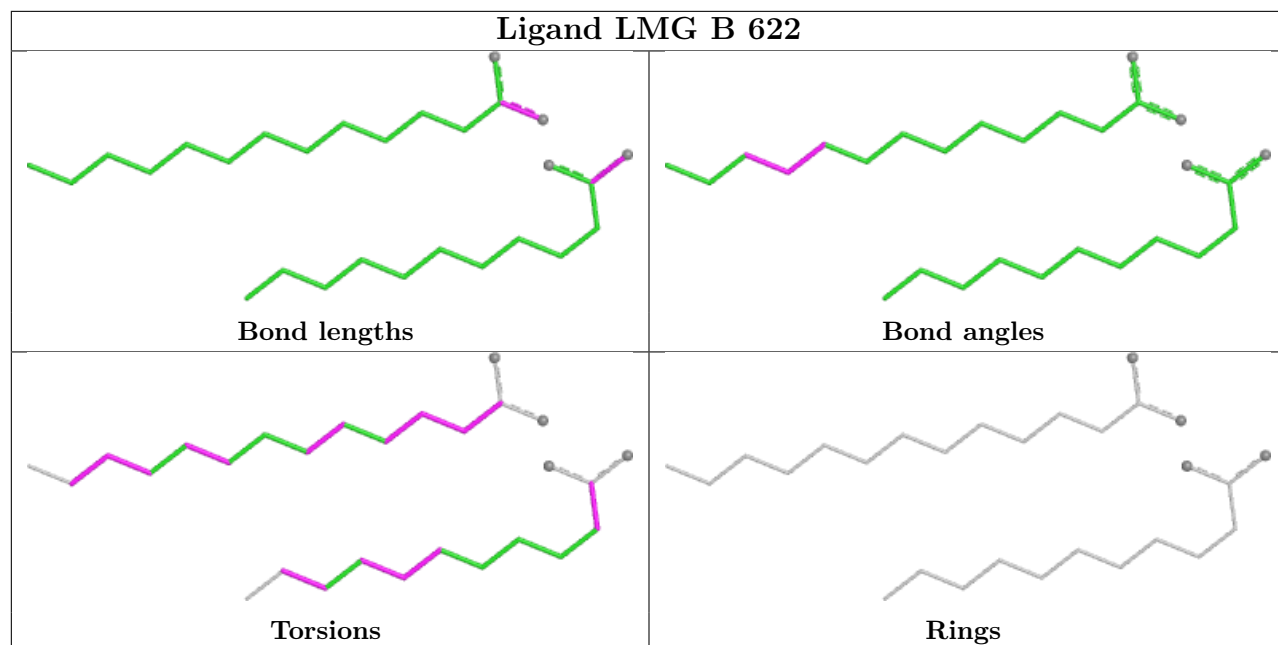


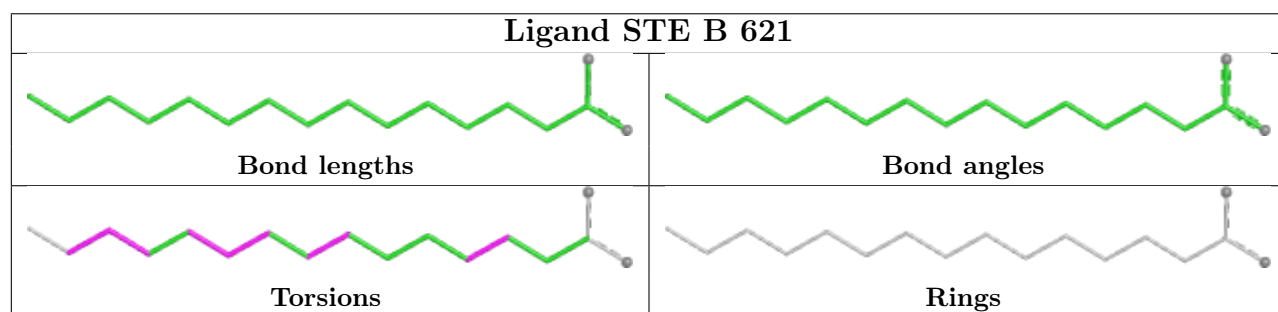
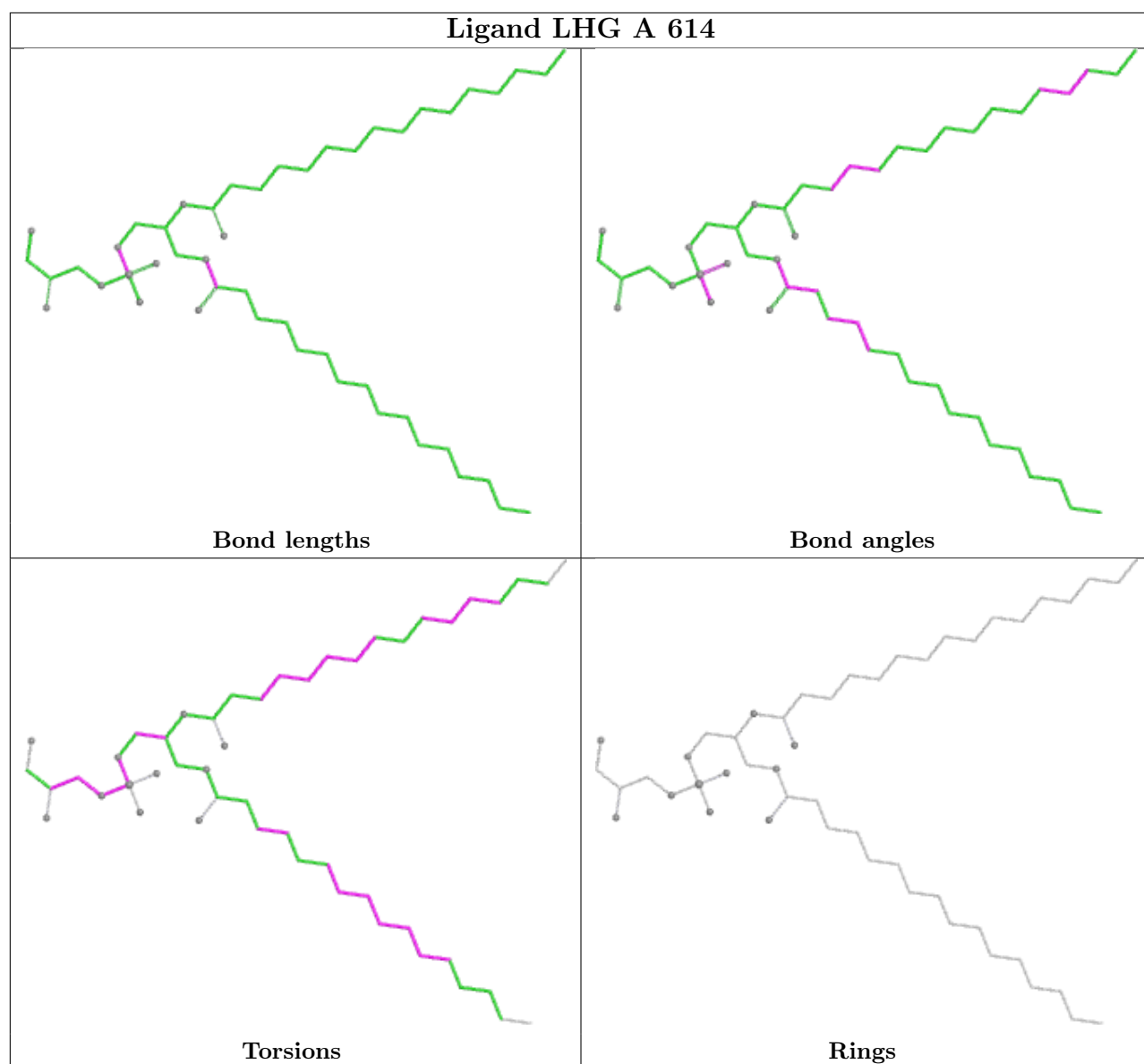


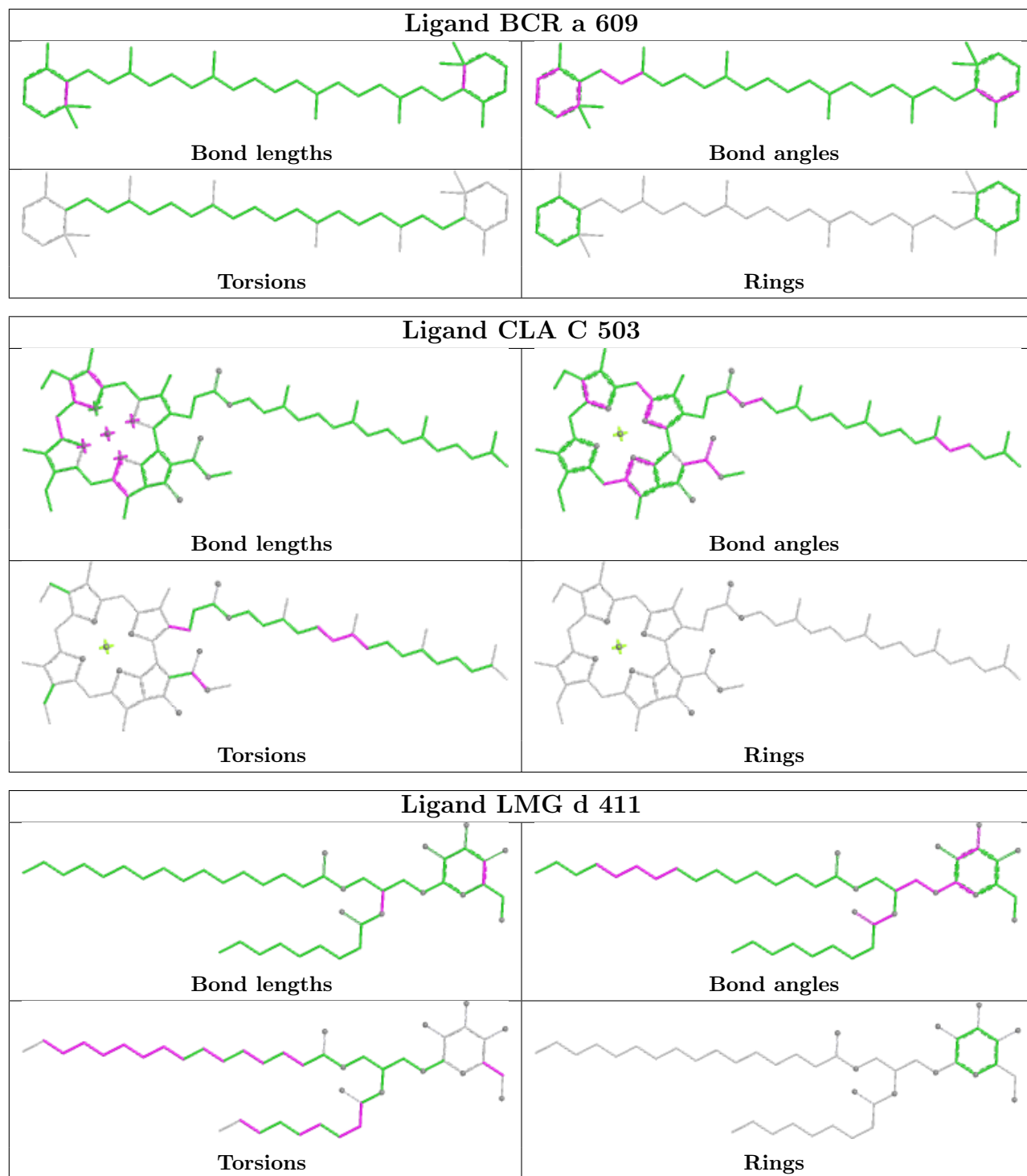


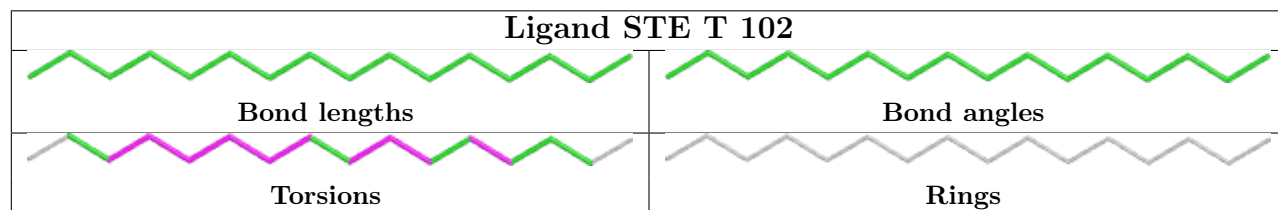
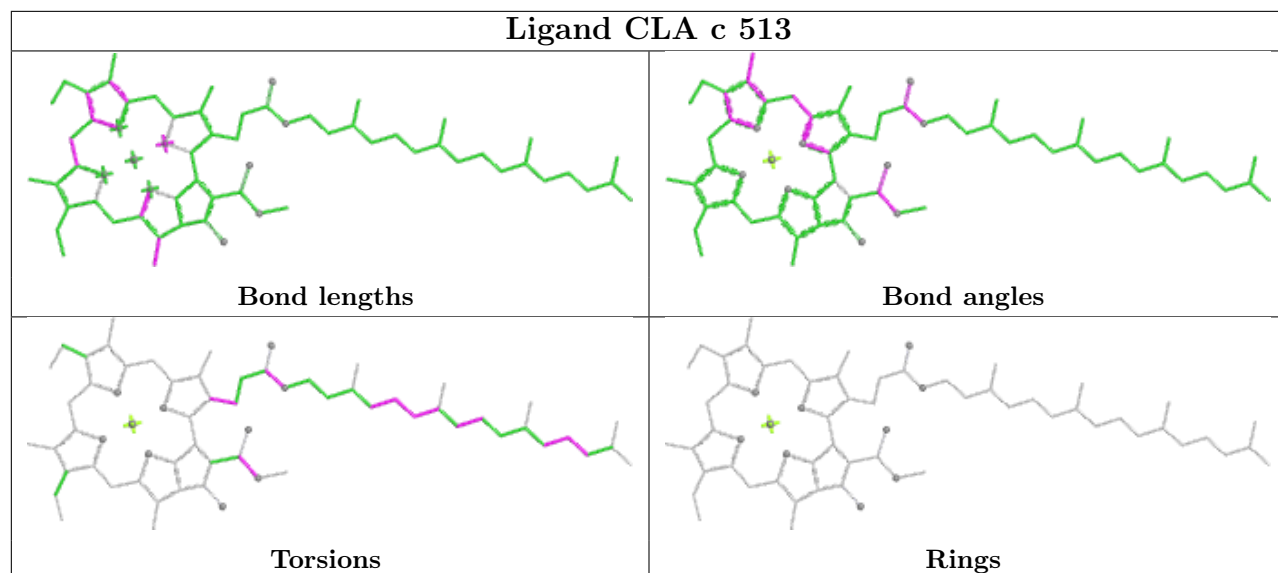
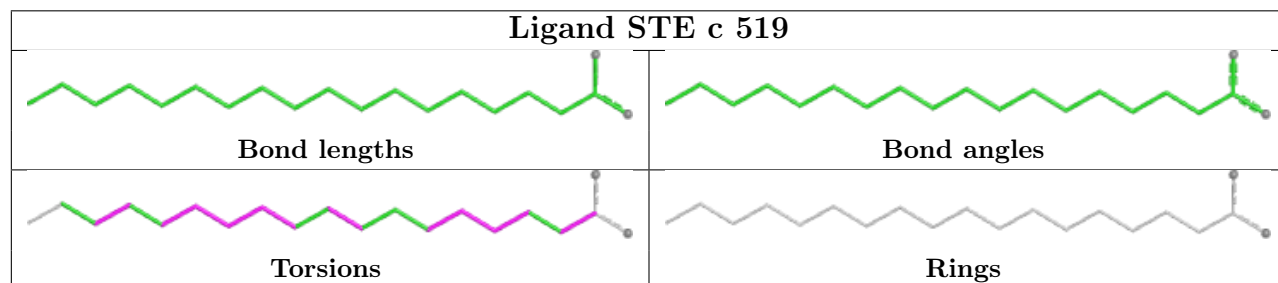
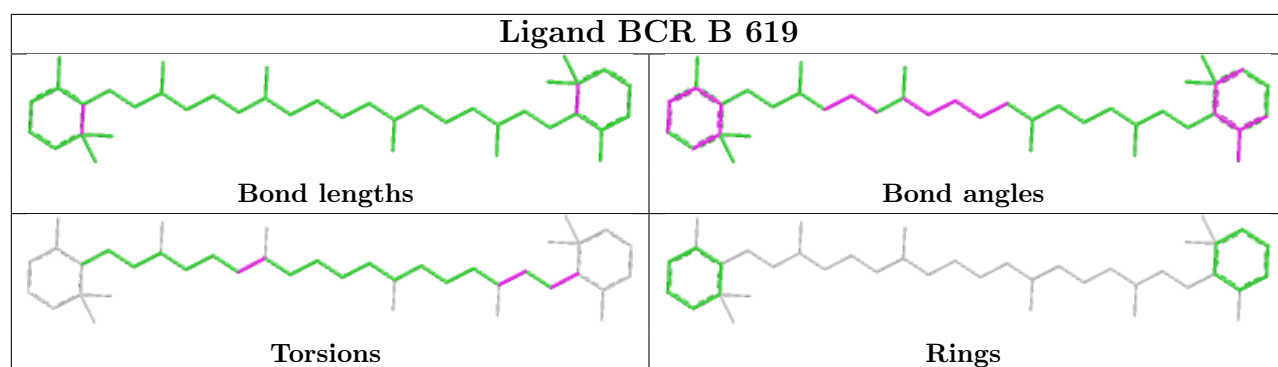


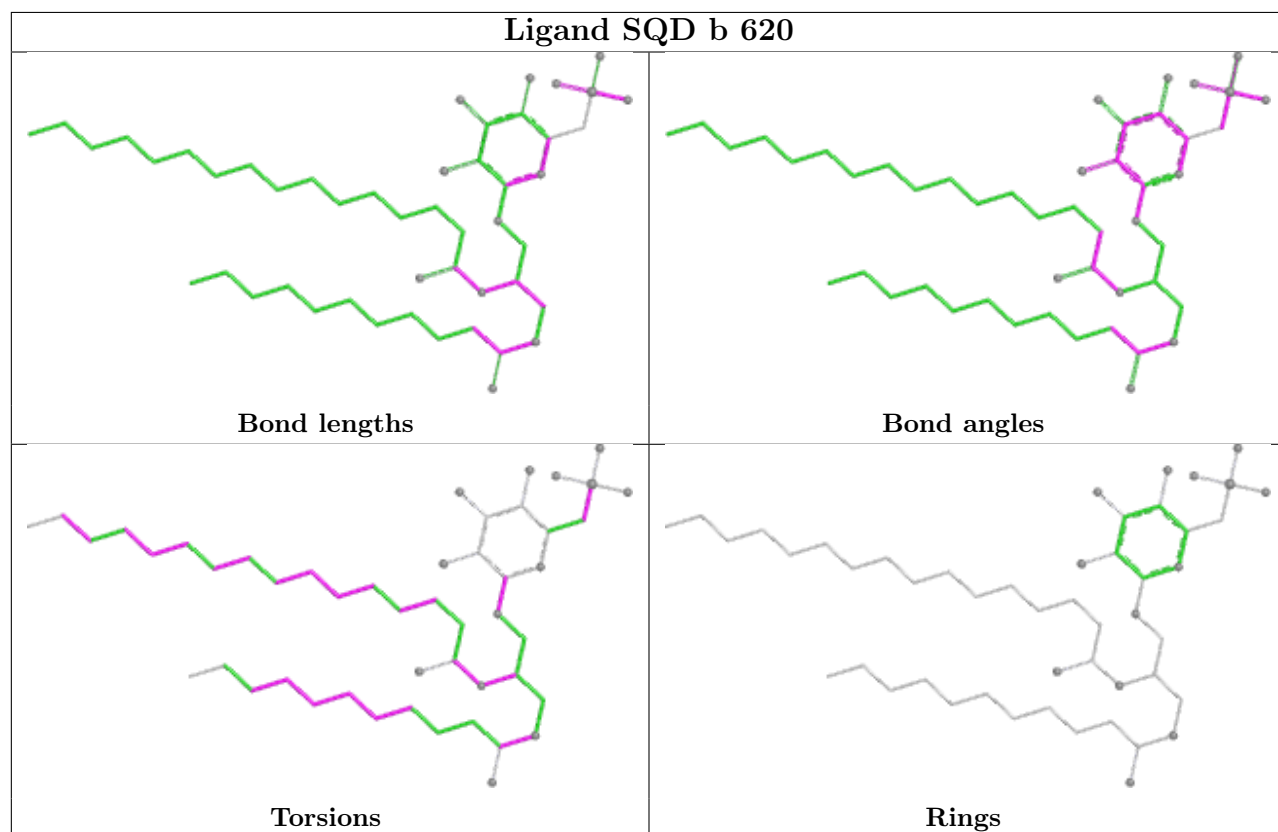
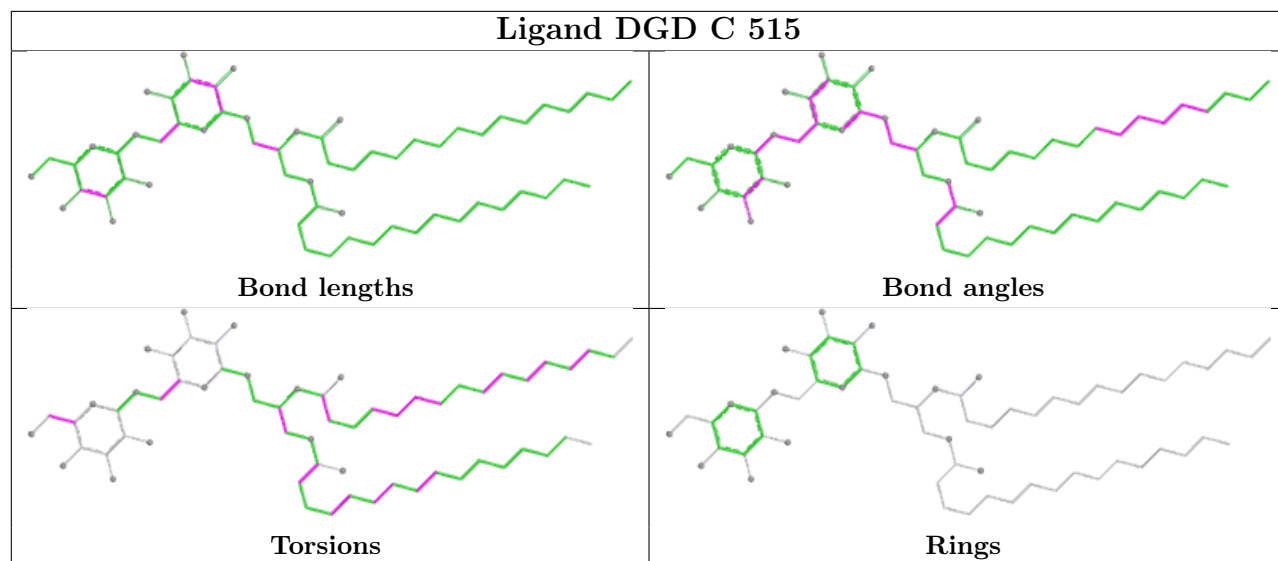


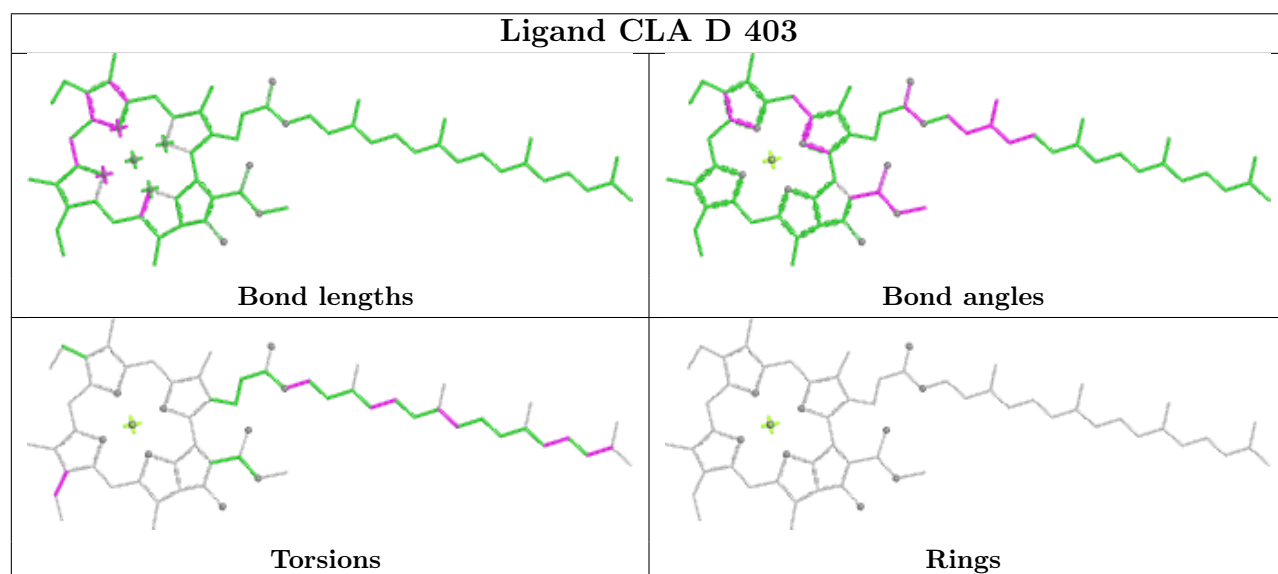
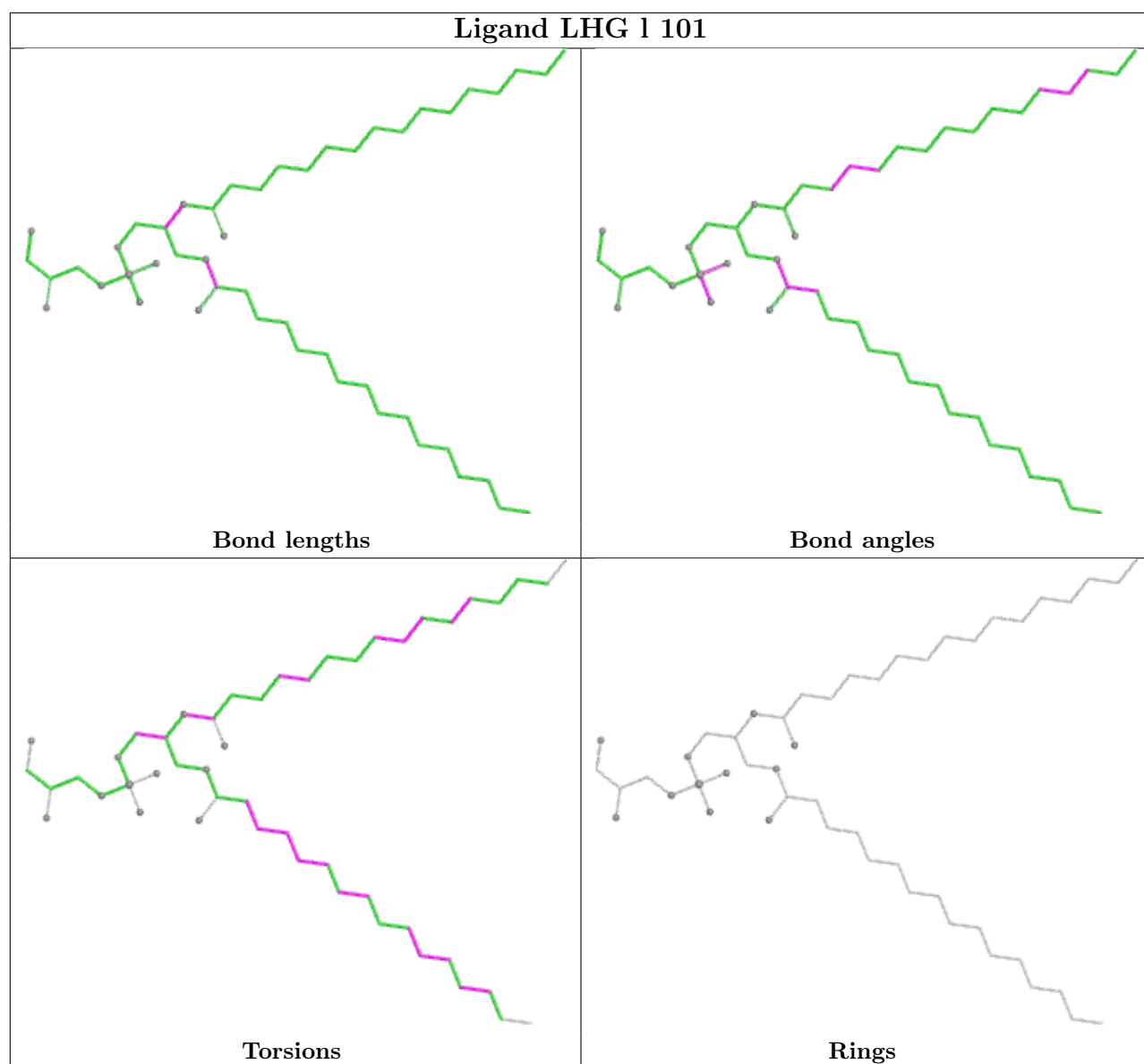


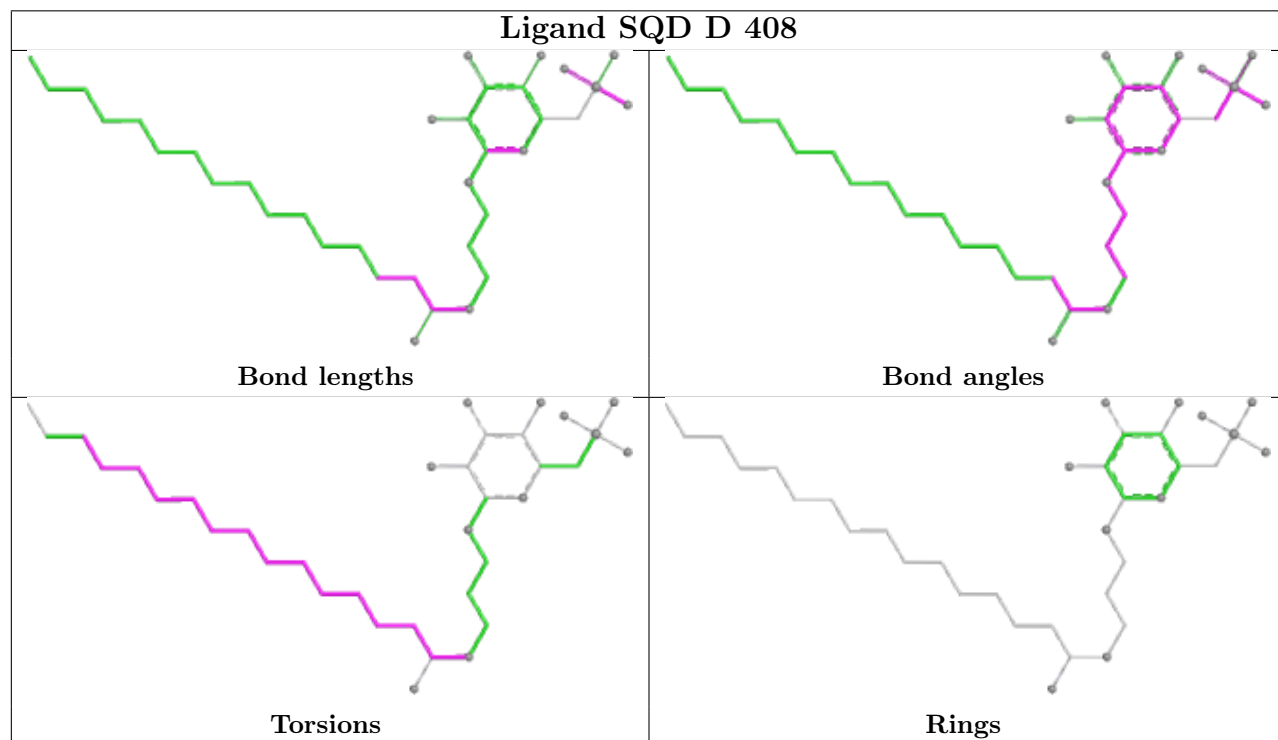
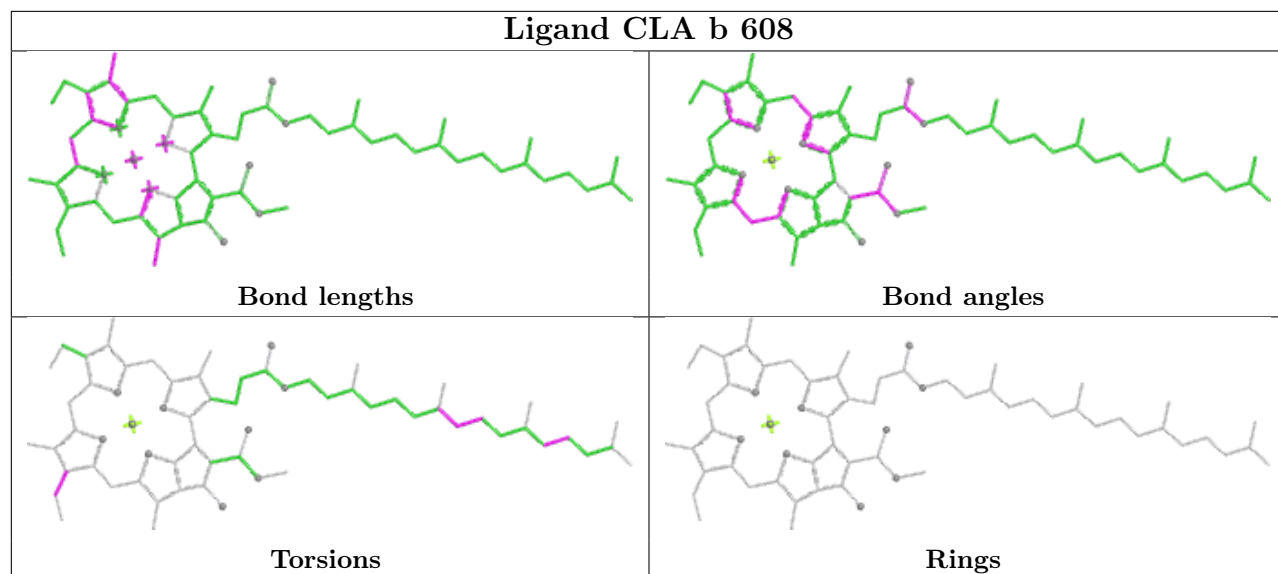


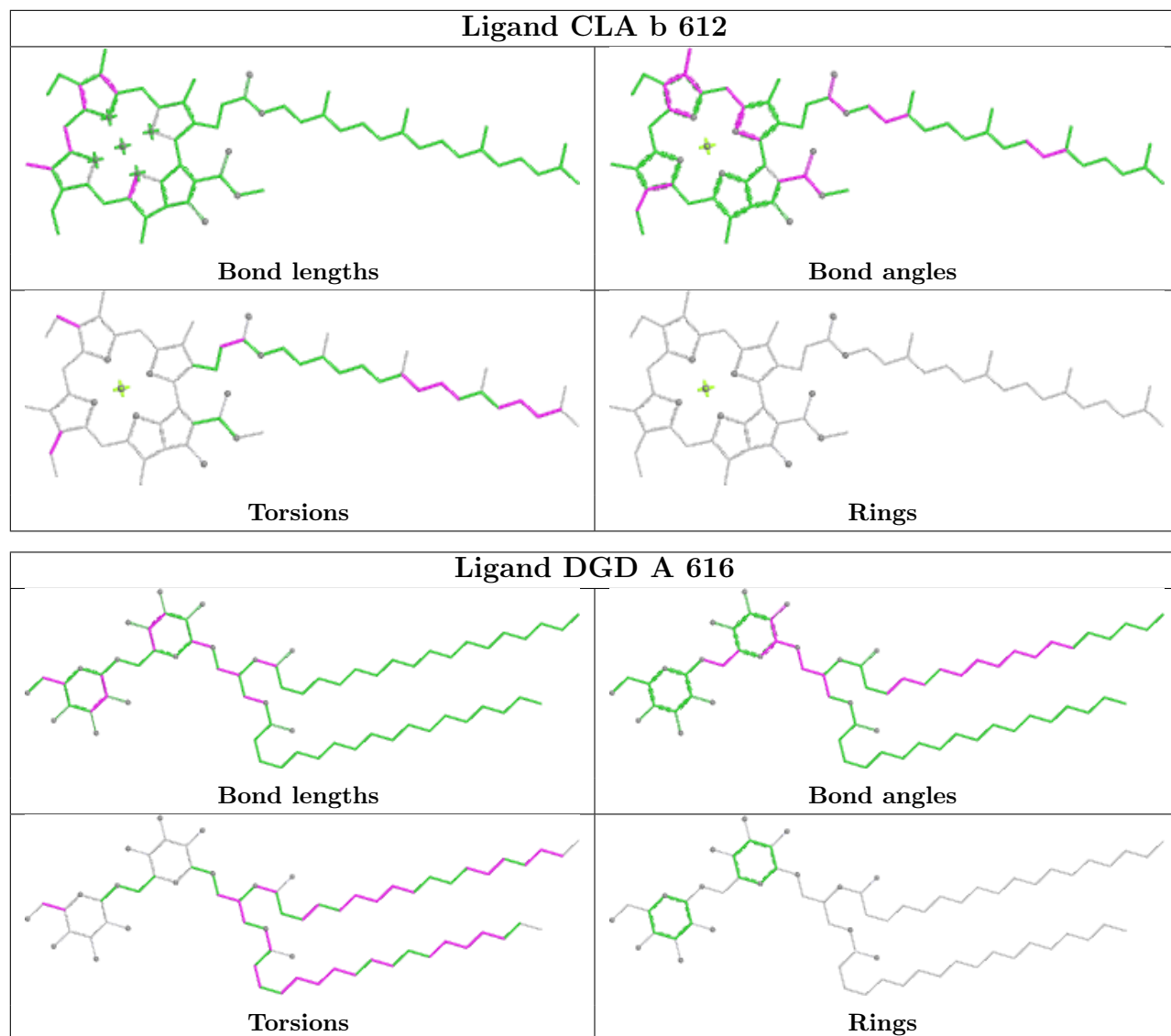


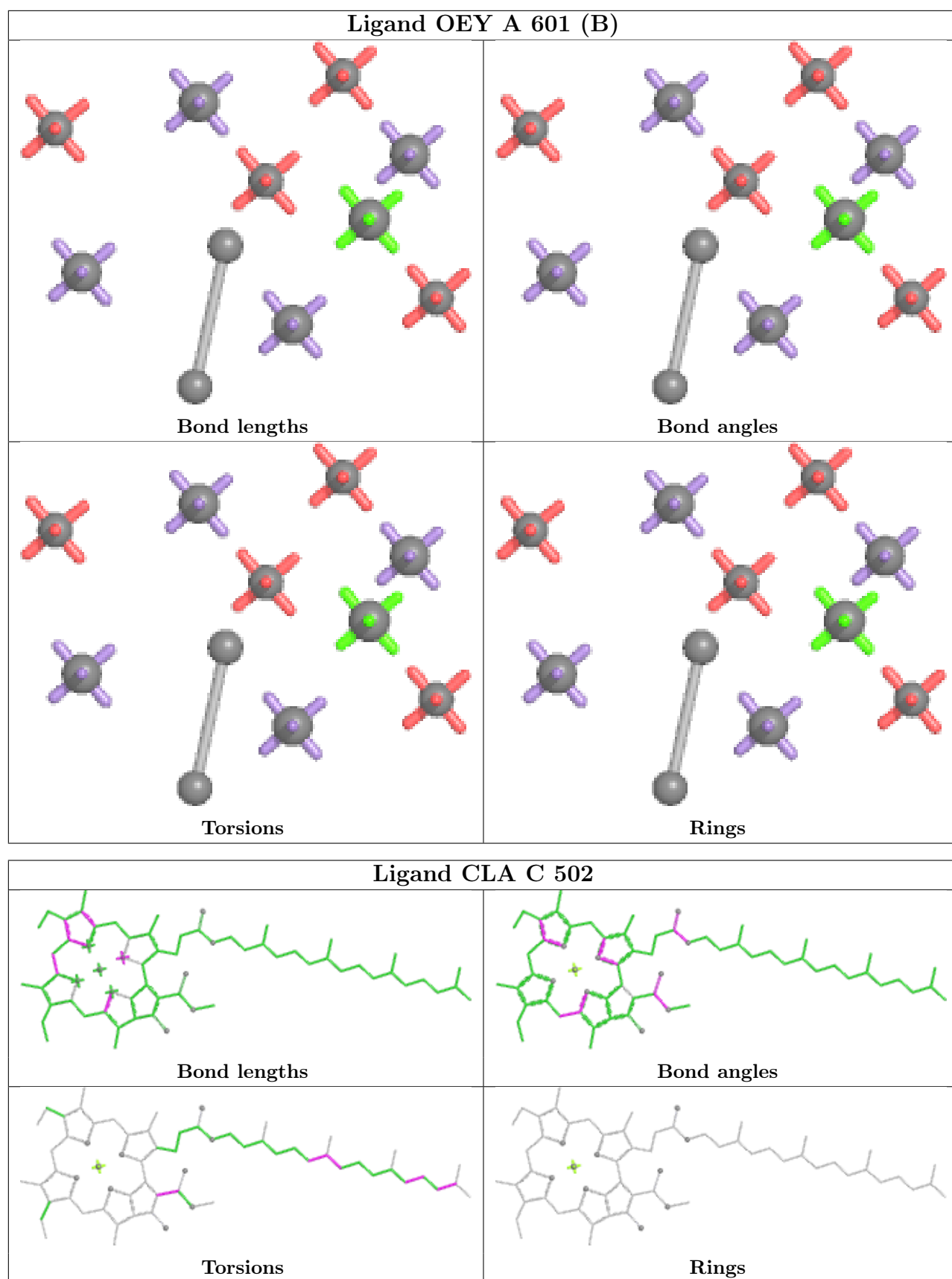


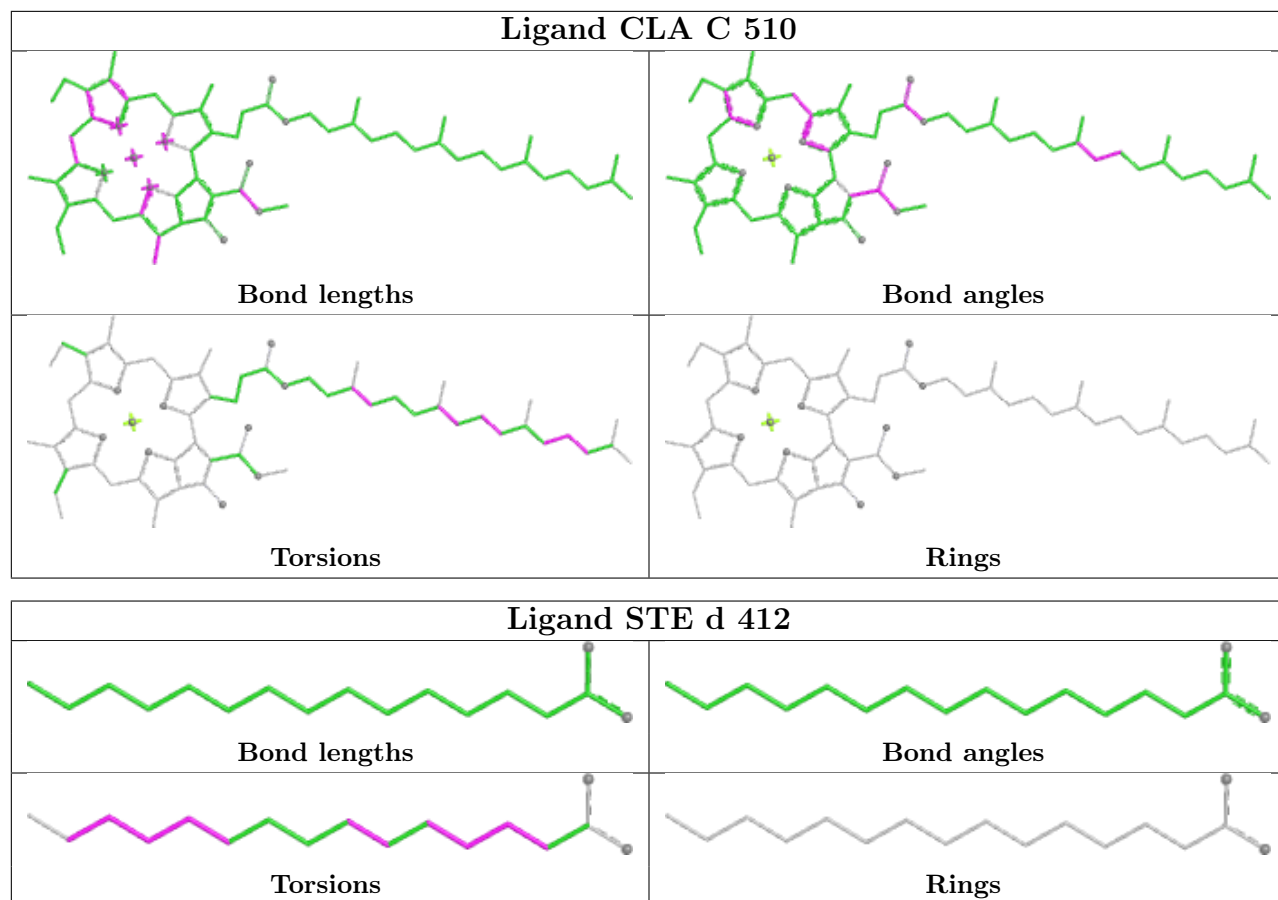


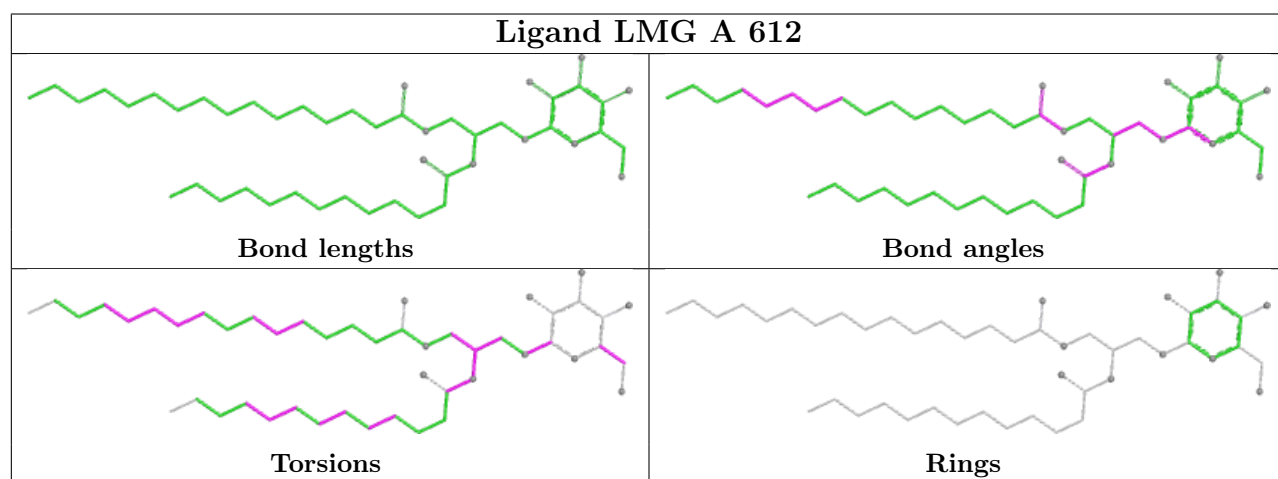
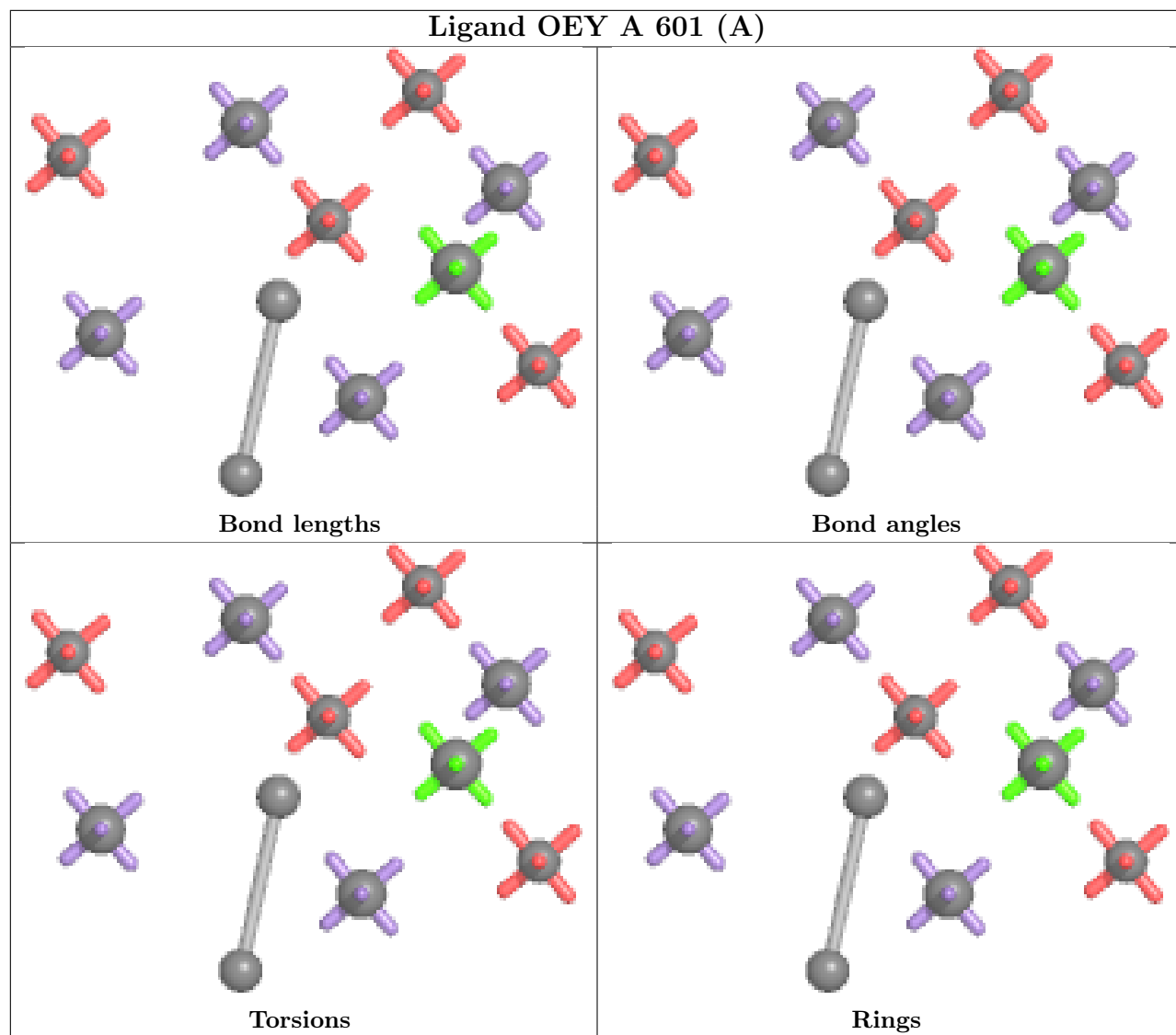


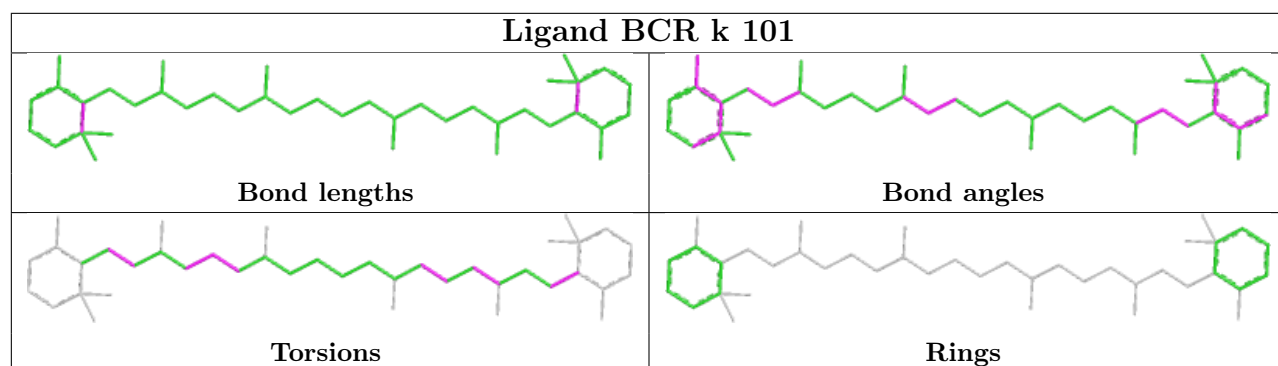
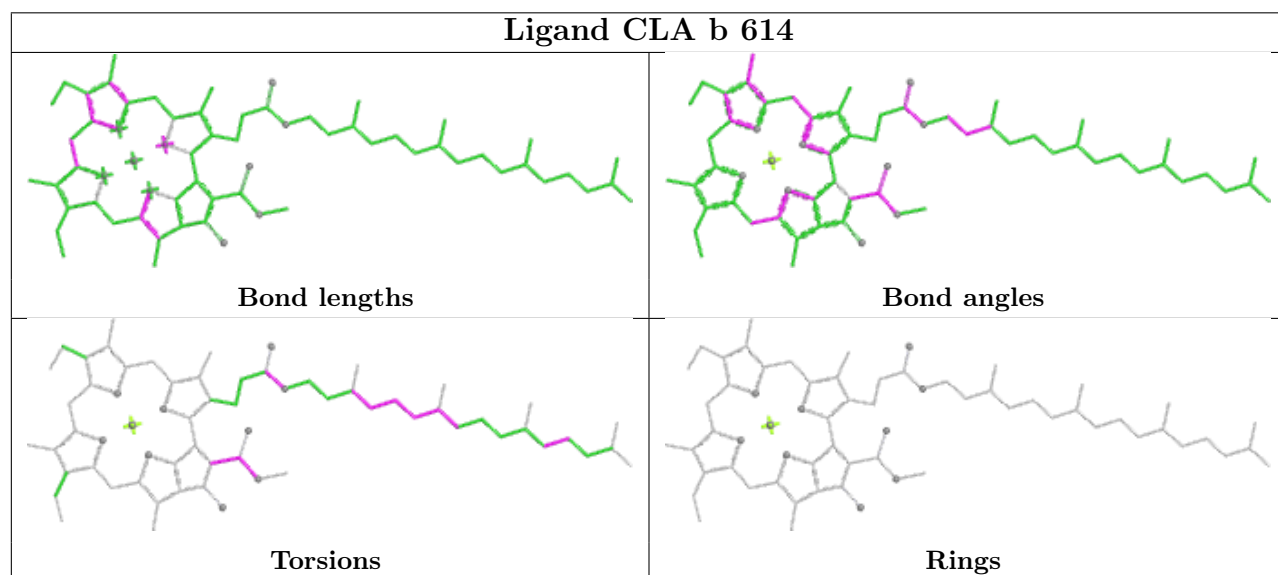
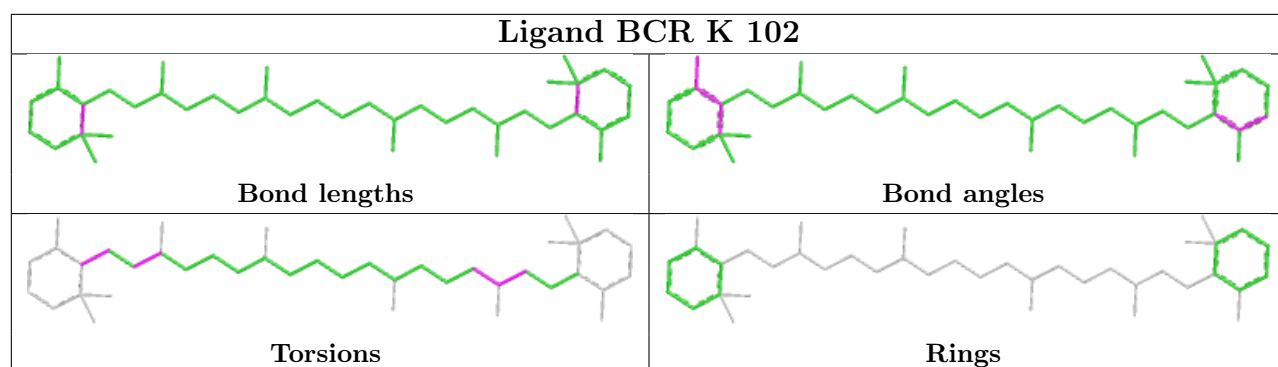


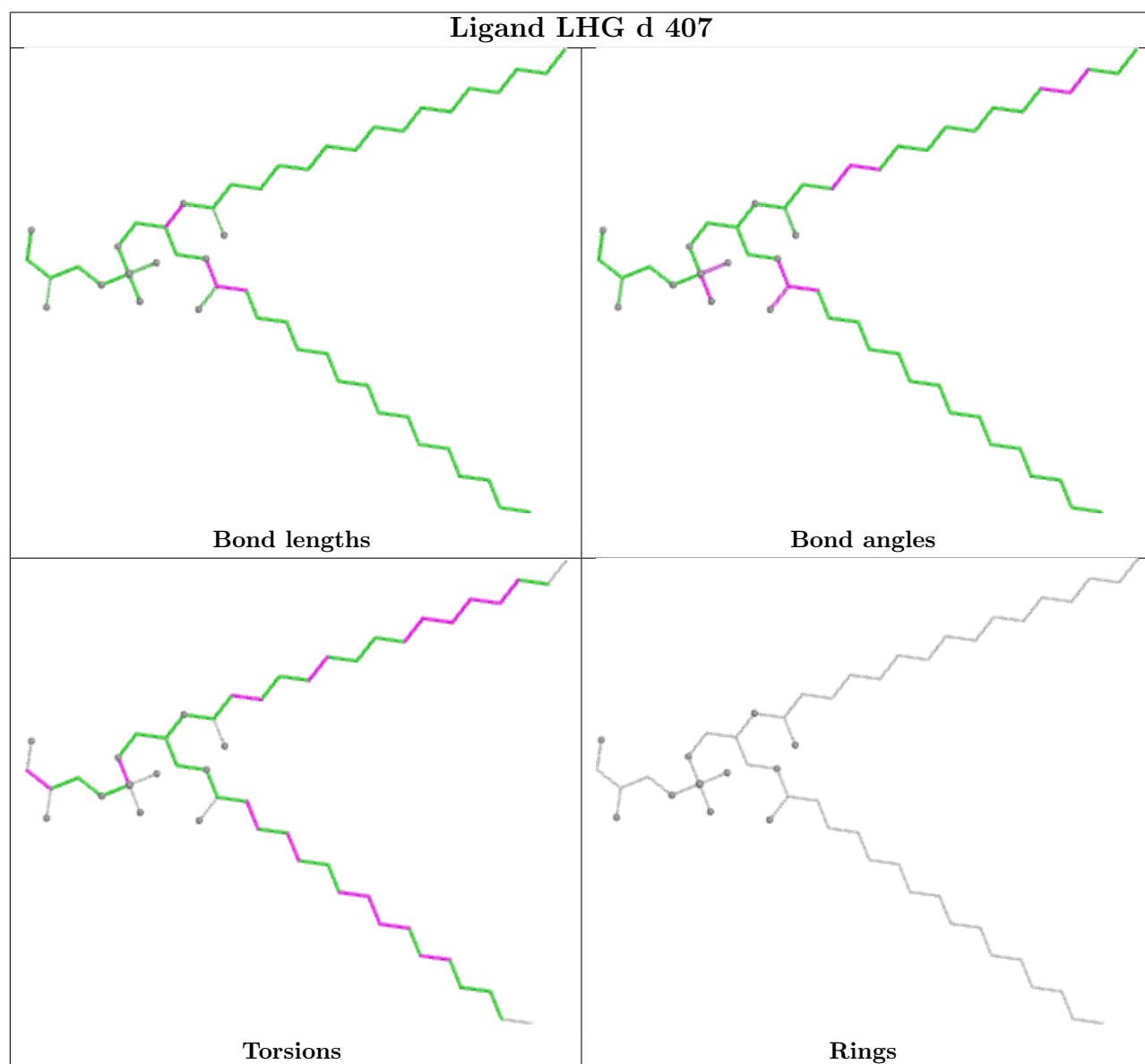
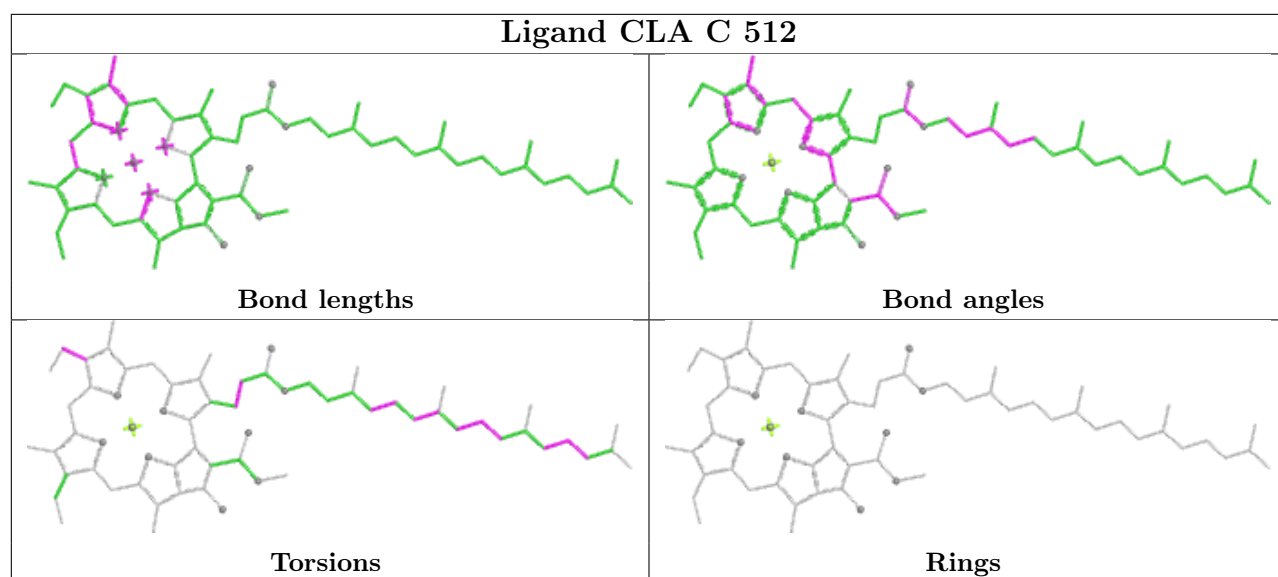


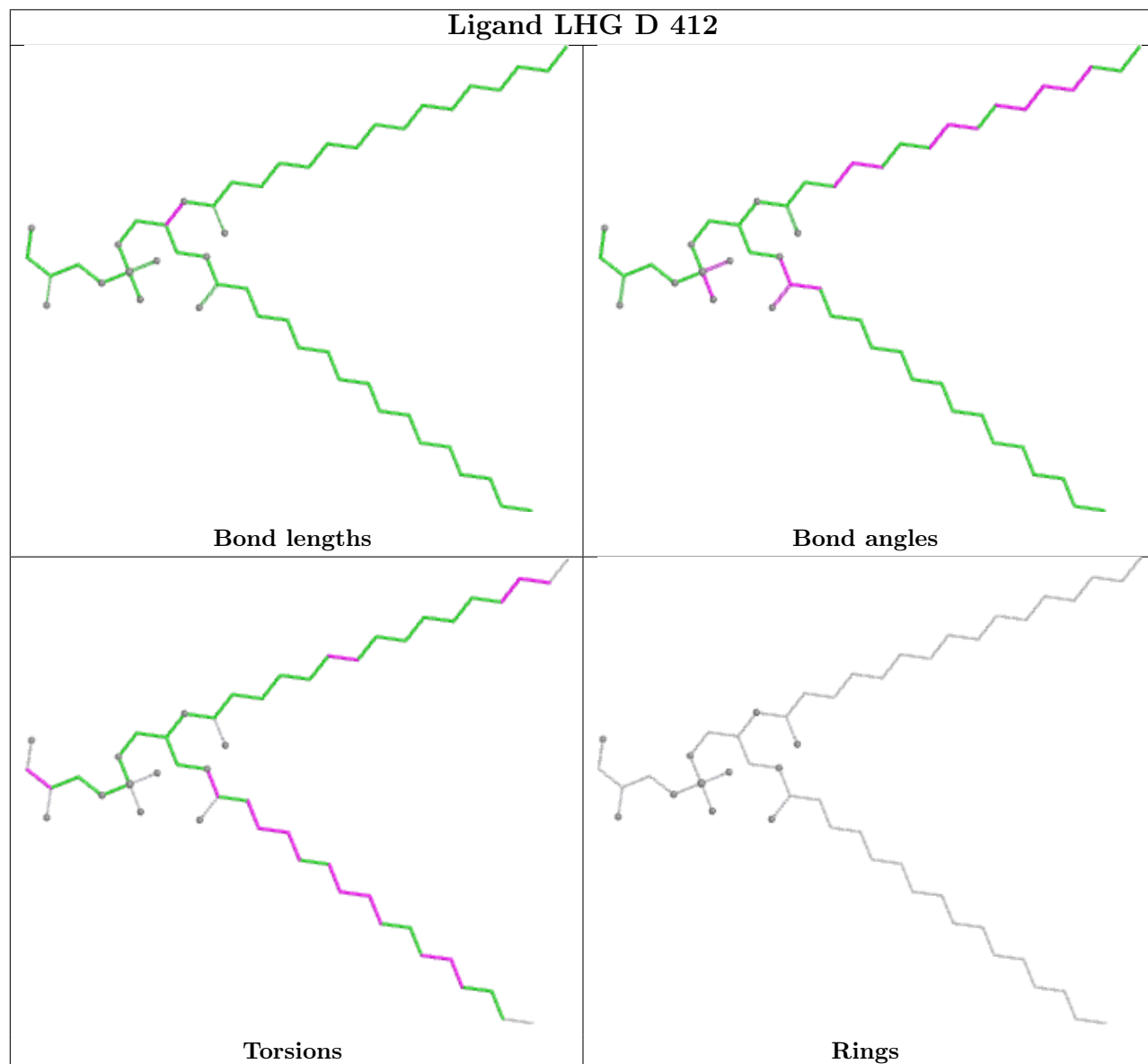
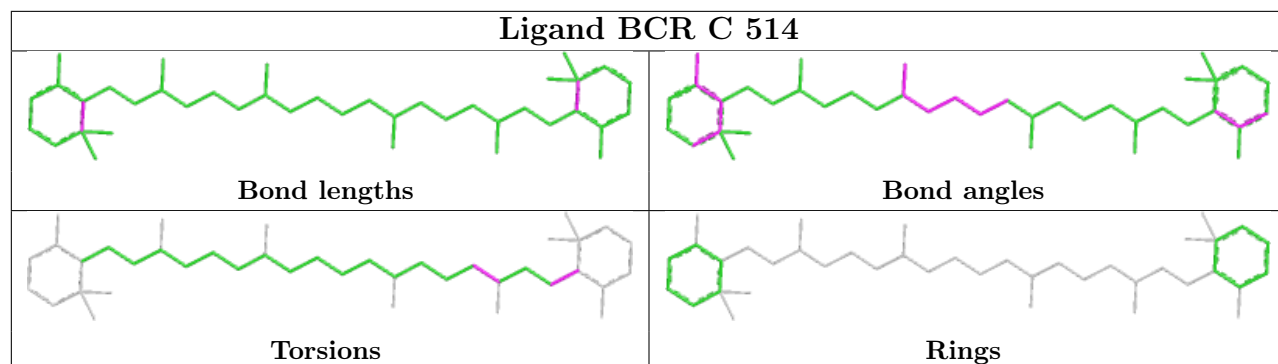


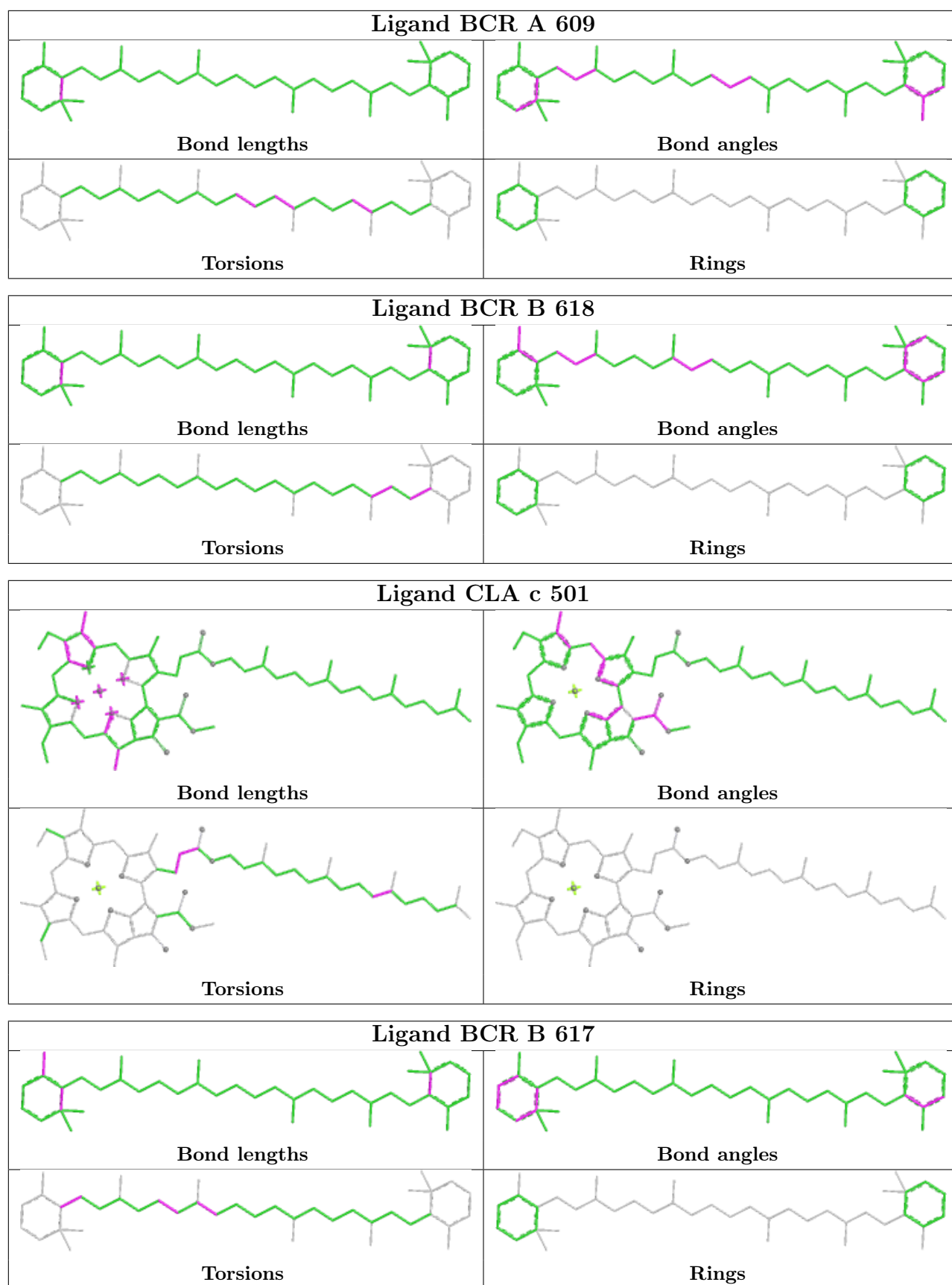


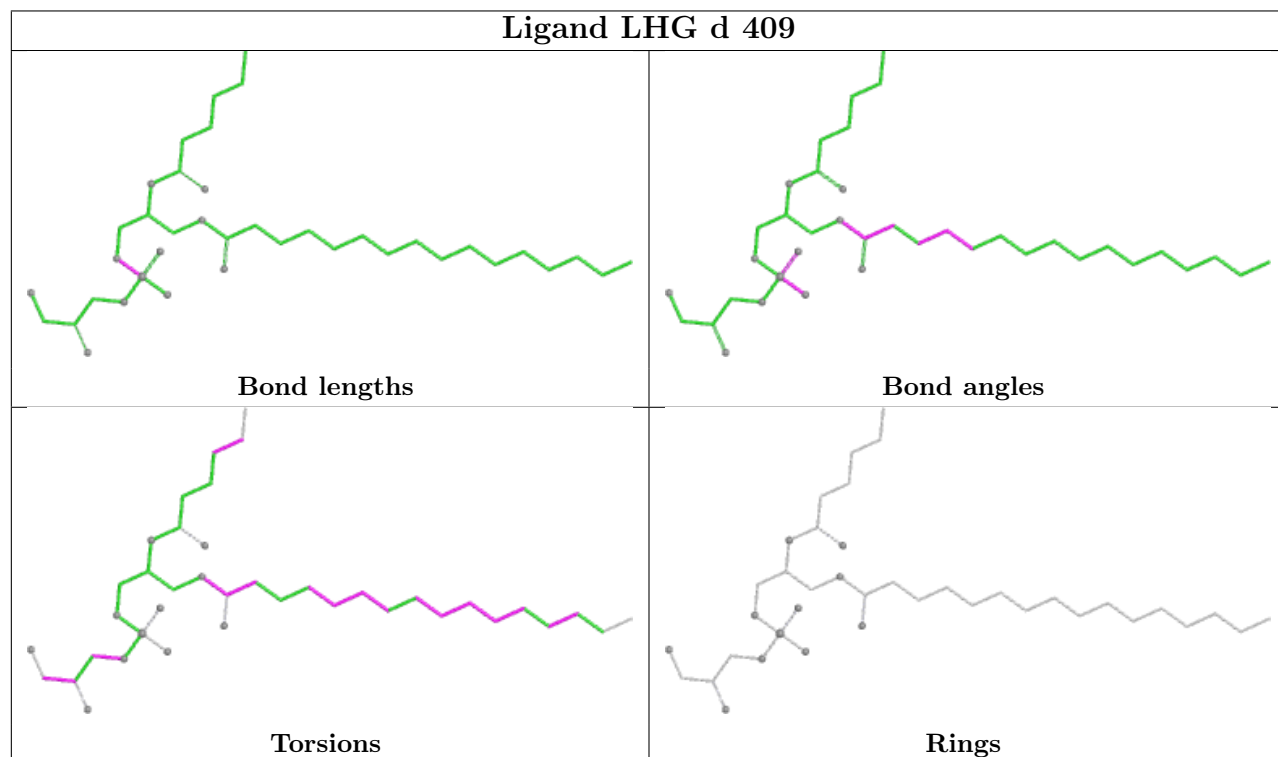
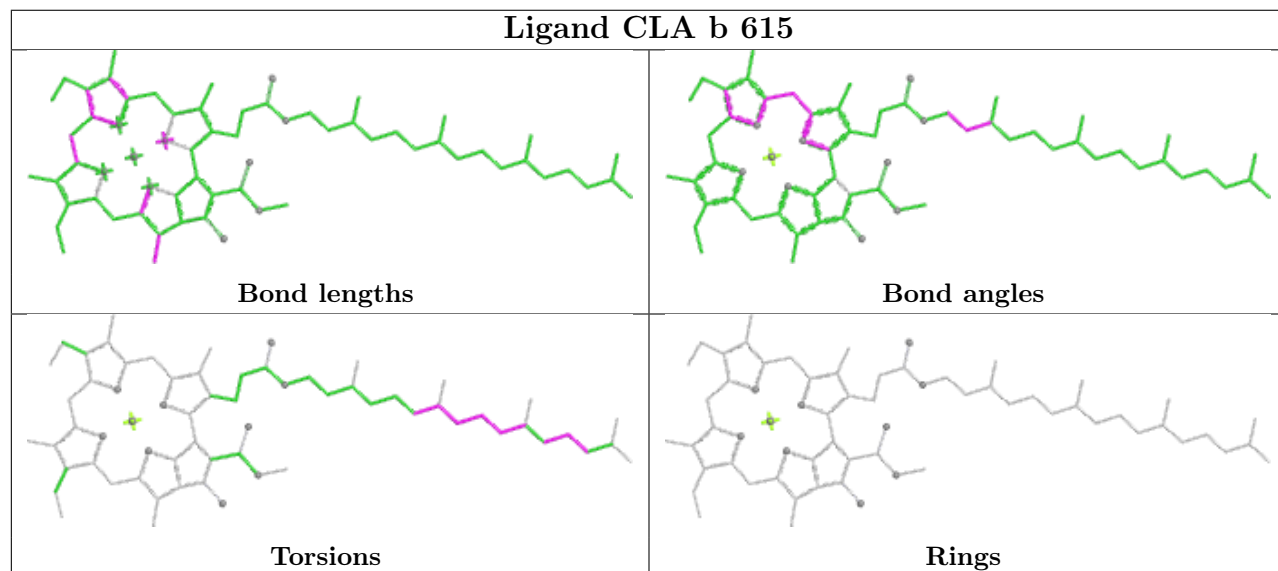
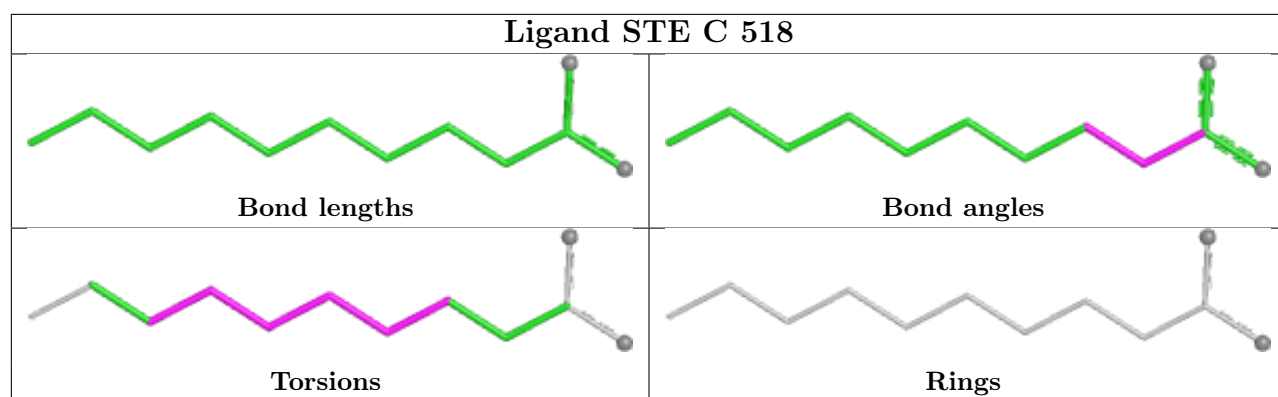


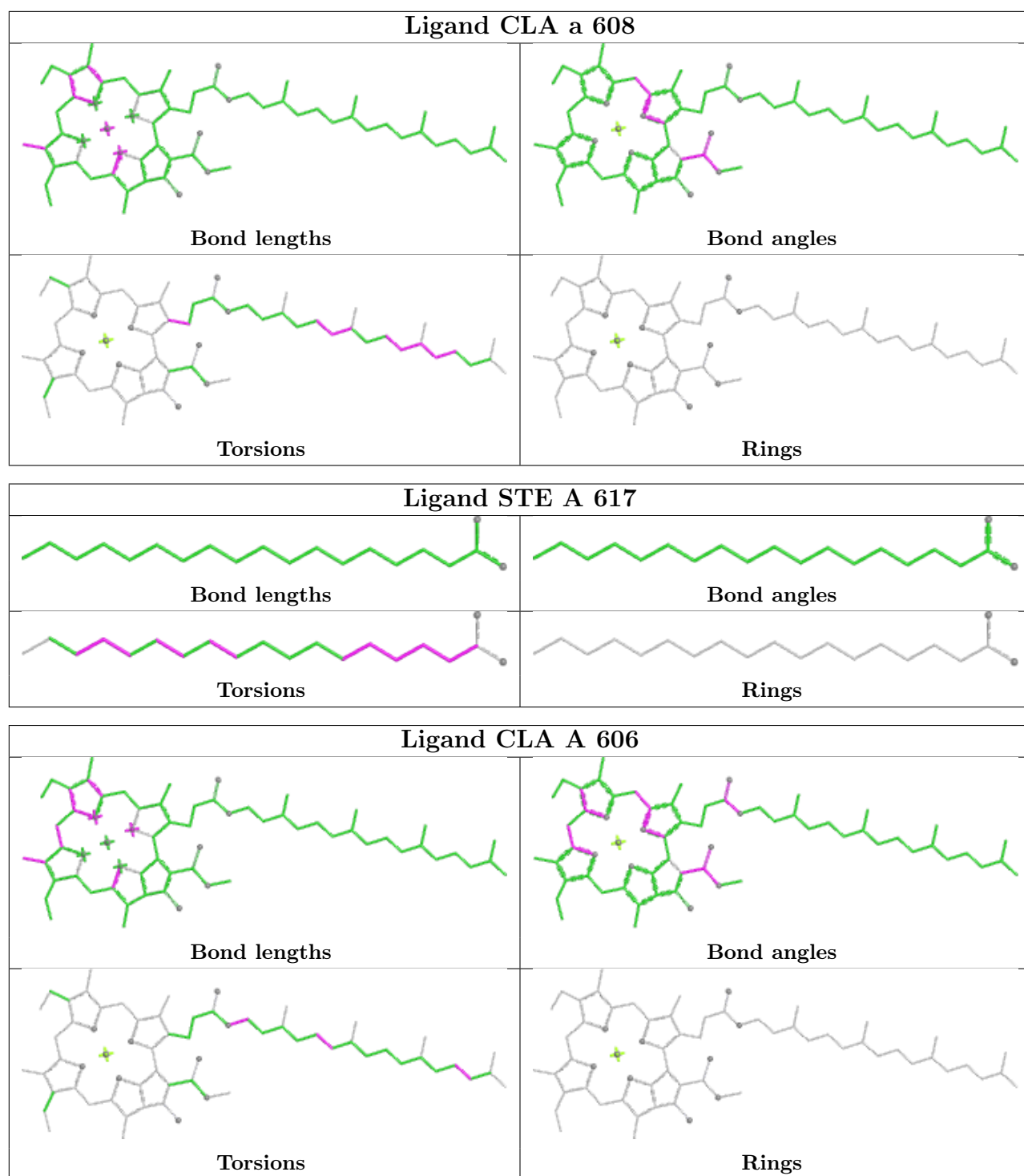


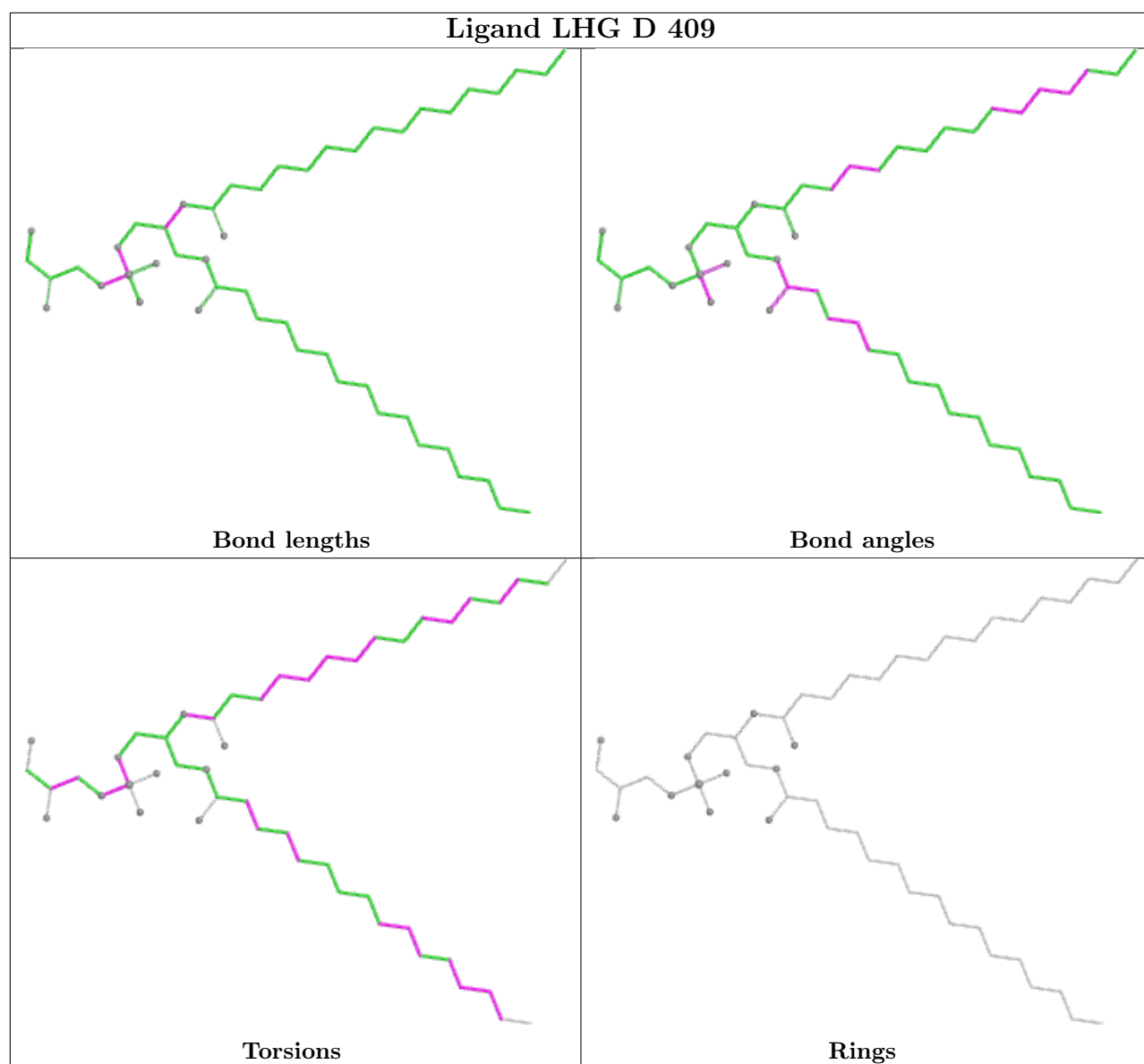












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data i

6.1 Protein, DNA and RNA chains i

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	334/344 (97%)	-0.33	2 (0%) 85 86	11, 28, 49, 77	64 (19%)
1	a	334/344 (97%)	-0.22	2 (0%) 85 86	11, 31, 57, 73	64 (19%)
2	B	505/510 (99%)	-0.21	4 (0%) 82 83	18, 32, 60, 86	4 (0%)
2	b	505/510 (99%)	-0.11	5 (0%) 79 80	26, 36, 69, 98	0
3	C	442/461 (95%)	-0.18	1 (0%) 91 91	13, 35, 50, 72	11 (2%)
3	c	451/461 (97%)	-0.03	1 (0%) 91 91	13, 40, 61, 86	12 (2%)
4	D	341/352 (96%)	-0.36	1 (0%) 90 90	14, 30, 47, 77	2 (0%)
4	d	341/352 (96%)	-0.21	1 (0%) 90 90	15, 34, 58, 75	3 (0%)
5	E	82/84 (97%)	0.43	1 (1%) 76 76	32, 50, 68, 82	1 (1%)
5	e	82/84 (97%)	0.70	2 (2%) 59 60	42, 61, 76, 84	0
6	F	34/45 (75%)	0.06	0 100 100	35, 42, 61, 80	0
6	f	34/45 (75%)	0.48	2 (5%) 28 27	43, 50, 77, 96	0
7	H	65/66 (98%)	0.05	1 (1%) 72 72	32, 41, 53, 68	0
7	h	63/66 (95%)	0.34	1 (1%) 70 70	40, 52, 60, 65	0
8	I	35/38 (92%)	-0.01	0 100 100	31, 38, 60, 73	0
8	i	35/38 (92%)	-0.02	0 100 100	30, 40, 64, 78	0
9	J	36/40 (90%)	0.38	1 (2%) 55 54	34, 49, 72, 83	0
9	j	36/40 (90%)	0.54	3 (8%) 17 16	39, 55, 88, 88	0
10	K	37/46 (80%)	0.20	0 100 100	41, 51, 65, 70	0
10	k	37/46 (80%)	0.43	0 100 100	49, 57, 75, 84	0
11	L	37/37 (100%)	-0.33	0 100 100	25, 29, 58, 66	0
11	l	36/37 (97%)	-0.41	0 100 100	27, 30, 58, 73	0
12	M	32/36 (88%)	-0.25	0 100 100	26, 33, 56, 69	0
12	m	31/36 (86%)	-0.28	0 100 100	29, 33, 52, 61	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	O	244/272 (89%)	0.03	2 (0%) 82 83	26, 41, 74, 127	1 (0%)
13	o	244/272 (89%)	0.03	3 (1%) 76 76	26, 40, 73, 103	0
14	T	29/32 (90%)	-0.40	1 (3%) 48 47	26, 31, 52, 67	0
14	t	29/32 (90%)	-0.31	0 100 100	26, 32, 65, 78	0
15	U	97/134 (72%)	0.02	0 100 100	33, 42, 69, 83	0
15	u	97/134 (72%)	-0.02	1 (1%) 79 80	30, 40, 54, 78	0
16	V	137/163 (84%)	-0.11	1 (0%) 84 84	29, 40, 53, 69	0
16	v	137/163 (84%)	0.13	0 100 100	34, 47, 69, 90	0
17	Y	27/46 (58%)	1.00	3 (11%) 10 9	51, 72, 91, 99	0
17	y	30/46 (65%)	0.91	0 100 100	64, 74, 87, 93	0
18	X	38/41 (92%)	0.31	2 (5%) 32 31	41, 51, 74, 75	0
18	x	39/41 (95%)	0.56	1 (2%) 57 57	50, 60, 82, 95	0
19	Z	62/62 (100%)	0.87	5 (8%) 18 17	51, 64, 102, 110	0
19	z	62/62 (100%)	1.04	6 (9%) 13 12	62, 74, 108, 118	0
20	R	34/41 (82%)	0.90	2 (5%) 28 27	56, 67, 76, 80	0
20	r	31/41 (75%)	1.20	4 (12%) 7 6	65, 78, 95, 98	0
All	All	5302/5700 (93%)	-0.04	59 (1%) 78 78	11, 38, 72, 127	162 (3%)

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
19	Z	62	VAL	4.1
19	Z	33	TRP	4.0
20	R	35	LEU	3.7
13	o	58	ASN	3.4
2	B	488	PRO	3.3

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
14	FME	t	1	10/11	0.89	0.10	32,34,49,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
12	FME	M	1	10/11	0.92	0.09	39,45,59,60	0
14	FME	T	1	10/11	0.95	0.09	28,32,52,66	0
8	FME	i	1	10/11	0.95	0.07	36,44,49,52	0
12	FME	m	1	10/11	0.95	0.08	34,47,55,64	0
8	FME	I	1	10/11	0.95	0.08	38,43,50,50	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
30	LHG	A	614	49/49	0.72	0.17	50,74,90,93	0
32	STE	H	103	18/20	0.72	0.17	48,62,67,71	0
32	STE	k	104	12/20	0.74	0.14	61,66,72,82	0
32	STE	L	102	12/20	0.76	0.19	50,55,63,64	0
27	PL9	A	610	55/55	0.77	0.16	35,58,68,70	0
28	LMG	c	520	48/55	0.77	0.15	45,66,74,78	0
32	STE	a	615	12/20	0.78	0.14	52,57,68,69	0
28	LMG	d	410	23/55	0.79	0.18	48,57,66,67	0
28	LMG	b	622	55/55	0.79	0.16	46,59,69,72	0
32	STE	d	412	17/20	0.79	0.15	46,51,67,67	0
25	CLA	b	601	65/65	0.79	0.14	47,66,83,86	0
32	STE	b	621	20/20	0.80	0.13	40,48,67,73	0
32	STE	b	625	10/20	0.80	0.18	44,53,65,68	0
31	DGD	a	614	44/66	0.80	0.14	37,49,60,70	0
29	SQD	a	613	36/54	0.80	0.14	41,53,65,70	0
32	STE	b	624	15/20	0.81	0.16	45,48,60,69	0
28	LMG	D	411	33/55	0.81	0.14	37,53,72,74	0
32	STE	B	625	18/20	0.82	0.16	39,52,69,76	0
32	STE	b	623	16/20	0.82	0.15	48,59,75,76	0
28	LMG	c	518	37/55	0.82	0.12	49,62,78,80	0
32	STE	B	621	17/20	0.83	0.13	36,47,63,65	0
32	STE	B	624	12/20	0.83	0.15	40,51,59,60	0
31	DGD	A	616	66/66	0.83	0.12	42,54,64,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
32	STE	B	626	12/20	0.83	0.14	47,54,63,63	0
32	STE	D	413	20/20	0.83	0.13	37,45,67,73	0
32	STE	c	519	20/20	0.83	0.14	41,49,76,82	0
27	PL9	a	610	55/55	0.83	0.15	42,61,72,74	0
32	STE	A	617	20/20	0.83	0.12	41,50,64,64	0
32	STE	B	627	16/20	0.84	0.14	42,49,60,61	0
32	STE	d	413	20/20	0.84	0.12	42,50,63,64	0
28	LMG	A	612	48/55	0.84	0.11	37,50,62,73	0
32	STE	C	518	12/20	0.85	0.13	36,44,54,57	0
32	STE	C	519	12/20	0.85	0.12	46,54,59,62	0
28	LMG	B	622	28/55	0.85	0.13	38,45,55,60	0
32	STE	E	102	12/20	0.85	0.13	51,63,72,74	0
32	STE	j	101	12/20	0.85	0.12	47,53,58,58	0
30	LHG	e	101	42/49	0.85	0.12	58,74,88,99	0
29	SQD	b	620	49/54	0.86	0.11	38,50,70,73	0
29	SQD	f	102	41/54	0.86	0.13	55,72,85,88	0
28	LMG	c	521	49/55	0.86	0.11	37,50,74,82	0
26	BCR	d	405	40/40	0.86	0.11	39,49,75,79	0
28	LMG	m	101	51/55	0.86	0.11	33,47,59,61	0
29	SQD	A	615	39/54	0.86	0.13	36,51,71,75	0
28	LMG	C	517	48/55	0.86	0.12	44,61,67,69	0
32	STE	t	102	14/20	0.86	0.11	37,43,50,53	0
32	STE	t	103	10/20	0.86	0.11	46,54,55,57	0
28	LMG	B	620	51/55	0.87	0.11	31,46,58,63	0
26	BCR	k	102	40/40	0.87	0.12	51,61,68,73	0
26	BCR	h	101	40/40	0.87	0.12	40,53,63,65	0
32	STE	T	102	16/20	0.87	0.13	39,47,55,57	0
26	BCR	k	101	40/40	0.88	0.11	45,56,63,66	0
32	STE	I	101	15/20	0.89	0.13	46,50,59,60	0
32	STE	J	102	12/20	0.89	0.11	48,53,60,61	0
25	CLA	B	601	65/65	0.89	0.10	41,53,69,75	0
26	BCR	D	405	40/40	0.89	0.10	34,42,66,71	0
32	STE	C	520	16/20	0.89	0.10	39,46,51,52	0
31	DGD	H	102	62/66	0.89	0.11	34,42,51,57	0
32	STE	m	102	18/20	0.89	0.14	32,42,61,63	0
29	SQD	B	623	54/54	0.89	0.10	39,52,71,82	0
29	SQD	D	408	36/54	0.89	0.12	44,60,68,70	0
29	SQD	a	612	54/54	0.90	0.10	38,57,66,72	0
26	BCR	K	101	40/40	0.90	0.11	44,50,59,62	0
31	DGD	c	516	62/66	0.90	0.10	36,45,70,78	0
26	BCR	k	103	40/40	0.90	0.13	45,51,62,64	0
26	BCR	K	102	40/40	0.90	0.10	41,47,59,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
25	CLA	c	512	65/65	0.90	0.11	47,53,65,72	0
26	BCR	B	618	40/40	0.90	0.09	24,37,45,45	0
25	CLA	C	513	65/65	0.90	0.10	41,52,73,76	0
28	LMG	D	407	51/55	0.91	0.11	32,44,66,69	0
26	BCR	b	619	40/40	0.91	0.09	29,43,57,60	0
25	CLA	c	513	65/65	0.91	0.10	43,60,78,84	0
26	BCR	H	101	40/40	0.91	0.09	31,40,52,53	0
31	DGD	C	516	62/66	0.91	0.10	30,43,72,87	0
26	BCR	B	619	40/40	0.91	0.08	28,37,51,56	0
32	STE	M	101	15/20	0.91	0.10	38,45,56,65	0
32	STE	M	102	10/20	0.91	0.12	41,44,53,54	0
26	BCR	C	514	40/40	0.91	0.09	26,35,47,48	0
26	BCR	T	101	40/40	0.91	0.08	29,36,47,50	0
31	DGD	h	102	62/66	0.91	0.10	35,44,54,56	0
29	SQD	A	613	52/54	0.92	0.10	34,50,68,75	0
30	LHG	d	407	49/49	0.92	0.10	34,43,59,64	0
26	BCR	t	101	40/40	0.92	0.08	29,35,45,49	0
25	CLA	C	512	65/65	0.92	0.09	35,46,70,72	0
26	BCR	b	618	40/40	0.92	0.07	26,35,44,49	0
25	CLA	c	511	65/65	0.93	0.10	42,52,60,67	0
25	CLA	C	508	65/65	0.93	0.09	25,35,67,76	0
30	LHG	d	409	39/49	0.93	0.10	35,40,54,55	0
26	BCR	K	103	40/40	0.93	0.11	37,47,58,59	0
24	BCT	d	401	4/4	0.93	0.08	33,34,43,43	0
26	BCR	b	617	40/40	0.93	0.08	28,40,45,48	0
26	BCR	A	609	40/40	0.93	0.07	22,31,36,37	0
25	CLA	B	606	65/65	0.93	0.09	25,33,54,60	0
26	BCR	c	514	40/40	0.93	0.09	31,44,51,55	0
31	DGD	c	517	62/66	0.93	0.09	32,45,62,72	0
25	CLA	C	503	65/65	0.93	0.08	29,36,42,53	0
25	CLA	b	614	65/65	0.93	0.09	28,35,59,64	0
25	CLA	c	503	65/65	0.93	0.09	34,41,47,52	0
25	CLA	c	510	65/65	0.93	0.08	33,42,51,55	0
25	CLA	C	501	65/65	0.94	0.07	24,32,43,44	0
30	LHG	D	410	47/49	0.94	0.09	28,39,59,63	0
30	LHG	D	412	49/49	0.94	0.09	28,38,53,55	0
24	BCT	A	605	4/4	0.94	0.07	28,32,34,34	0
25	CLA	C	506	65/65	0.94	0.09	29,37,64,72	0
25	CLA	b	606	65/65	0.94	0.08	26,37,56,69	0
30	LHG	l	101	49/49	0.94	0.09	33,40,48,54	0
26	BCR	B	617	40/40	0.94	0.08	28,37,45,46	0
31	DGD	C	515	62/66	0.94	0.09	23,33,60,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
25	CLA	b	609	65/65	0.94	0.09	34,42,56,64	0
25	CLA	B	616	60/65	0.94	0.10	26,34,63,70	0
31	DGD	J	101	62/66	0.94	0.09	28,39,66,75	0
25	CLA	b	616	60/65	0.94	0.09	31,39,71,75	0
31	DGD	c	515	62/66	0.94	0.09	24,37,60,72	0
28	LMG	d	411	44/55	0.94	0.09	37,47,70,72	0
25	CLA	C	510	65/65	0.94	0.08	28,37,47,57	0
25	CLA	c	504	60/65	0.94	0.09	31,40,63,68	0
25	CLA	c	505	65/65	0.94	0.08	27,36,50,52	0
27	PL9	D	406	55/55	0.94	0.07	20,29,37,39	0
25	CLA	c	508	64/65	0.94	0.09	32,40,73,83	0
27	PL9	d	406	55/55	0.94	0.07	25,32,39,40	0
25	CLA	c	509	65/65	0.94	0.09	33,43,54,58	0
25	CLA	C	511	65/65	0.94	0.10	34,45,57,63	0
26	BCR	a	609	40/40	0.94	0.07	22,30,39,44	0
33	PHO	d	402	64/64	0.94	0.07	28,37,43,45	0
25	CLA	a	606	65/65	0.95	0.08	25,35,74,77	0
25	CLA	a	608	65/65	0.95	0.09	22,30,63,67	0
25	CLA	d	403	65/65	0.95	0.07	22,28,48,53	0
25	CLA	d	404	65/65	0.95	0.09	28,38,73,79	0
25	CLA	B	610	65/65	0.95	0.07	22,28,37,39	0
25	CLA	b	602	65/65	0.95	0.08	29,38,49,55	0
25	CLA	C	504	59/65	0.95	0.07	28,37,67,70	0
25	CLA	b	608	65/65	0.95	0.07	29,39,54,57	0
25	CLA	C	505	65/65	0.95	0.07	26,34,53,59	0
25	CLA	b	610	65/65	0.95	0.08	29,35,43,46	0
25	CLA	b	613	65/65	0.95	0.08	23,30,58,67	0
25	CLA	B	611	65/65	0.95	0.06	23,28,38,44	0
25	CLA	b	615	65/65	0.95	0.07	29,37,49,52	0
25	CLA	C	507	65/65	0.95	0.08	26,34,46,52	0
25	CLA	c	501	65/65	0.95	0.07	29,36,47,53	0
25	CLA	c	502	65/65	0.95	0.07	31,36,48,52	0
25	CLA	B	614	65/65	0.95	0.08	23,34,58,63	0
25	CLA	C	509	65/65	0.95	0.09	27,35,52,54	0
25	CLA	B	615	65/65	0.95	0.08	27,33,50,55	0
25	CLA	c	506	65/65	0.95	0.08	35,42,67,73	0
25	CLA	c	507	65/65	0.95	0.08	32,39,48,51	0
25	CLA	B	602	65/65	0.95	0.07	23,32,51,55	0
25	CLA	B	607	65/65	0.95	0.08	20,27,51,56	0
25	CLA	C	502	65/65	0.95	0.07	25,33,46,55	0
33	PHO	a	607	64/64	0.95	0.07	21,28,34,37	0
25	CLA	a	605	65/65	0.95	0.07	22,28,36,43	0

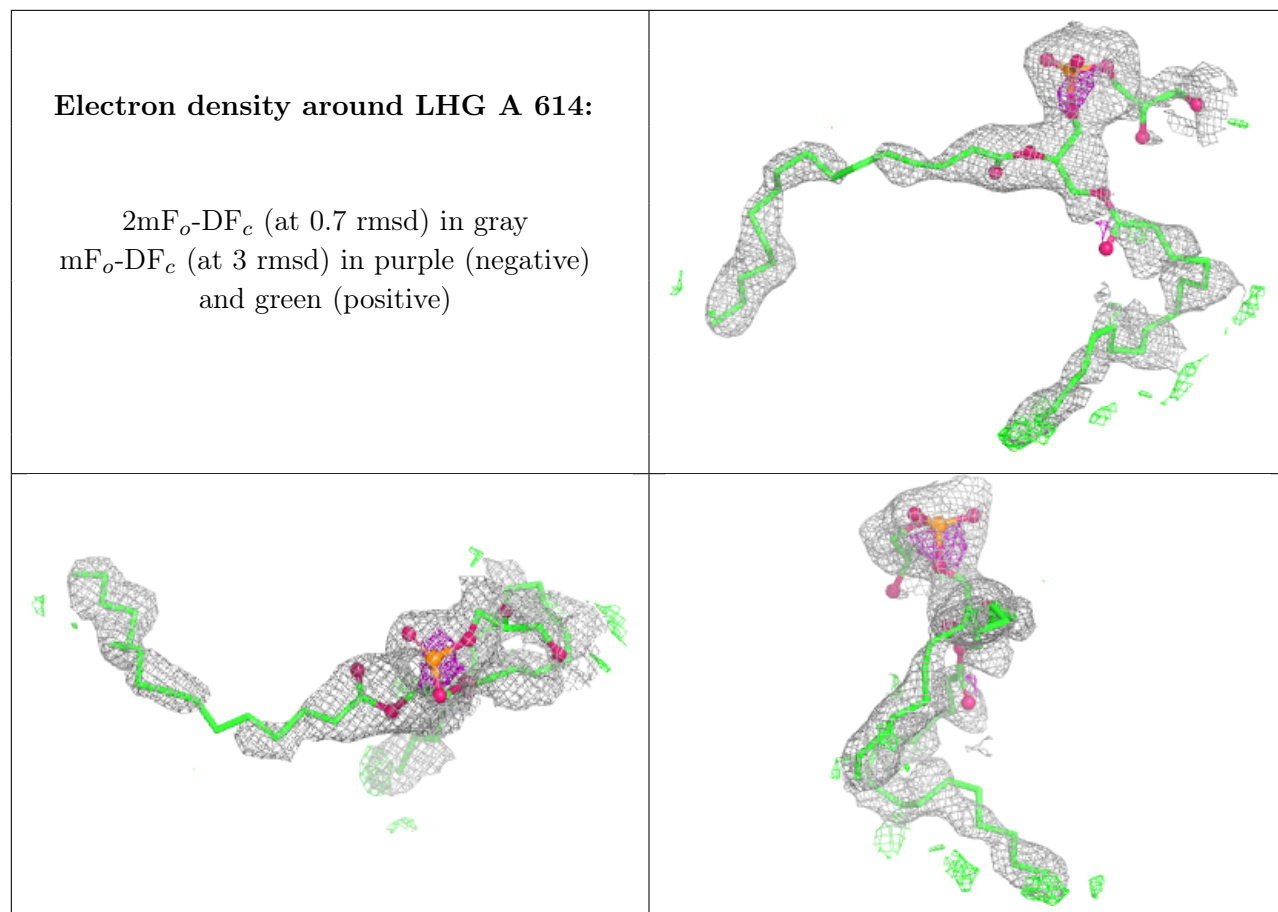
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
25	CLA	B	604	65/65	0.96	0.07	21,27,59,65	0
25	CLA	a	611	65/65	0.96	0.06	19,28,39,46	0
25	CLA	B	605	65/65	0.96	0.07	20,28,40,44	0
25	CLA	A	611	65/65	0.96	0.06	17,25,34,37	0
25	CLA	b	603	65/65	0.96	0.07	21,31,53,59	0
25	CLA	b	604	65/65	0.96	0.07	22,30,56,61	0
25	CLA	b	605	65/65	0.96	0.07	23,31,39,43	0
25	CLA	A	606	65/65	0.96	0.06	19,26,36,44	0
25	CLA	b	607	65/65	0.96	0.07	22,30,52,58	0
25	CLA	B	608	65/65	0.96	0.07	25,31,49,59	0
25	CLA	B	609	65/65	0.96	0.07	23,34,52,58	0
30	LHG	L	101	49/49	0.96	0.07	28,36,43,55	0
25	CLA	A	607	65/65	0.96	0.09	22,29,77,81	0
30	LHG	d	408	49/49	0.96	0.08	27,37,44,50	0
25	CLA	b	611	65/65	0.96	0.07	24,30,42,49	0
25	CLA	b	612	65/65	0.96	0.07	24,32,40,46	0
25	CLA	D	403	65/65	0.96	0.07	19,25,41,56	0
25	CLA	D	404	65/65	0.96	0.08	27,33,73,82	0
33	PHO	D	401	64/64	0.96	0.06	19,26,33,38	0
33	PHO	D	402	64/64	0.96	0.06	24,31,35,37	0
25	CLA	B	603	65/65	0.96	0.07	20,27,49,55	0
25	CLA	B	612	65/65	0.96	0.06	21,27,38,41	0
34	HEM	E	101	43/43	0.96	0.09	38,45,55,63	0
34	HEM	f	101	43/43	0.96	0.09	47,56,67,76	0
25	CLA	A	608	54/65	0.97	0.06	19,26,50,54	0
30	LHG	D	409	49/49	0.97	0.07	24,35,44,49	0
25	CLA	B	613	65/65	0.97	0.06	20,26,54,58	0
35	HEC	V	201	43/43	0.98	0.06	24,30,38,43	0
35	HEC	v	201	43/43	0.98	0.06	29,35,42,46	0
23	CL	a	603	1/1	0.99	0.03	31,31,31,31	0
23	CL	a	604	1/1	0.99	0.09	32,32,32,32	0
21	OEY	A	601[A]	11/11	0.99	0.03	29,32,36,36	11
21	OEY	A	601[B]	11/11	0.99	0.03	23,28,31,31	11
21	OEY	a	601[A]	11/11	0.99	0.03	28,31,33,35	11
21	OEY	a	601[B]	11/11	0.99	0.03	24,29,29,31	11
22	FE2	A	602	1/1	0.99	0.01	29,29,29,29	0
22	FE2	a	602	1/1	0.99	0.02	32,32,32,32	0
23	CL	A	603	1/1	0.99	0.04	27,27,27,27	0
23	CL	A	604	1/1	0.99	0.02	29,29,29,29	0

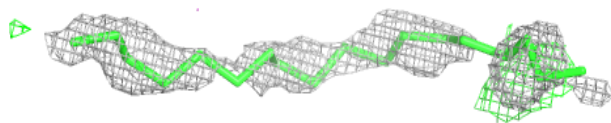
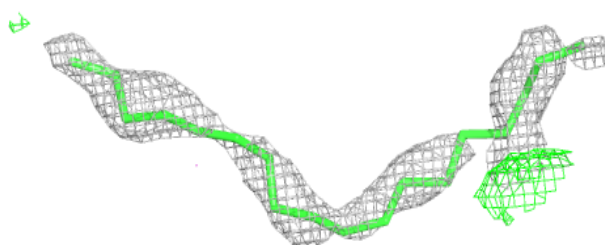
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different

orientation to approximate a three-dimensional view.

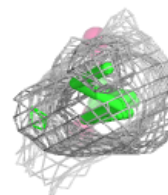
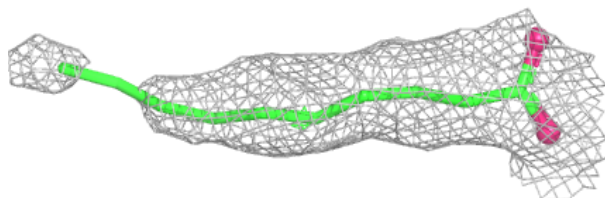


Electron density around STE H 103:

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

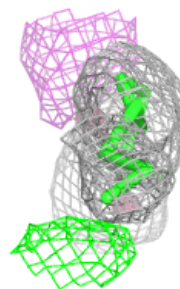
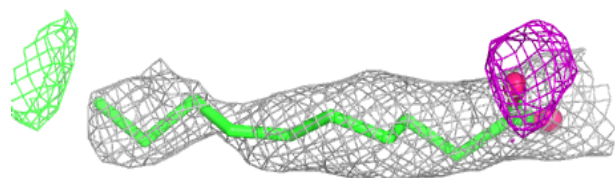
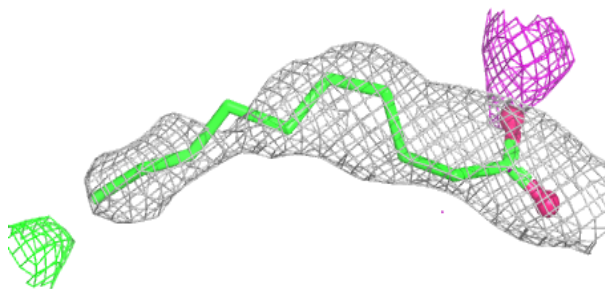
**Electron density around STE k 104:**

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

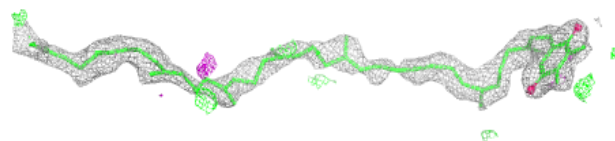
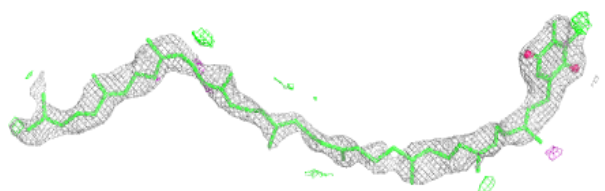


Electron density around STE L 102:

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

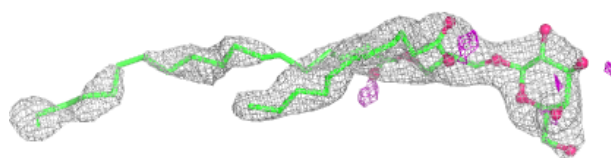
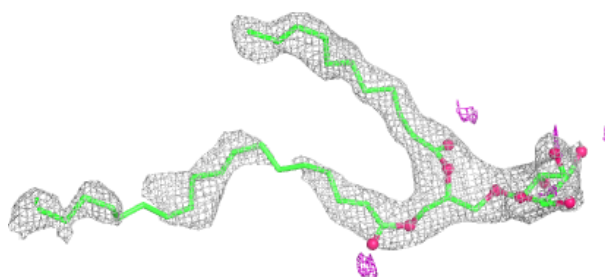
**Electron density around PL9 A 610:**

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

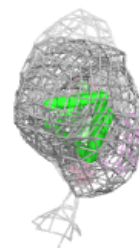
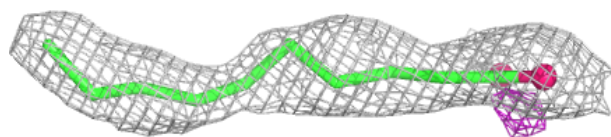
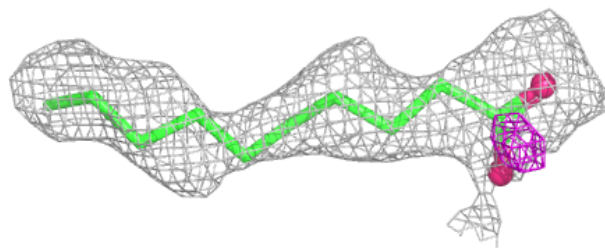


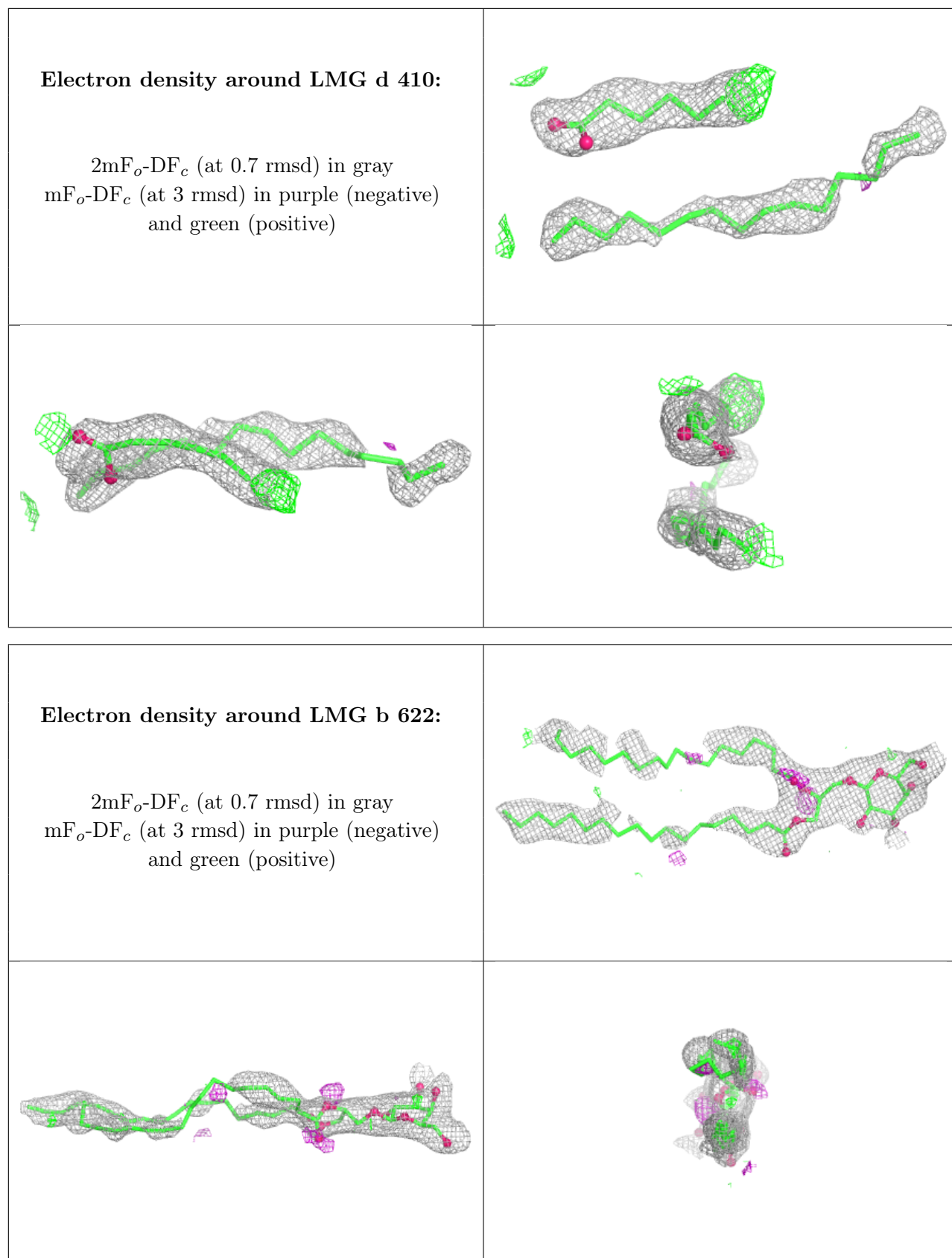
Electron density around LMG c 520:

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

**Electron density around STE a 615:**

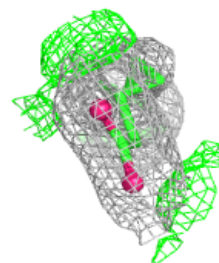
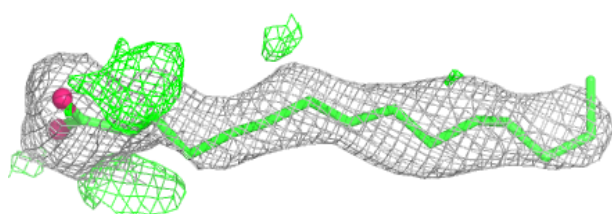
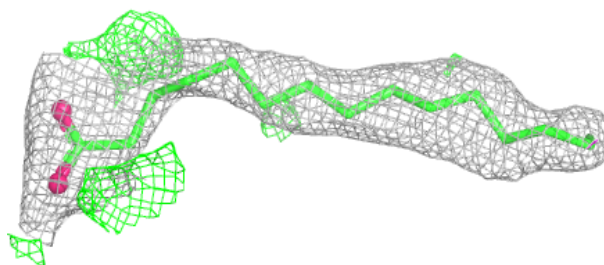
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



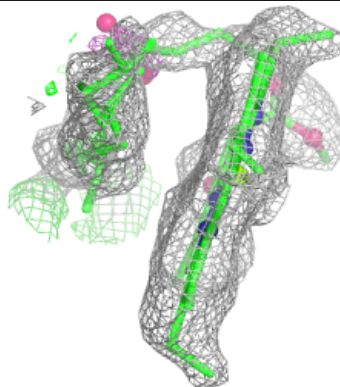
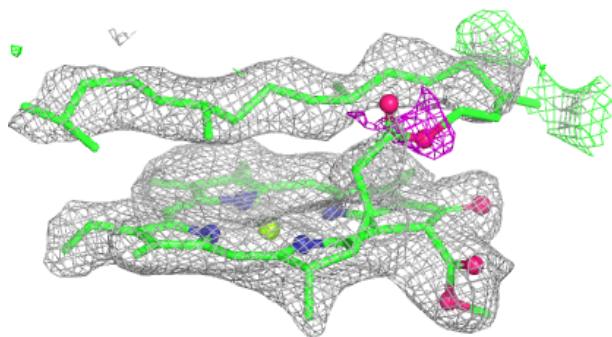
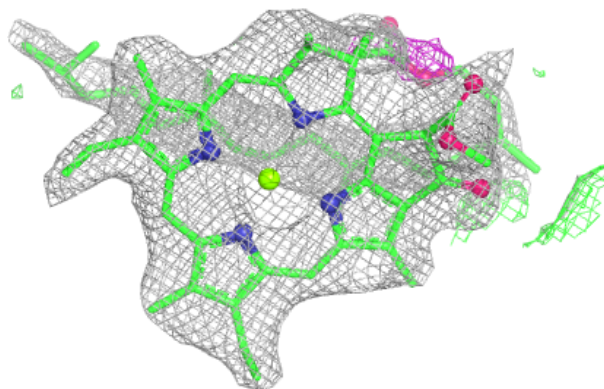


Electron density around STE d 412:

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

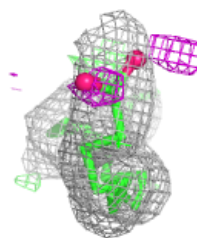
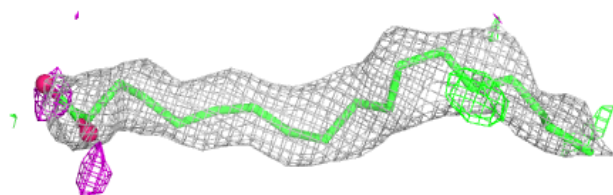
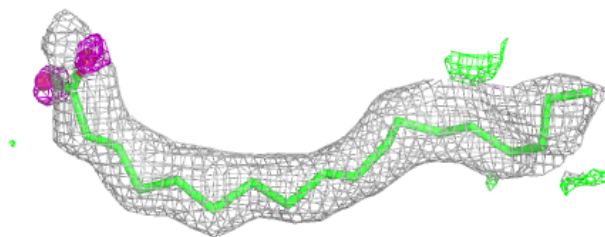
**Electron density around CLA b 601:**

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

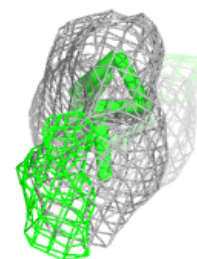
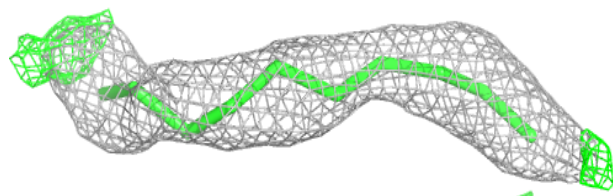
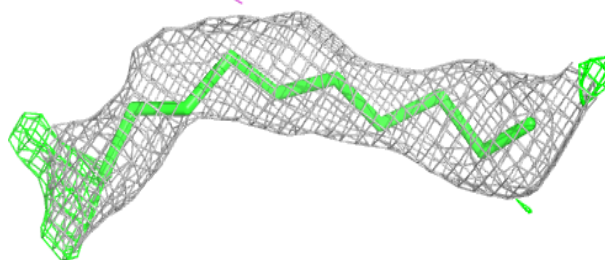


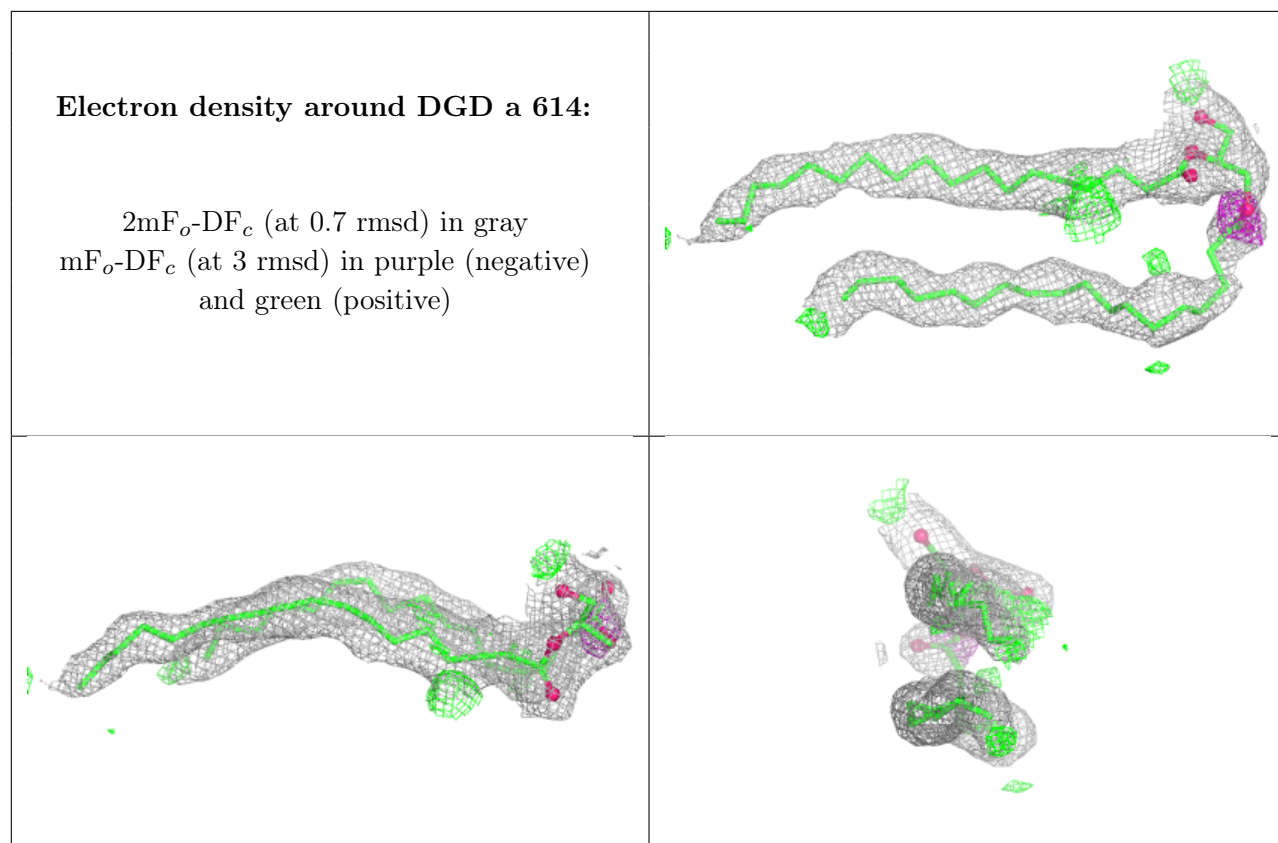
Electron density around STE b 621:

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

**Electron density around STE b 625:**

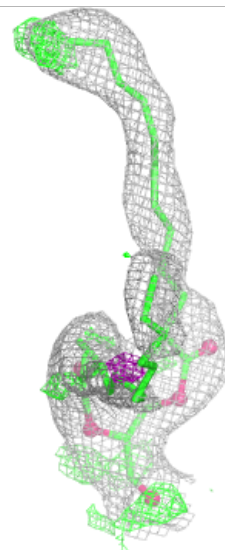
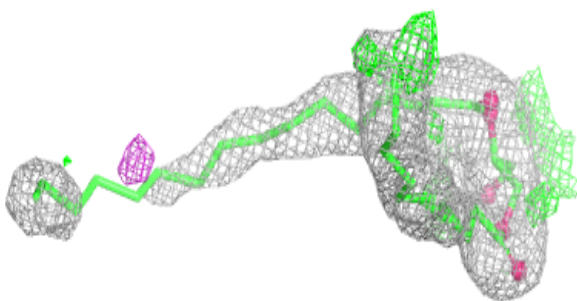
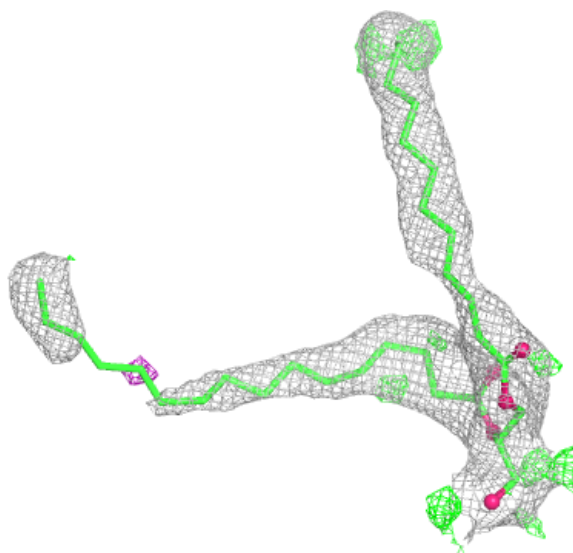
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





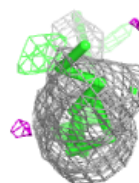
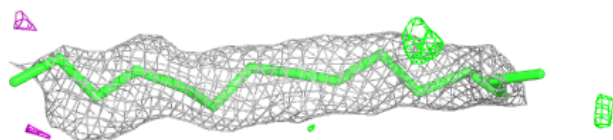
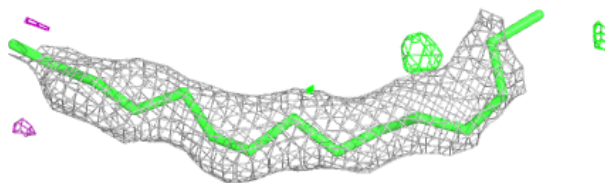
Electron density around SQD a 613:

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

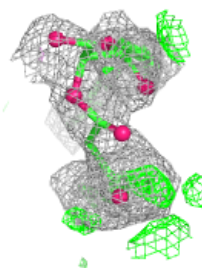
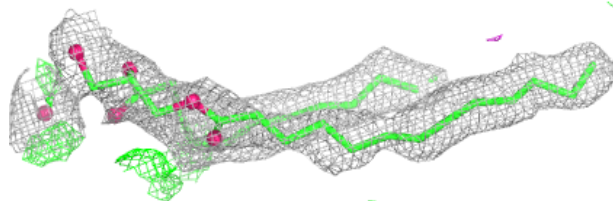
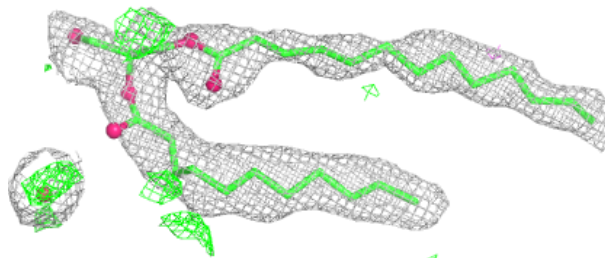


Electron density around STE b 624:

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

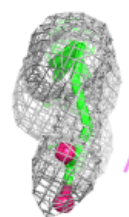
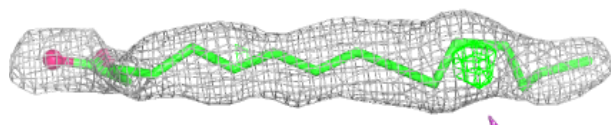
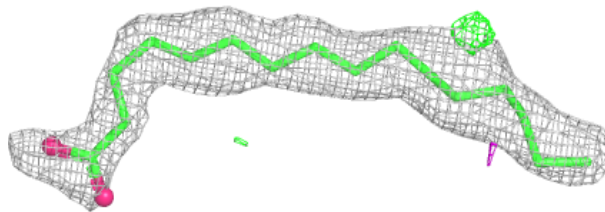
**Electron density around LMG D 411:**

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

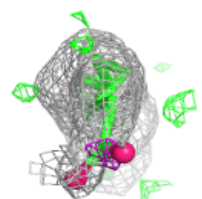
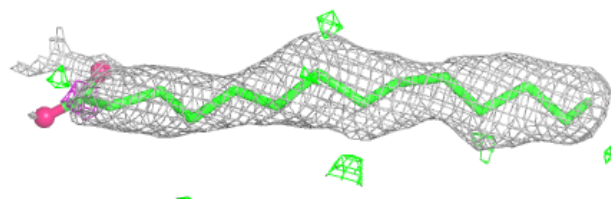
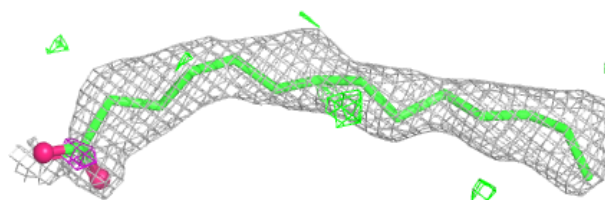


Electron density around STE B 625:

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

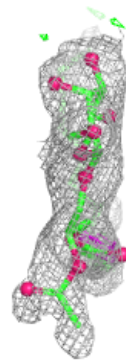
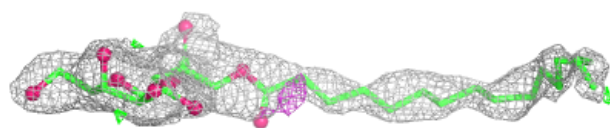
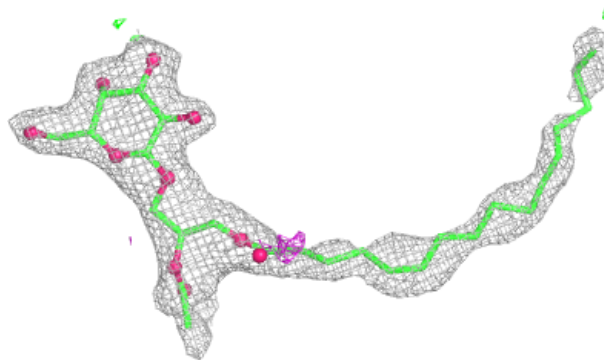
**Electron density around STE b 623:**

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

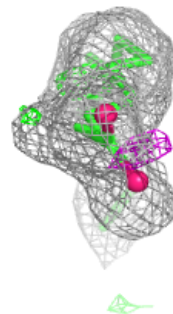
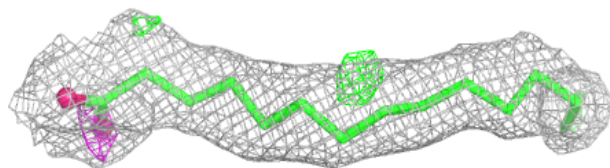
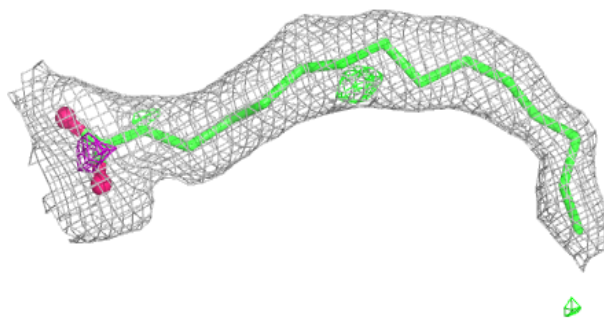


Electron density around LMG c 518:

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

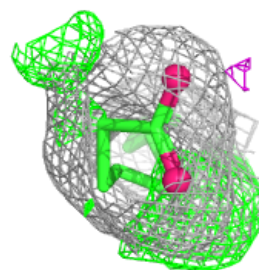
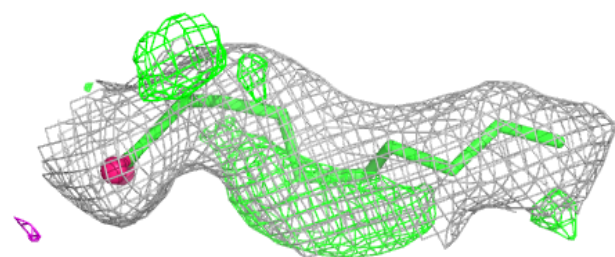
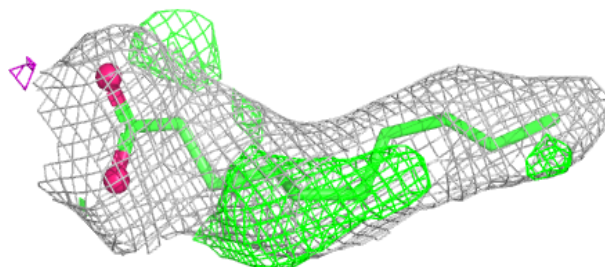
**Electron density around STE B 621:**

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

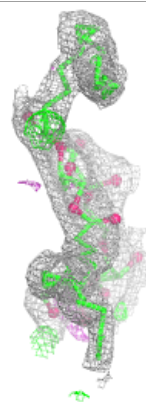
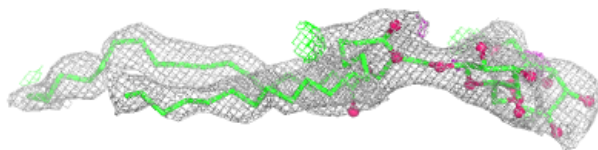
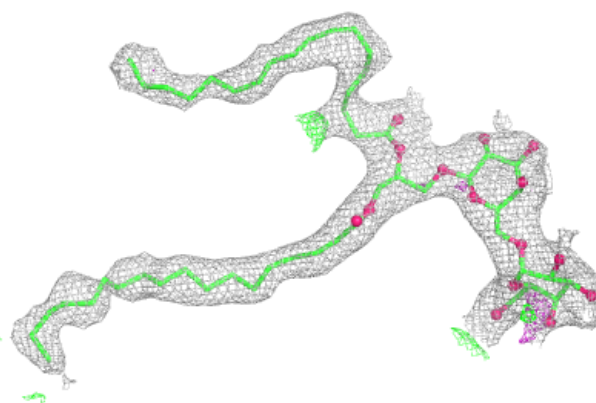


Electron density around STE B 624:

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

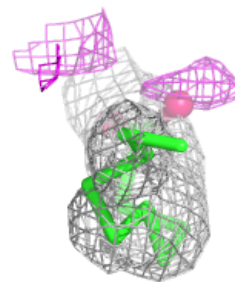
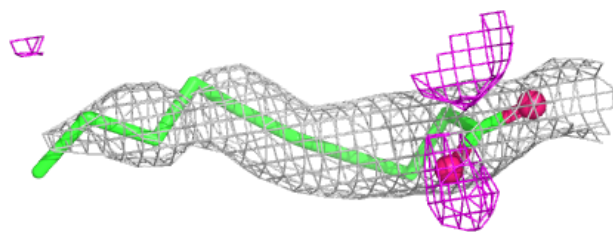
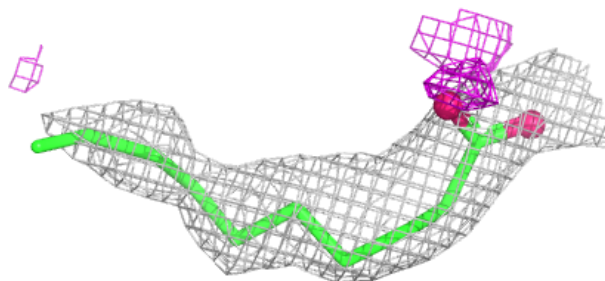
**Electron density around DGD A 616:**

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

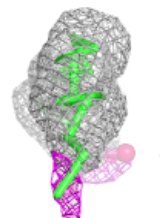
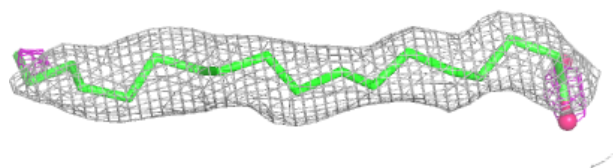
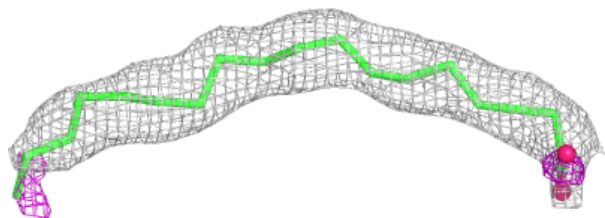


Electron density around STE B 626:

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

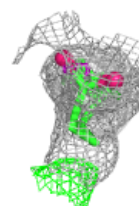
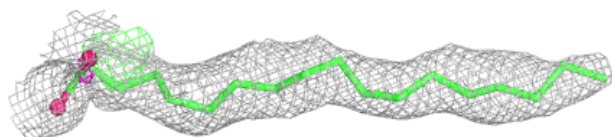
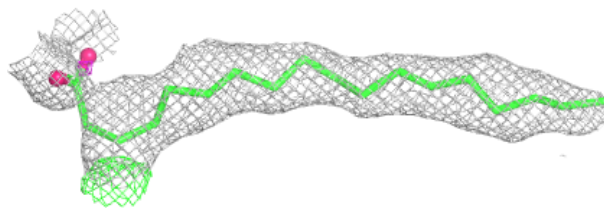
**Electron density around STE D 413:**

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

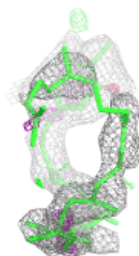
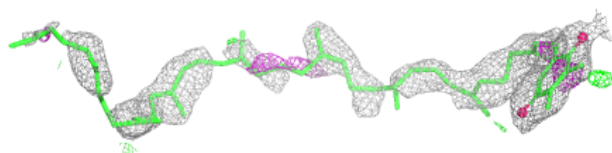
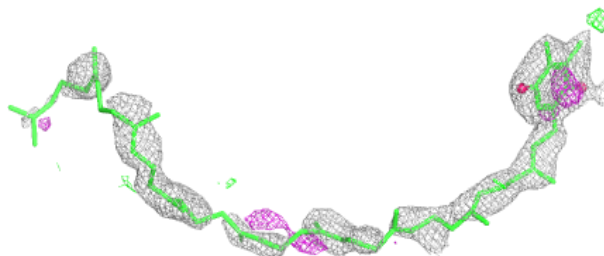


Electron density around STE c 519:

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

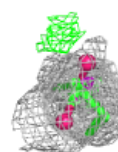
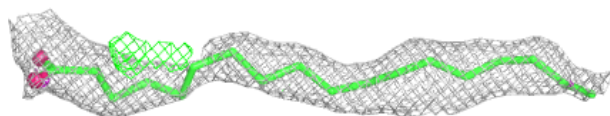
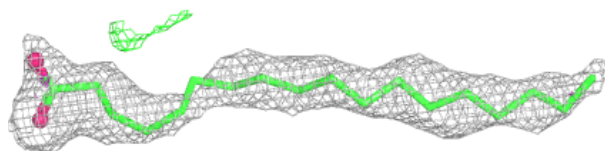
**Electron density around PL9 a 610:**

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

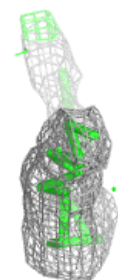
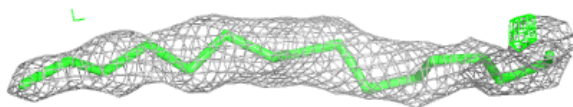
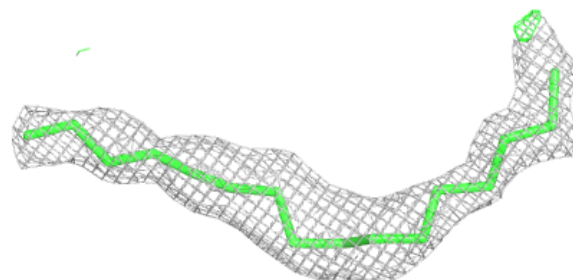


Electron density around STE A 617:

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

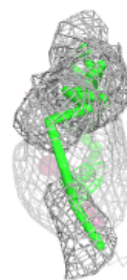
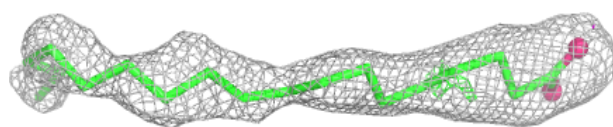
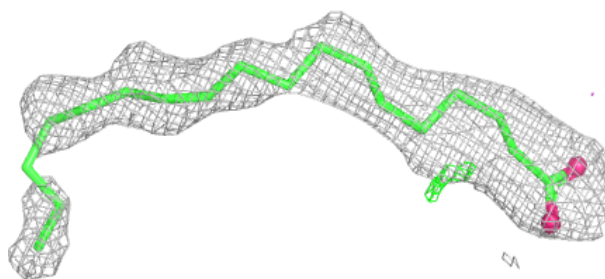
**Electron density around STE B 627:**

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

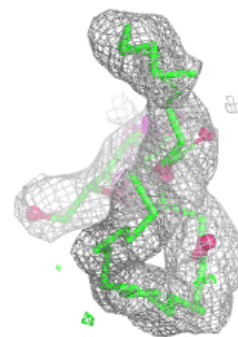
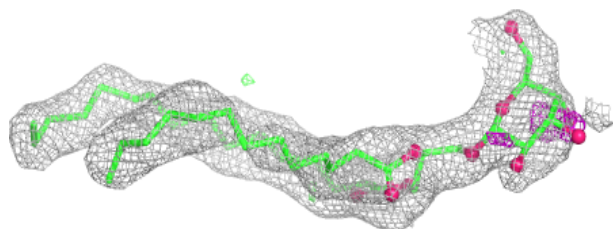
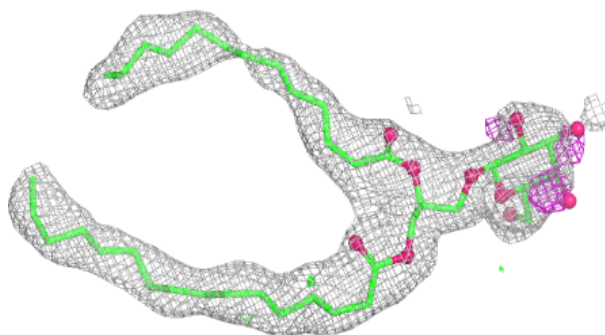


Electron density around STE d 413:

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

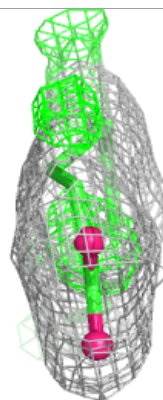
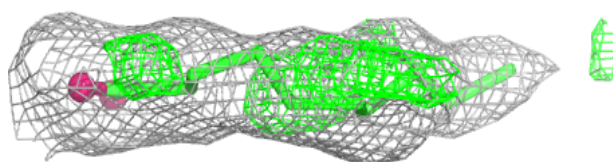
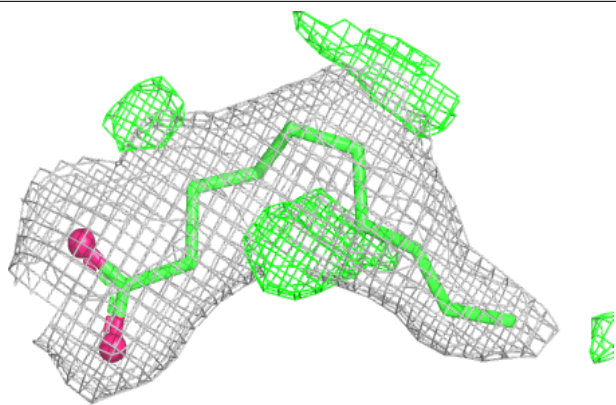
**Electron density around LMG A 612:**

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

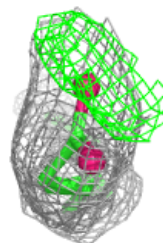
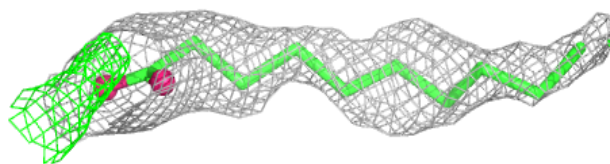
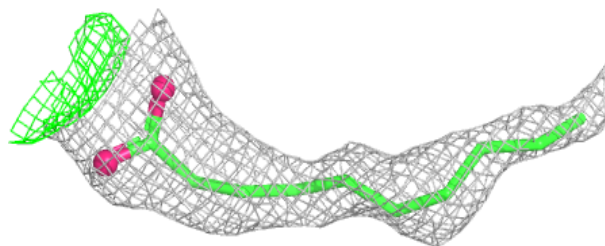


Electron density around STE C 518:

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

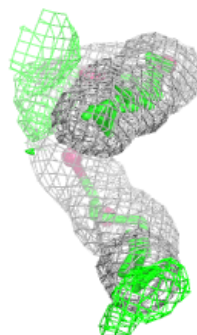
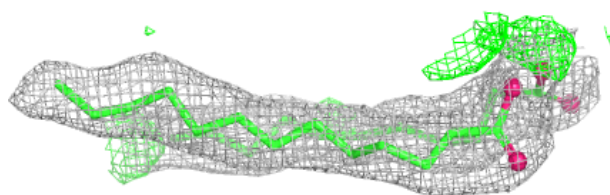
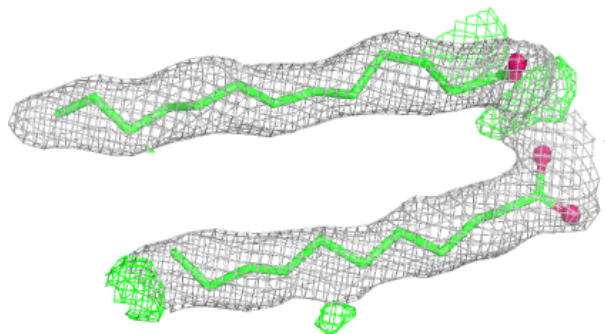
**Electron density around STE C 519:**

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

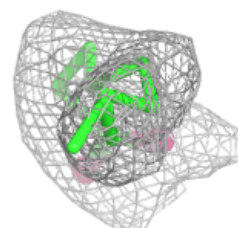
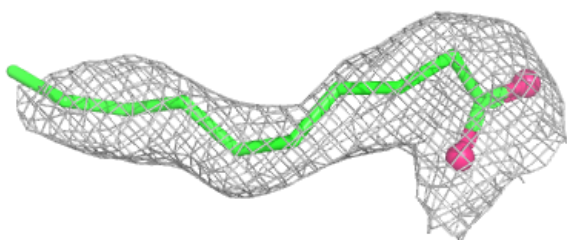
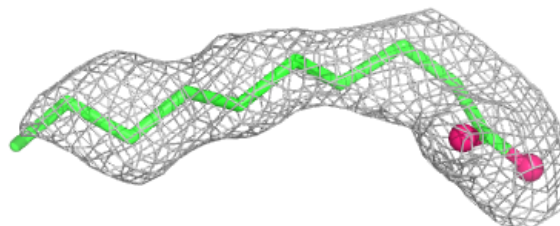


Electron density around LMG B 622:

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

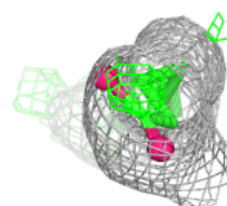
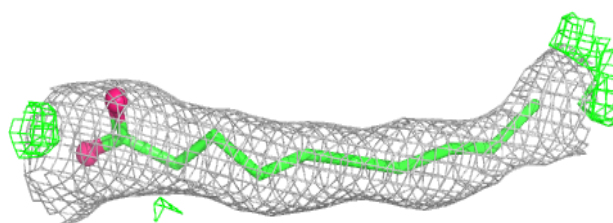
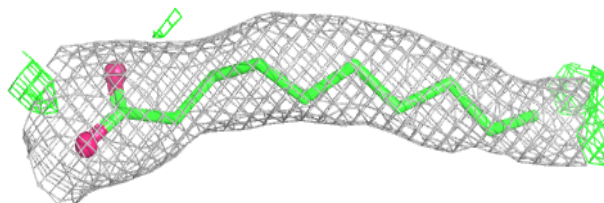
**Electron density around STE E 102:**

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

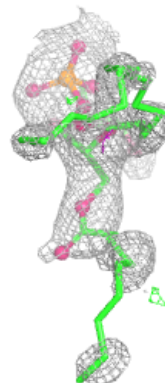
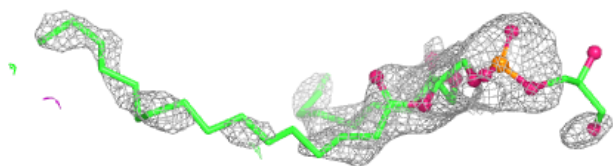
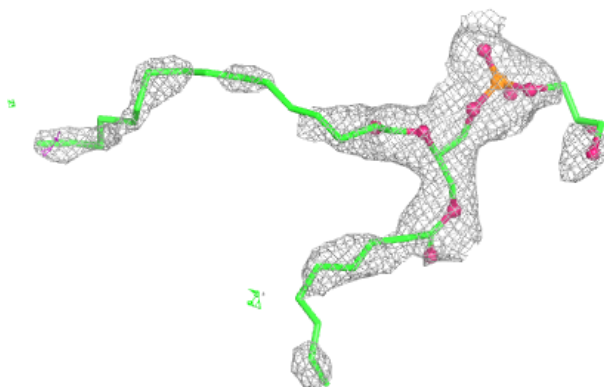


Electron density around STE j 101:

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

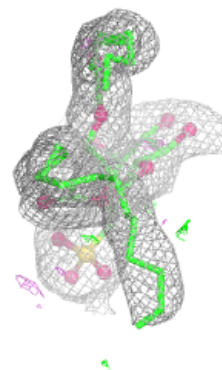
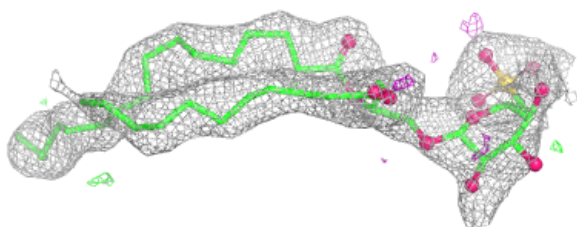
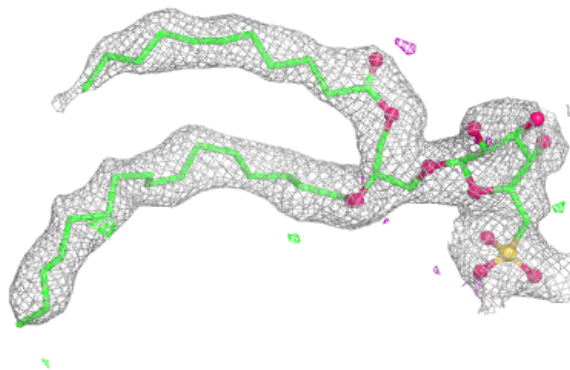
**Electron density around LHG e 101:**

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

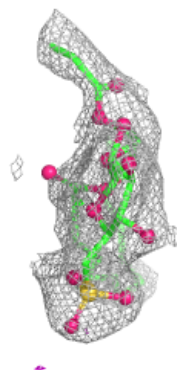
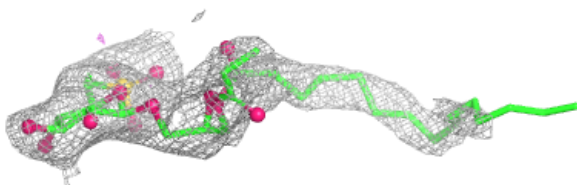
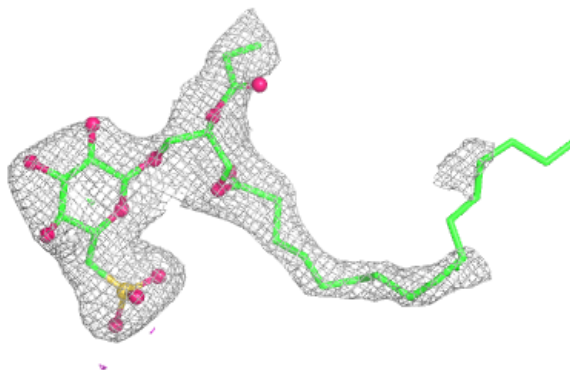


Electron density around SQD b 620:

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

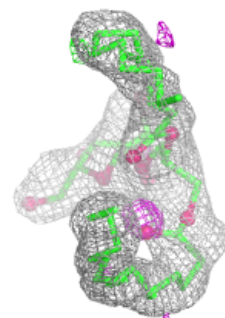
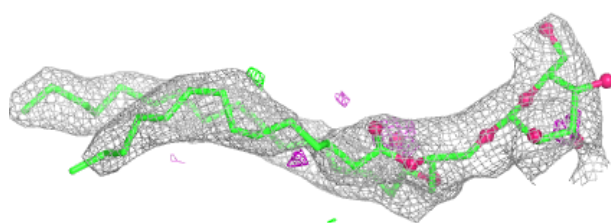
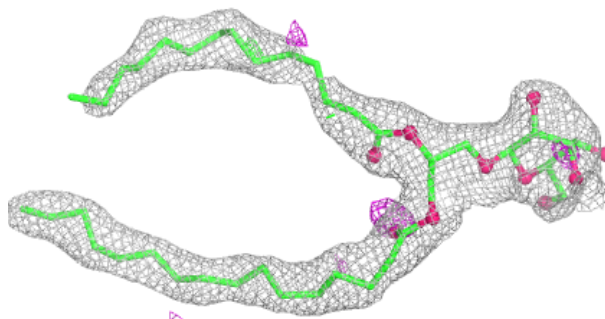
**Electron density around SQD f 102:**

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

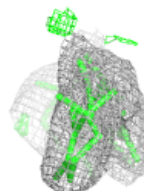
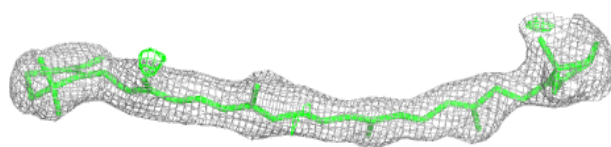
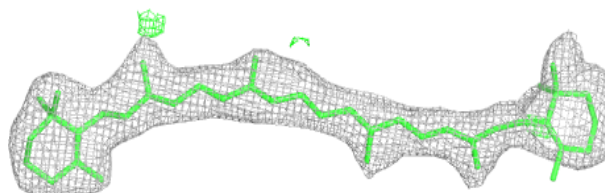


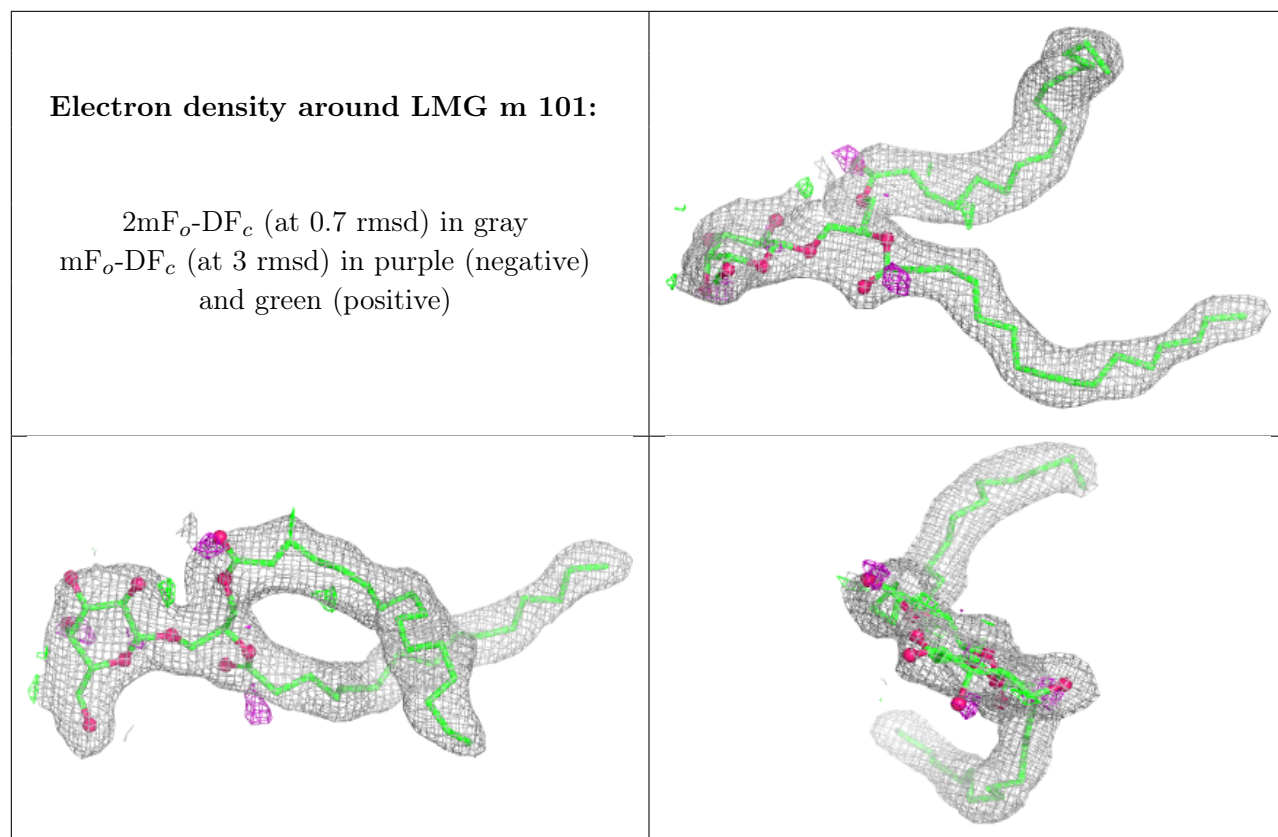
Electron density around LMG c 521:

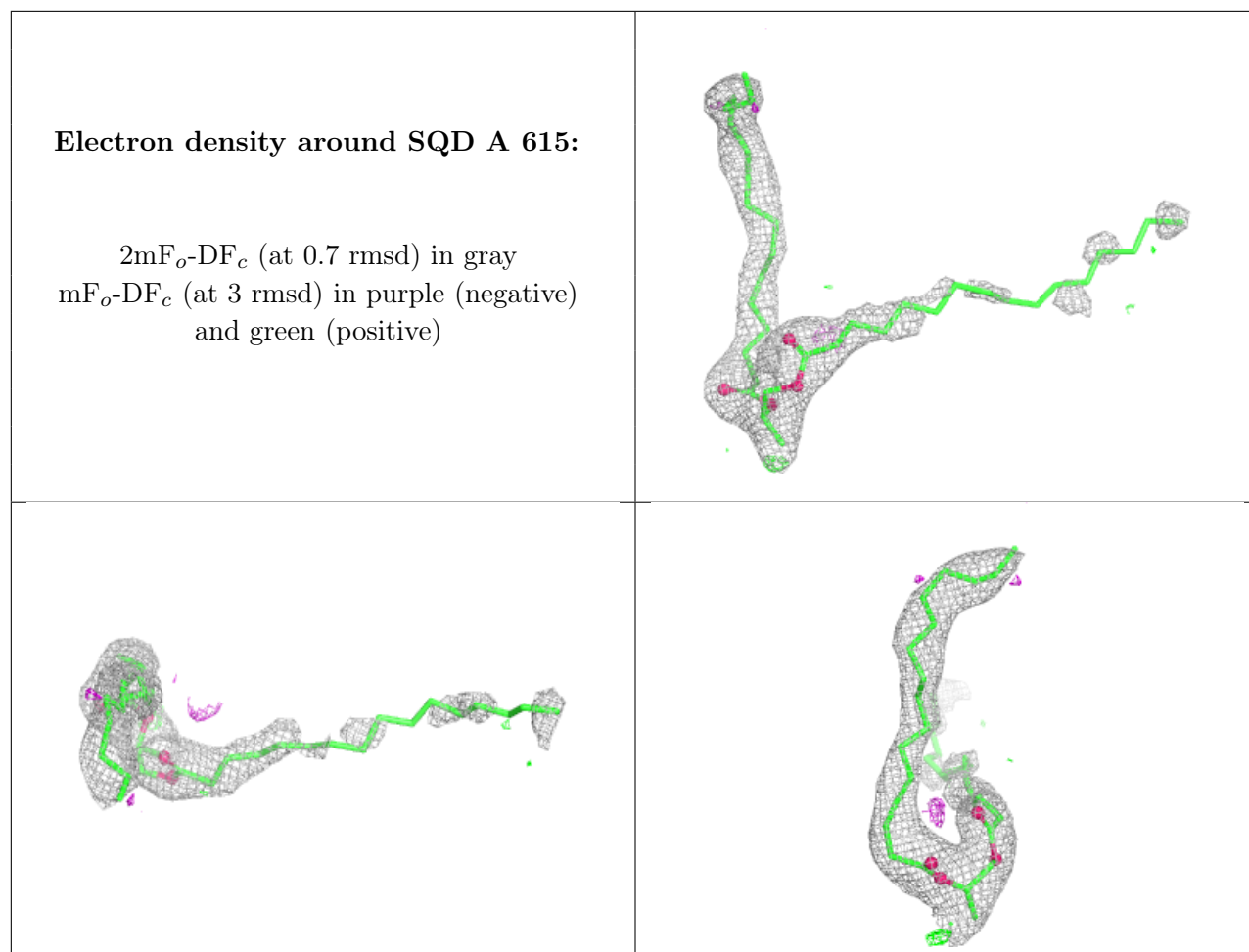
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around BCR d 405:**

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

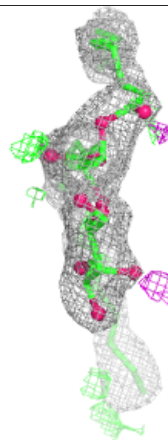
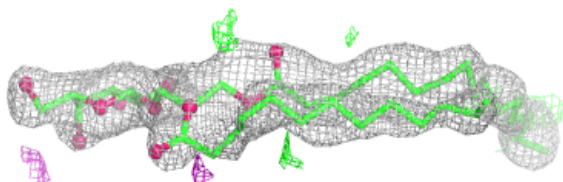
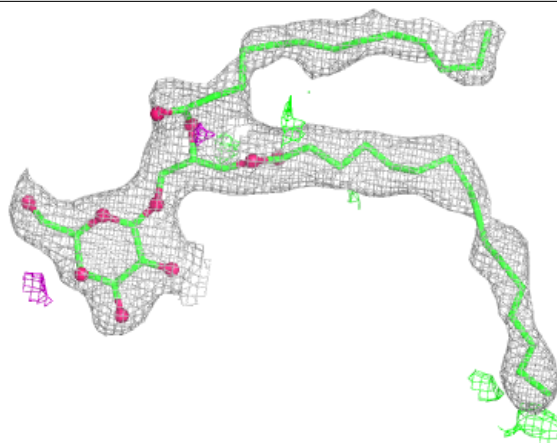




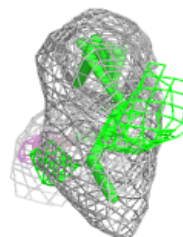
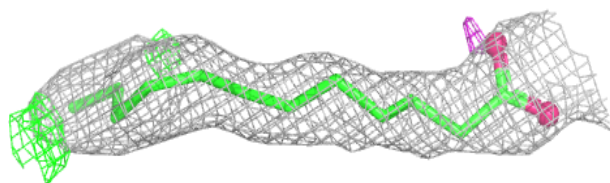
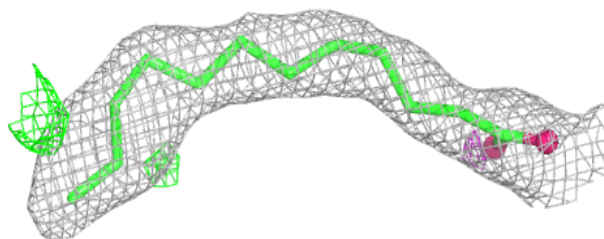


Electron density around LMG C 517:

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

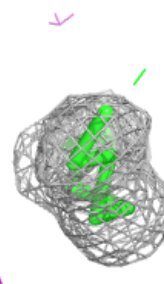
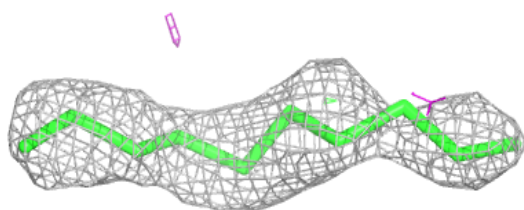
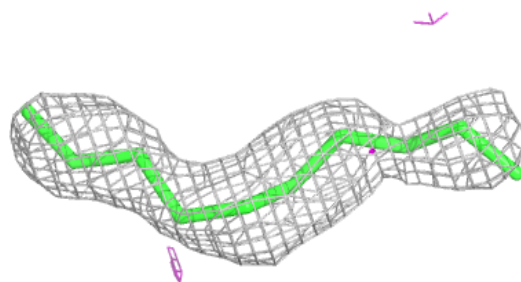
**Electron density around STE t 102:**

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

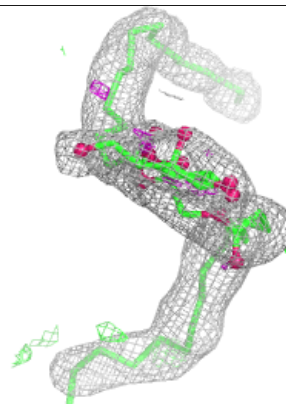
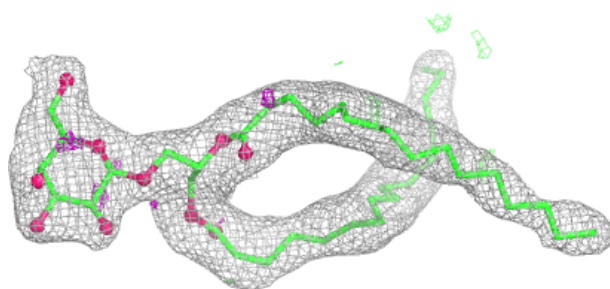
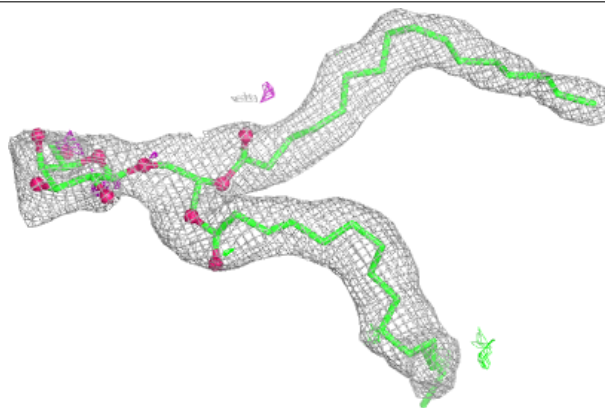


Electron density around STE t 103:

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

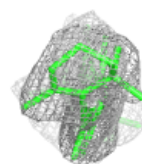
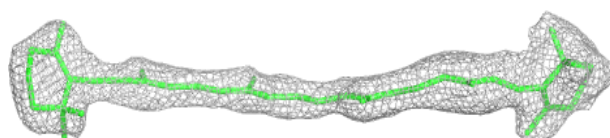
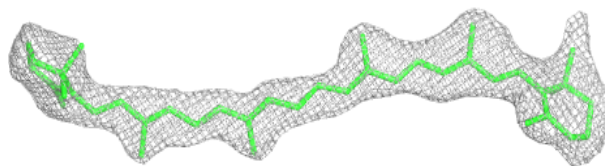
**Electron density around LMG B 620:**

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

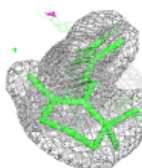
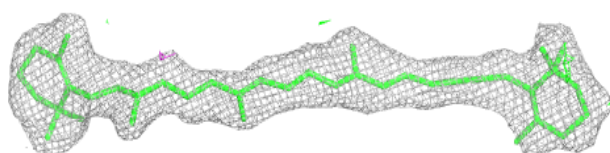
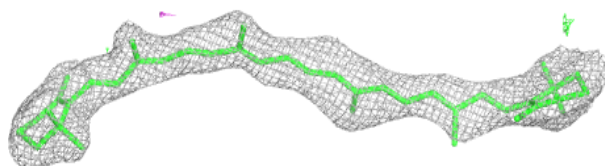


Electron density around BCR k 102:

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

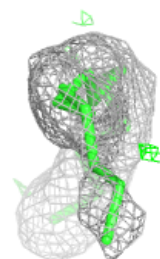
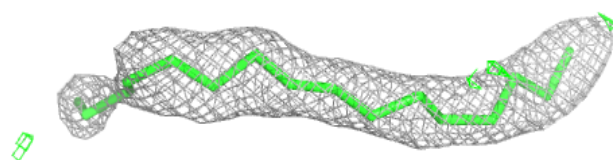
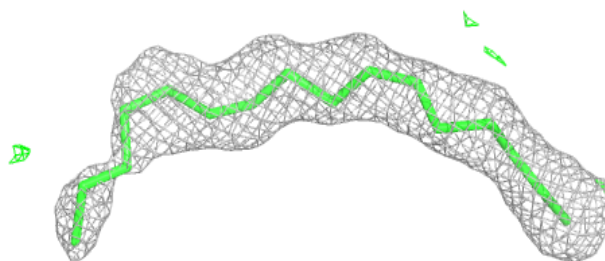
**Electron density around BCR h 101:**

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

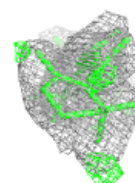
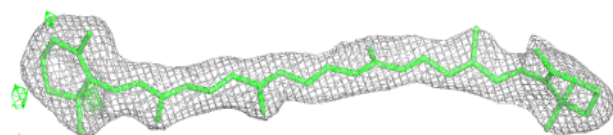
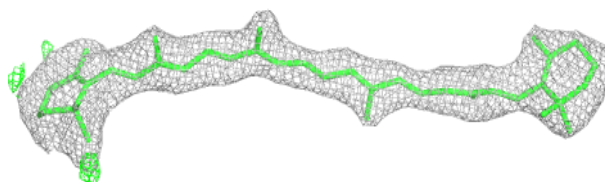


Electron density around STE T 102:

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

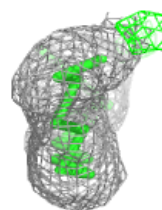
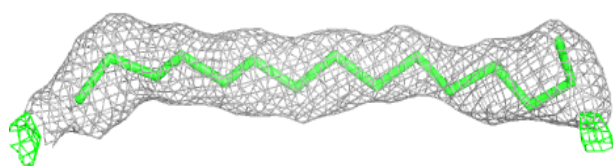
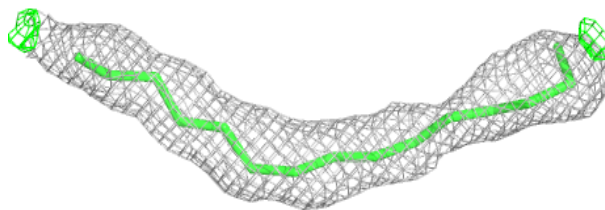
**Electron density around BCR k 101:**

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

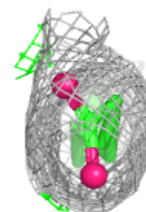
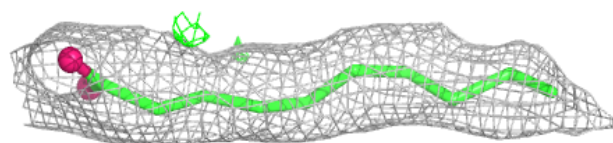
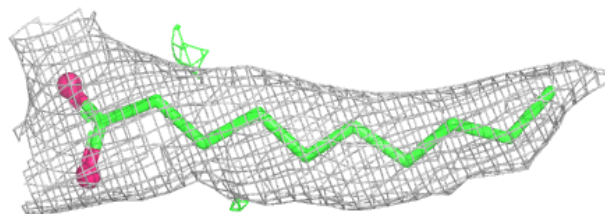


Electron density around STE I 101:

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

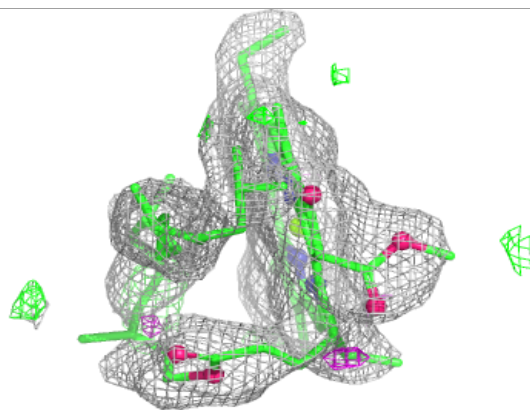
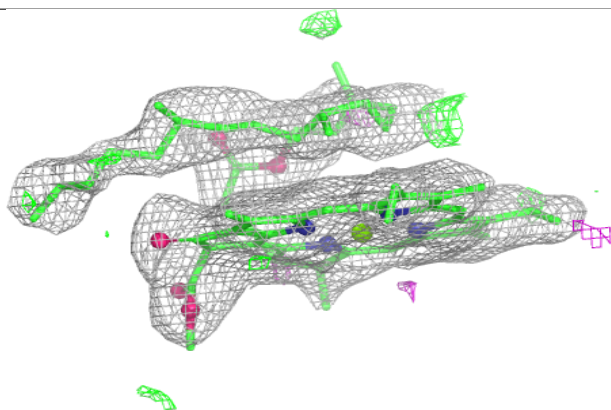
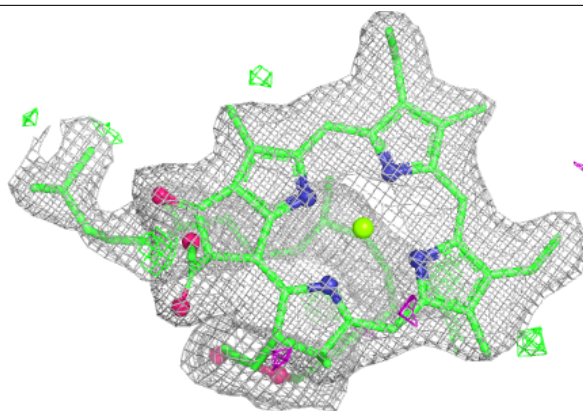
**Electron density around STE J 102:**

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

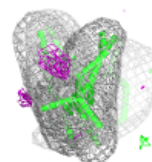
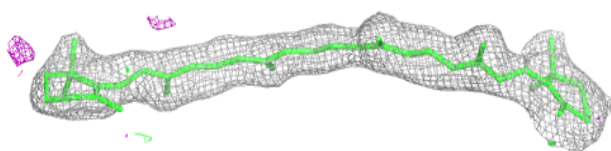
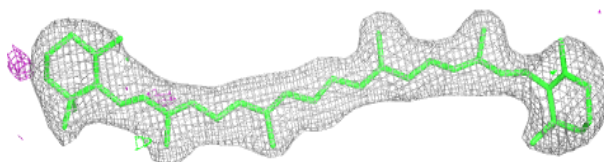


Electron density around CLA B 601:

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

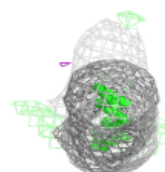
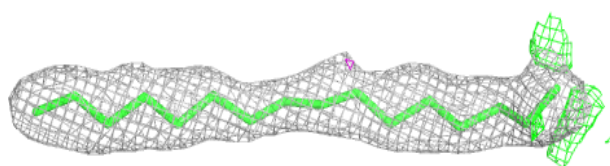
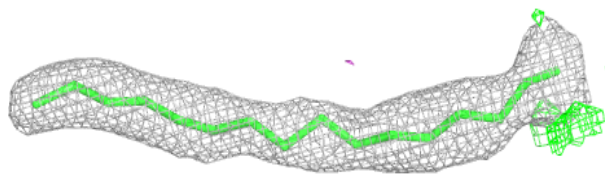
**Electron density around BCR D 405:**

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

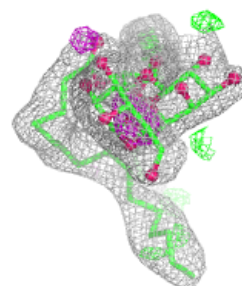
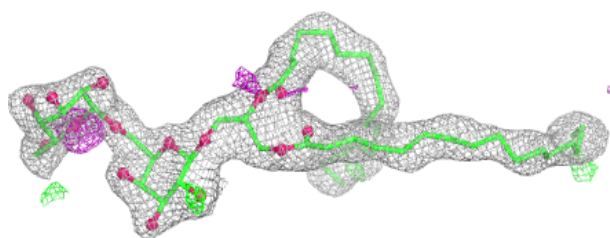
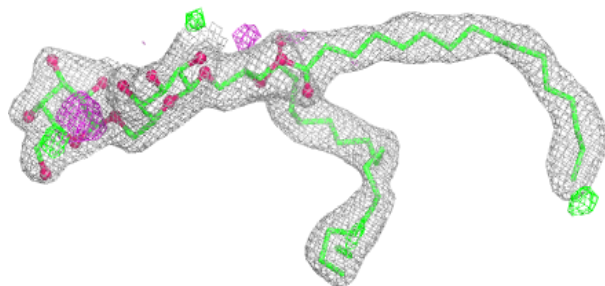


Electron density around STE C 520:

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

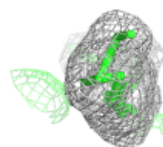
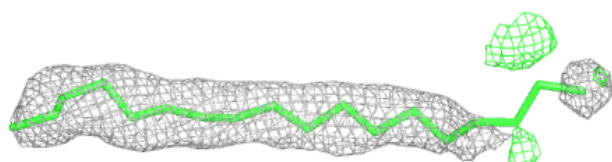
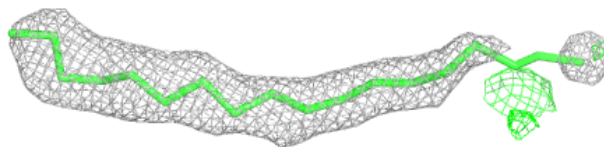
**Electron density around DGD H 102:**

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

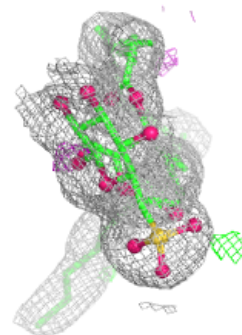
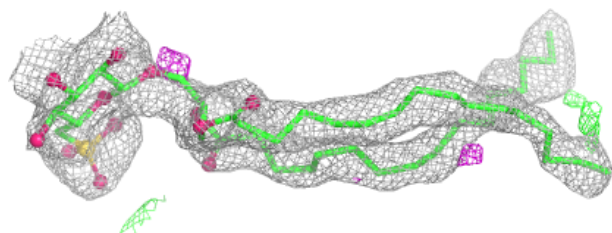
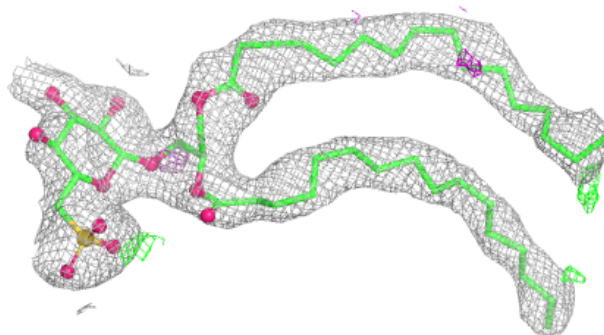


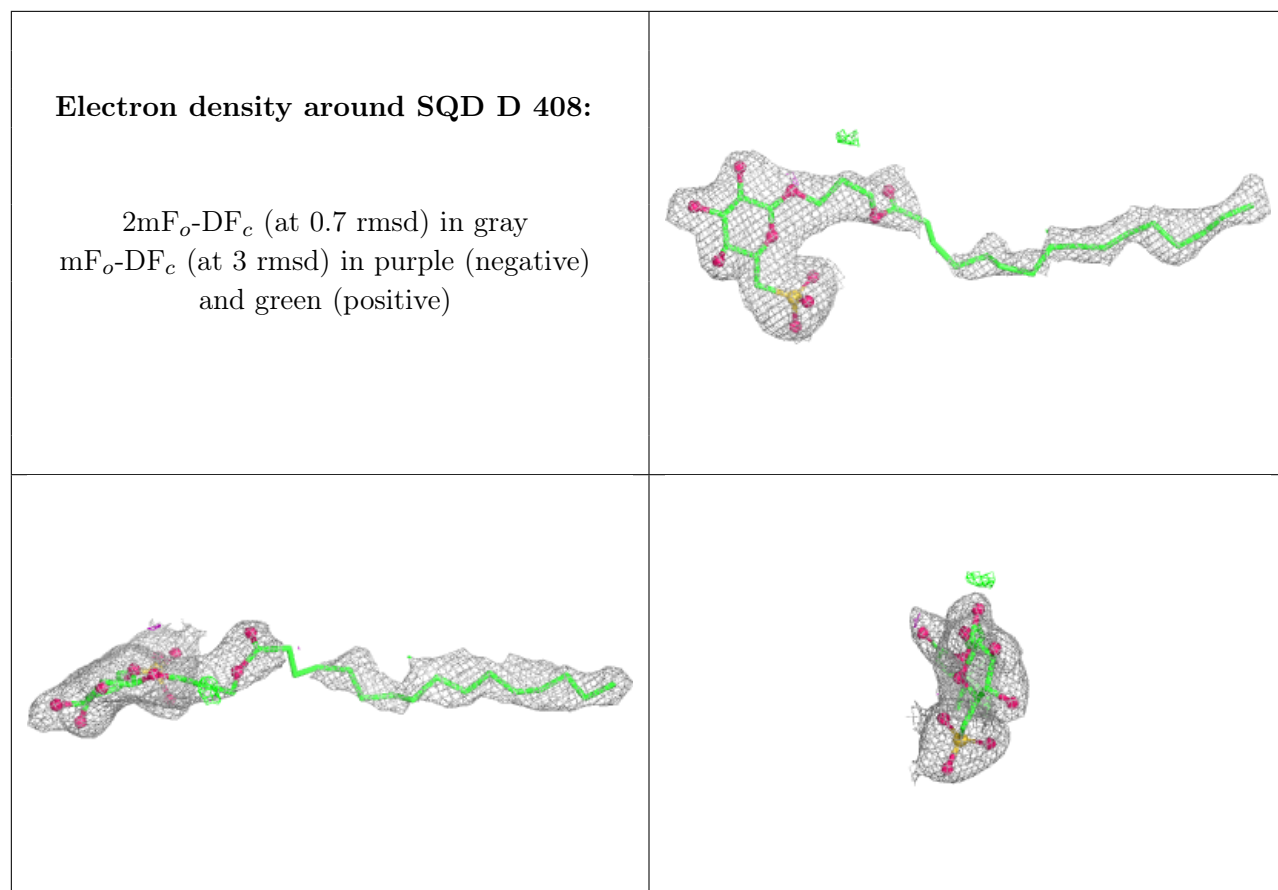
Electron density around STE m 102:

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

**Electron density around SQD B 623:**

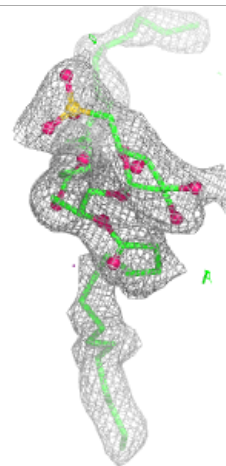
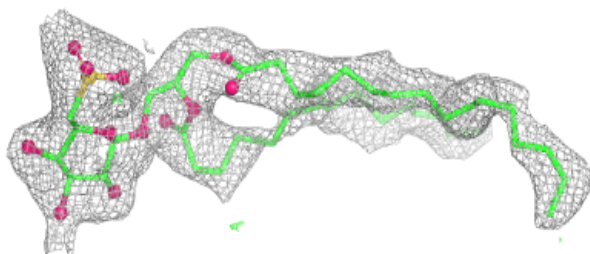
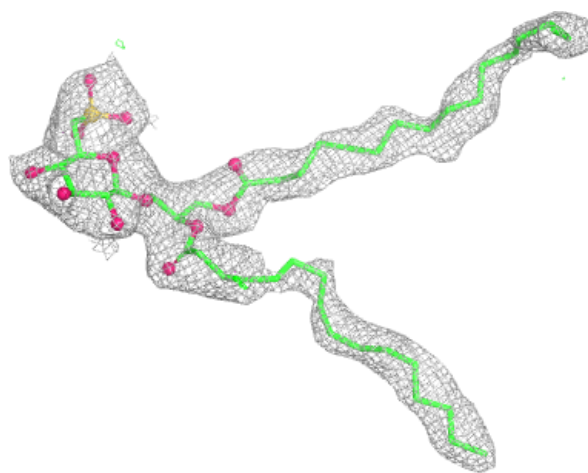
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





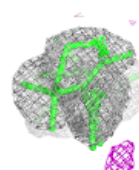
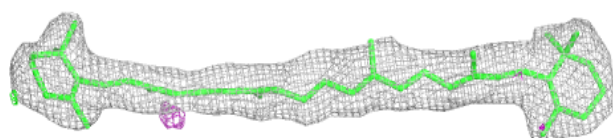
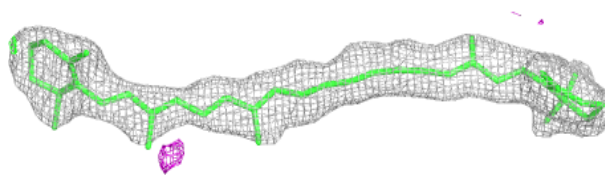
Electron density around SQD a 612:

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

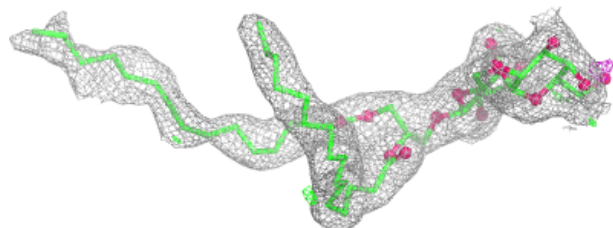
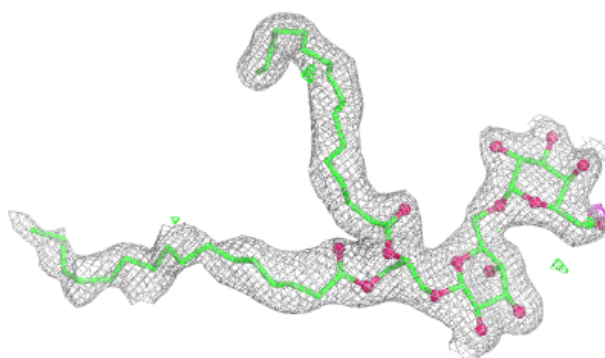


Electron density around BCR K 101:

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

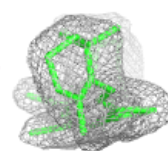
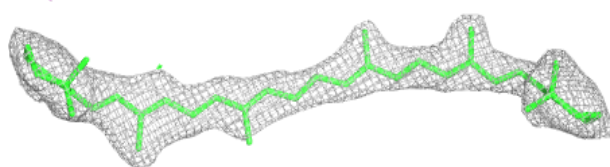
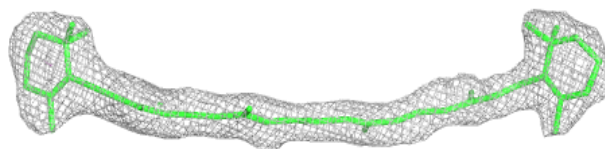
**Electron density around DGD c 516:**

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

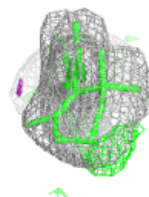
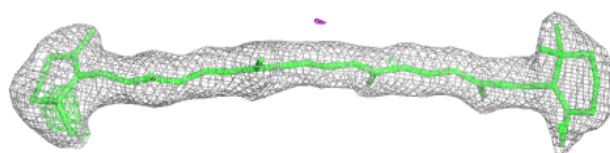
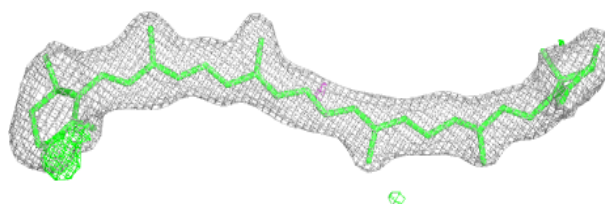


Electron density around BCR k 103:

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

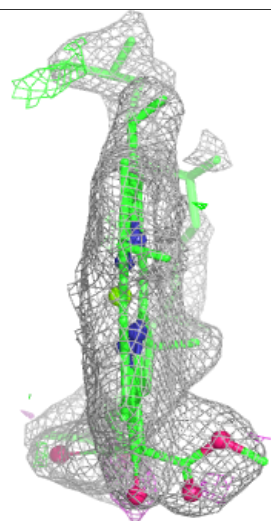
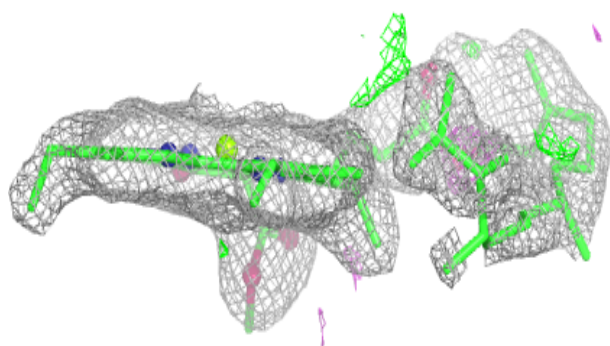
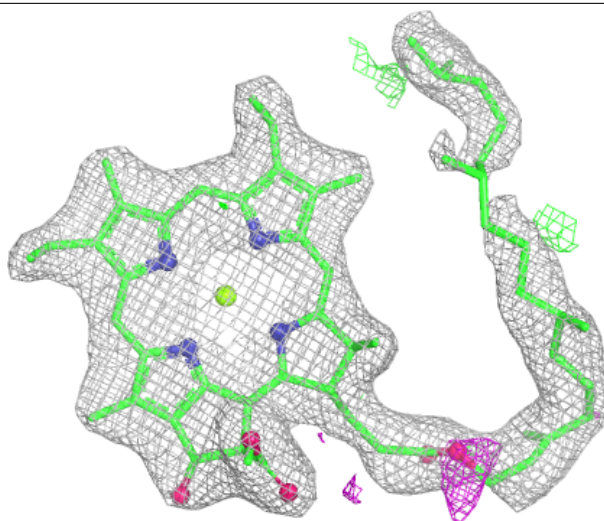
**Electron density around BCR K 102:**

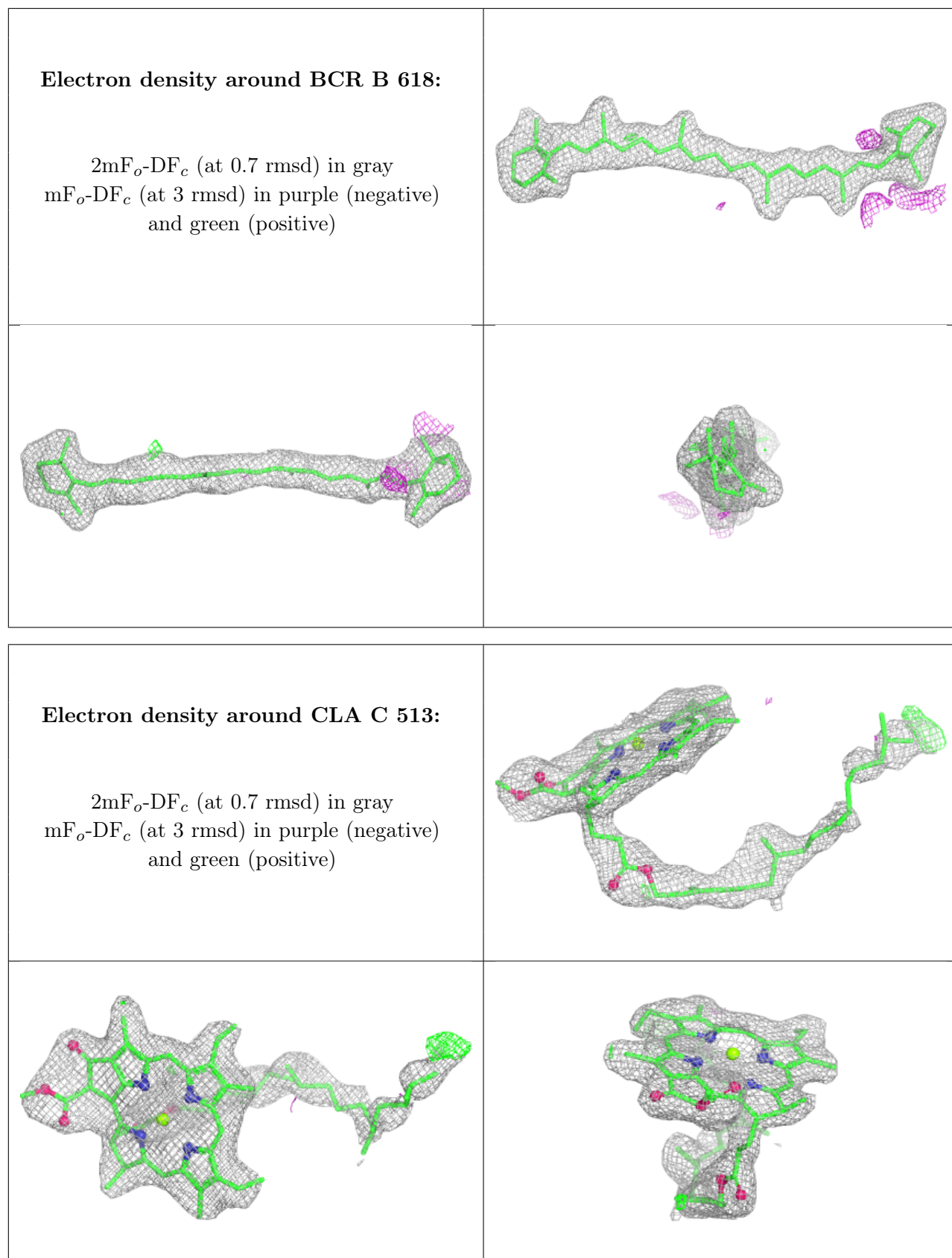
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CLA c 512:

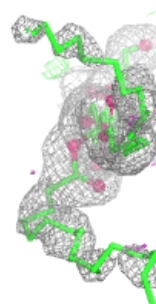
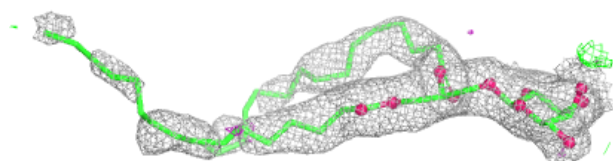
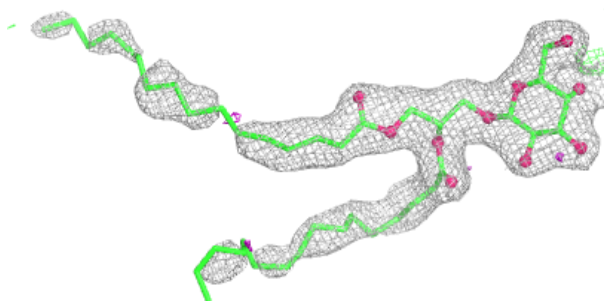
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



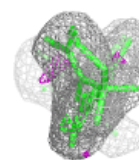
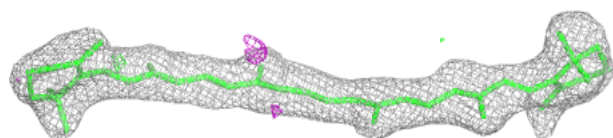
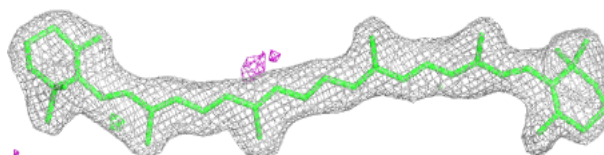


Electron density around LMG D 407:

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

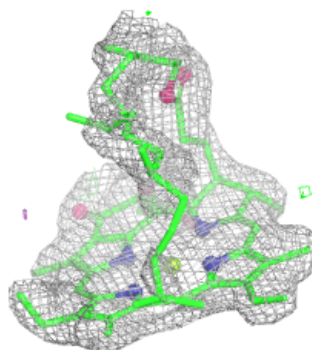
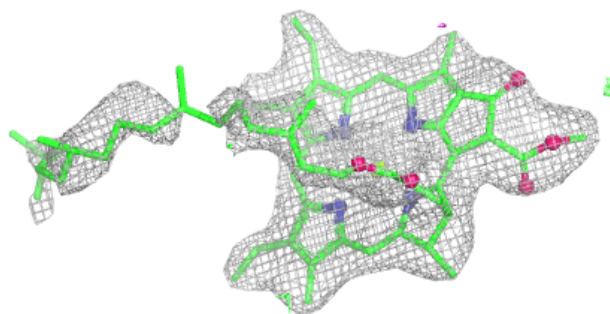
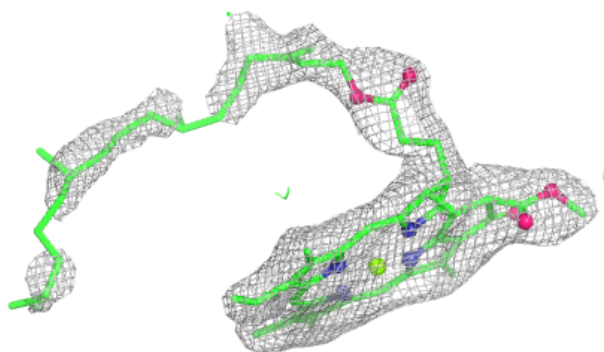
**Electron density around BCR b 619:**

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

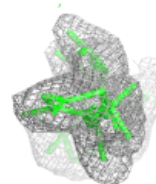
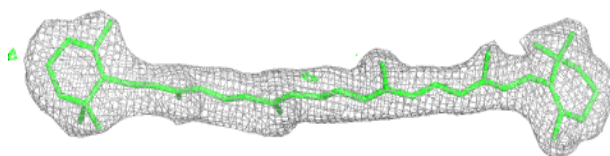
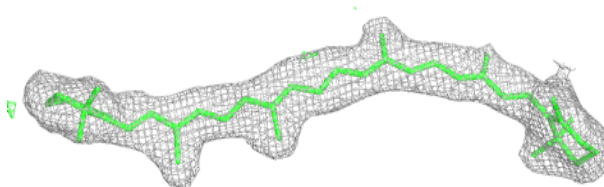


Electron density around CLA c 513:

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

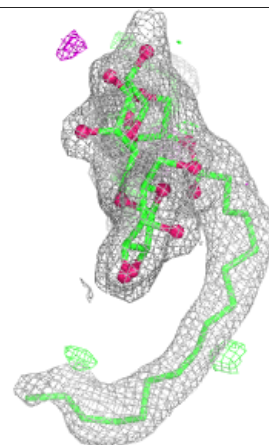
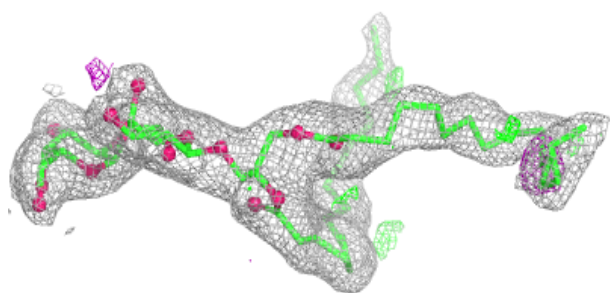
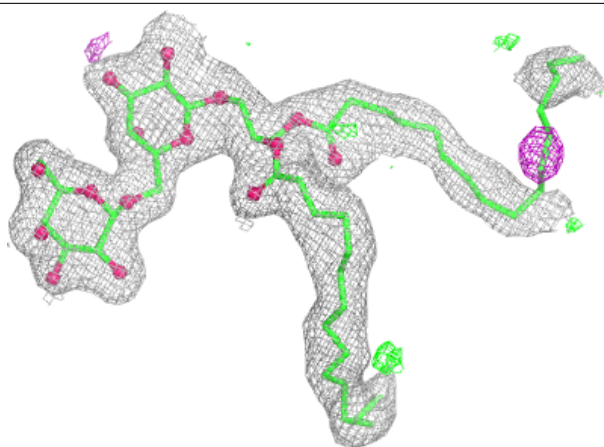
**Electron density around BCR H 101:**

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

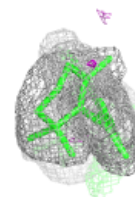
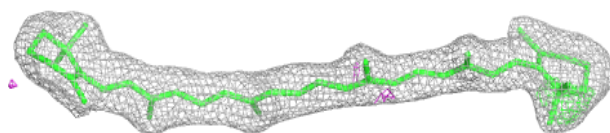
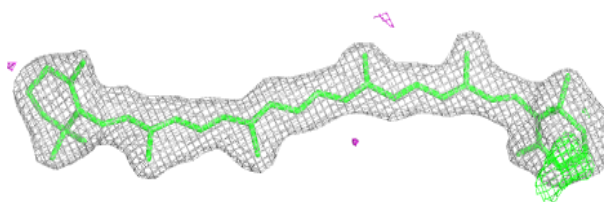


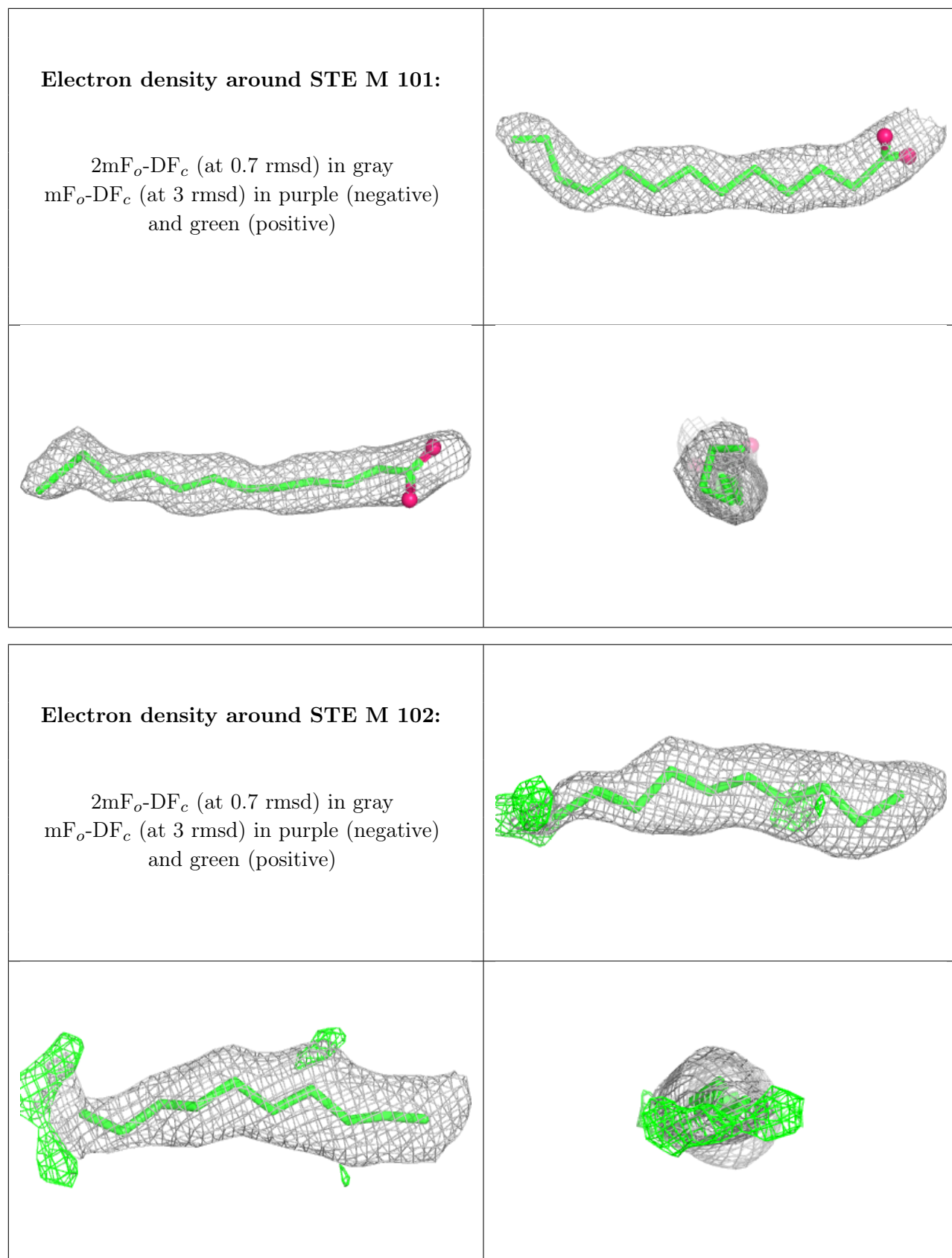
Electron density around DGD C 516:

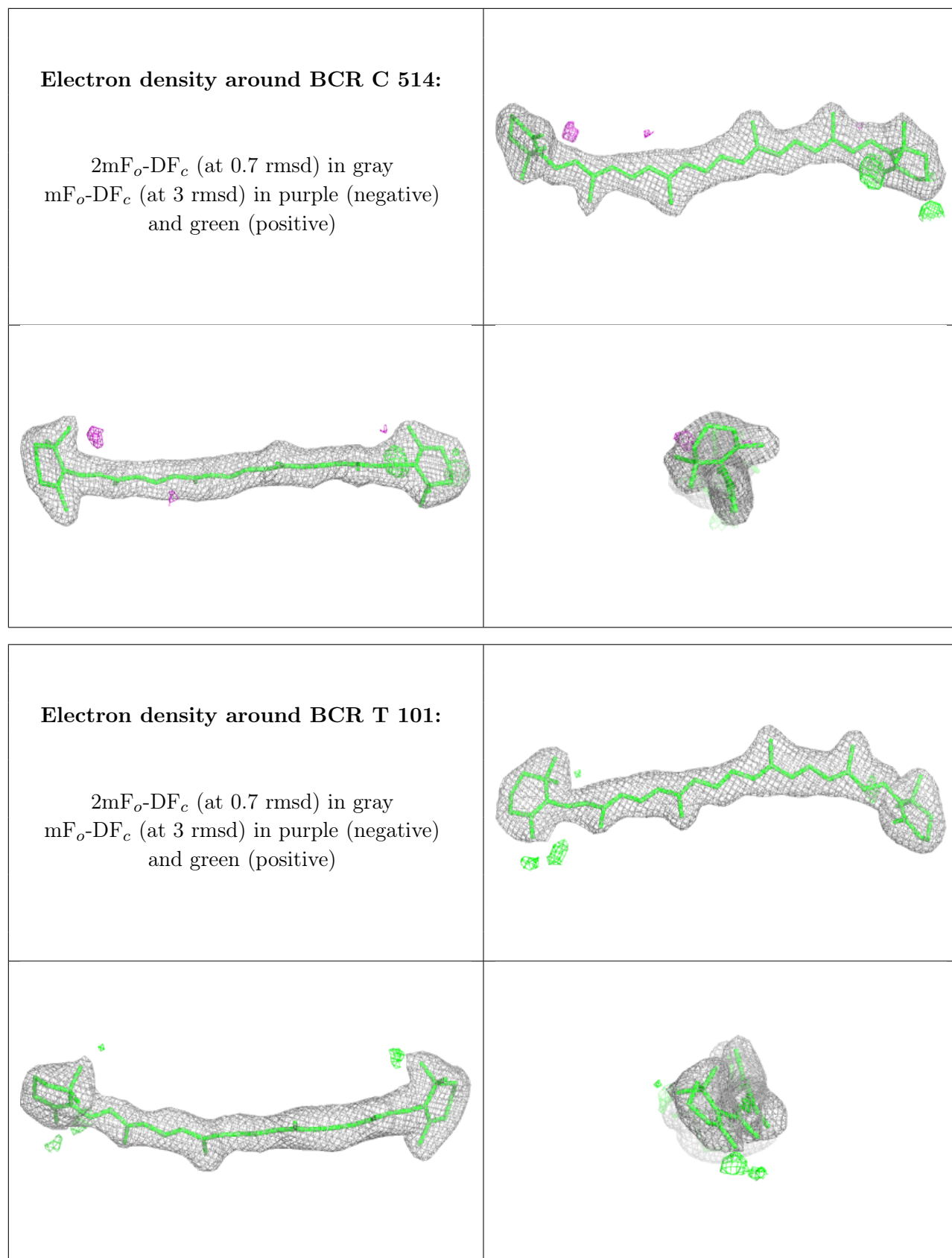
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

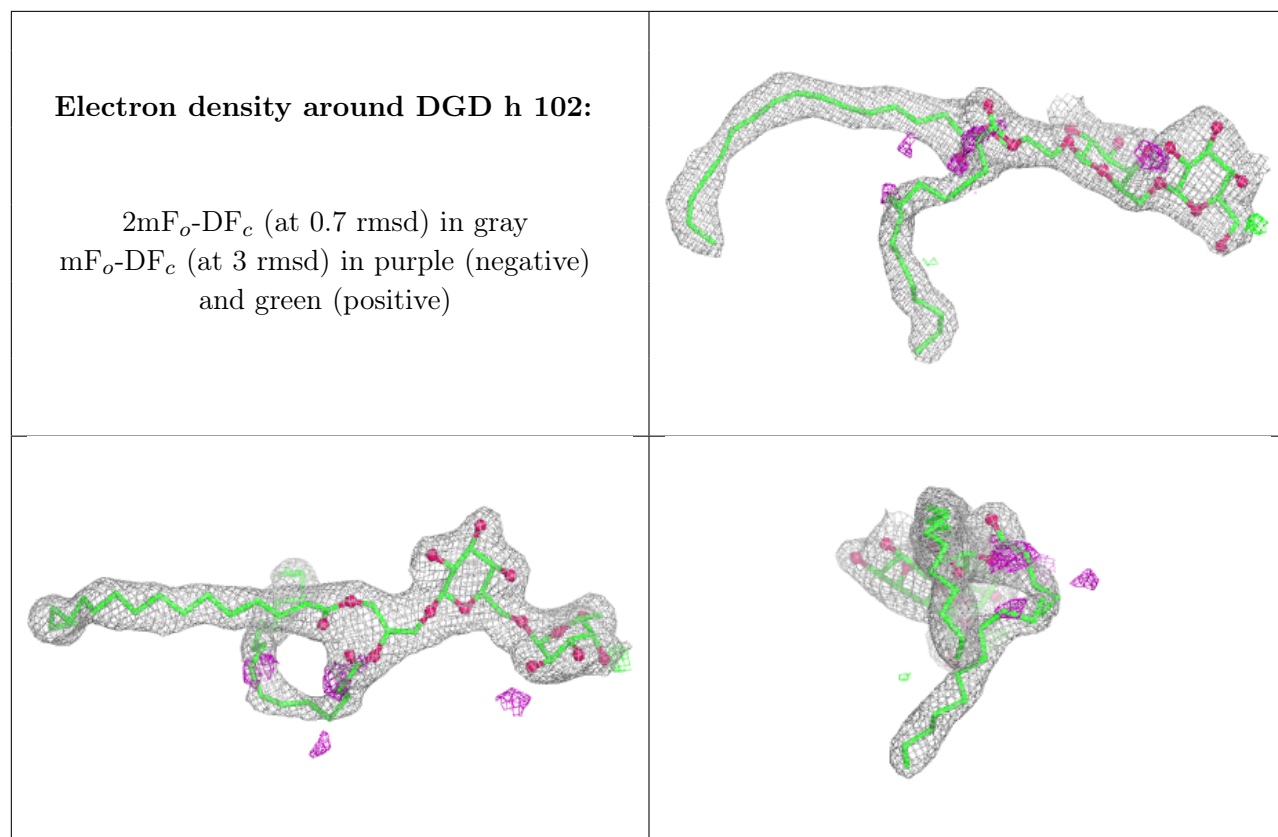
**Electron density around BCR B 619:**

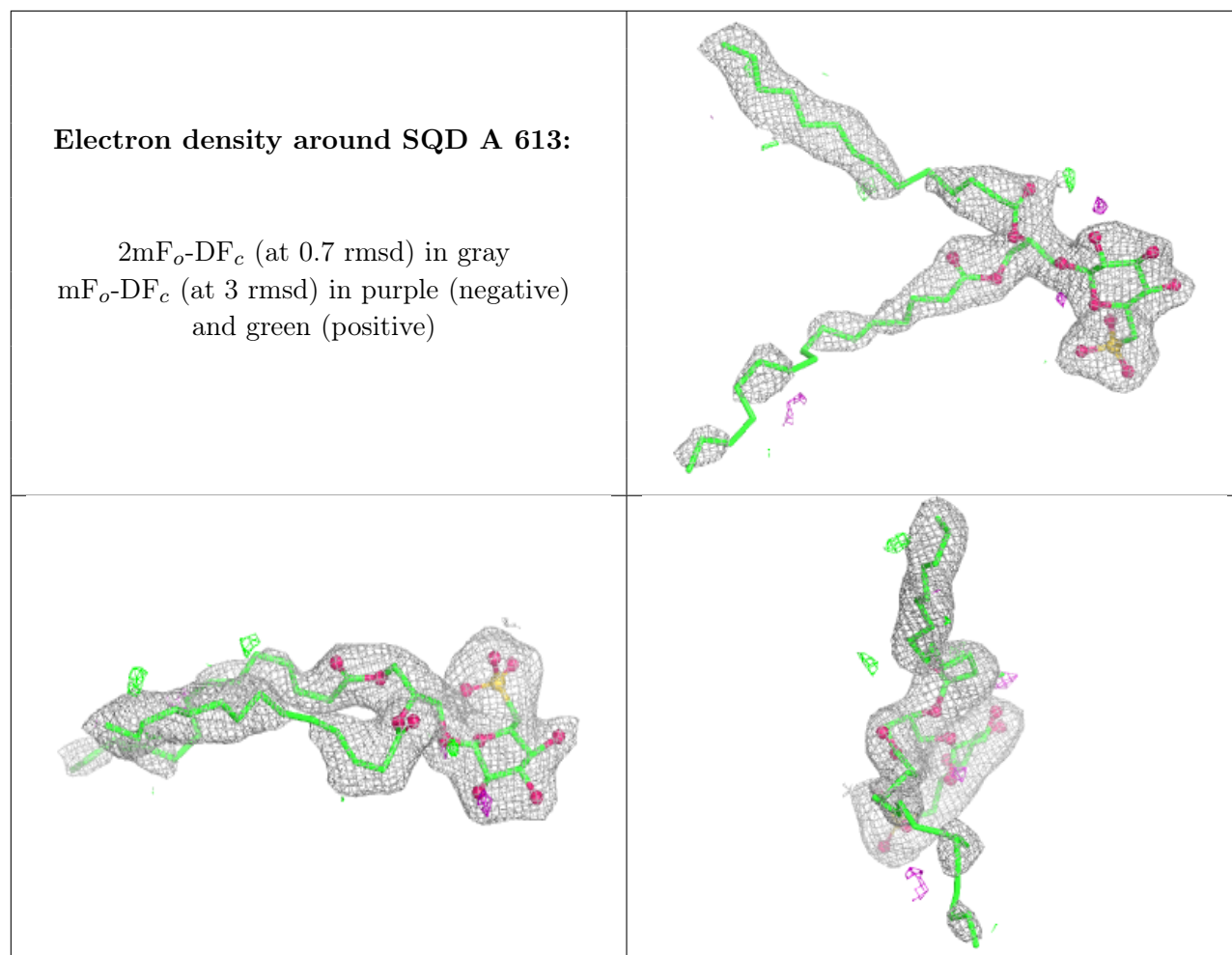
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





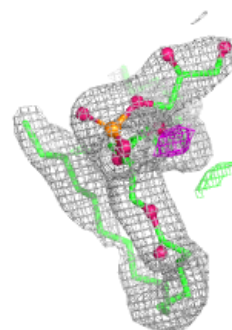
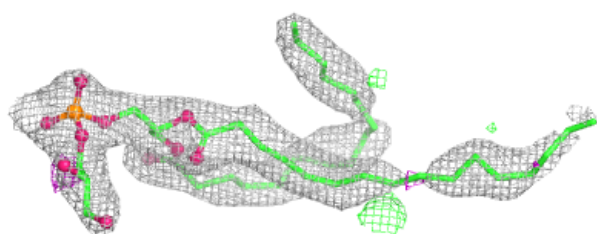
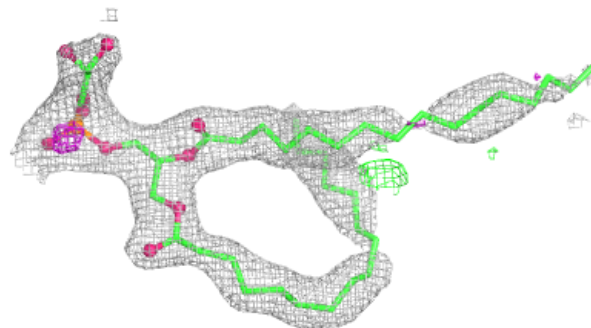




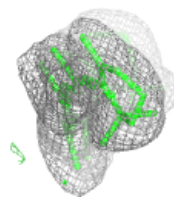
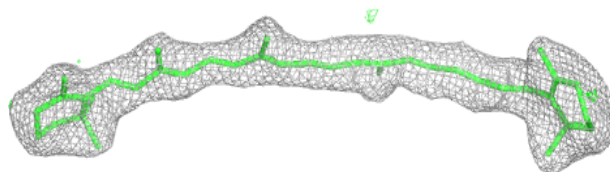
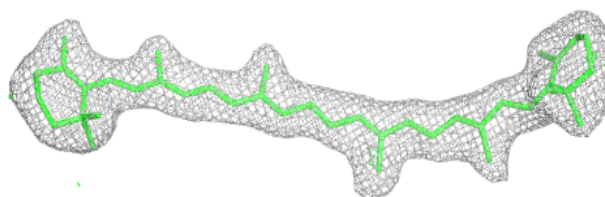


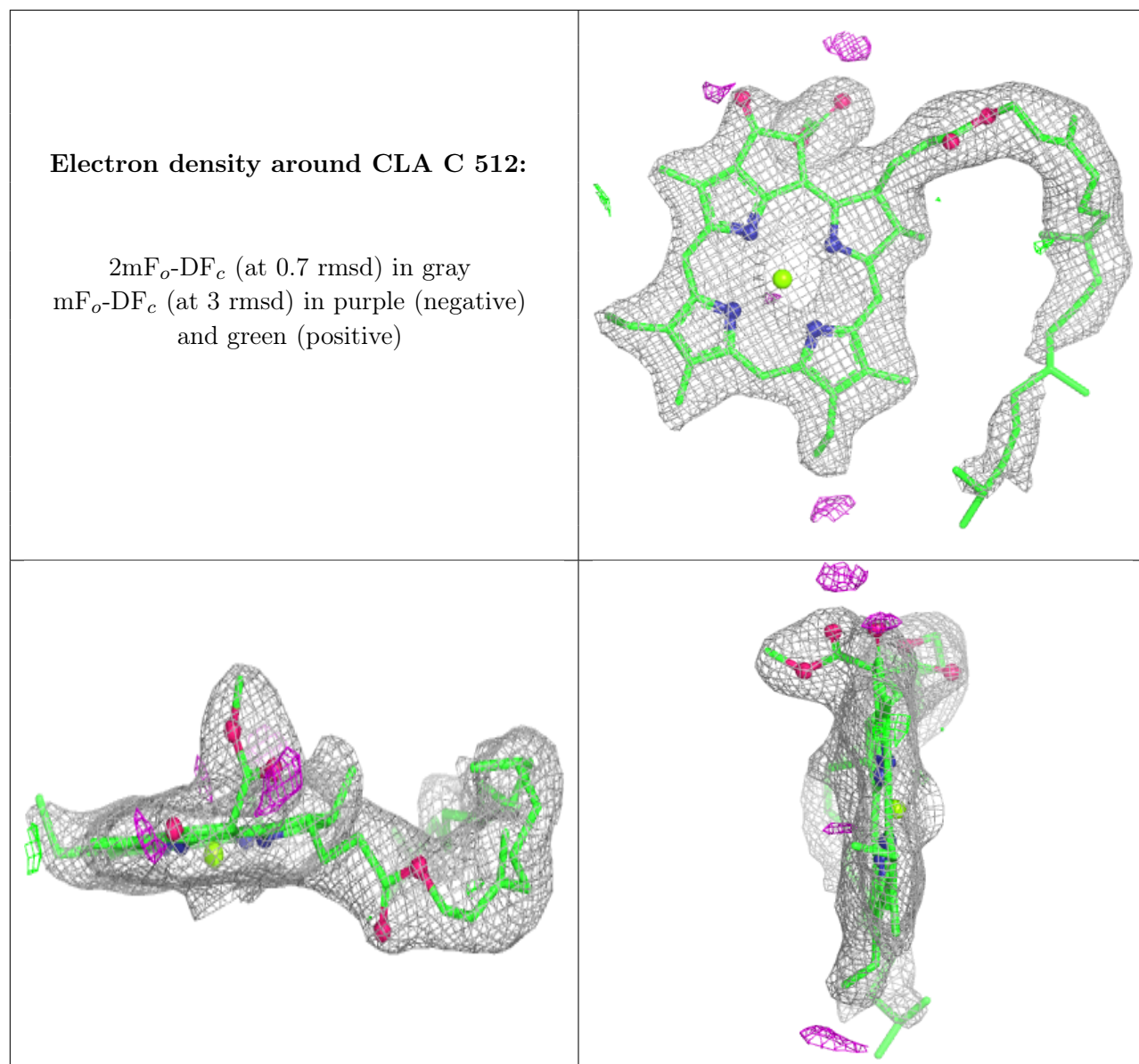
Electron density around LHG d 407:

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

**Electron density around BCR t 101:**

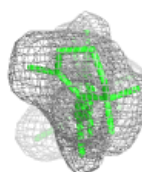
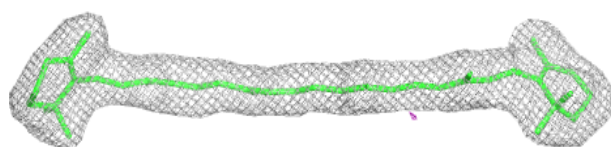
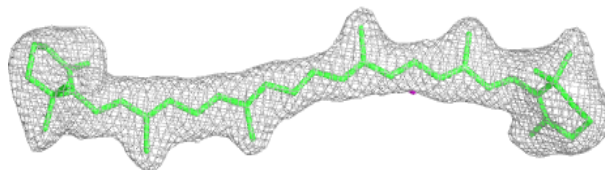
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



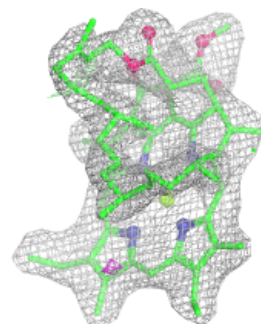
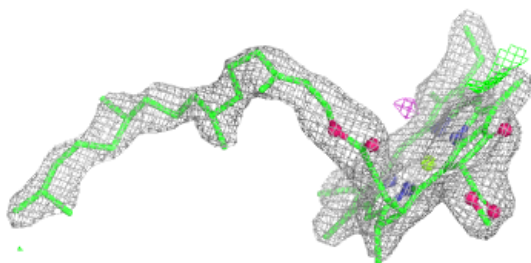
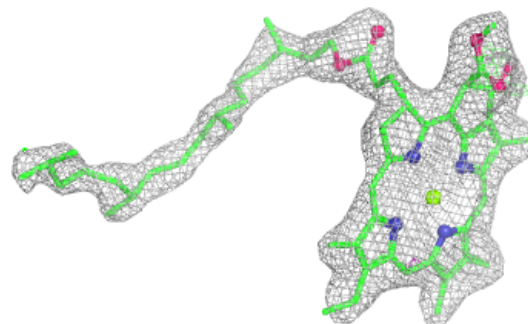


Electron density around BCR b 618:

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

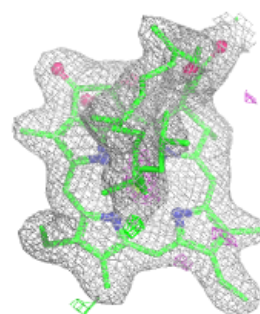
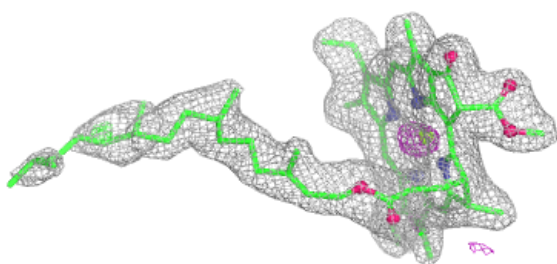
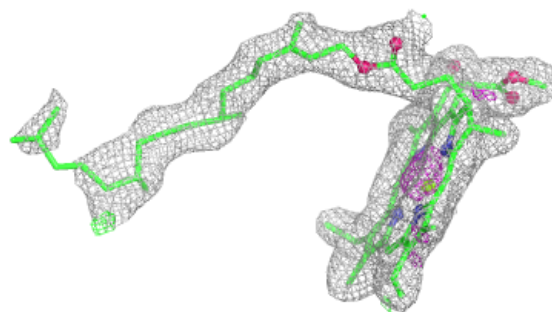
**Electron density around CLA c 511:**

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

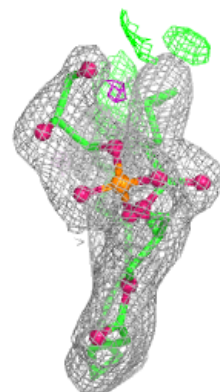
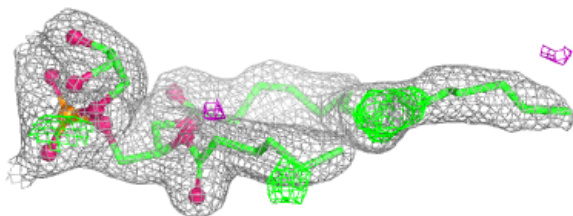
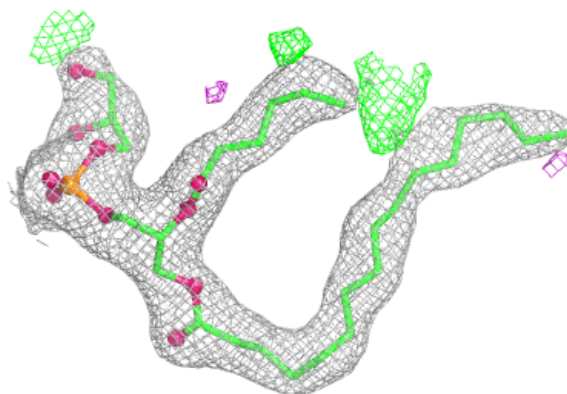


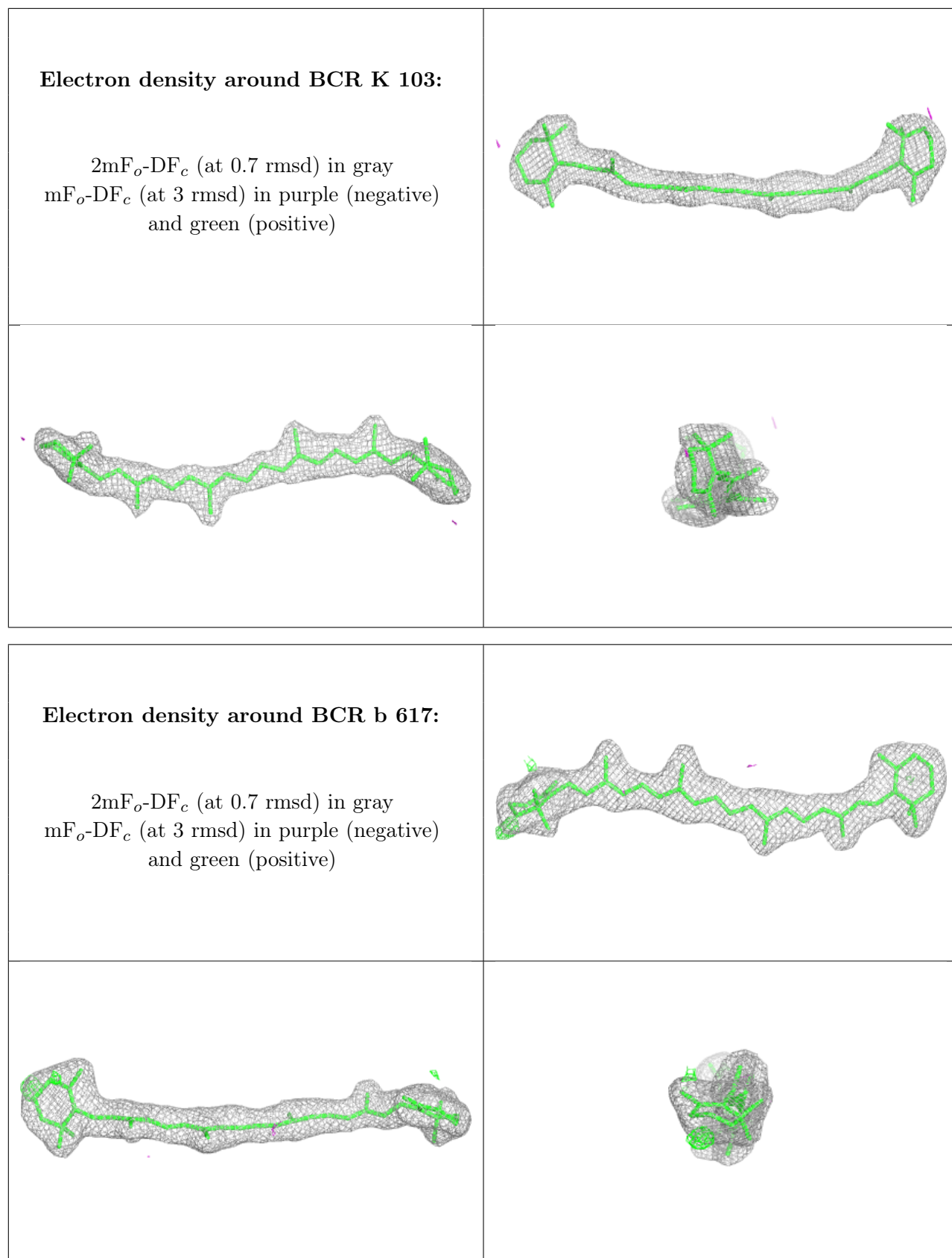
Electron density around CLA C 508:

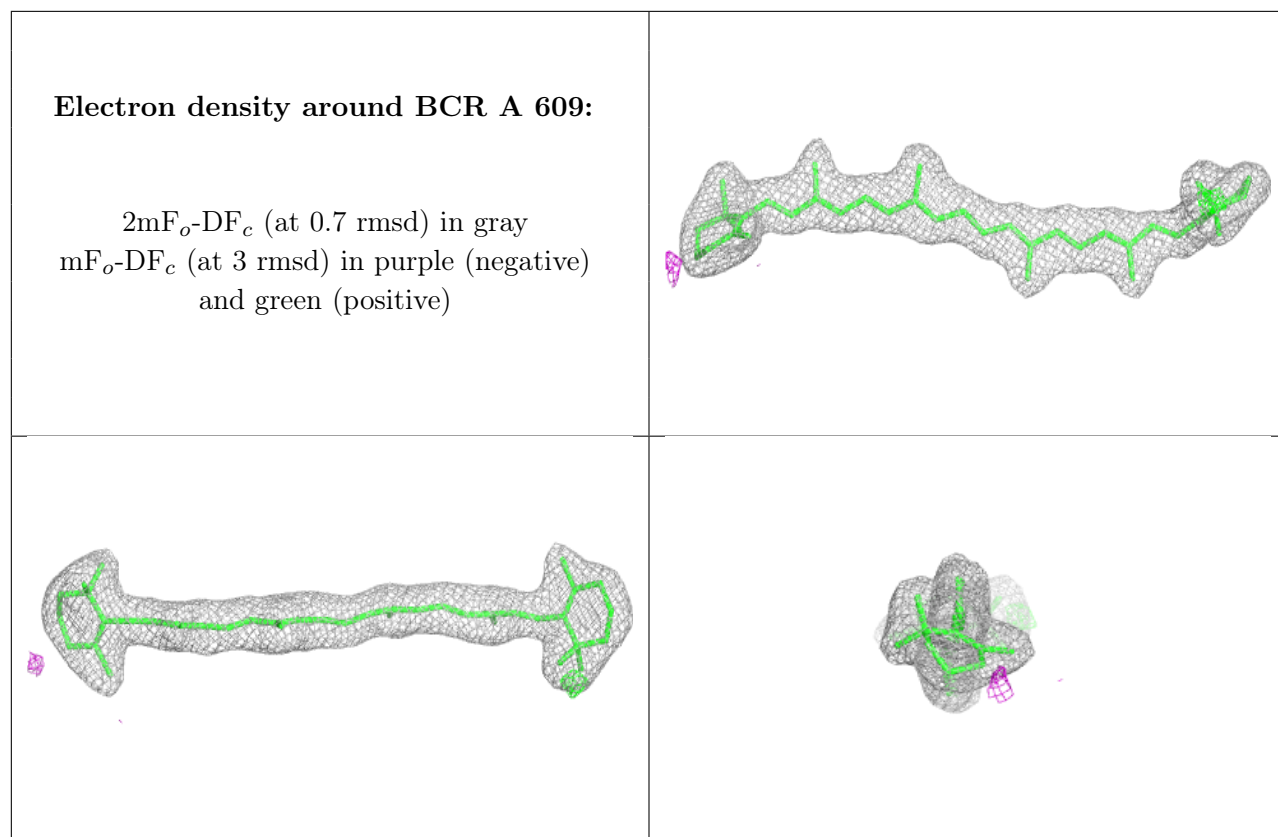
$2mF_o-DF_c$ (at 0.7 rnsd) in gray
 mF_o-DF_c (at 3 rnsd) in purple (negative)
and green (positive)

**Electron density around LHG d 409:**

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

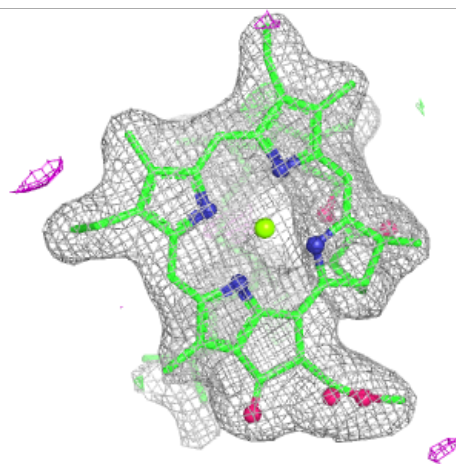
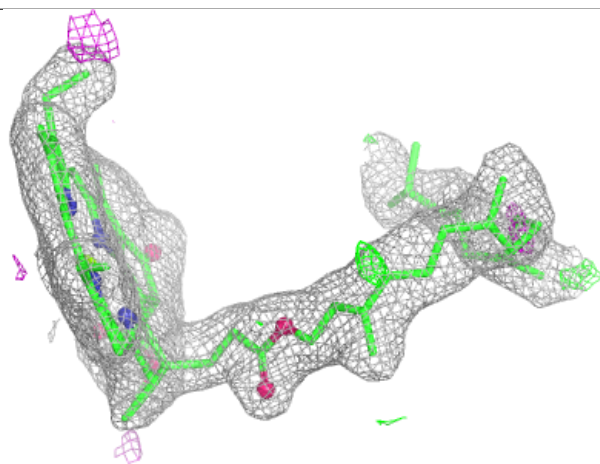
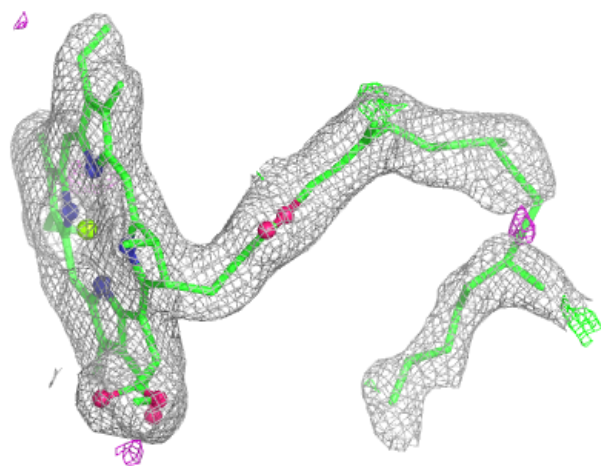






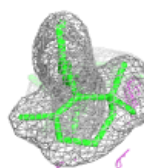
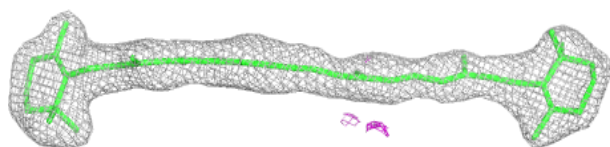
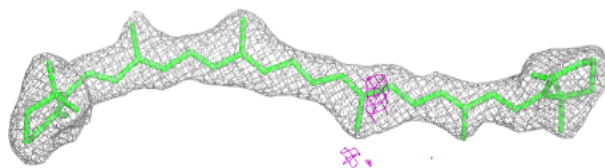
Electron density around CLA B 606:

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

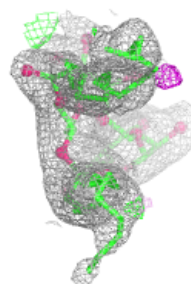
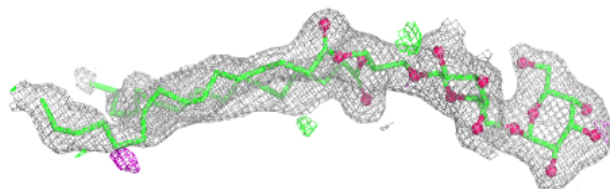
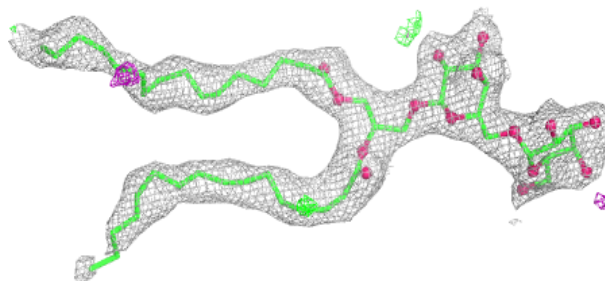


Electron density around BCR c 514:

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

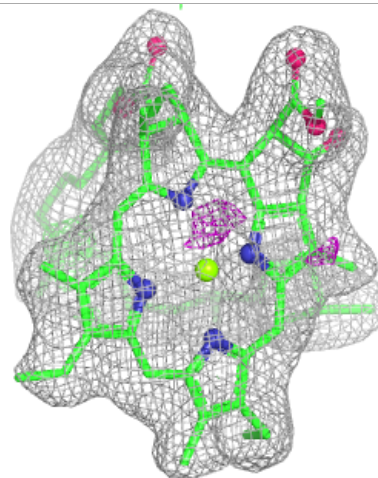
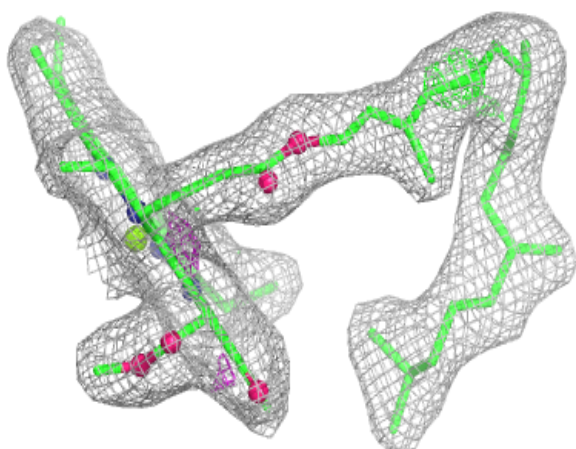
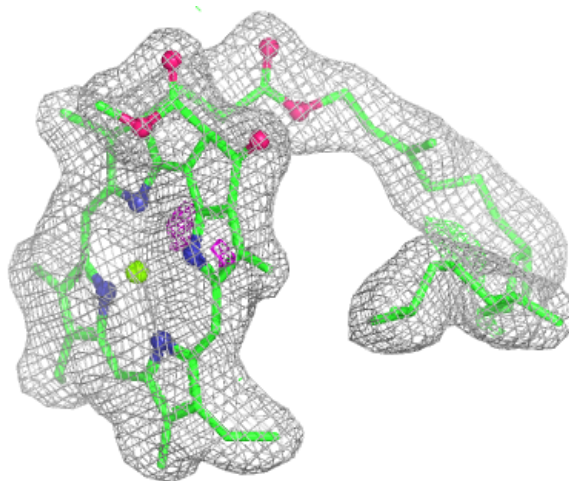
**Electron density around DGD c 517:**

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



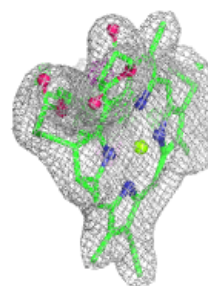
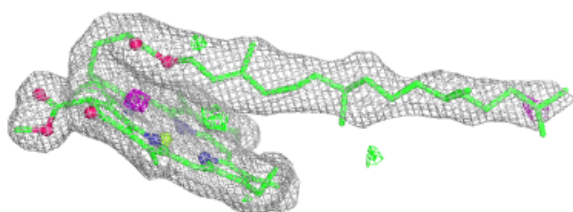
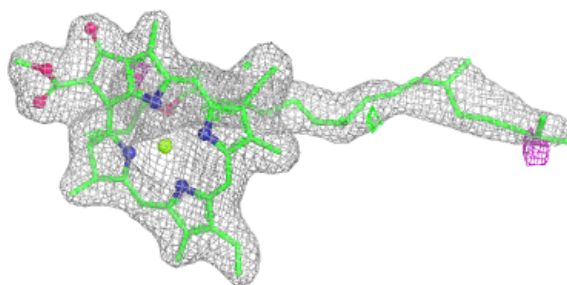
Electron density around CLA C 503:

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



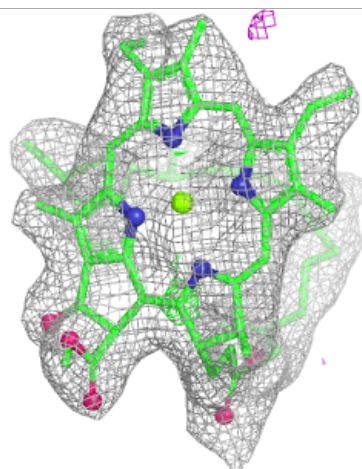
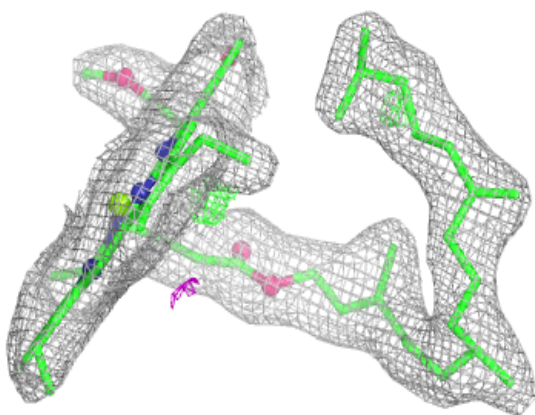
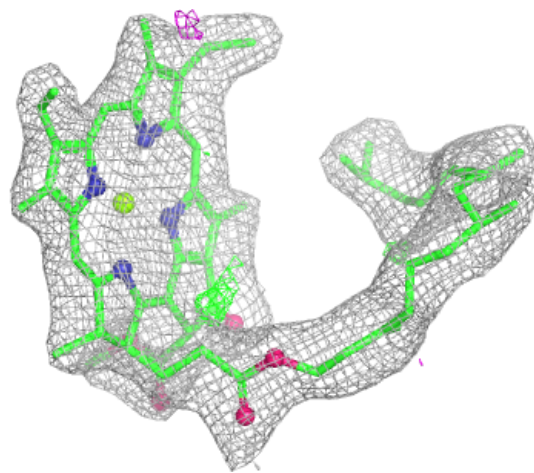
Electron density around CLA b 614:

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



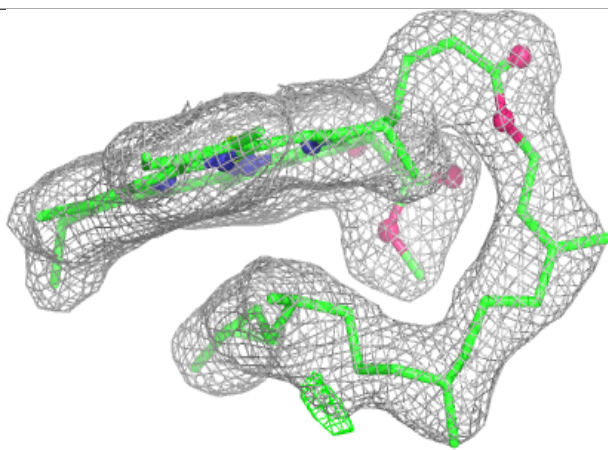
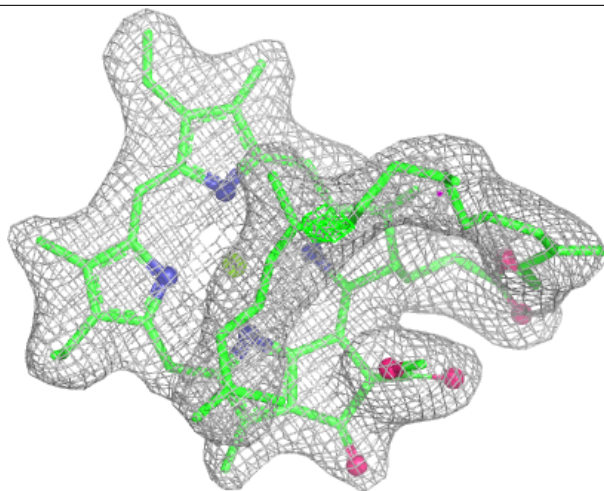
Electron density around CLA c 503:

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



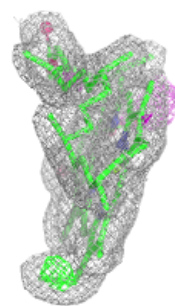
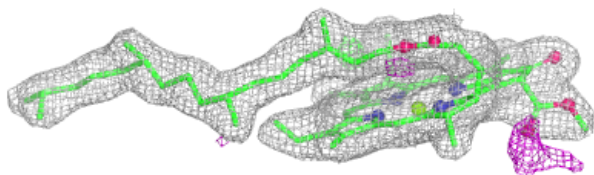
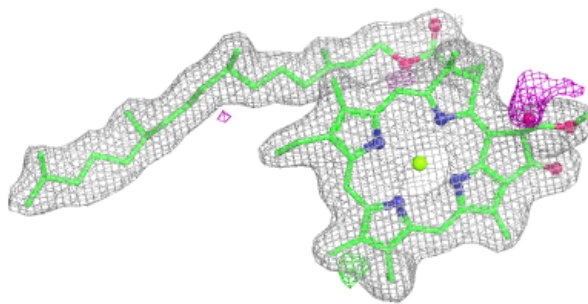
Electron density around CLA c 510:

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

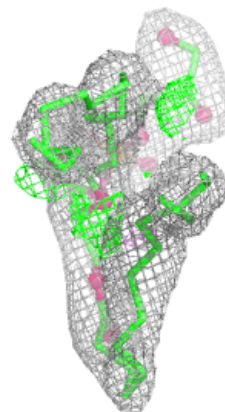
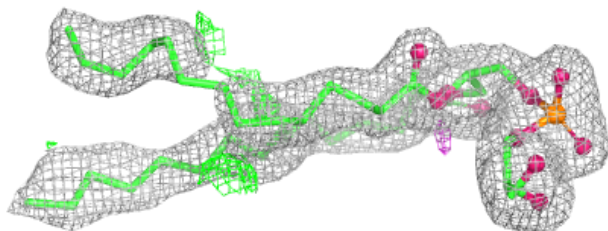
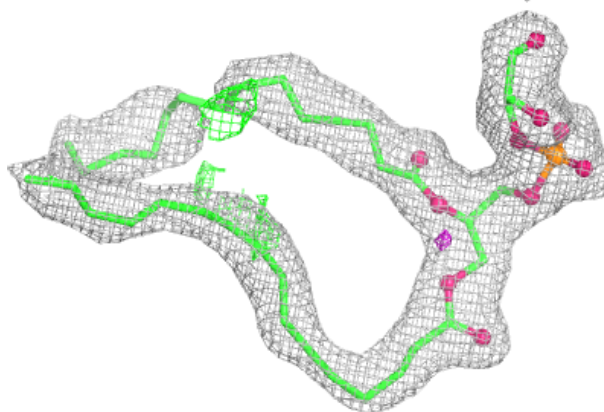


Electron density around CLA C 501:

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

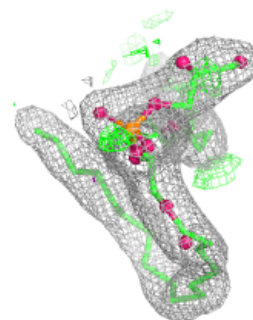
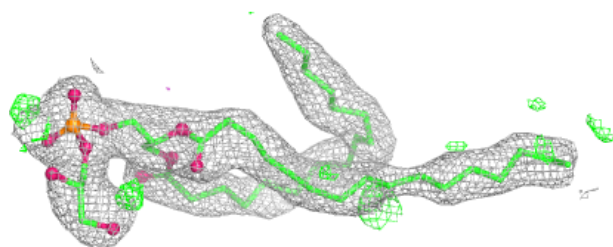
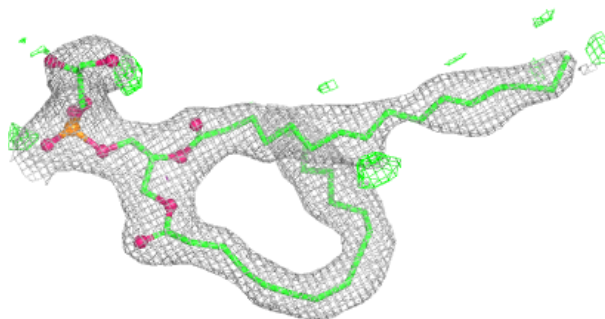
**Electron density around LHG D 410:**

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

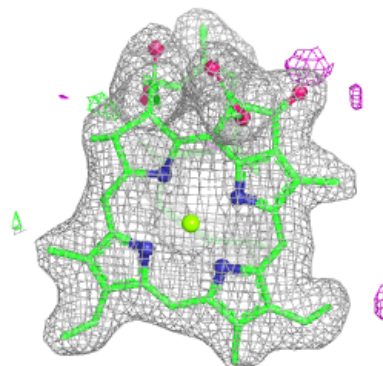
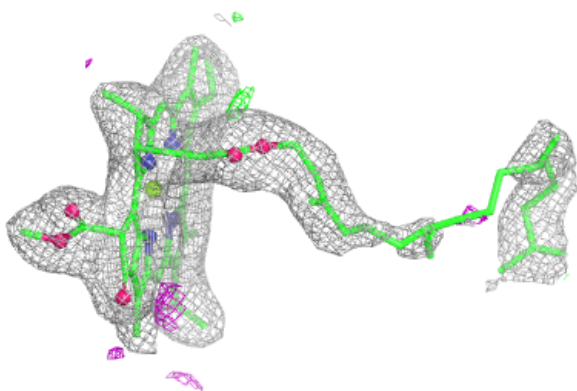
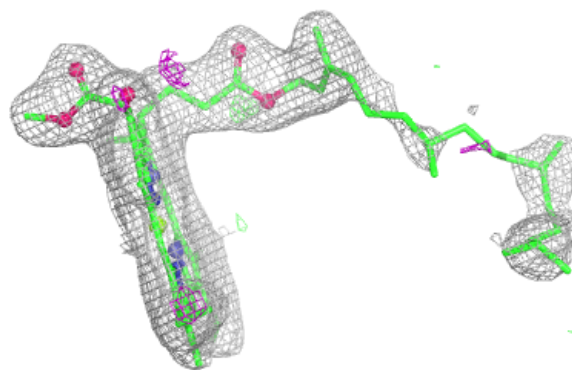


Electron density around LHG D 412:

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

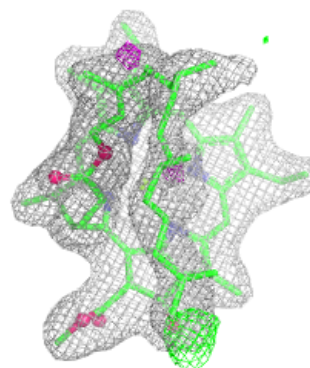
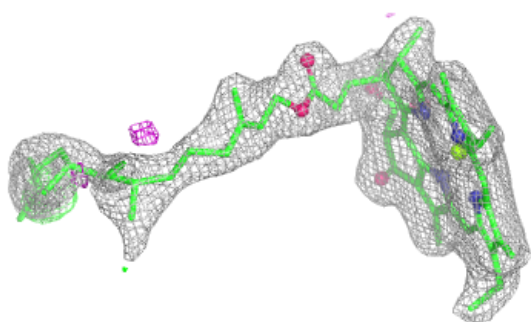
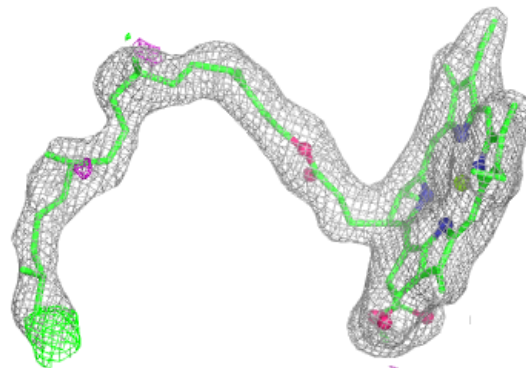
**Electron density around CLA C 506:**

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



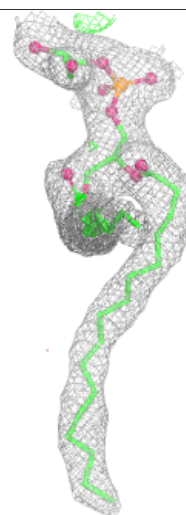
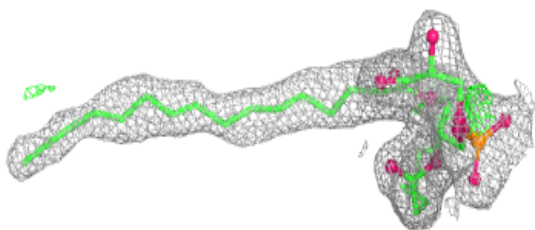
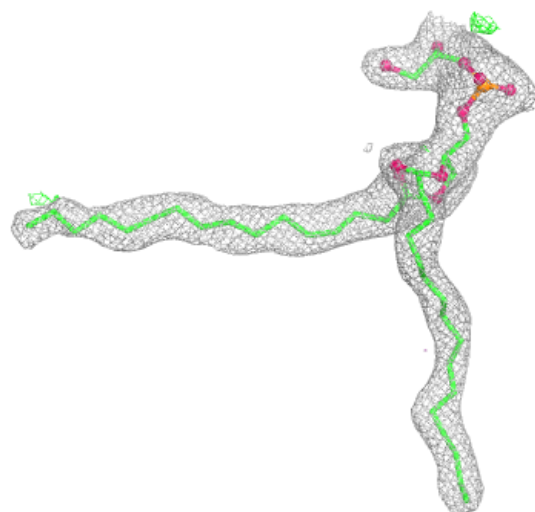
Electron density around CLA b 606:

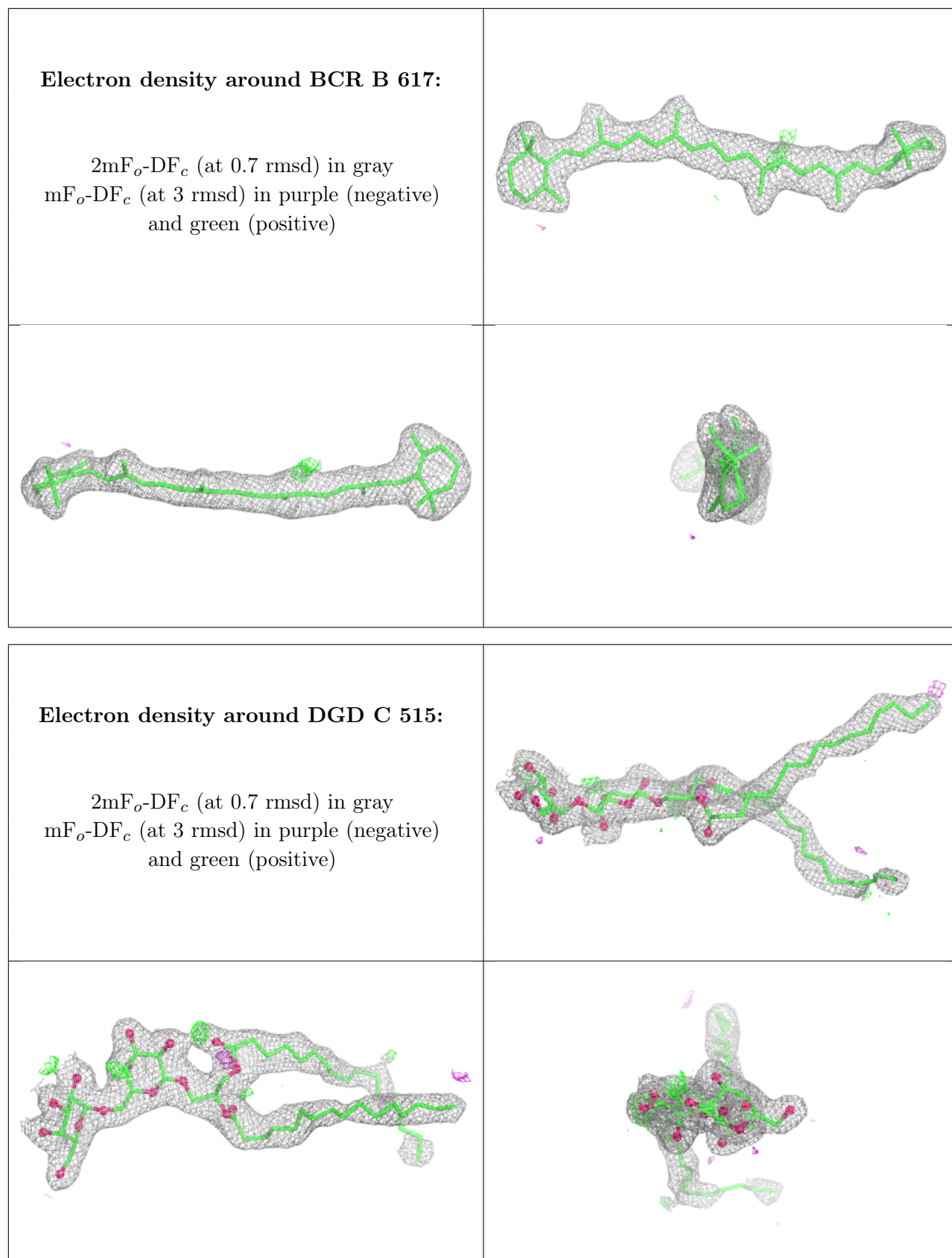
$2mF_o-DF_c$ (at 0.7 rnsd) in gray
 mF_o-DF_c (at 3 rnsd) in purple (negative)
and green (positive)



Electron density around LHG 1 101:

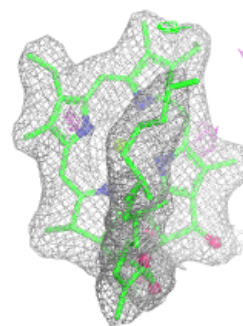
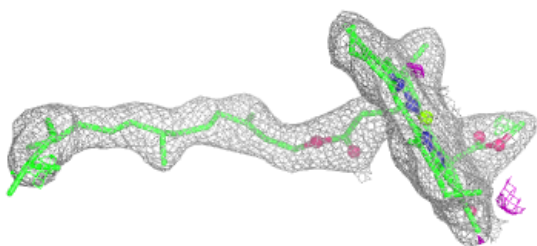
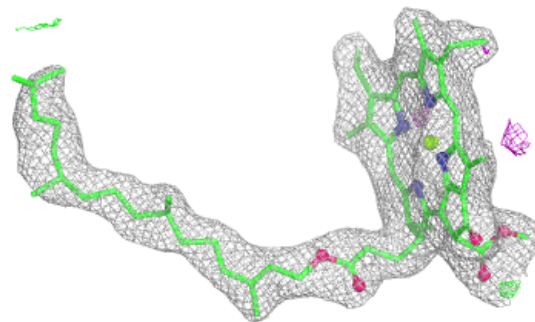
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





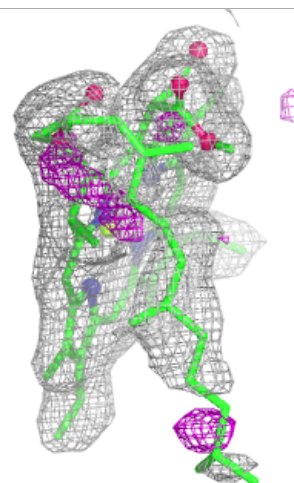
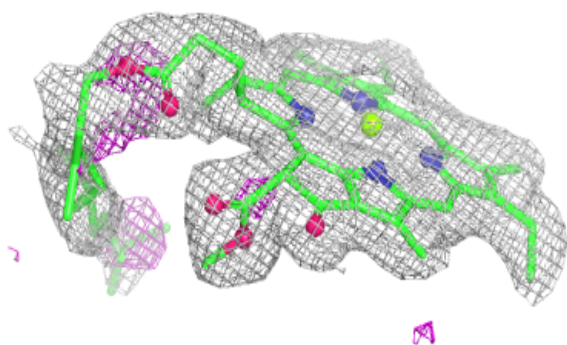
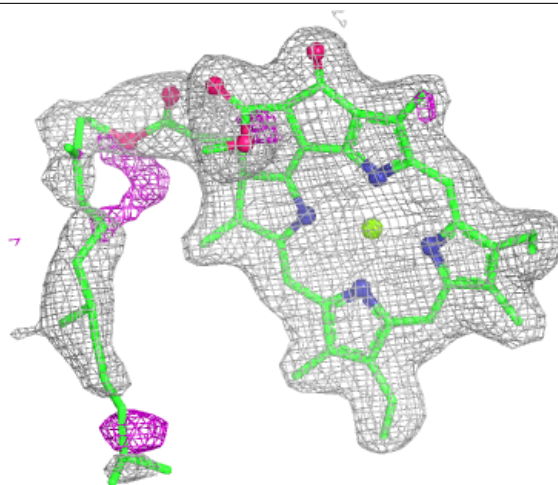
Electron density around CLA b 609:

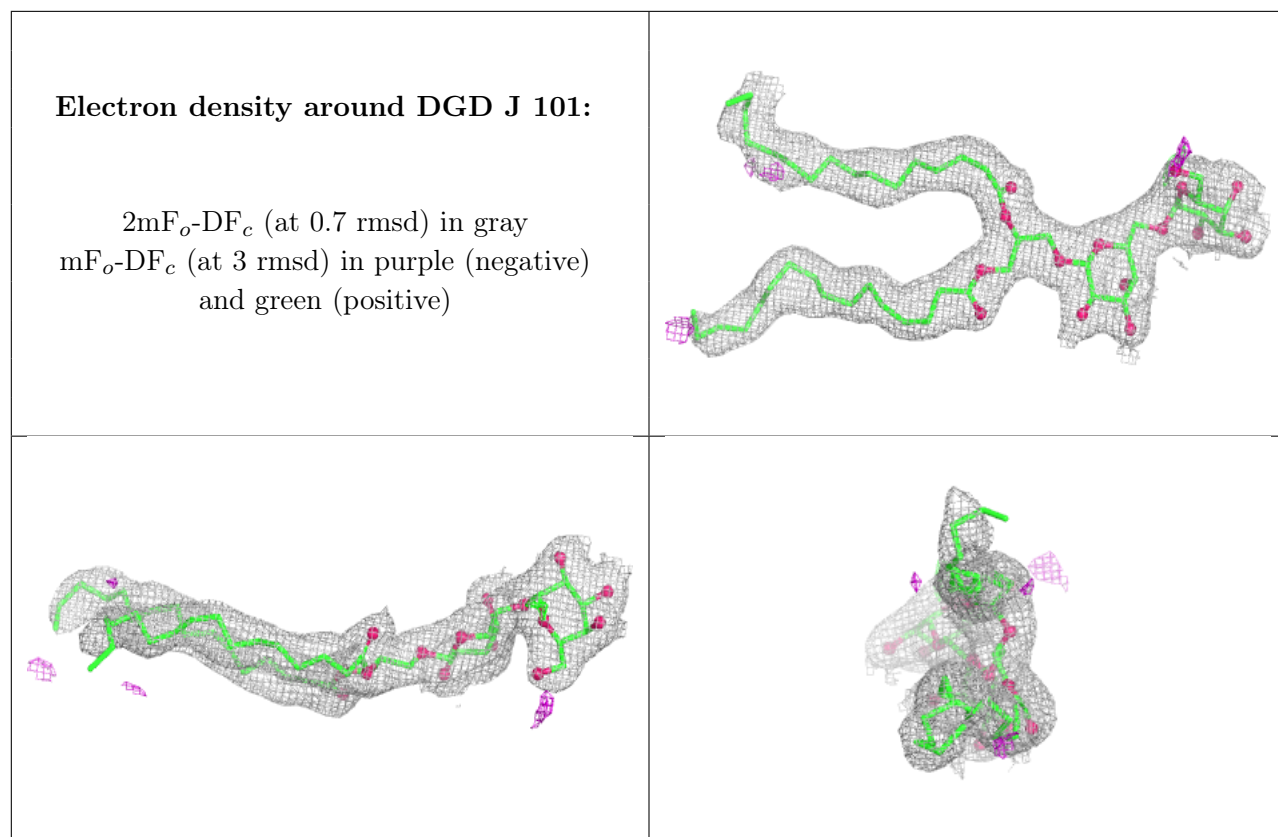
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CLA B 616:

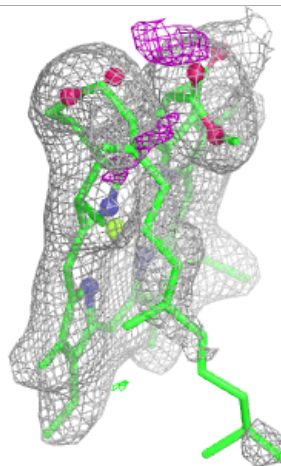
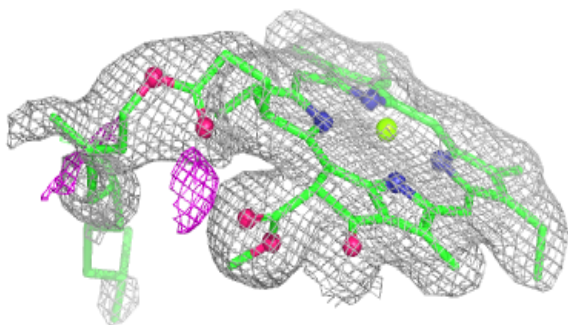
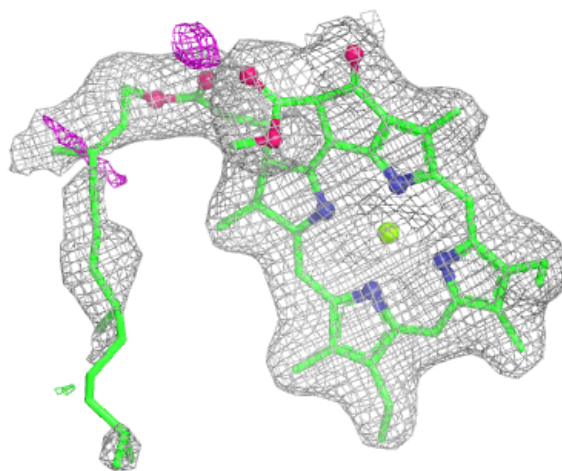
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





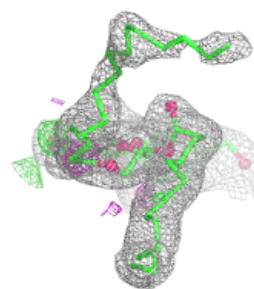
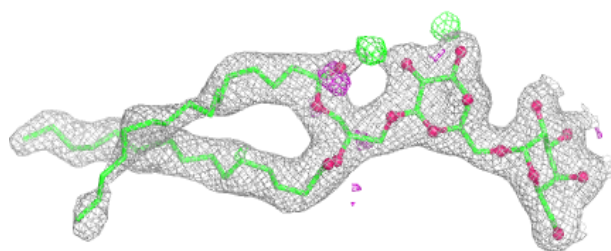
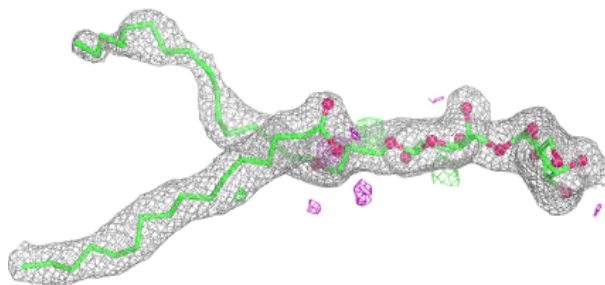
Electron density around CLA b 616:

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

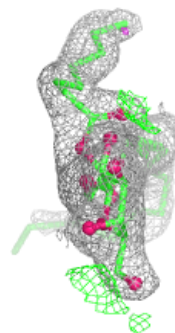
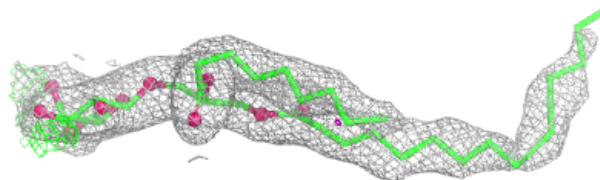
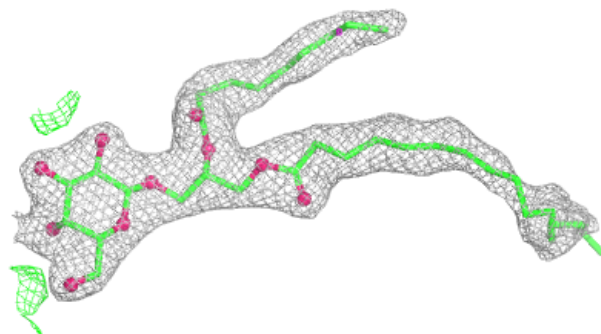


Electron density around DGD c 515:

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

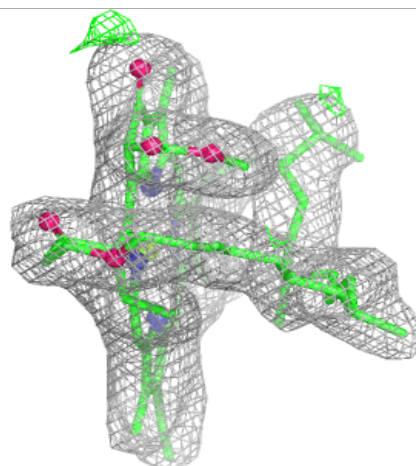
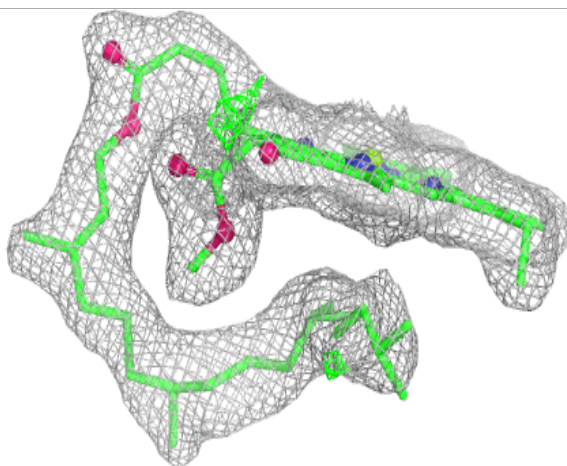
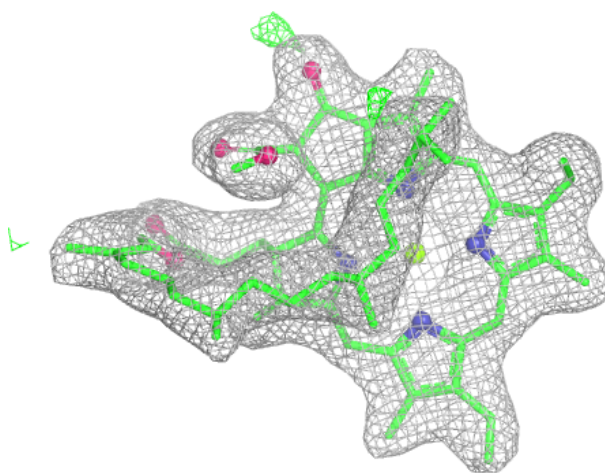
**Electron density around LMG d 411:**

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



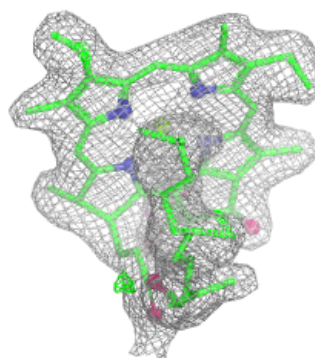
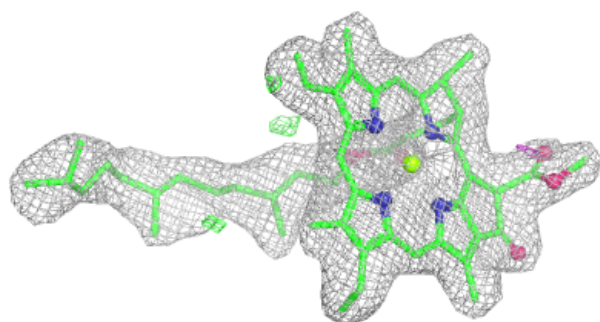
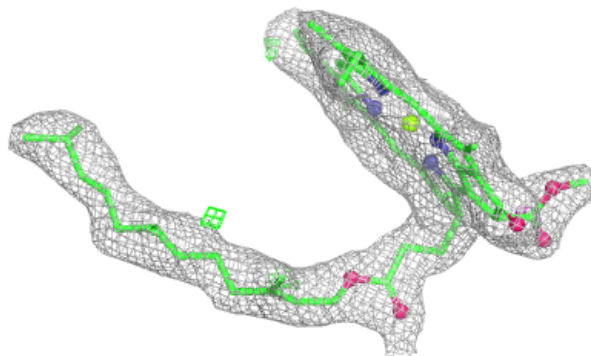
Electron density around CLA C 510:

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

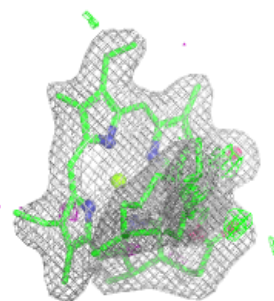
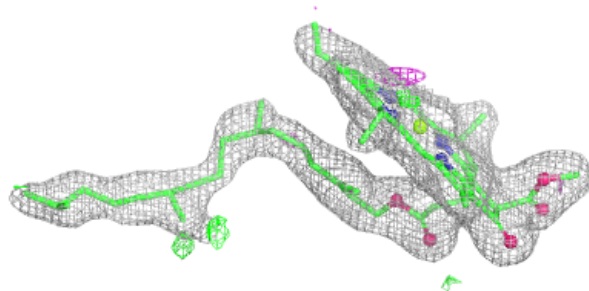
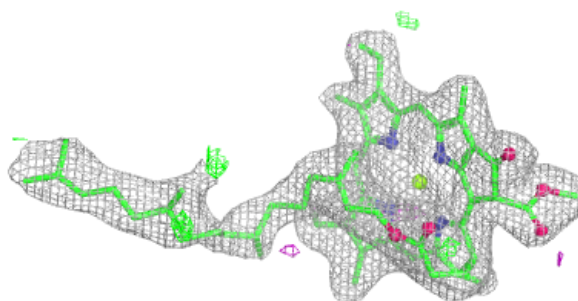


Electron density around CLA c 504:

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

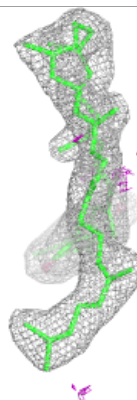
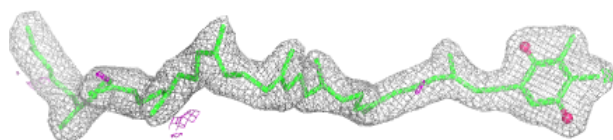
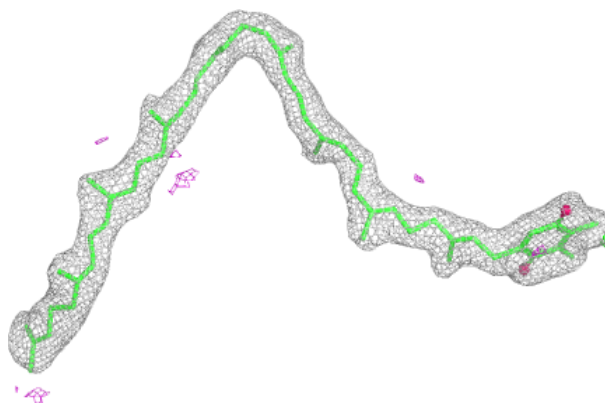
**Electron density around CLA c 505:**

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

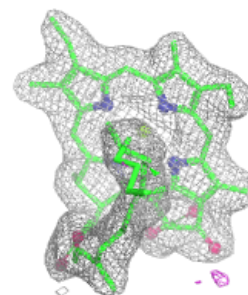
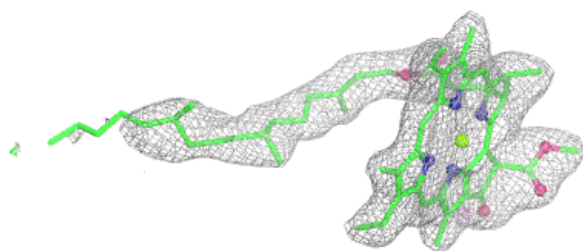
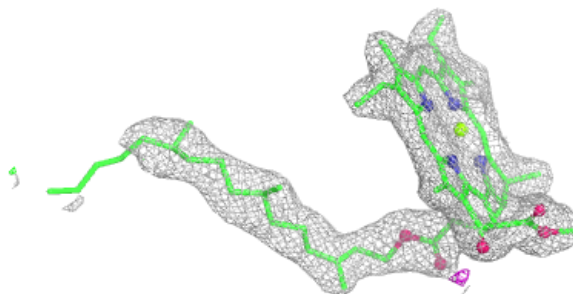


Electron density around PL9 D 406:

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

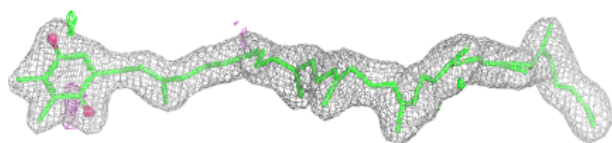
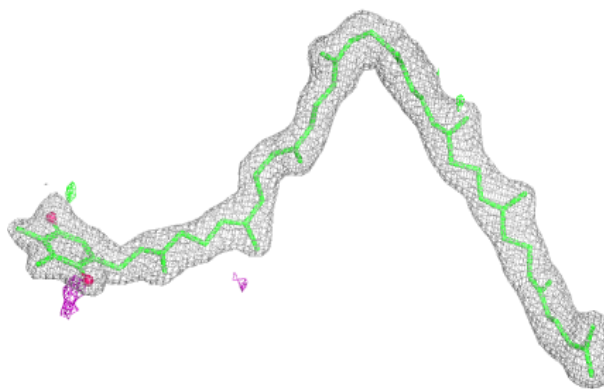
**Electron density around CLA c 508:**

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

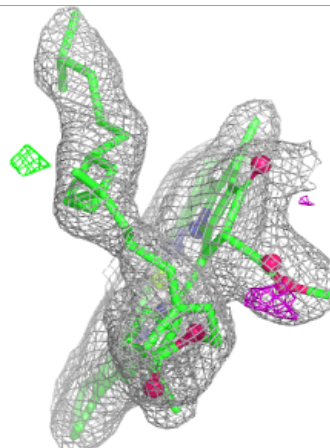
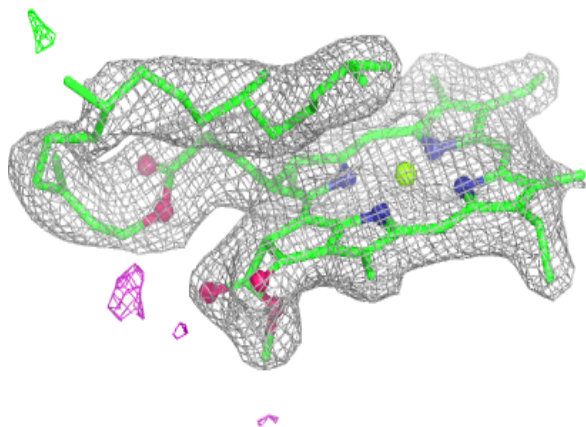
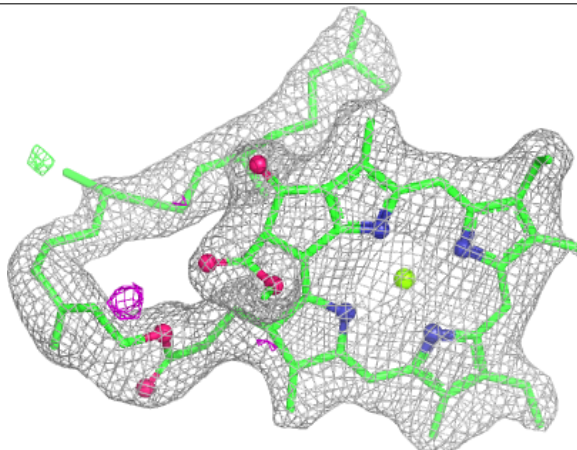


Electron density around PL9 d 406:

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

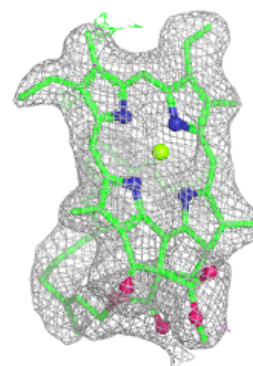
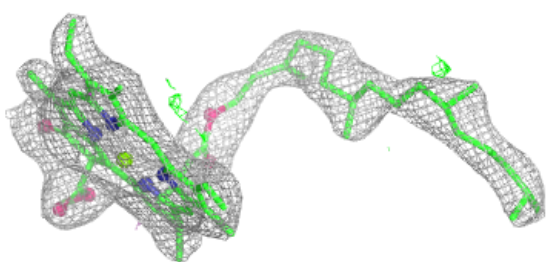
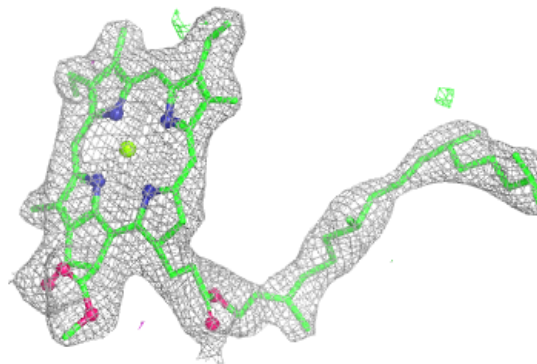
**Electron density around CLA c 509:**

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

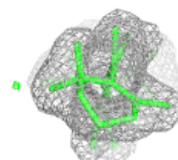
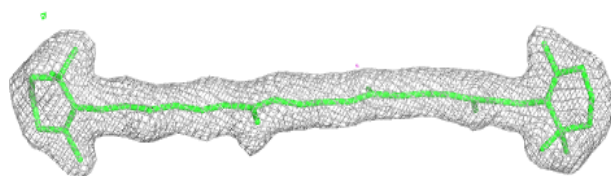
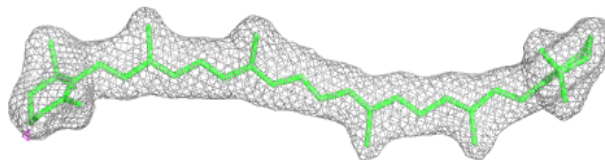


Electron density around CLA C 511:

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

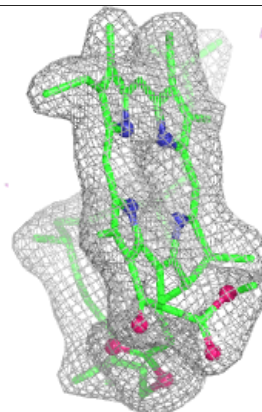
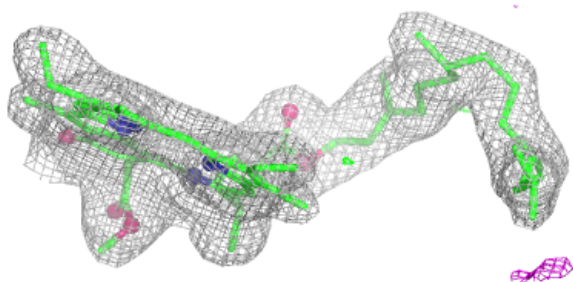
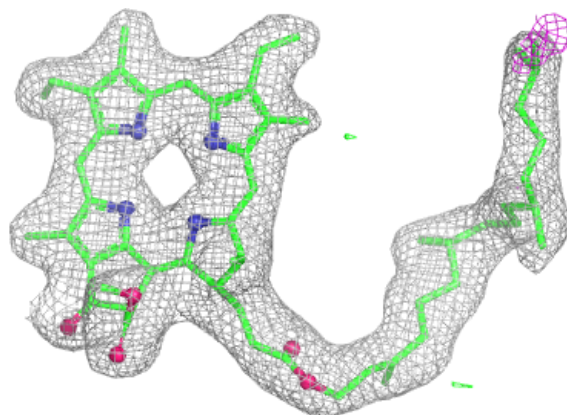
**Electron density around BCR a 609:**

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

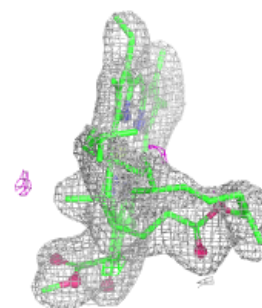
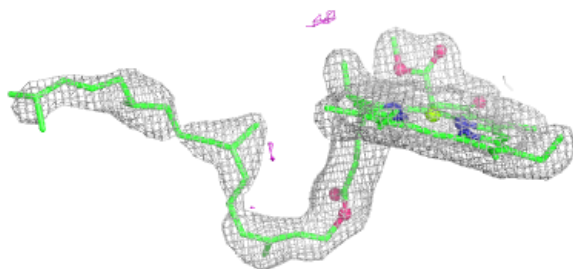
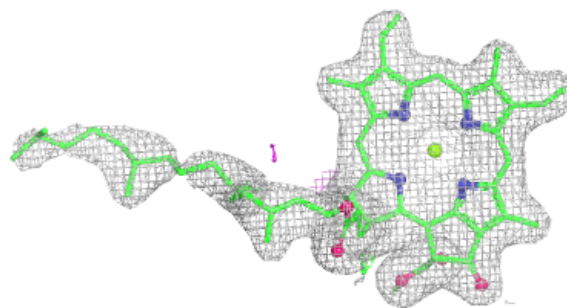


Electron density around PHO d 402:

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

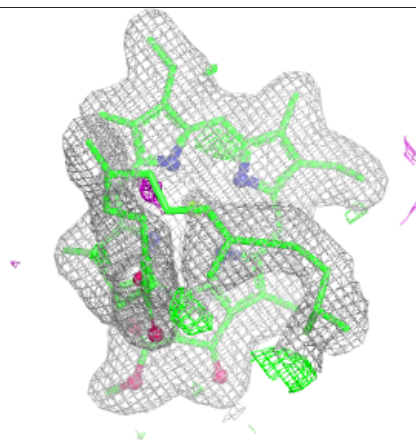
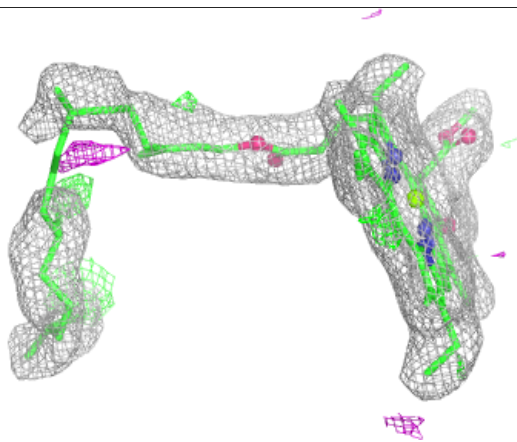
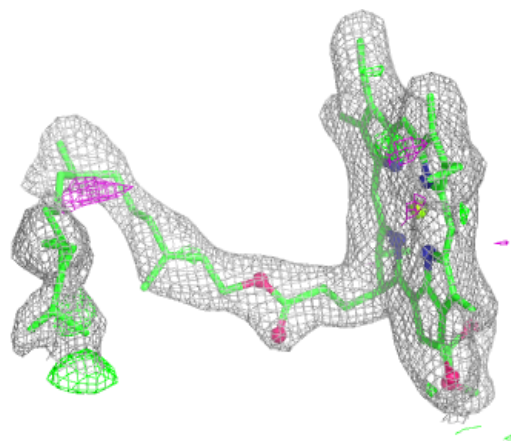
**Electron density around CLA a 606:**

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



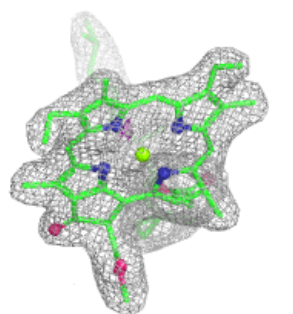
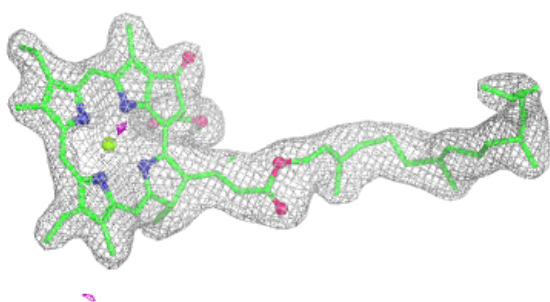
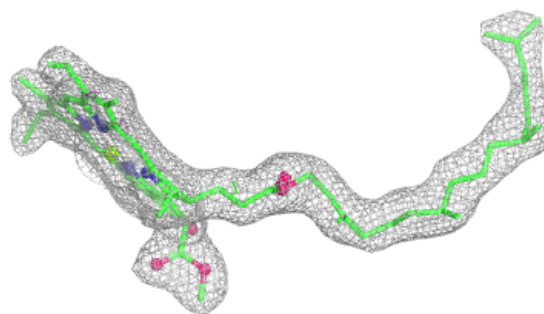
Electron density around CLA a 608:

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

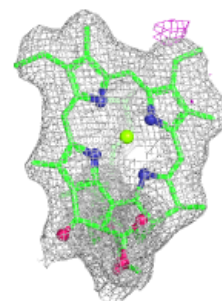
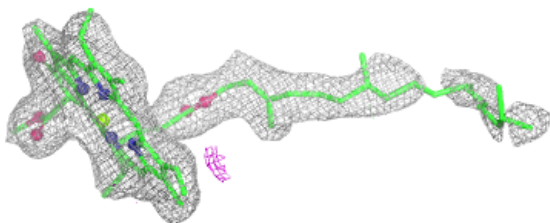
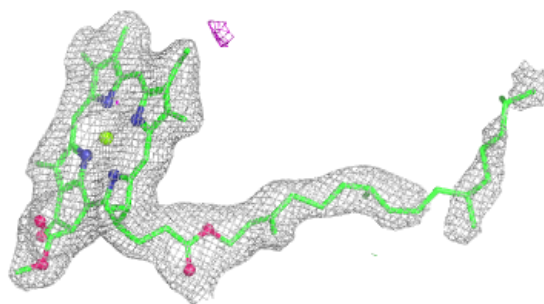


Electron density around CLA d 403:

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

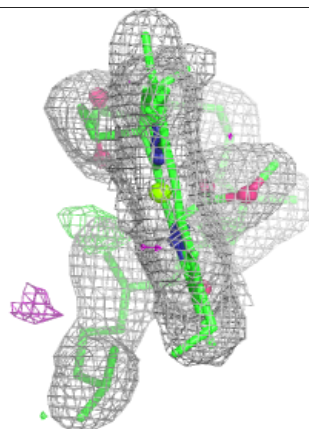
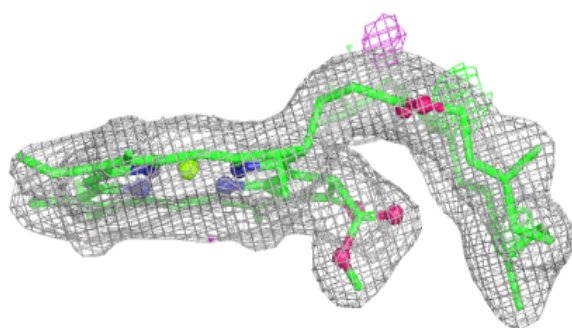
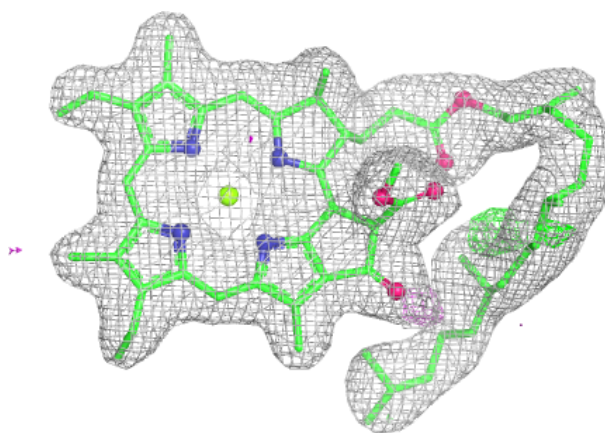
**Electron density around CLA d 404:**

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

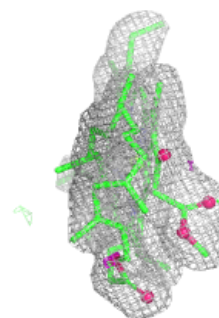
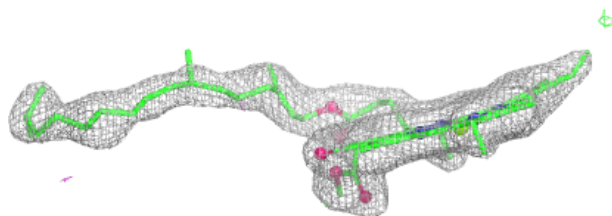
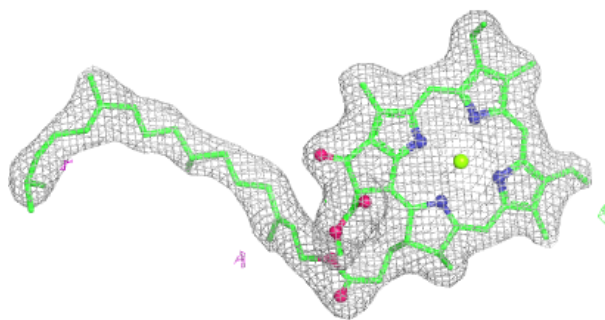


Electron density around CLA B 610:

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

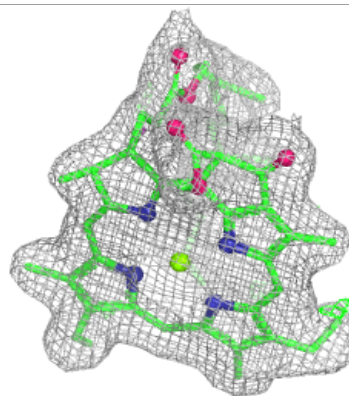
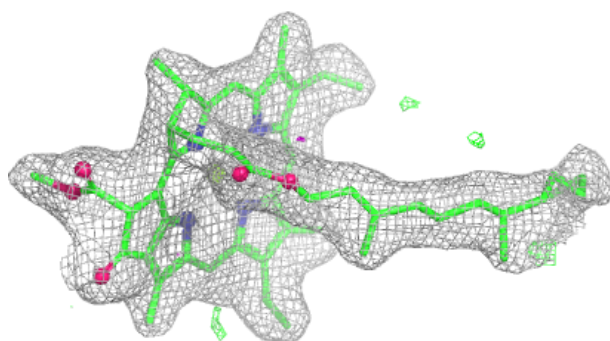
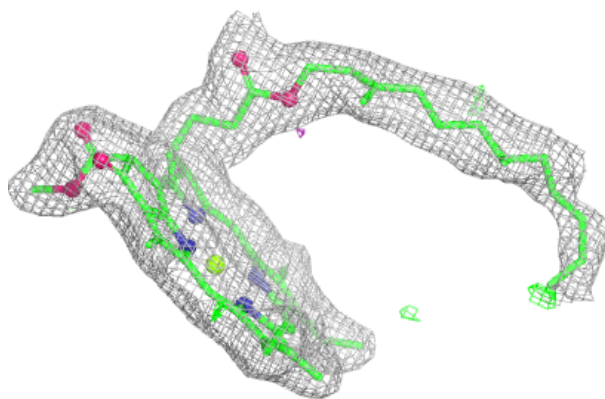
**Electron density around CLA b 602:**

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

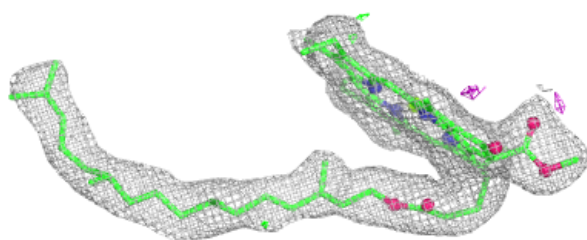
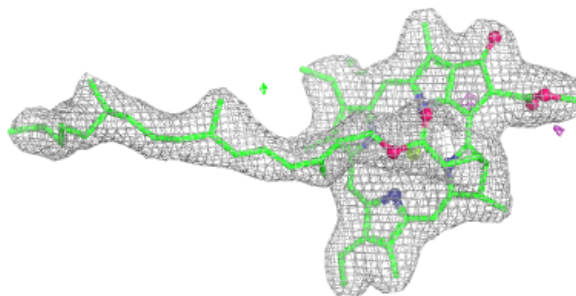


Electron density around CLA C 504:

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

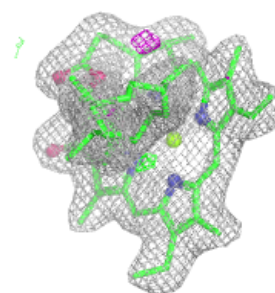
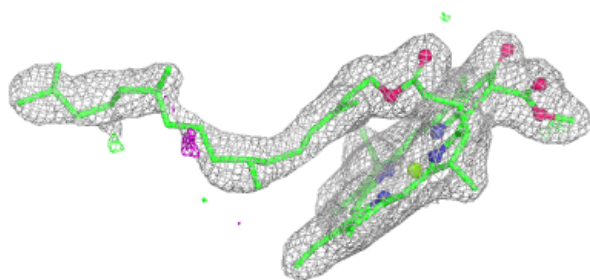
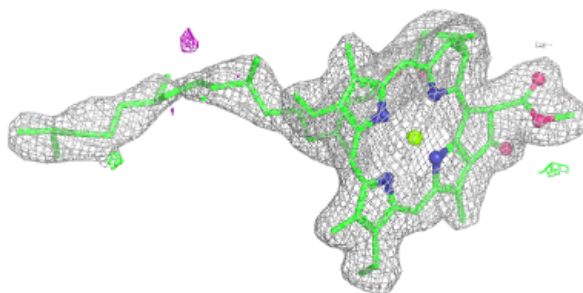
**Electron density around CLA b 608:**

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



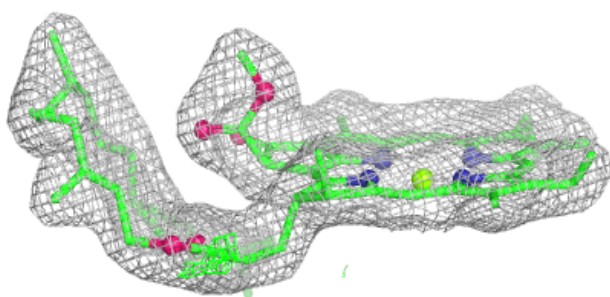
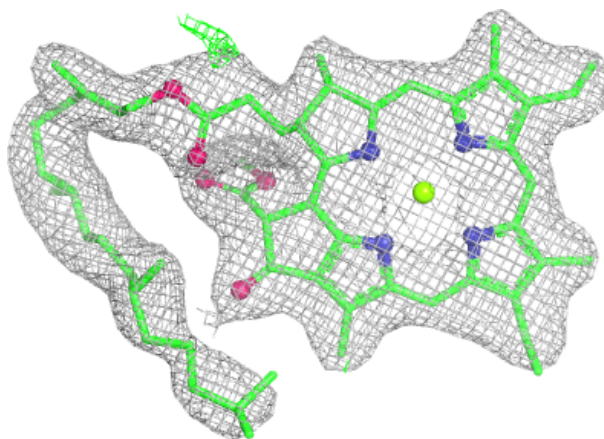
Electron density around CLA C 505:

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



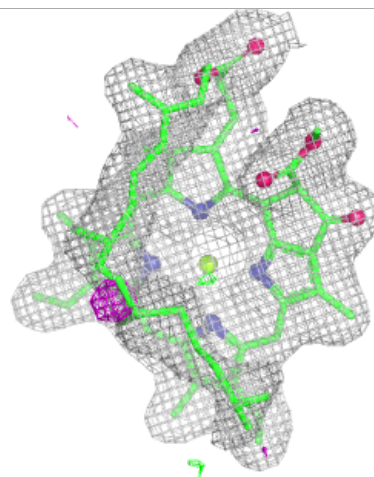
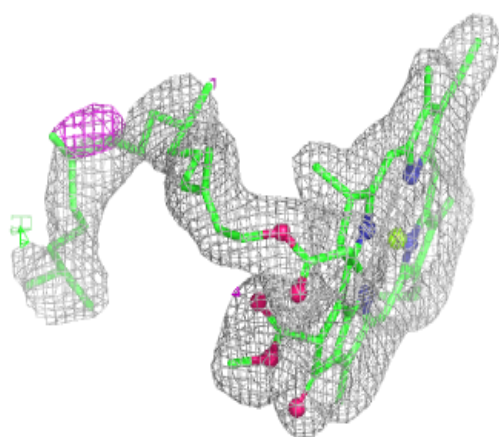
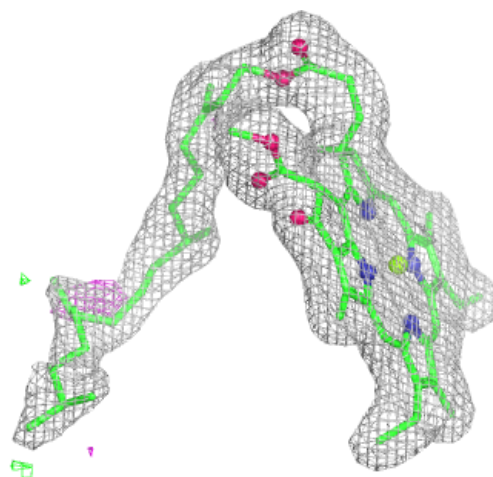
Electron density around CLA b 610:

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



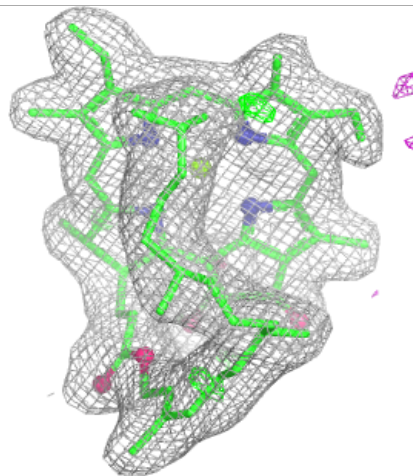
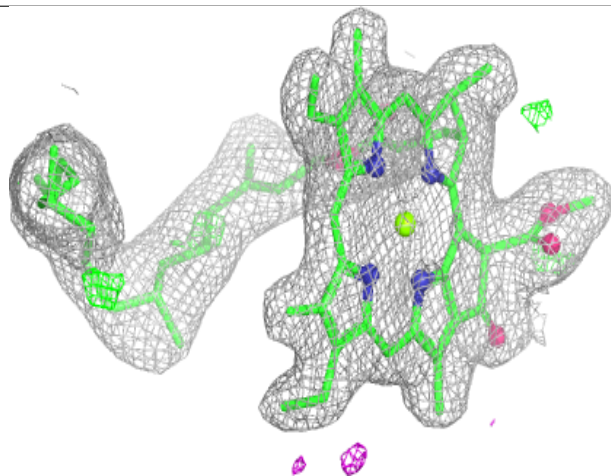
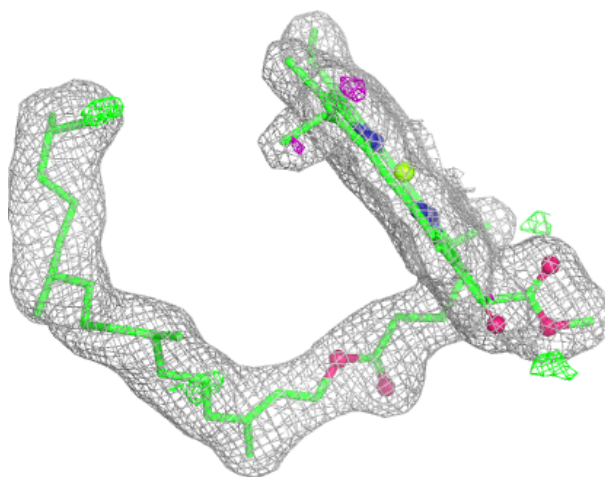
Electron density around CLA b 613:

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



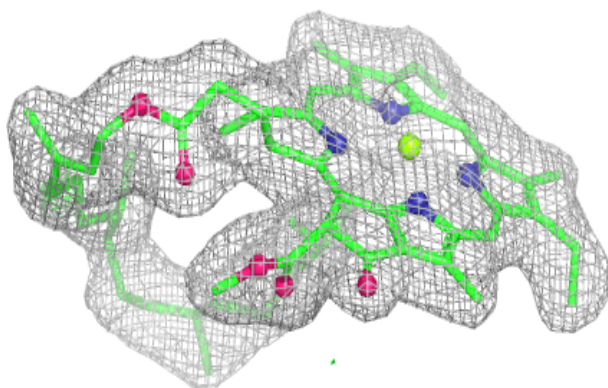
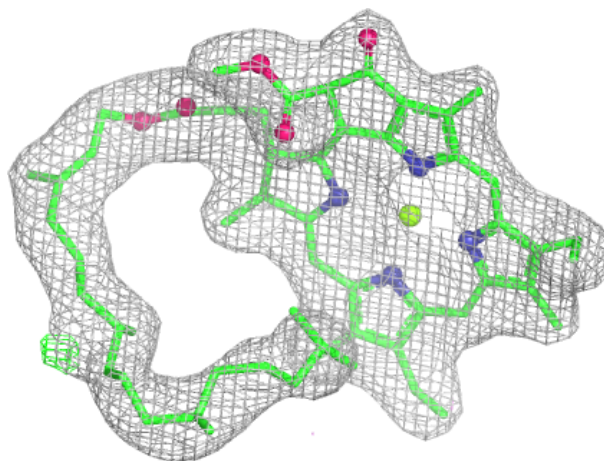
Electron density around CLA B 611:

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



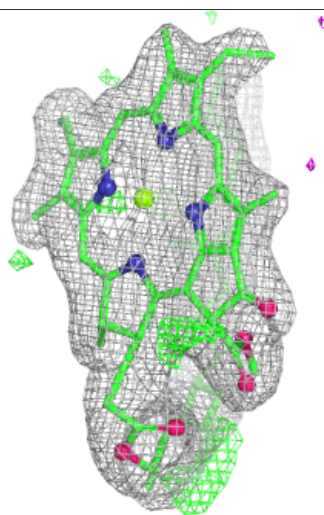
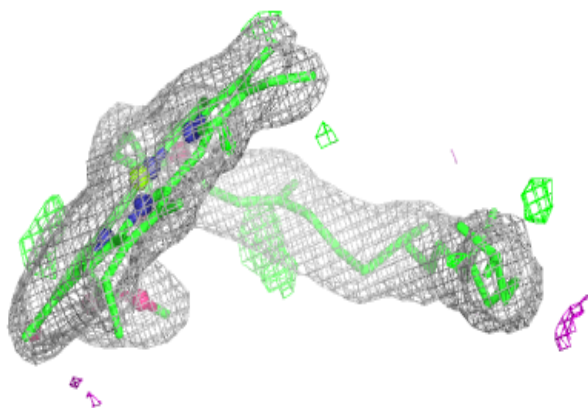
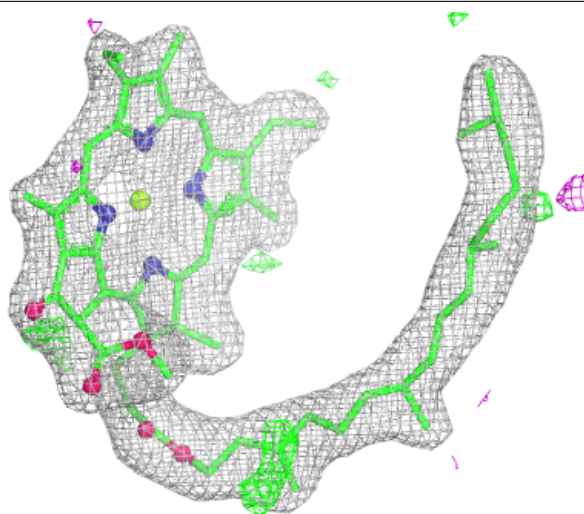
Electron density around CLA b 615:

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



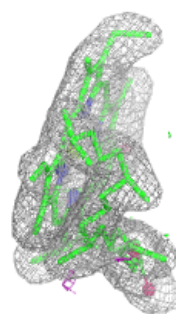
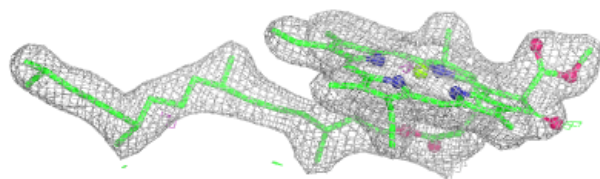
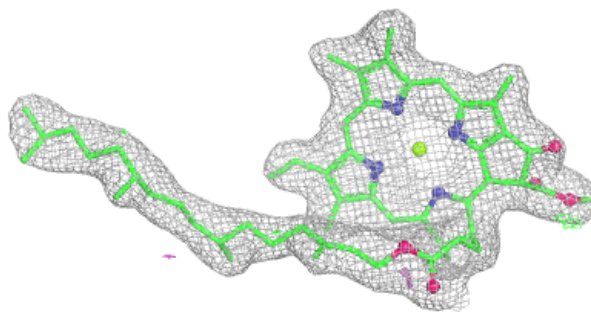
Electron density around CLA C 507:

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

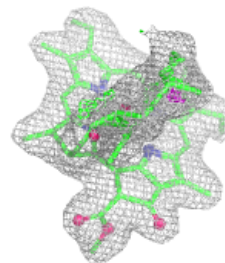
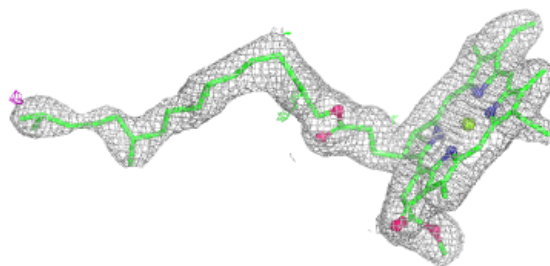


Electron density around CLA c 501:

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

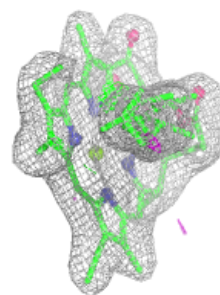
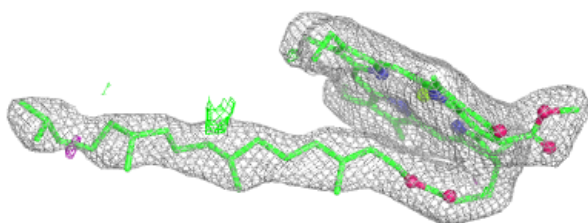
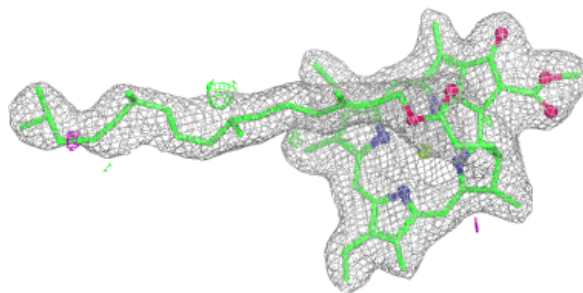
**Electron density around CLA c 502:**

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



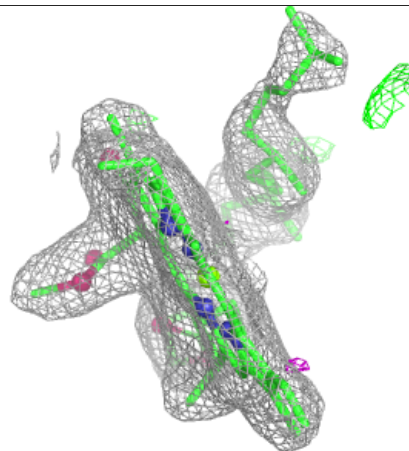
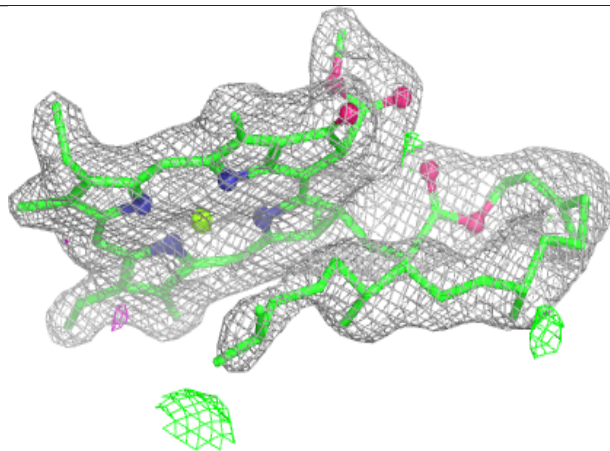
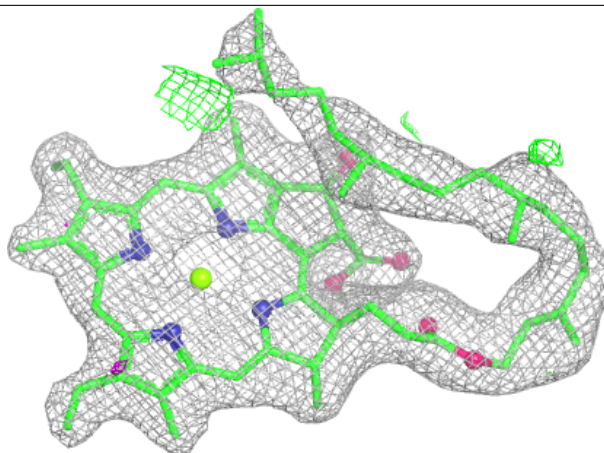
Electron density around CLA B 614:

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



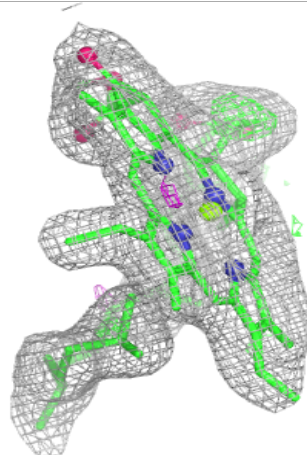
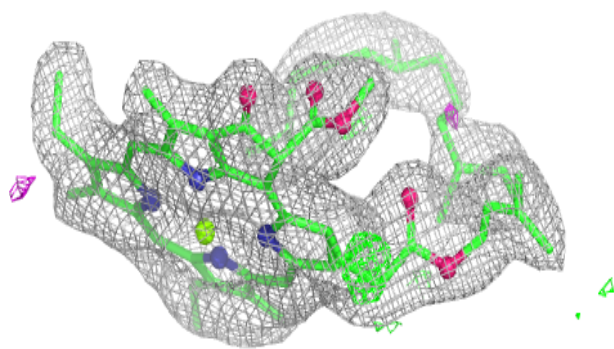
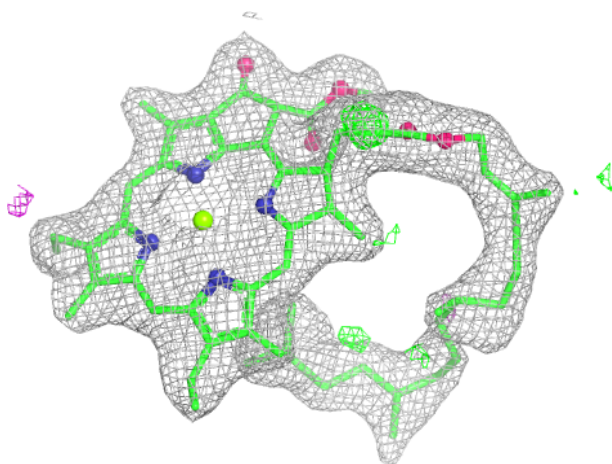
Electron density around CLA C 509:

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



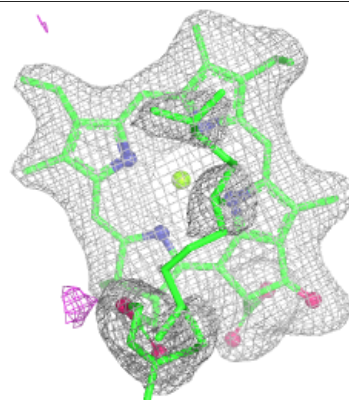
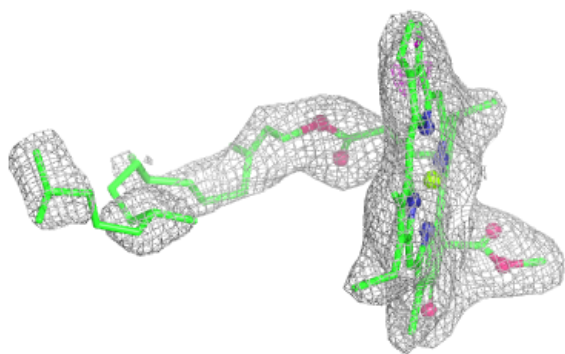
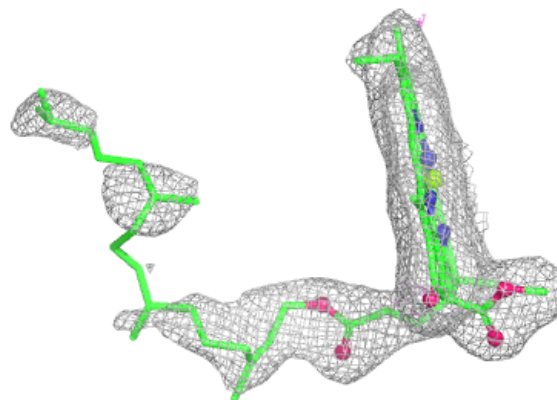
Electron density around CLA B 615:

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



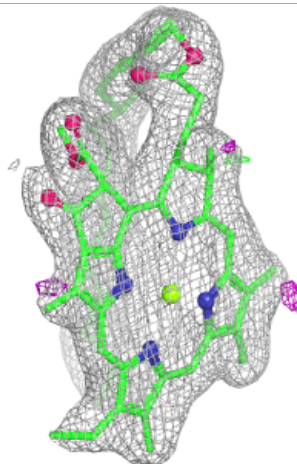
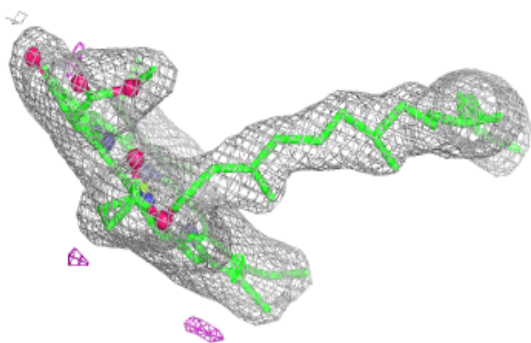
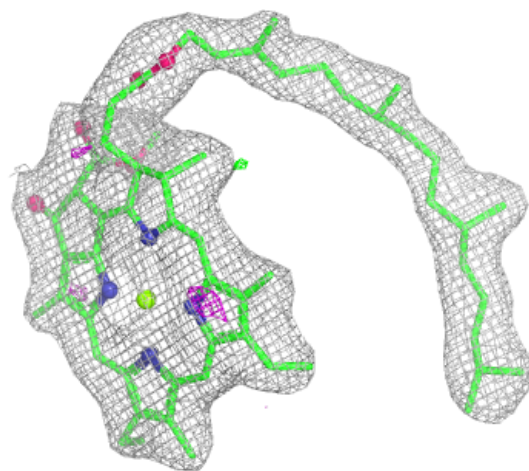
Electron density around CLA c 506:

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



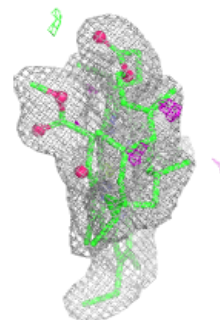
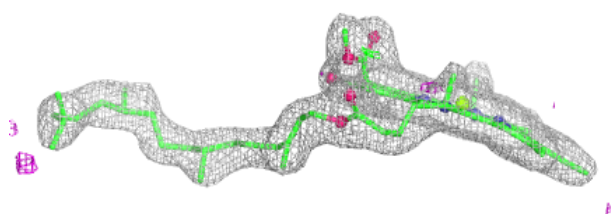
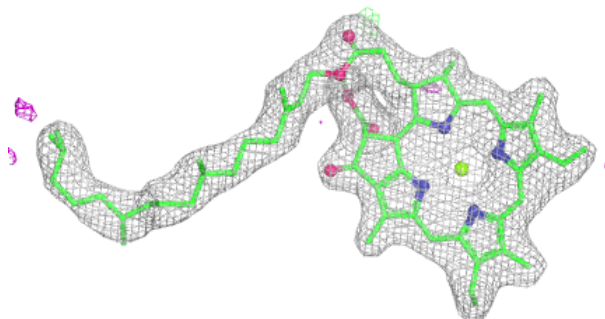
Electron density around CLA c 507:

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

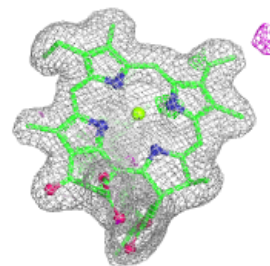
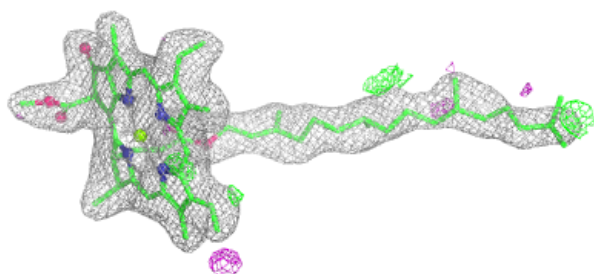
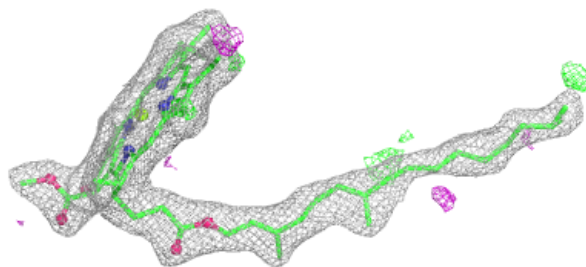


Electron density around CLA B 602:

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

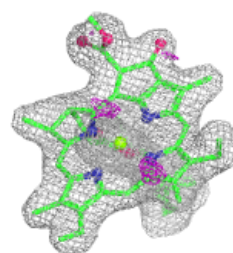
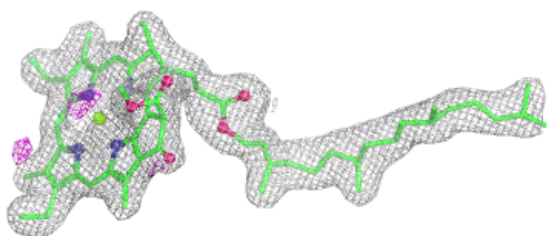
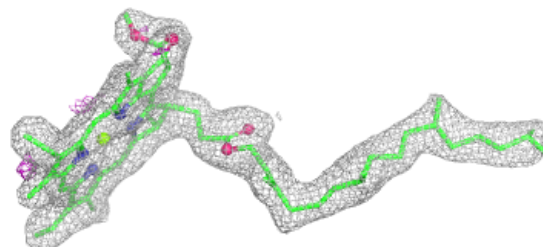
**Electron density around CLA B 607:**

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



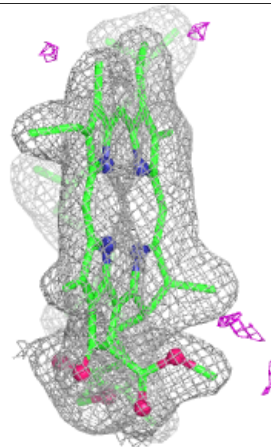
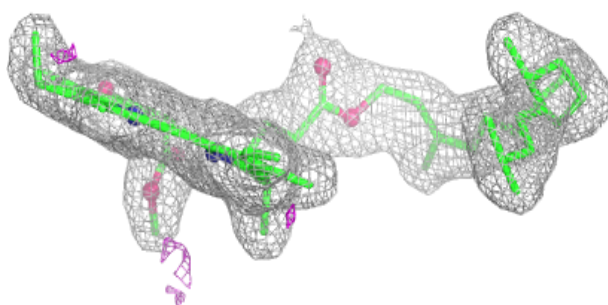
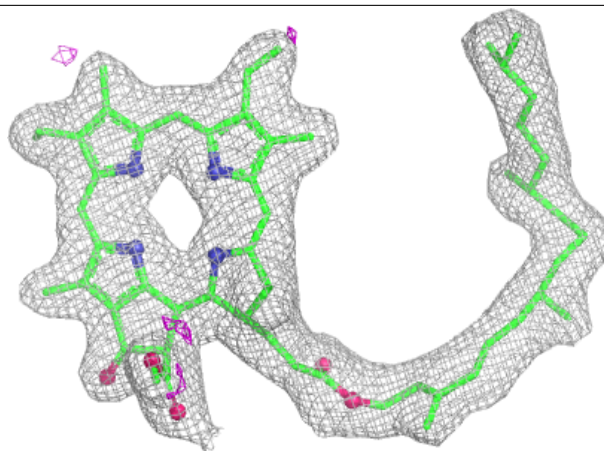
Electron density around CLA C 502:

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



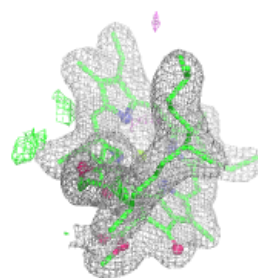
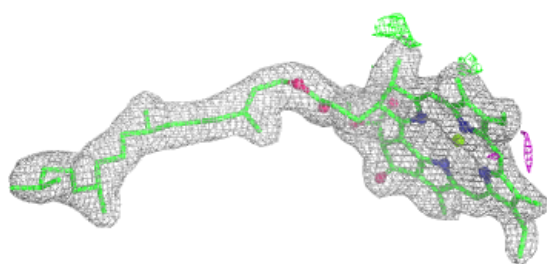
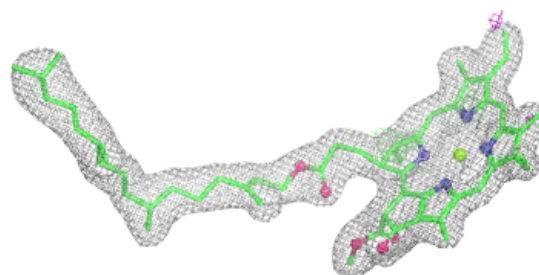
Electron density around PHO a 607:

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

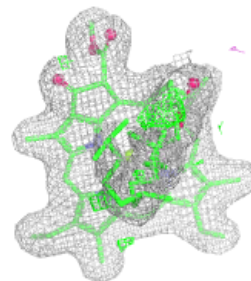
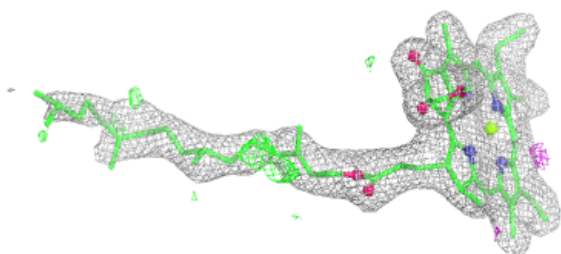
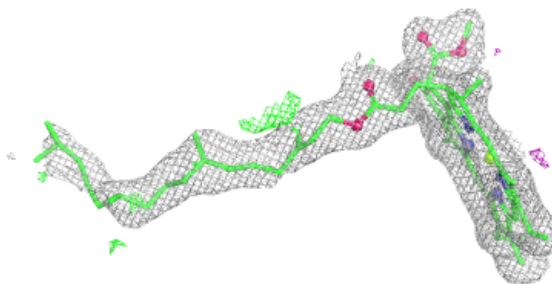


Electron density around CLA a 605:

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

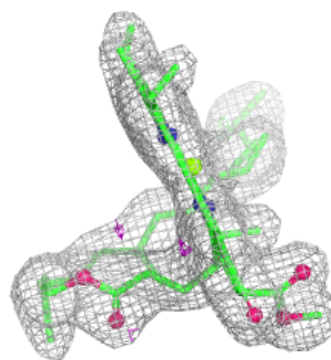
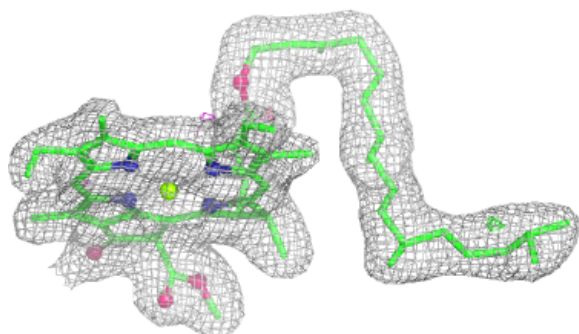
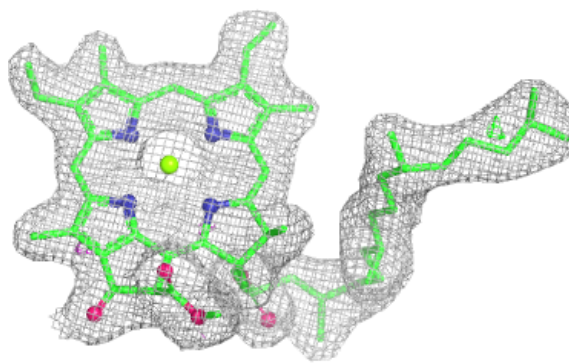
**Electron density around CLA B 604:**

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

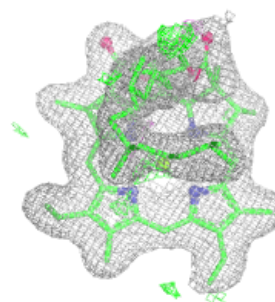
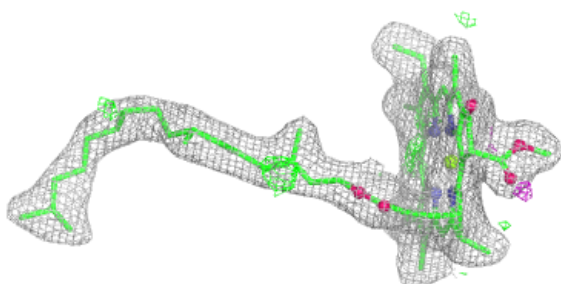
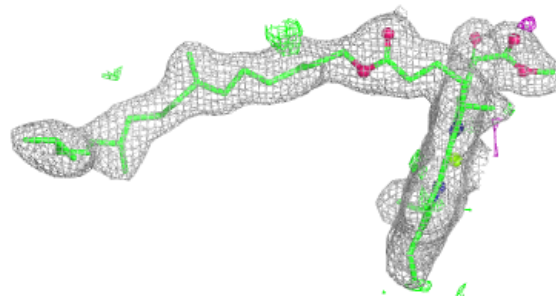


Electron density around CLA a 611:

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

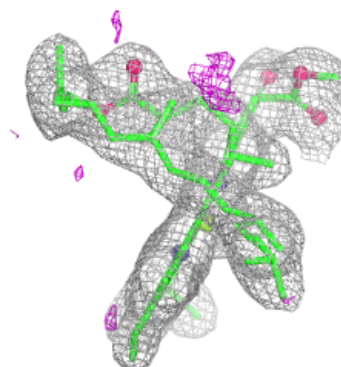
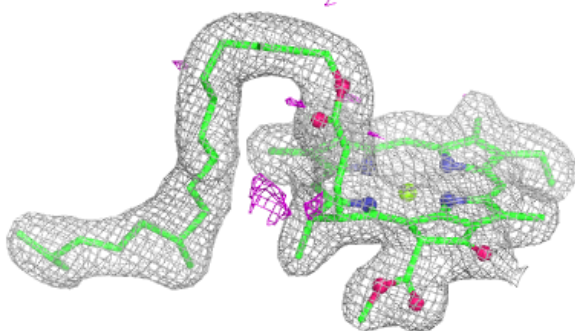
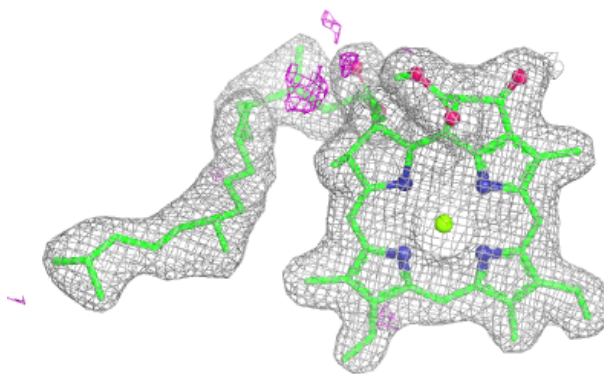
**Electron density around CLA B 605:**

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

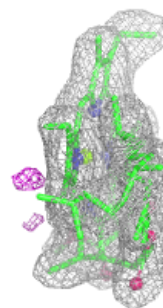
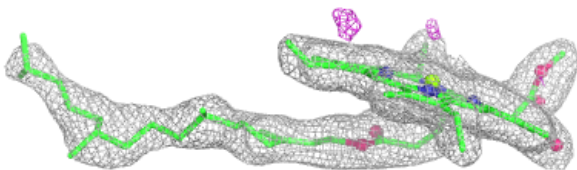
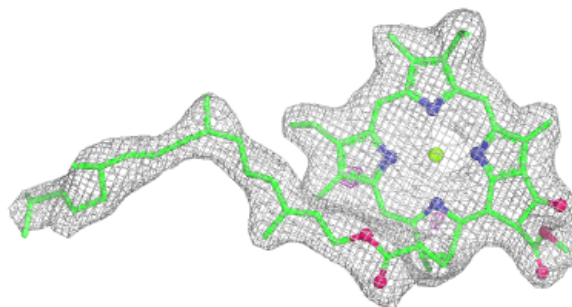


Electron density around CLA A 611:

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

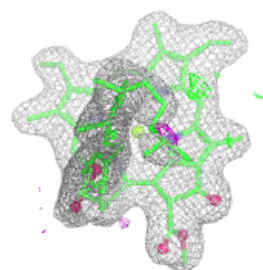
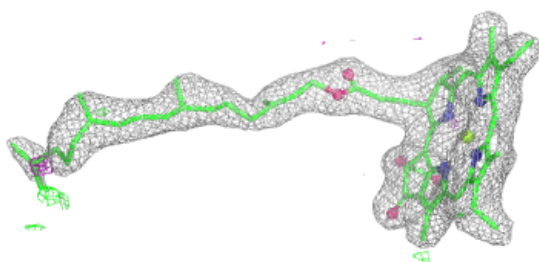
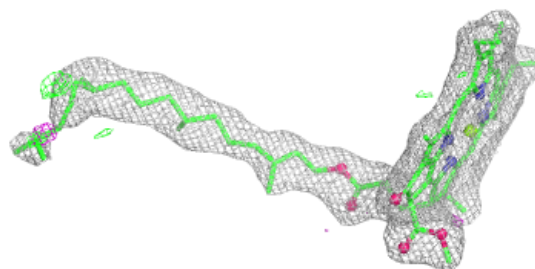
**Electron density around CLA b 603:**

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

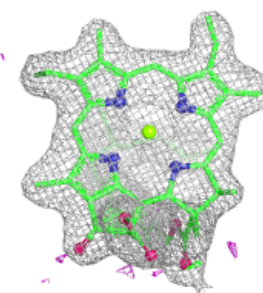
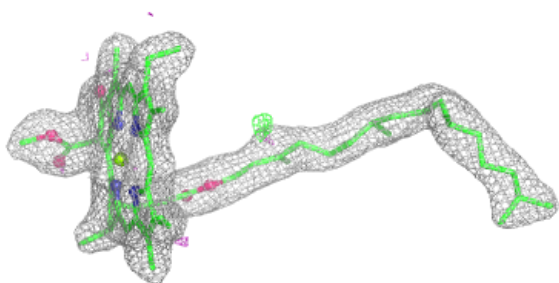
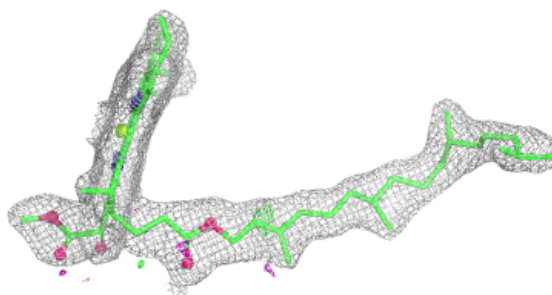


Electron density around CLA b 604:

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

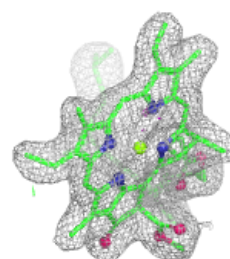
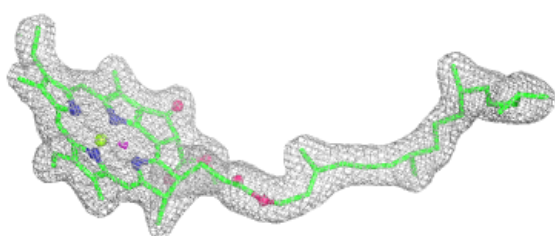
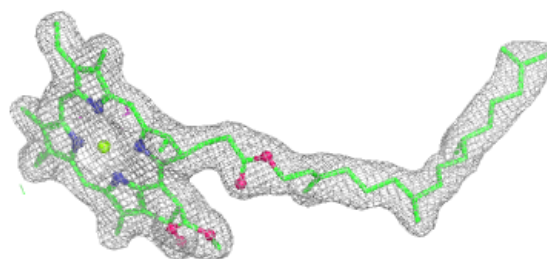
**Electron density around CLA b 605:**

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

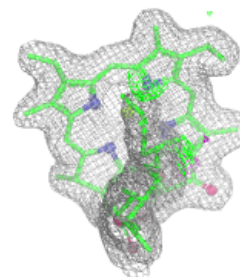
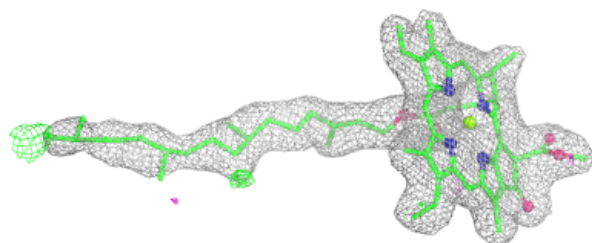
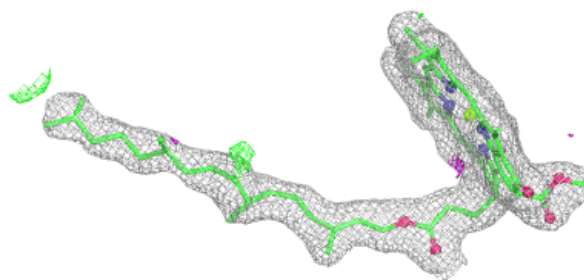


Electron density around CLA A 606:

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

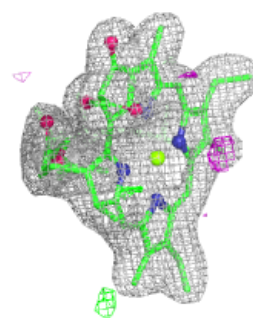
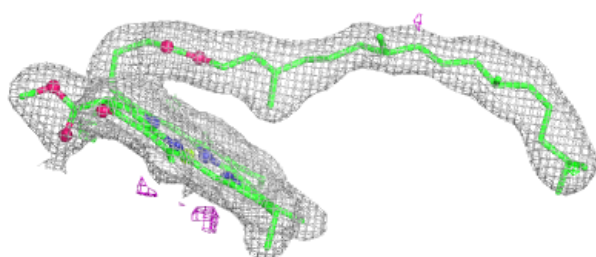
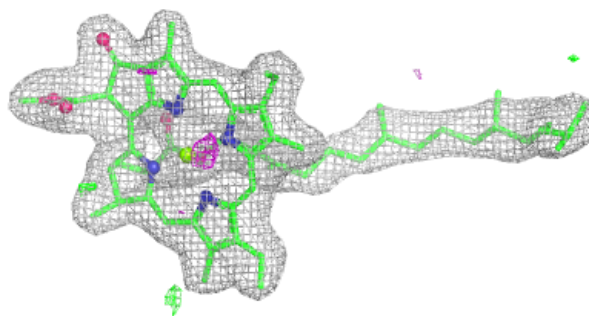
**Electron density around CLA b 607:**

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

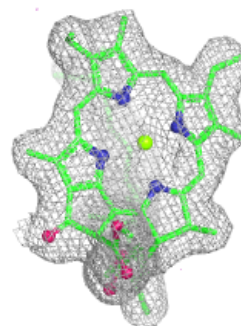
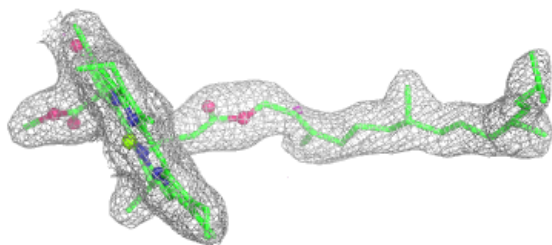
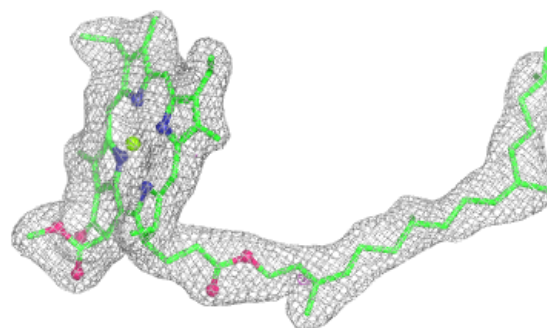


Electron density around CLA B 608:

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

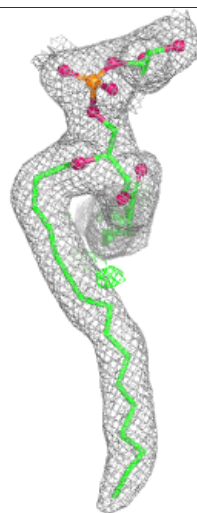
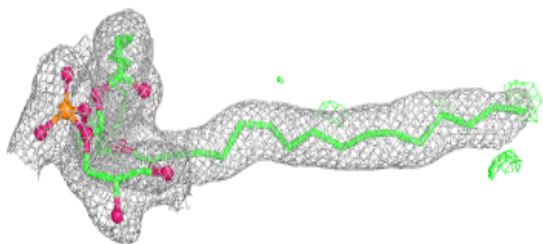
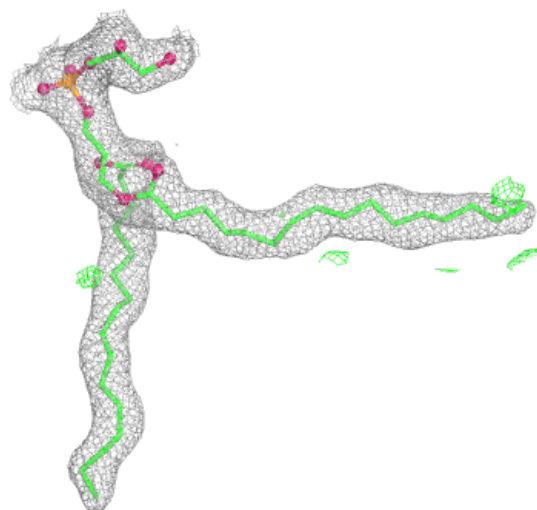
**Electron density around CLA B 609:**

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



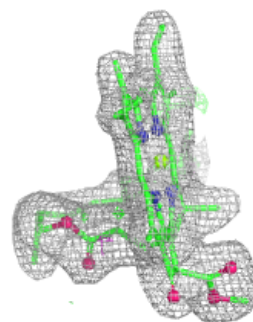
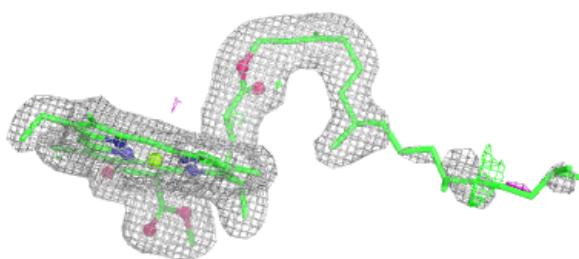
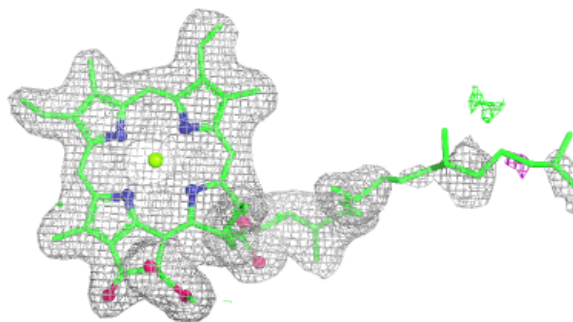
Electron density around LHG L 101:

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

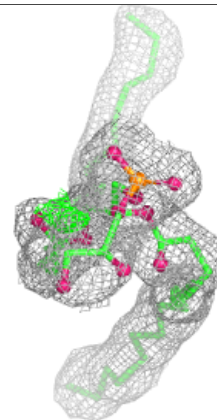
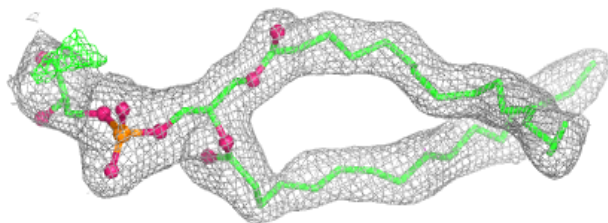
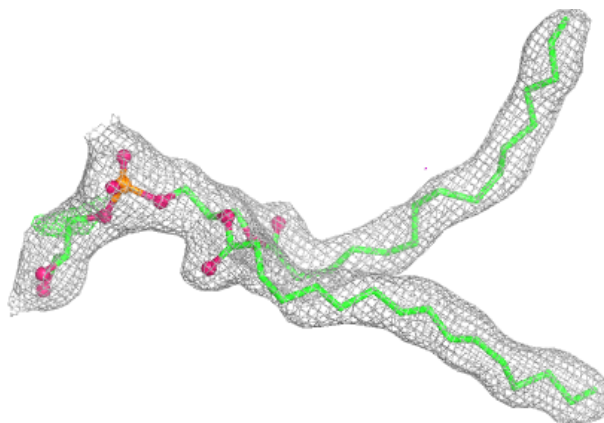


Electron density around CLA A 607:

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

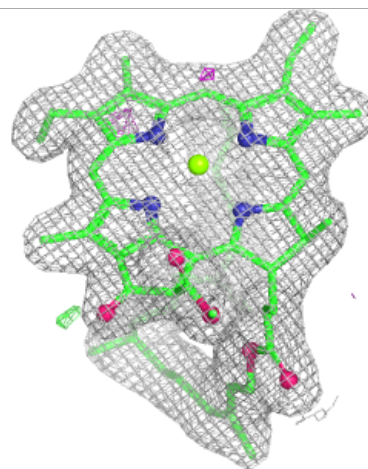
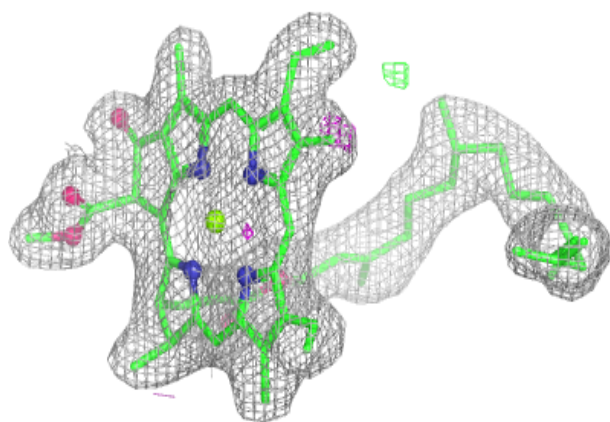
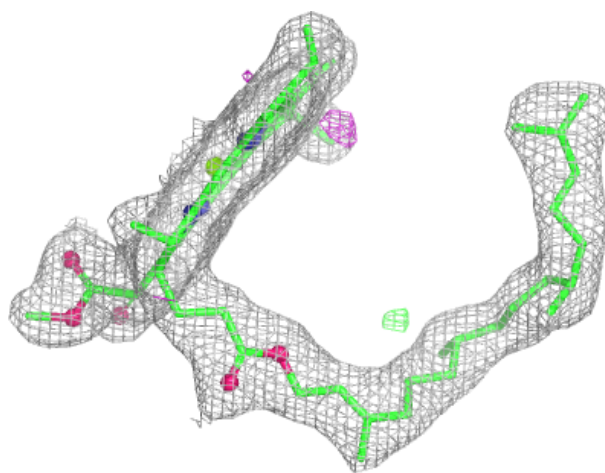
**Electron density around LHG d 408:**

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



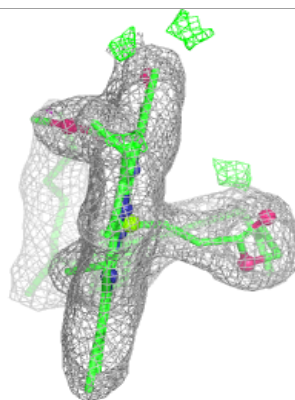
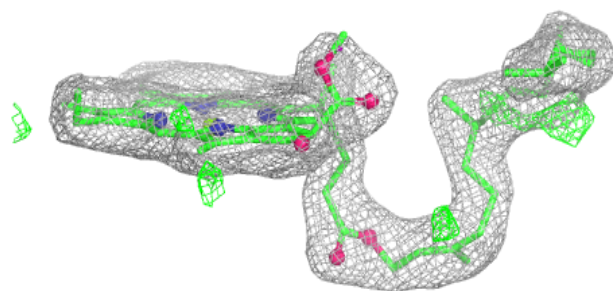
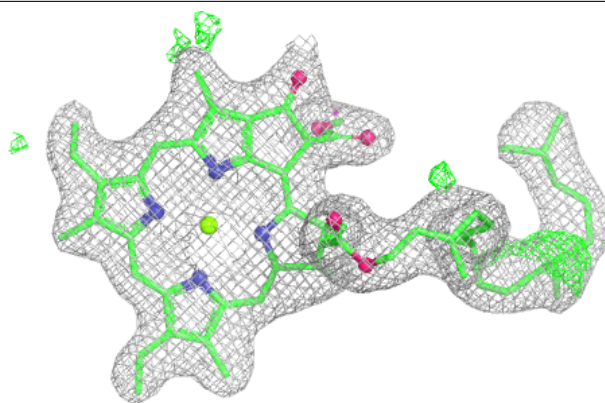
Electron density around CLA b 611:

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

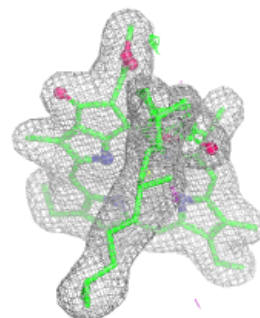
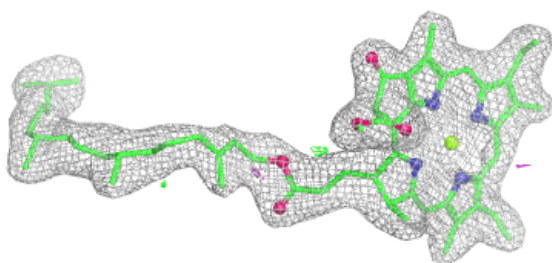
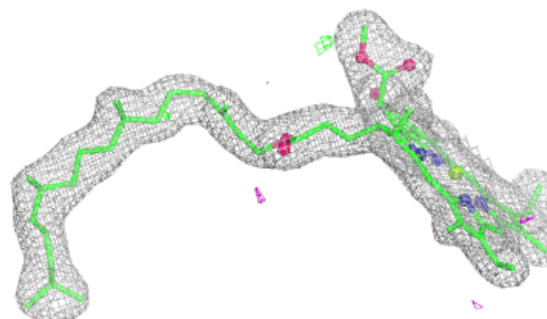


Electron density around CLA b 612:

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

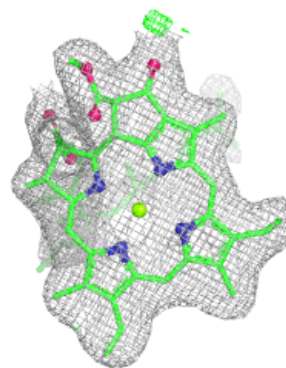
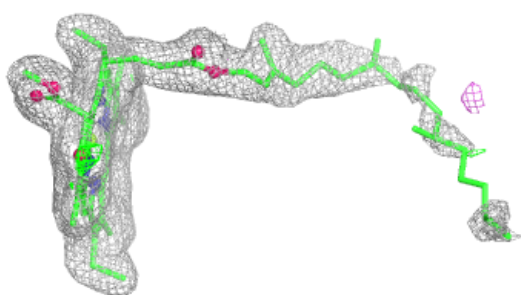
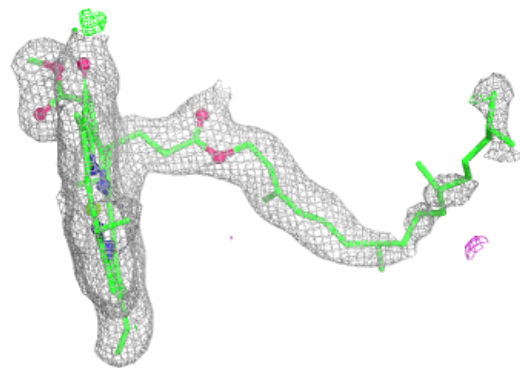
**Electron density around CLA D 403:**

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

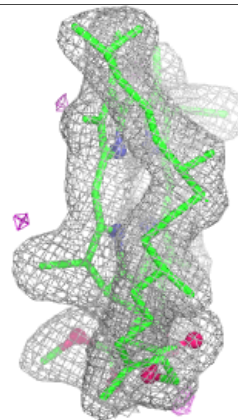
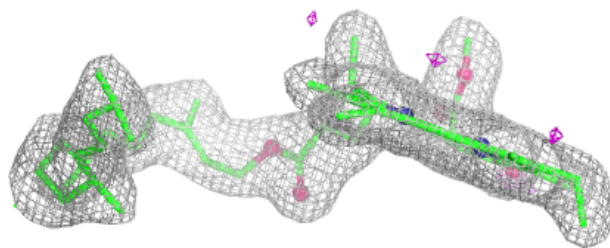
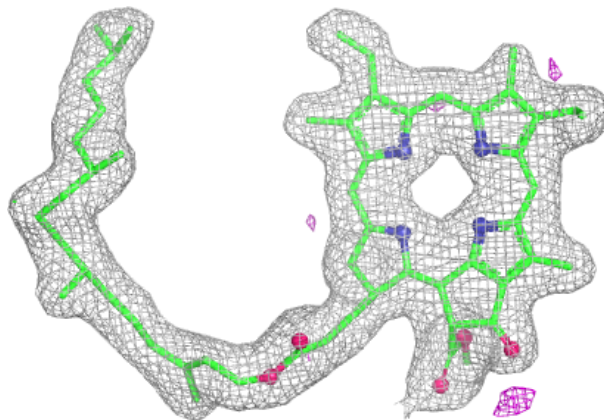


Electron density around CLA D 404:

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

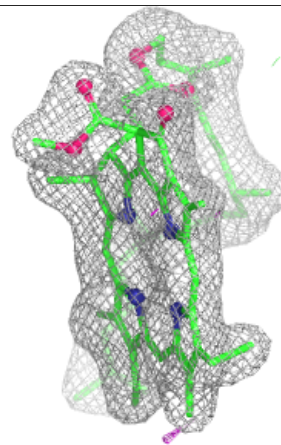
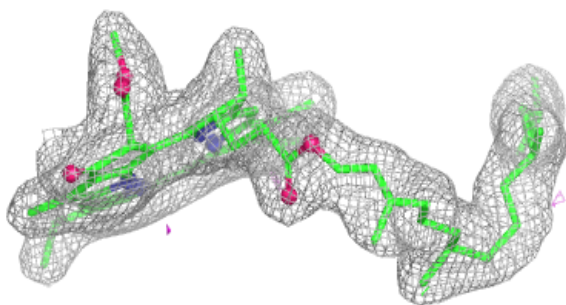
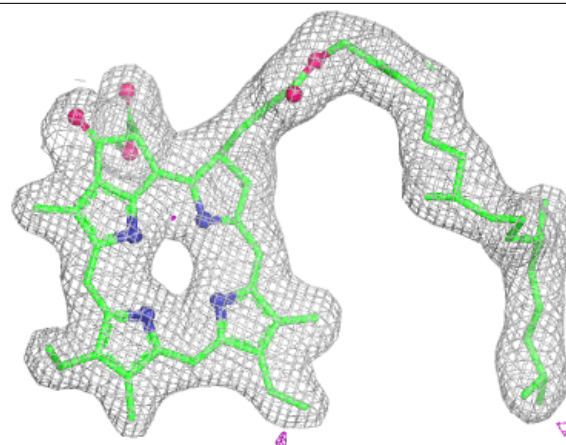
**Electron density around PHO D 401:**

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



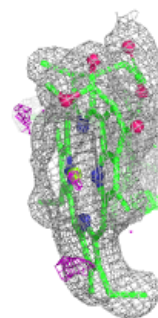
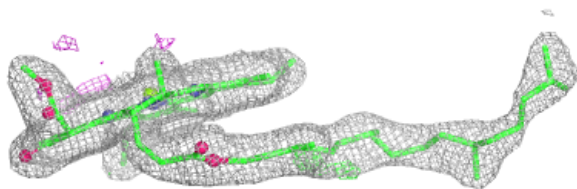
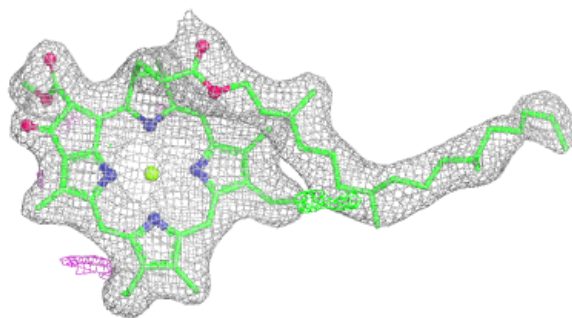
Electron density around PHO D 402:

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

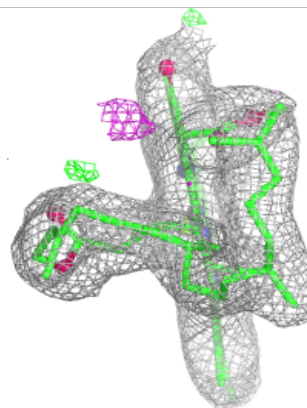
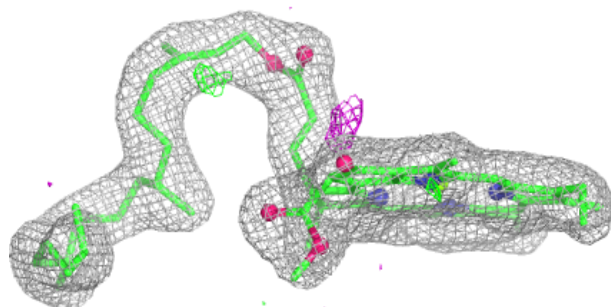
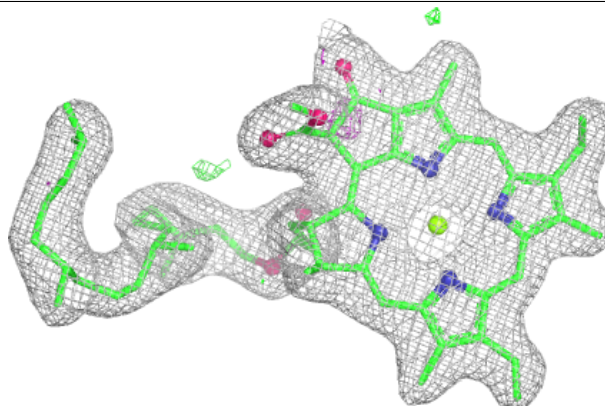


Electron density around CLA B 603:

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

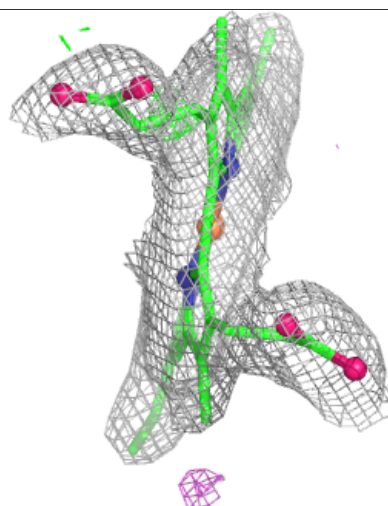
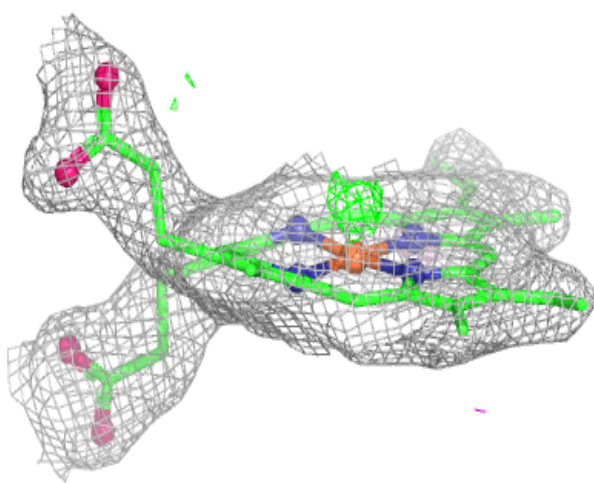
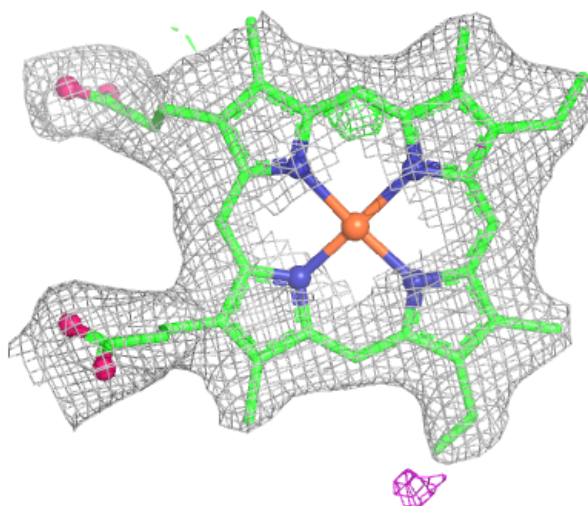
**Electron density around CLA B 612:**

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



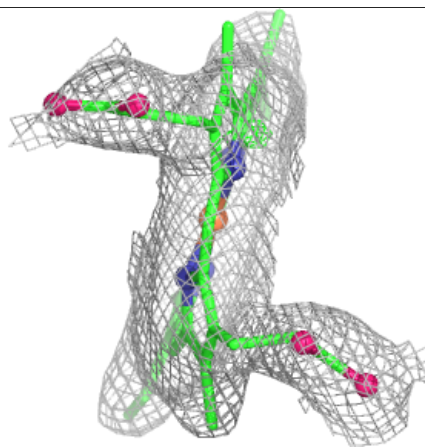
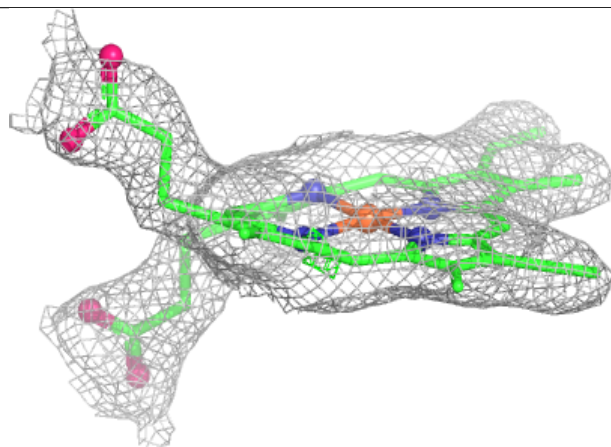
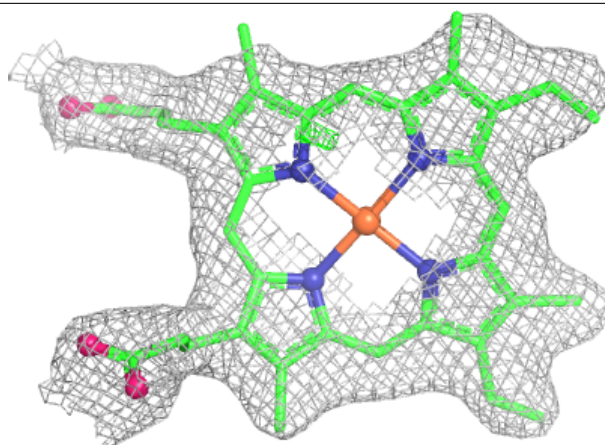
Electron density around HEM E 101:

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



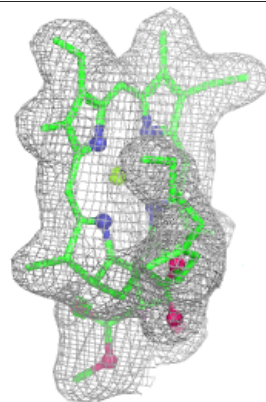
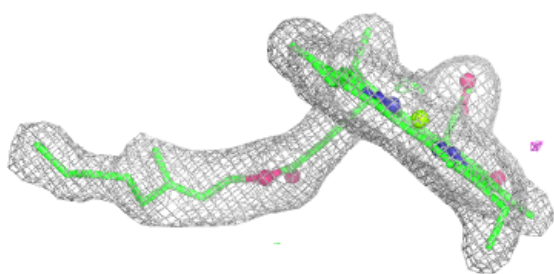
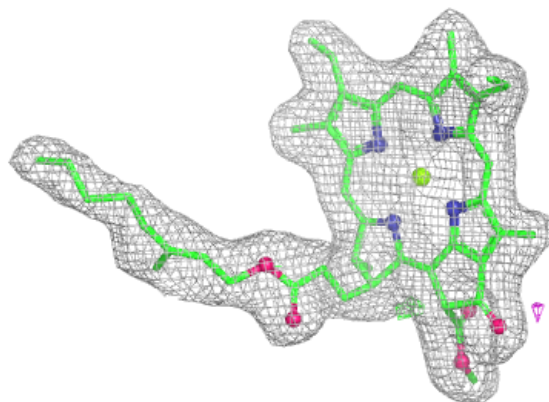
Electron density around HEM f 101:

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

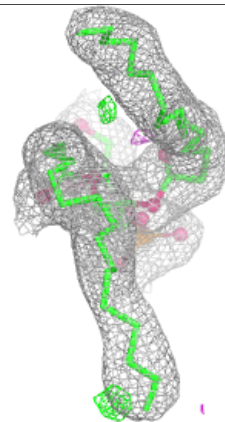
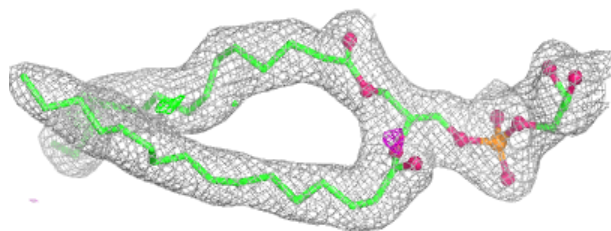
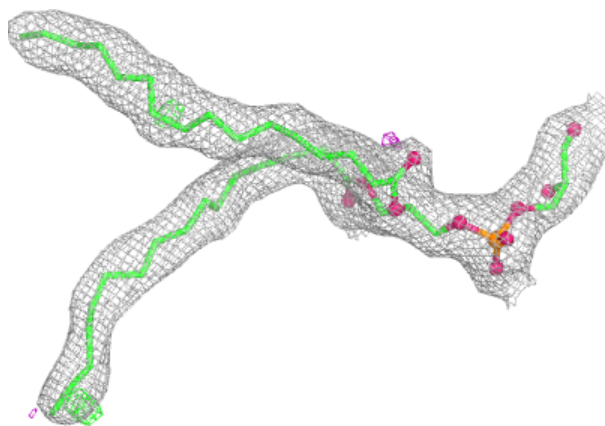


Electron density around CLA A 608:

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

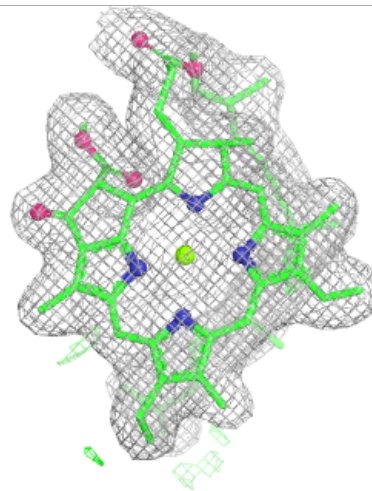
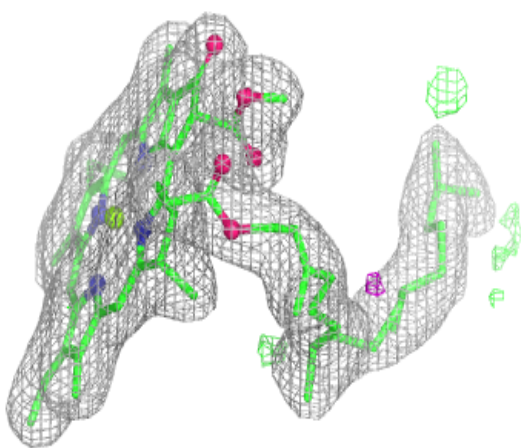
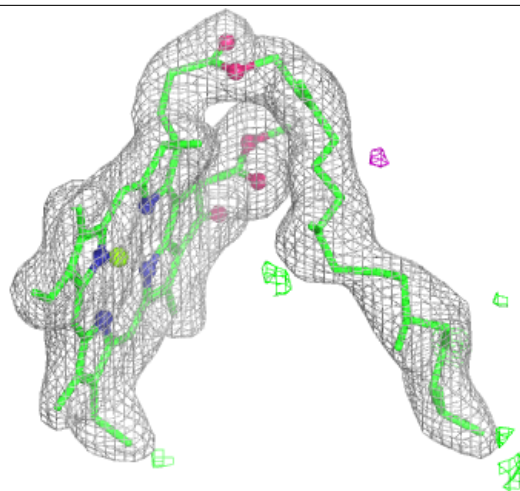
**Electron density around LHG D 409:**

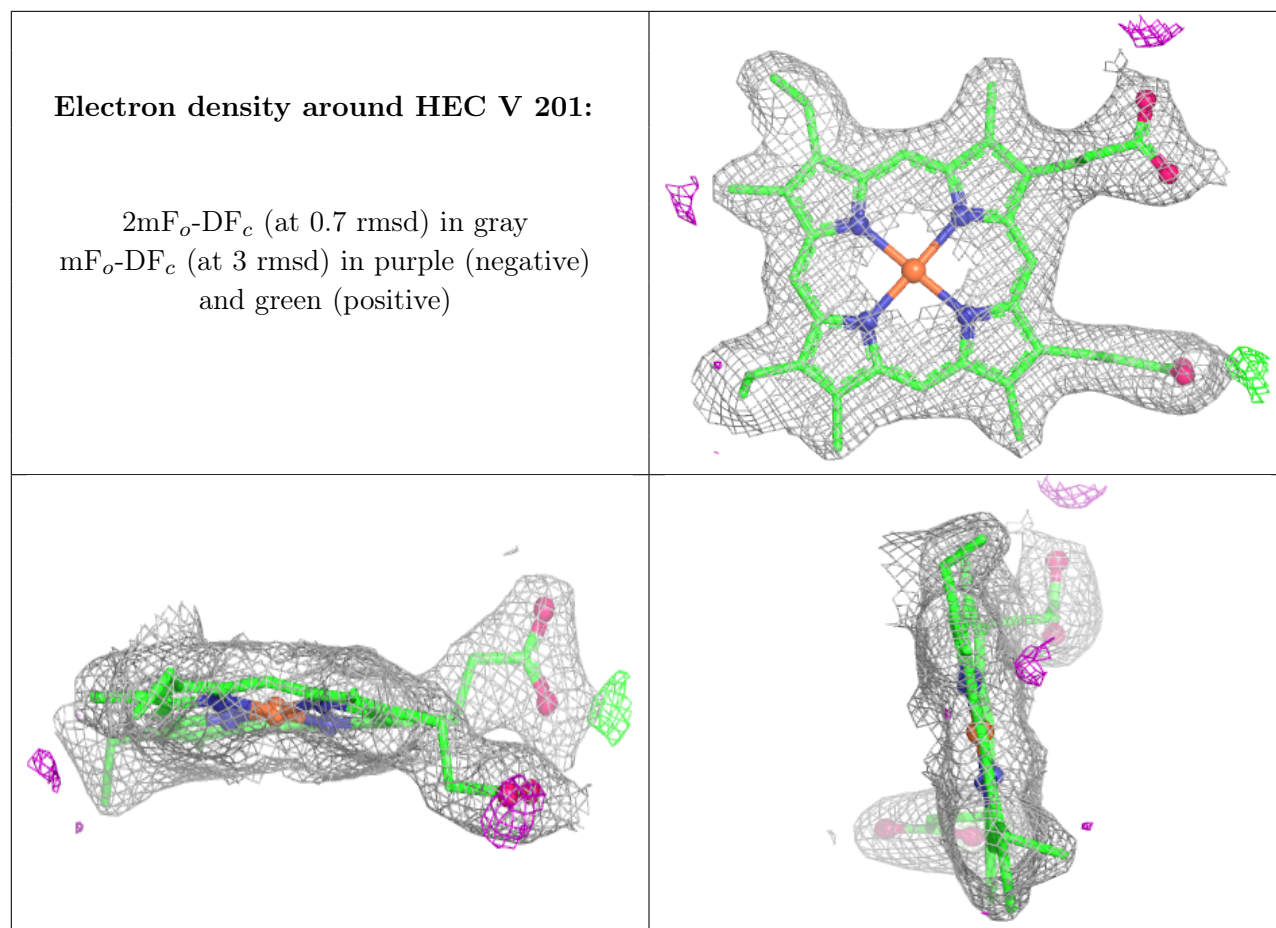
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CLA B 613:

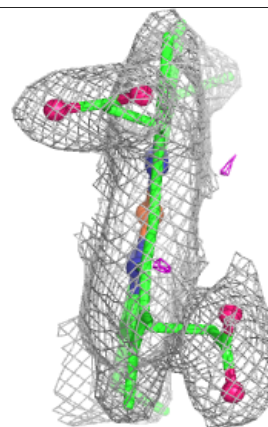
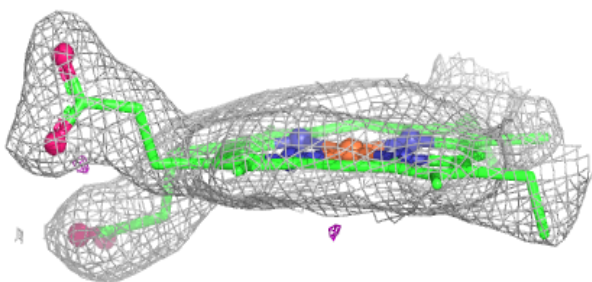
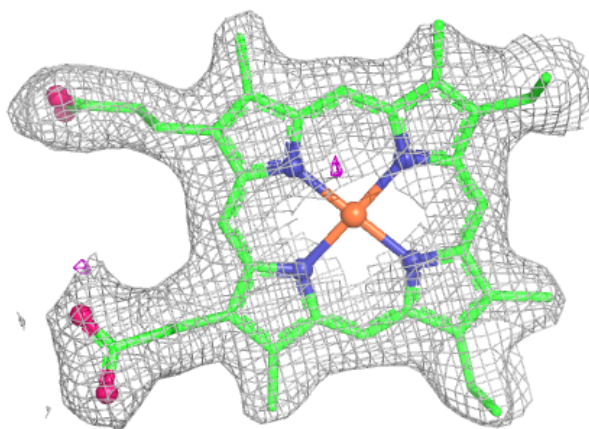
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





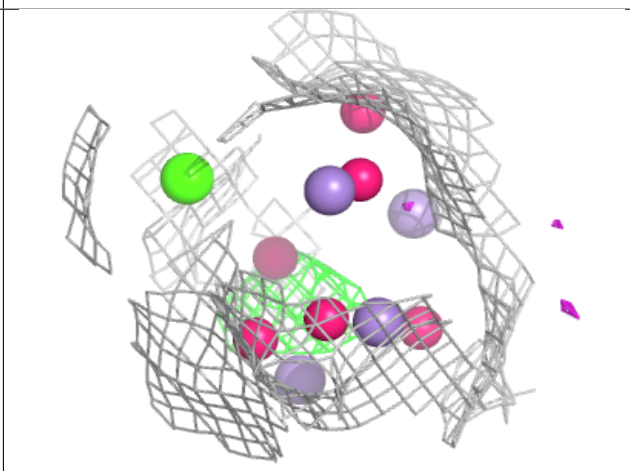
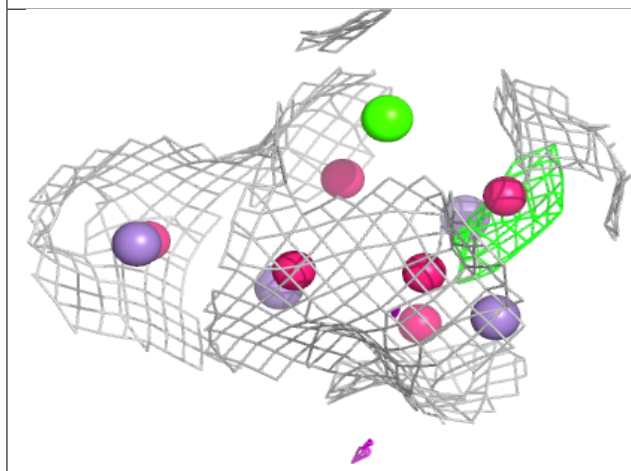
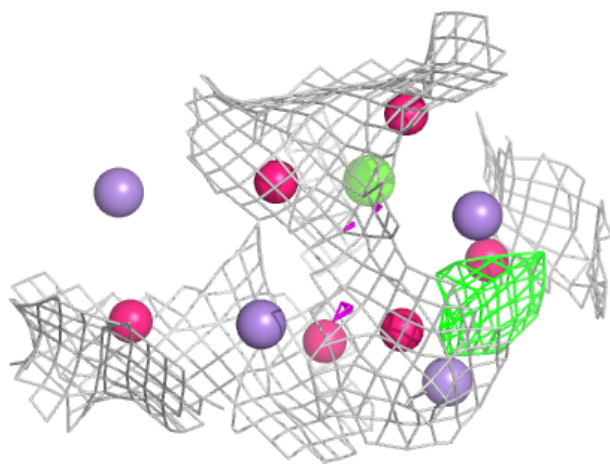
Electron density around HEC v 201:

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



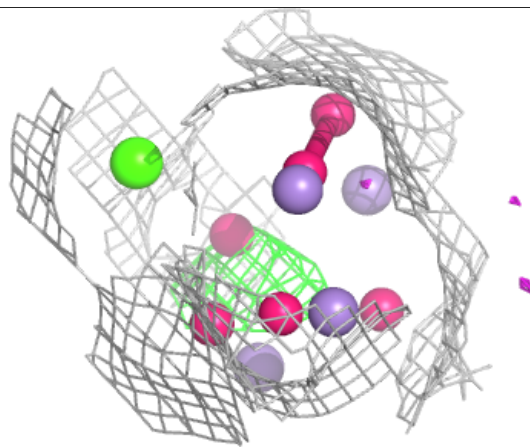
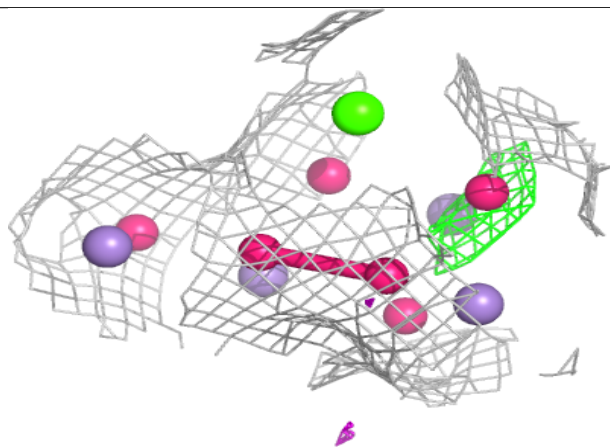
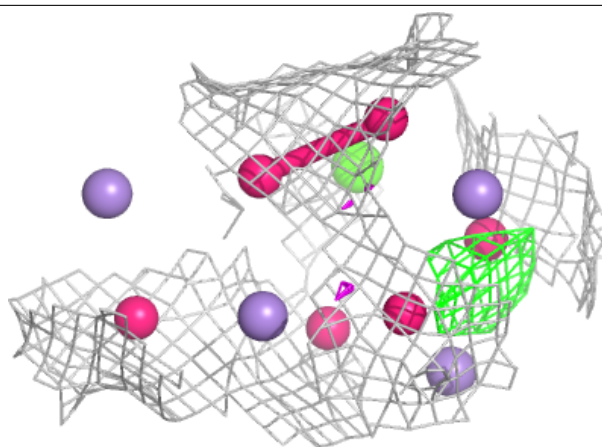
Electron density around OEY A 601 (A):

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



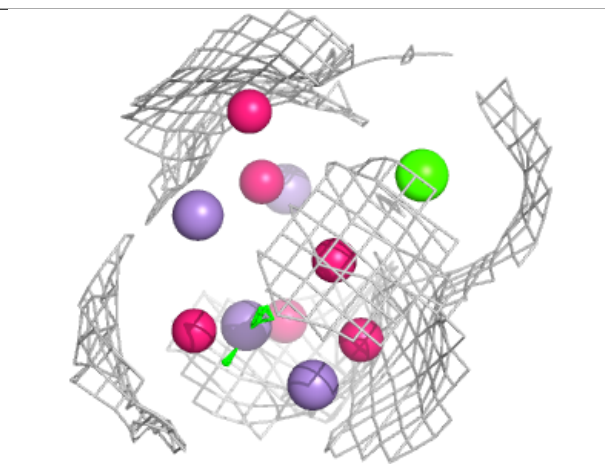
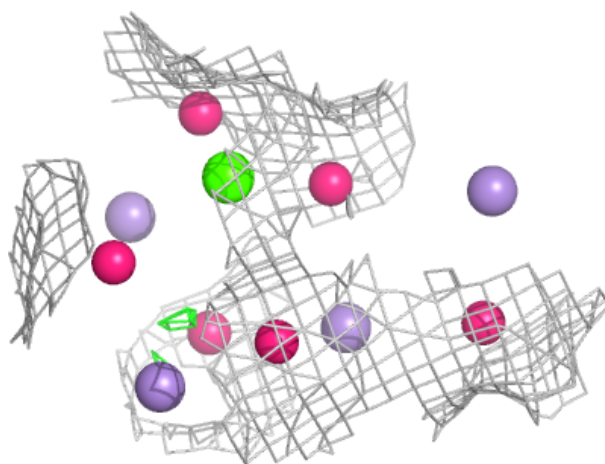
Electron density around OEY A 601 (B):

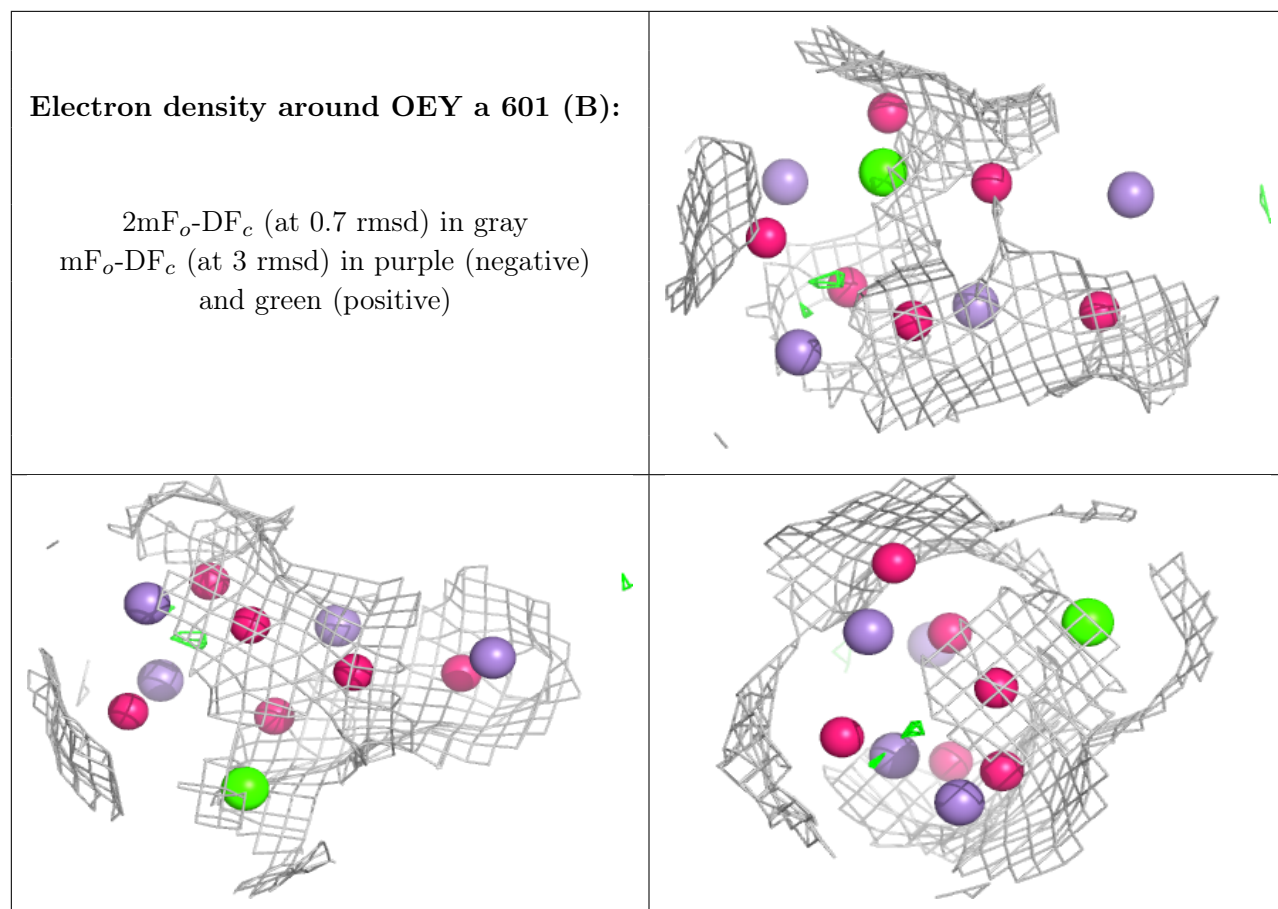
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around OEY a 601 (A):

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





6.5 Other polymers [i](#)

There are no such residues in this entry.