



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 3, 2026 – 11:43 PM EDT

PDB ID : 1S5L / pdb_00001s5l
Title : Architecture of the photosynthetic oxygen evolving center
Authors : Ferreira, K.N.; Iverson, T.M.; Maghlaoui, K.; Barber, J.; Iwata, S.
Deposited on : 2004-01-21
Resolution : 3.50 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

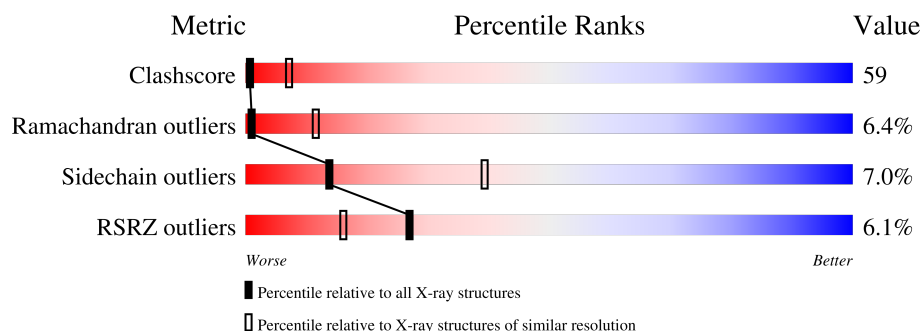
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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.



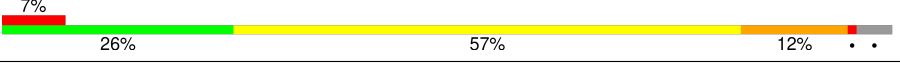
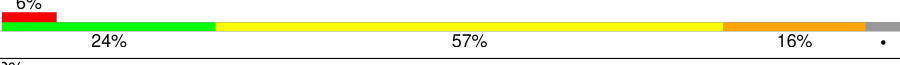
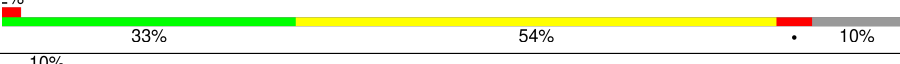
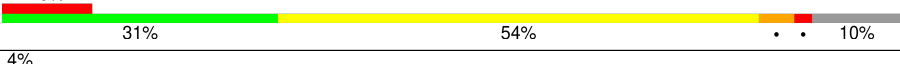
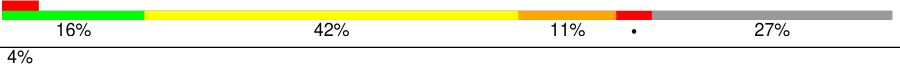
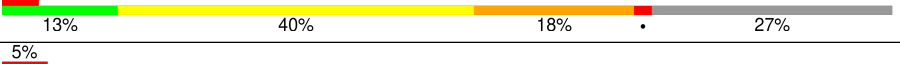
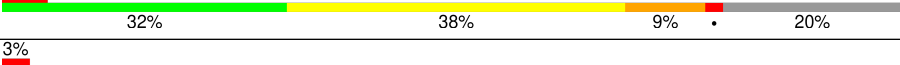
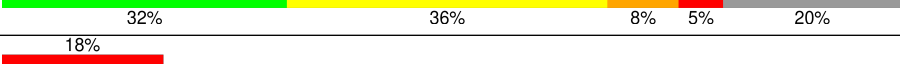
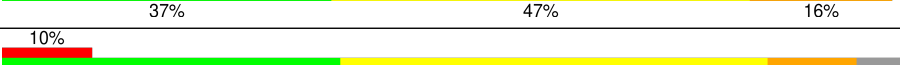
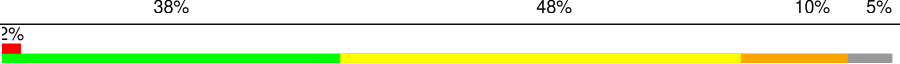
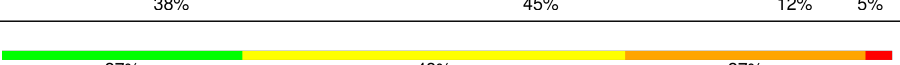
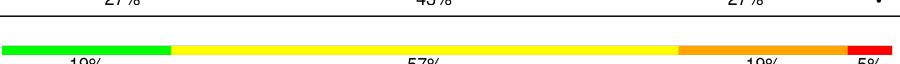
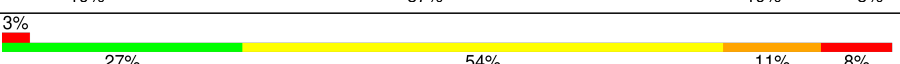
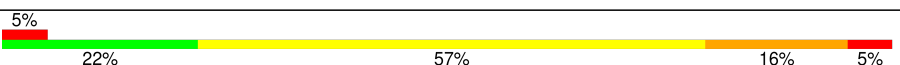
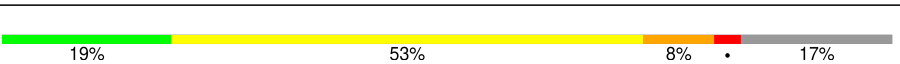
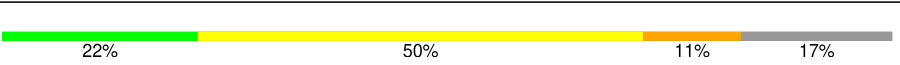
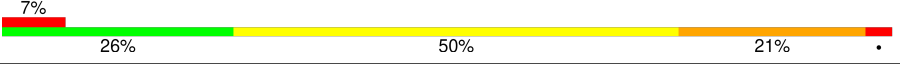
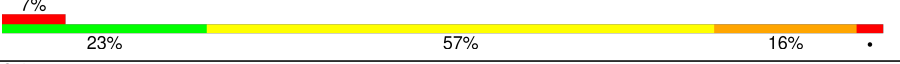
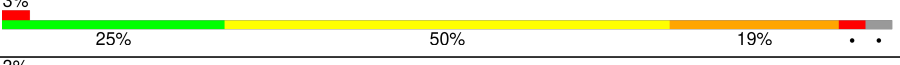
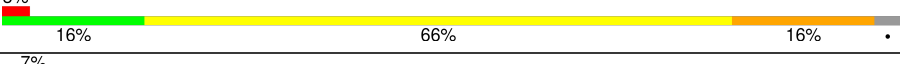
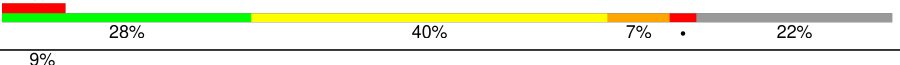
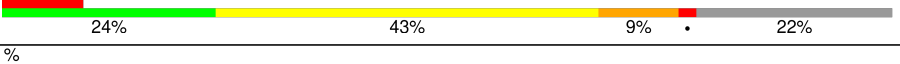
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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	5% 23% 55% 17% • •
1	a	344	6% 24% 52% 19% • •
2	B	510	7% 27% 54% 12% • 7%
2	b	510	5% 28% 52% 13% • 7%
3	C	473	5% 18% 56% 14% • 11%
3	c	473	6% 22% 54% 13% • 11%

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Mol	Chain	Length	Quality of chain
4	D	352	
4	d	352	
5	E	84	
5	e	84	
6	F	45	
6	f	45	
7	H	66	
7	h	66	
8	I	38	
8	i	38	
9	J	40	
9	j	40	
10	K	37	
10	k	37	
11	L	37	
11	l	37	
12	M	36	
12	m	36	
13	O	246	
13	o	246	
14	T	32	
14	t	32	
15	U	134	
15	u	134	
16	V	137	

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Mol	Chain	Length	Quality of chain
16	v	137	
17	X	50	
17	x	50	
18	N	37	
18	n	37	
19	Z	62	
19	z	62	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	CLA	B	524	-	-	X	-
23	CLA	b	2524	-	-	X	-
23	CLA	c	2486	-	-	X	-
28	HEC	E	84	X	-	-	-
28	HEC	V	138	X	-	-	-
28	HEC	e	2084	X	-	-	-
28	HEC	v	2138	X	-	-	-

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 45945 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 Q(B) protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	0	0
			2617	1714	430	458	15			
1	a	333	Total	C	N	O	S	0	0	0
			2616	1714	430	457	15			

- Molecule 2 is a protein called photosystem II core light harvesting protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	476	Total	C	N	O	S	0	0	0
			3739	2455	625	646	13			
2	b	476	Total	C	N	O	S	0	0	0
			3739	2455	625	646	13			

- Molecule 3 is a protein called photosystem II CP43 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	421	Total	C	N	O	S	0	0	0
			3253	2140	544	557	12			
3	c	421	Total	C	N	O	S	0	0	0
			3253	2140	544	557	12			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	MET	-	insertion	UNP Q8DIF8
C	2	LYS	-	insertion	UNP Q8DIF8
C	3	THR	-	insertion	UNP Q8DIF8
C	4	LEU	-	insertion	UNP Q8DIF8
C	5	SER	-	insertion	UNP Q8DIF8
C	6	SER	-	insertion	UNP Q8DIF8
C	7	GLN	-	insertion	UNP Q8DIF8
C	8	LYS	-	insertion	UNP Q8DIF8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	9	ARG	-	insertion	UNP Q8DIF8
C	10	TYR	-	insertion	UNP Q8DIF8
C	11	SER	-	insertion	UNP Q8DIF8
C	12	PRO	-	insertion	UNP Q8DIF8
C	13	VAL	-	insertion	UNP Q8DIF8
c	2001	MET	-	insertion	UNP Q8DIF8
c	2002	LYS	-	insertion	UNP Q8DIF8
c	2003	THR	-	insertion	UNP Q8DIF8
c	2004	LEU	-	insertion	UNP Q8DIF8
c	2005	SER	-	insertion	UNP Q8DIF8
c	2006	SER	-	insertion	UNP Q8DIF8
c	2007	GLN	-	insertion	UNP Q8DIF8
c	2008	LYS	-	insertion	UNP Q8DIF8
c	2009	ARG	-	insertion	UNP Q8DIF8
c	2010	TYR	-	insertion	UNP Q8DIF8
c	2011	SER	-	insertion	UNP Q8DIF8
c	2012	PRO	-	insertion	UNP Q8DIF8
c	2013	VAL	-	insertion	UNP Q8DIF8

- Molecule 4 is a protein called photosystem II reaction center D2 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	339	Total	C	N	O	S	0	0	0
			2702	1792	439	459	12			
4	d	339	Total	C	N	O	S	0	0	0
			2702	1792	439	459	12			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	76	Total	C	N	O	0	0	0
			624	411	99	114			
5	e	76	Total	C	N	O	0	0	0
			624	411	99	114			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	33	Total	C	N	O	S	0	0	0
			269	184	44	40	1			
6	f	33	Total	C	N	O	S	0	0	0
			269	184	44	40	1			

- Molecule 7 is a protein called photosystem II PsbH protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	53	Total	C	N	O	S	0	0	0
			409	276	60	71	2			
7	h	53	Total	C	N	O	S	0	0	0
			409	276	60	71	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	38	Total	C	N	O	S	0	0	0
			312	210	48	53	1			
8	i	38	Total	C	N	O	S	0	0	0
			312	210	48	53	1			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	L	37	Total	C	N	O	S	0	0	0
			304	202	48	53	1			
11	l	37	Total	C	N	O	S	0	0	0
			304	202	48	53	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	M	30	Total	C	N	O	S	0	0	0
			234	159	33	41	1			
12	m	30	Total	C	N	O	S	0	0	0
			234	159	33	41	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	O	246	Total	C	N	O	S	0	0	0
			1888	1179	320	385	4			
13	o	246	Total	C	N	O	S	0	0	0
			1888	1179	320	385	4			

- Molecule 14 is a protein called photosystem II PsbT protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	T	31	Total	C	N	O	S	0	0	0
			265	186	38	39	2			
14	t	31	Total	C	N	O	S	0	0	0
			265	186	38	39	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	U	105	Total	C	N	O		0	0	0
			827	521	137	169				
15	u	105	Total	C	N	O		0	0	0
			827	521	137	169				

- 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 PsbX protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	X	40	Total	C	N	O	0	0	0
			296	197	47	52			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	x	40	Total	C	N	O	0	0	0
			296	197	47	52			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	1	MET	-	insertion	UNP Q9F1R6
X	2	ILE	-	insertion	UNP Q9F1R6
X	3	GLN	-	insertion	UNP Q9F1R6
X	4	SER	-	insertion	UNP Q9F1R6
X	5	ALA	-	insertion	UNP Q9F1R6
X	6	SER	-	insertion	UNP Q9F1R6
X	7	SER	-	insertion	UNP Q9F1R6
X	8	LEU	-	insertion	UNP Q9F1R6
X	9	LEU	-	insertion	UNP Q9F1R6
X	10	LEU	-	insertion	UNP Q9F1R6
x	2001	MET	-	insertion	UNP Q9F1R6
x	2002	ILE	-	insertion	UNP Q9F1R6
x	2003	GLN	-	insertion	UNP Q9F1R6
x	2004	SER	-	insertion	UNP Q9F1R6
x	2005	ALA	-	insertion	UNP Q9F1R6
x	2006	SER	-	insertion	UNP Q9F1R6
x	2007	SER	-	insertion	UNP Q9F1R6
x	2008	LEU	-	insertion	UNP Q9F1R6
x	2009	LEU	-	insertion	UNP Q9F1R6
x	2010	LEU	-	insertion	UNP Q9F1R6

- Molecule 18 is a protein called Photosystem II PsbN protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	N	37	Total	C	N	O	0	0	0
			186	111	37	38			
18	n	37	Total	C	N	O	0	0	0
			186	111	37	38			

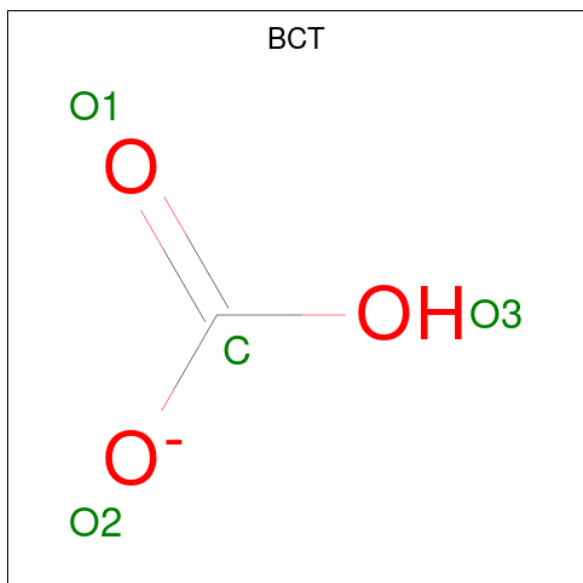
- Molecule 19 is a protein called Photosystem II reaction center Z protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	Z	58	Total	C	N	O	S	0	0	0
			442	300	68	72	2			
19	z	58	Total	C	N	O	S	0	0	0
			442	300	68	72	2			

- Molecule 20 is FE (III) ION (CCD ID: FE) (formula: Fe).

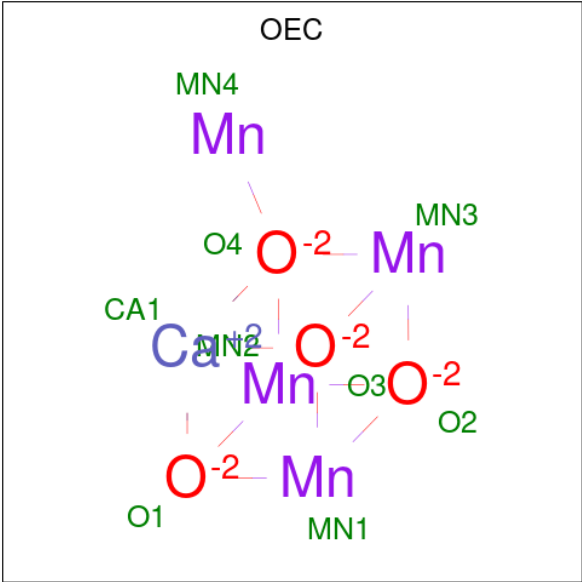
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	A	1	Total	Fe	0	0
			1	1		
20	a	1	Total	Fe	0	0
			1	1		

- Molecule 21 is BICARBONATE ION (CCD ID: BCT) (formula: CHO_3).



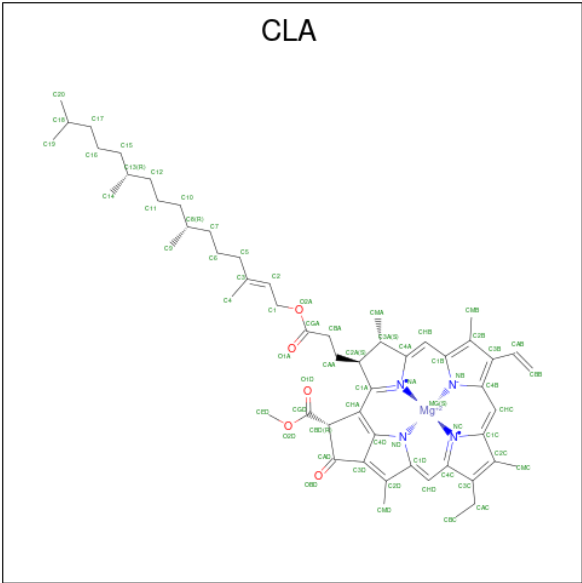
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	A	1	Total	C	O	0	0
			4	1	3		
21	D	1	Total	C	O	0	0
			4	1	3		
21	a	1	Total	C	O	0	0
			4	1	3		
21	d	1	Total	C	O	0	0
			4	1	3		

- Molecule 22 is OXYGEN EVOLVING SYSTEM (CCD ID: OEC) (formula: CaMn_4O_4).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
22	A	1	Total	Ca	Mn	O	0	0
			9	1	4	4		
22	a	1	Total	Ca	Mn	O	0	0
			9	1	4	4		

- Molecule 23 is CHLOROPHYLL A (CCD ID: CLA) (formula: $C_{55}H_{72}MgN_4O_5$).



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

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

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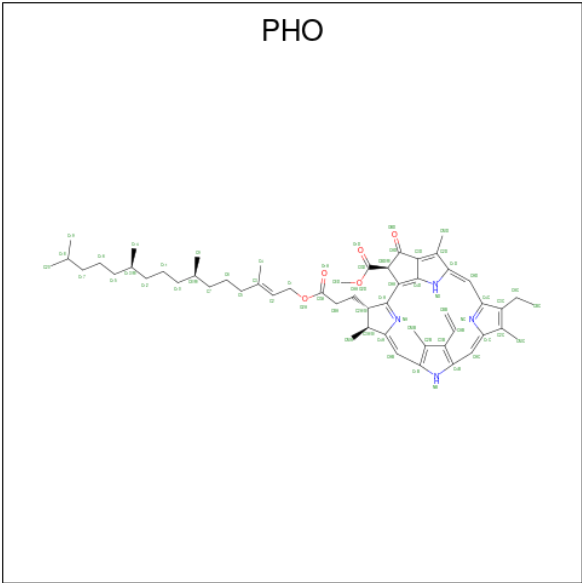
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
23	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
23	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
23	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
23	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
23	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
23	b	1	Total 65	C 55	Mg 1	N 4	O 5	0	0
23	b	1	Total 65	C 55	Mg 1	N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

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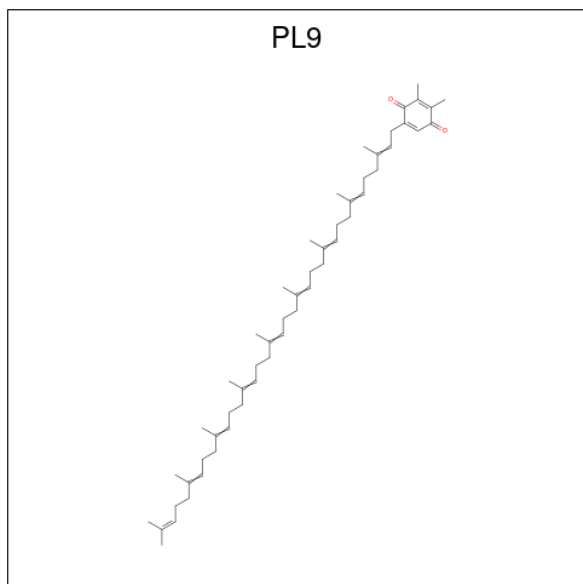
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	d	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	d	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5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

- Molecule 24 is PHEOPHYTIN A (CCD ID: PHO) (formula: C₅₅H₇₄N₄O₅).



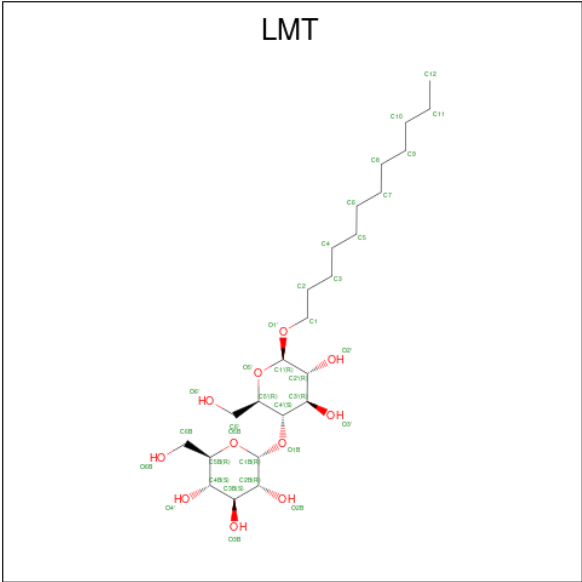
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
24	A	1	Total	C	N	O	0	0
			64	55	4	5		
24	D	1	Total	C	N	O	0	0
			64	55	4	5		
24	a	1	Total	C	N	O	0	0
			64	55	4	5		
24	d	1	Total	C	N	O	0	0
			64	55	4	5		

- Molecule 25 is 2,3-DIMETHYL-5-(3,7,11,15,19,23,27,31,35-NONAMETHYL-2,6,10,14,18,22,26,30,34-HEXATRIACONTANONAENYL-2,5-CYCLOHEXADIENE-1,4-DIONE-2,3-DIMETHYL-5-SOLANESYL-1,4-BENZOQUINONE (CCD ID: PL9) (formula: $C_{53}H_{80}O_2$).



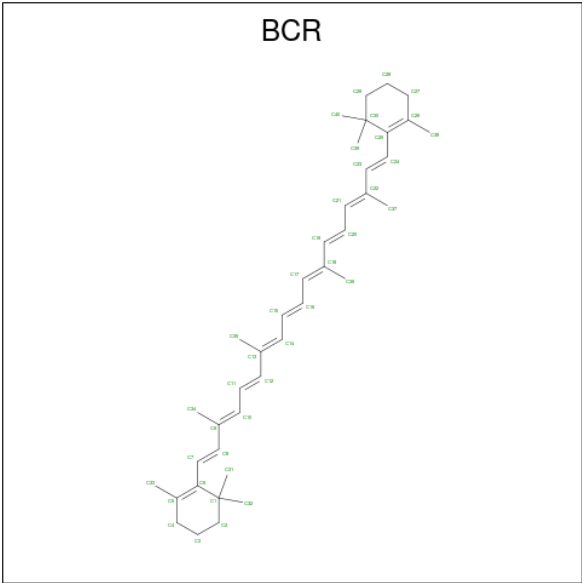
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
25	A	1	Total	C	O	0	0
			45	43	2		
25	D	1	Total	C	O	0	0
			45	43	2		
25	a	1	Total	C	O	0	0
			45	43	2		
25	d	1	Total	C	O	0	0
			45	43	2		

- Molecule 26 is DODECYL-BETA-D-MALTOSE (CCD ID: LMT) (formula: $C_{24}H_{46}O_{11}$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	B	1	Total	C	O	0
			35	24	11	
26	d	1	Total	C	O	0
			35	24	11	

- Molecule 27 is BETA-CAROTENE (CCD ID: BCR) (formula: $C_{40}H_{56}$).



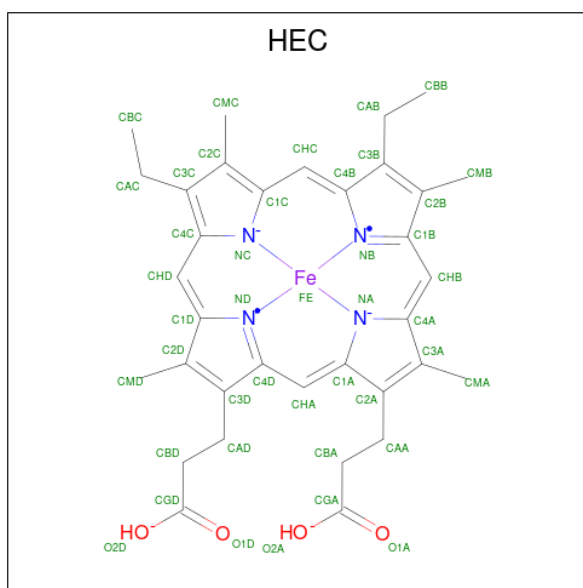
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
27	B	1	Total	C		0
			40	40		
27	B	1	Total	C		0
			40	40		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
27	C	1	Total C 40 40	0	0
27	C	1	Total C 40 40	0	0
27	F	1	Total C 40 40	0	0
27	J	1	Total C 40 40	0	0
27	K	1	Total C 40 40	0	0
27	b	1	Total C 40 40	0	0
27	b	1	Total C 40 40	0	0
27	c	1	Total C 40 40	0	0
27	c	1	Total C 40 40	0	0
27	d	1	Total C 40 40	0	0
27	j	1	Total C 40 40	0	0
27	k	1	Total C 40 40	0	0

- Molecule 28 is HEME C (CCD ID: HEC) (formula: $\text{C}_{34}\text{H}_{36}\text{FeN}_4\text{O}_4$).

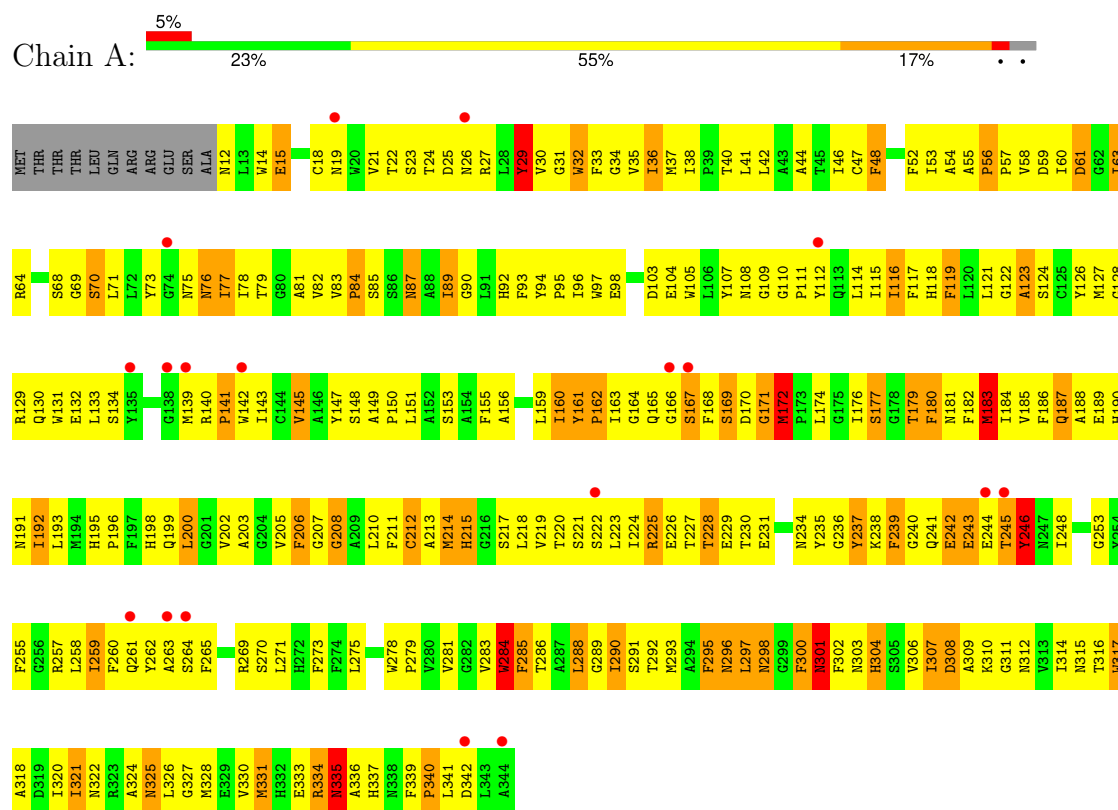


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
28	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
28	V	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
28	e	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
28	v	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

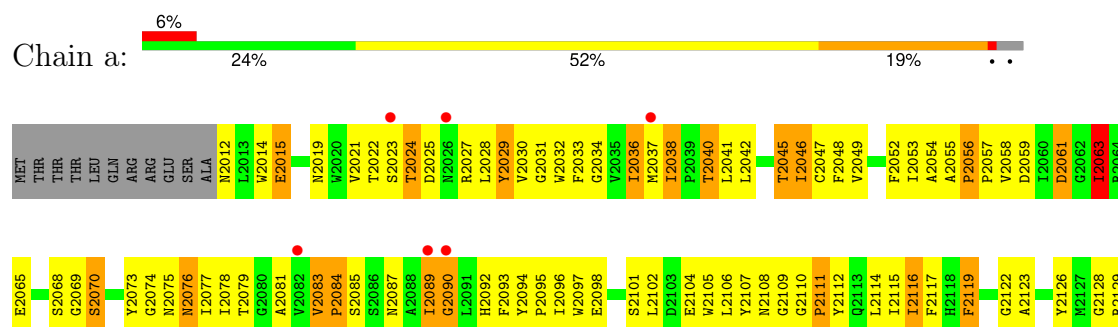
3 Residue-property plots [i](#)

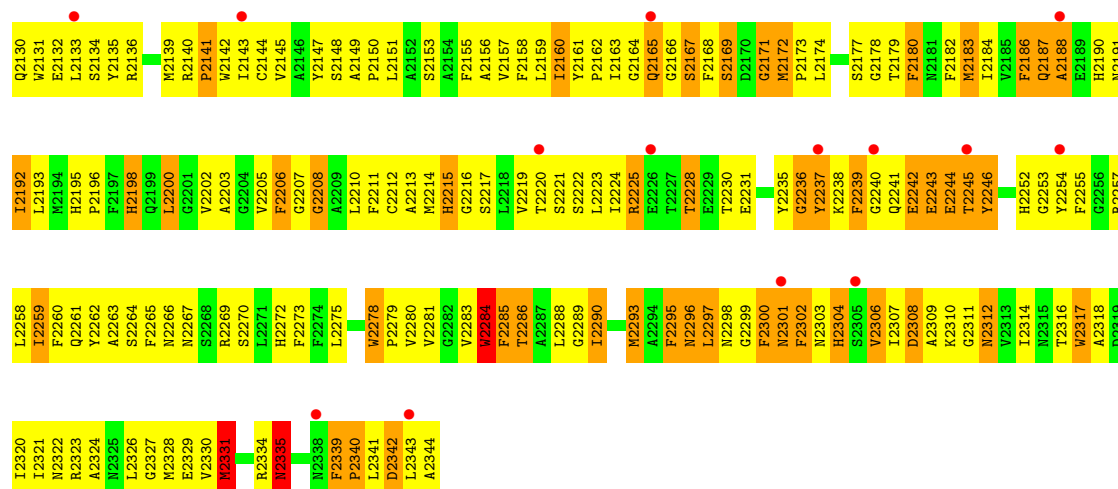
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 Q(B) protein

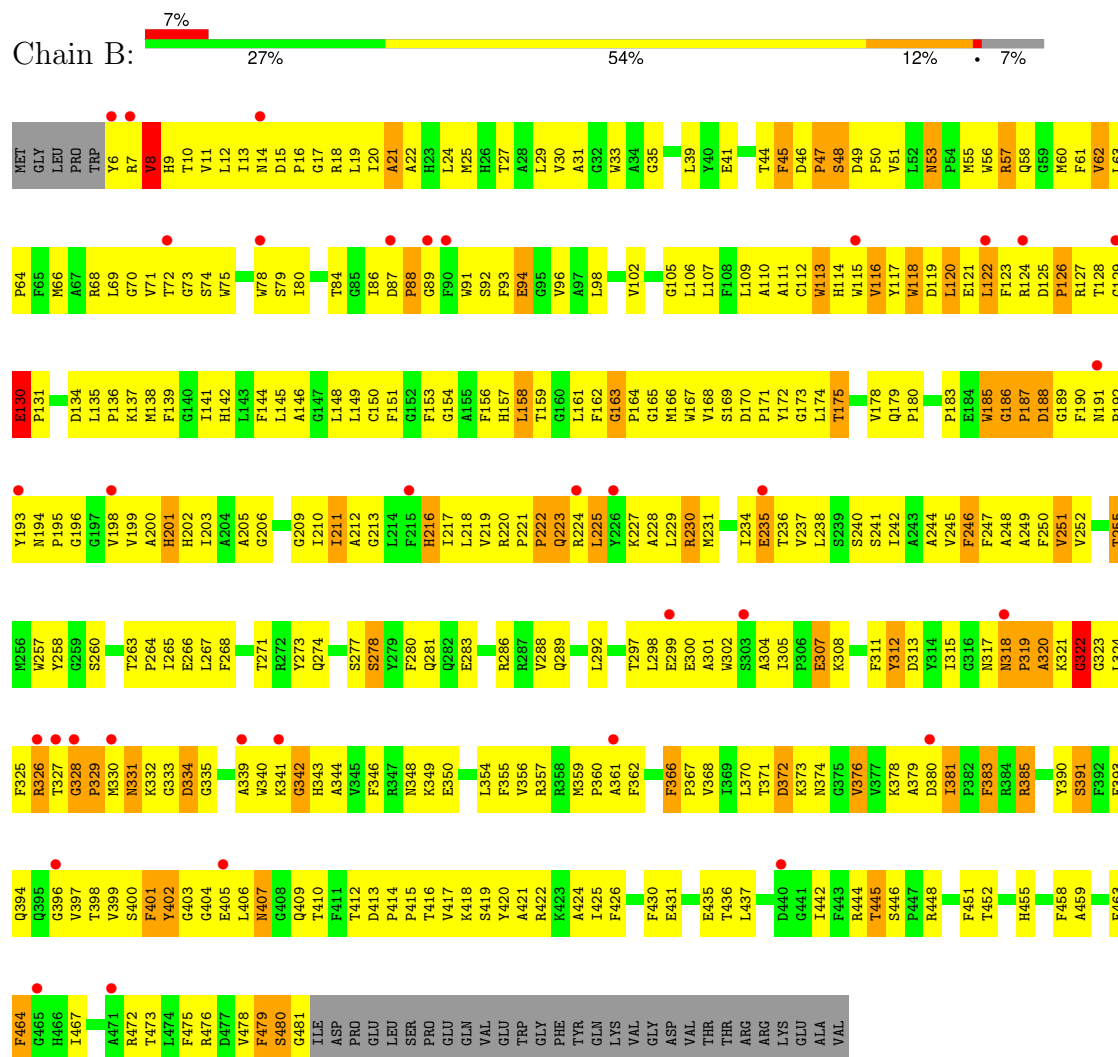


• Molecule 1: Photosystem Q(B) protein





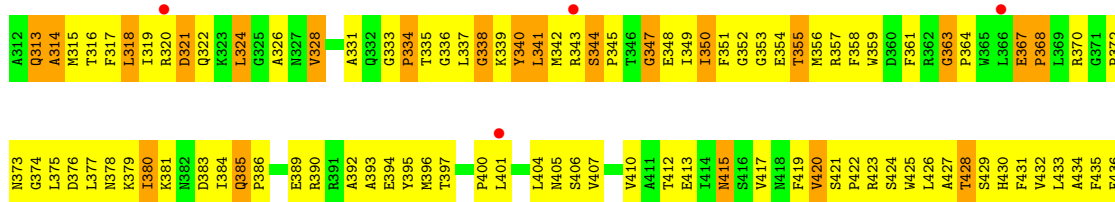
• Molecule 2: photosystem II core light harvesting protein



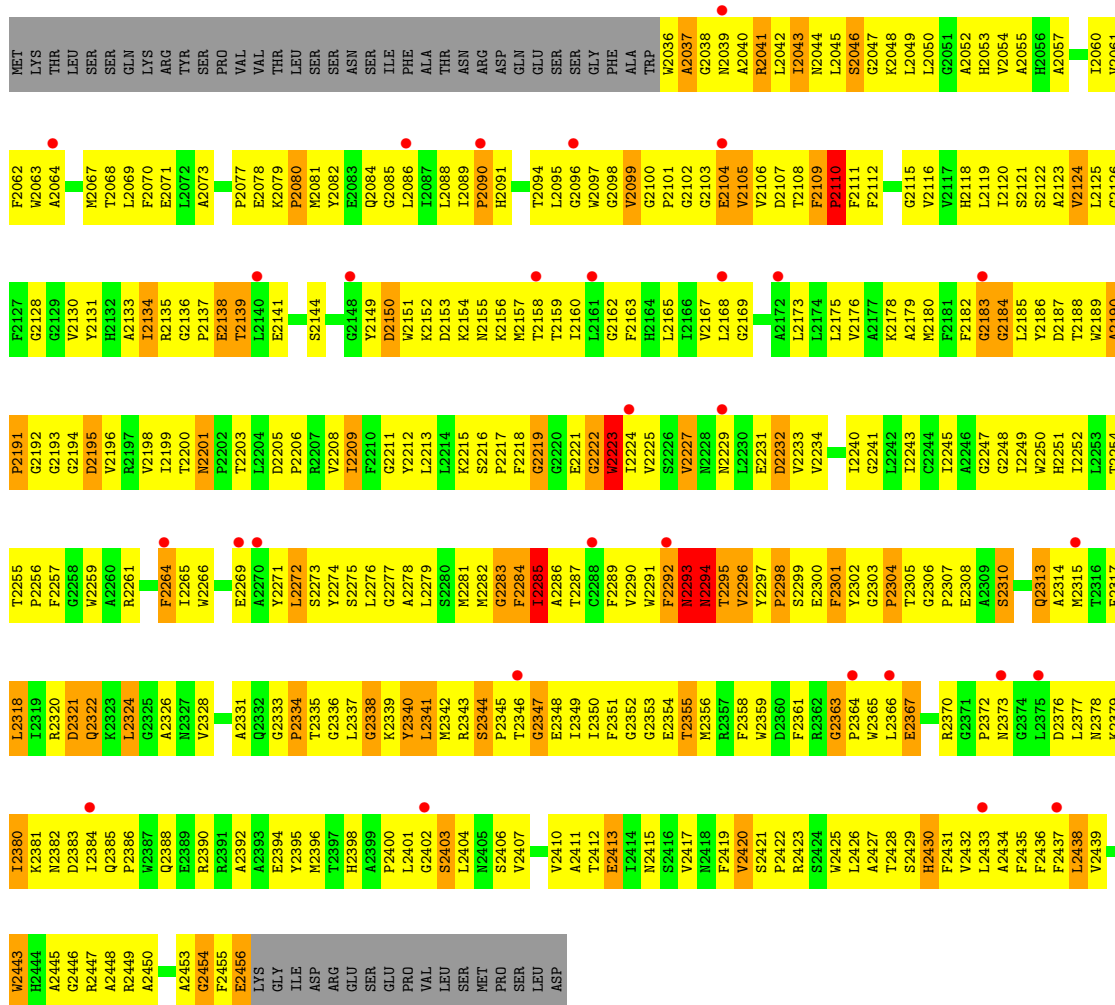
• Molecule 2: photosystem II core light harvesting protein







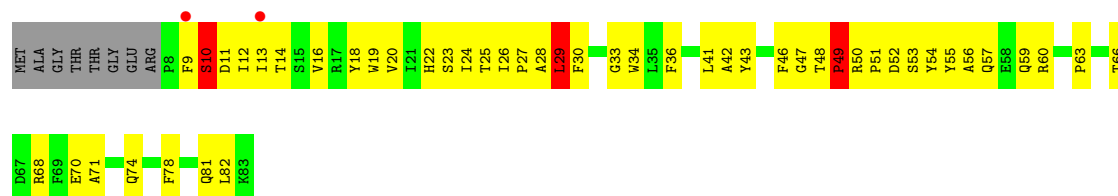
• Molecule 3: photosystem II CP43 protein



• Molecule 4: photosystem II reaction center D2 protein







• Molecule 5: Cytochrome b559 alpha subunit



• Molecule 6: Cytochrome b559 beta subunit



• Molecule 6: Cytochrome b559 beta subunit



• Molecule 7: photosystem II PsbH protein

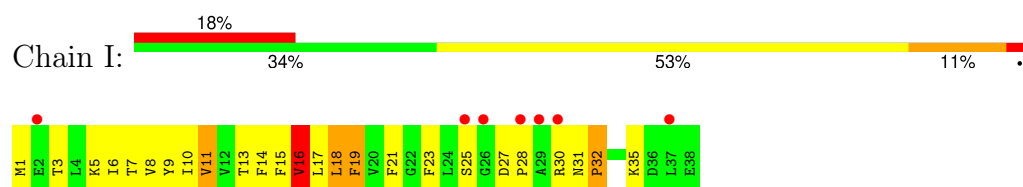


• Molecule 7: photosystem II PsbH protein

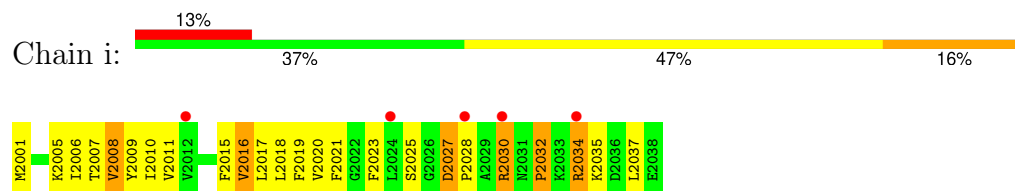


• Molecule 8: Photosystem II reaction center I protein

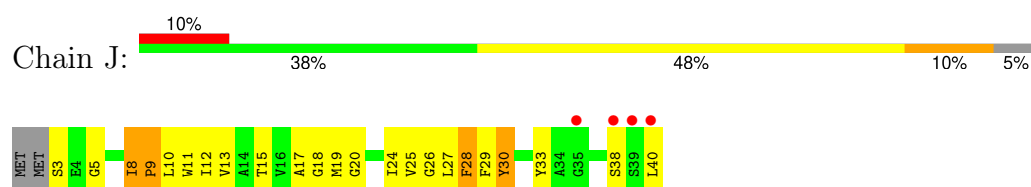




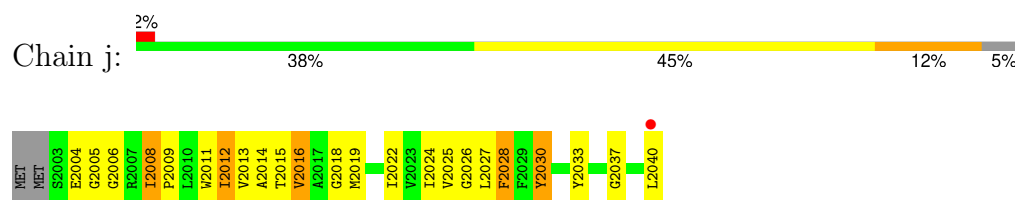
• Molecule 8: Photosystem II reaction center I protein



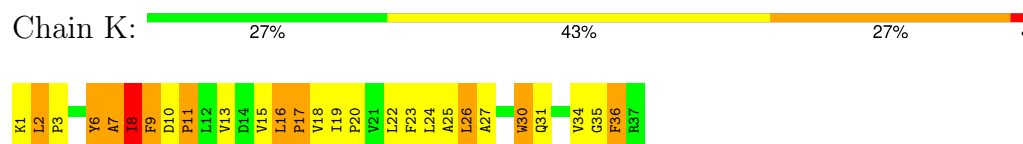
• Molecule 9: Photosystem II reaction center J protein



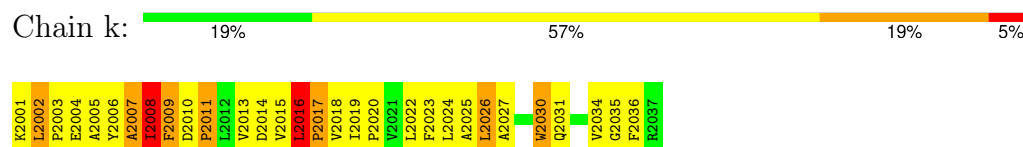
• Molecule 9: Photosystem II reaction center J protein



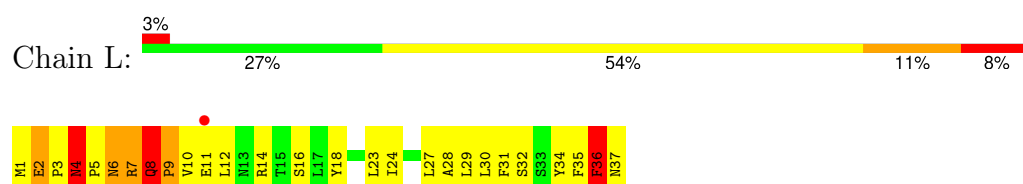
• Molecule 10: Photosystem II reaction center protein K



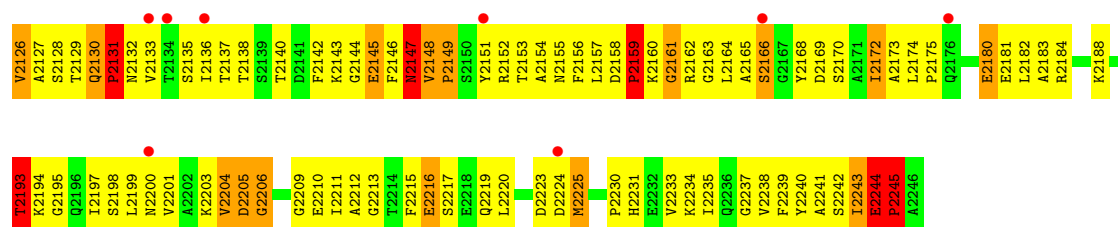
• Molecule 10: Photosystem II reaction center protein K



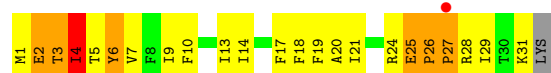
• Molecule 11: Photosystem II reaction center L protein



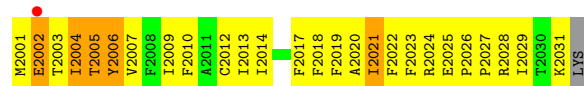
- | |
|-------|
| F2065 | V2066 | P2067 | K2068 | L2070 | V2071 | T2072 | E2073 | T2075 | T2076 | S2077 | L2078 | D2079 | Q2080 | Q2081 | Q2082 | G2083 | E2084 | L2085 | N2088 | S2089 | D2090 | G2091 | S2092 | L2093 | T2094 | F2095 | V2096 | E2097 | E2098 | D2099 | G2100 | L2101 | D2102 | F2103 | Q2104 | P2105 | T2106 | T2107 | V2108 | Q2109 | M2110 | A2111 | G2112 | E2114 | R2115 | T2116 | P2117 | L2118 | L2119 | F2120 | T2121 | V2122 | K2123 | L2124 | L2125 |
|-------|



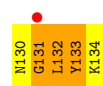
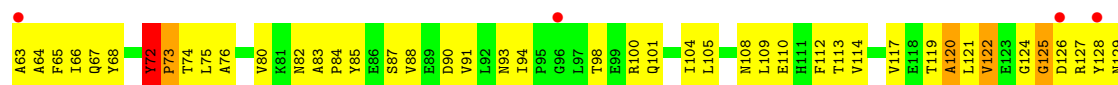
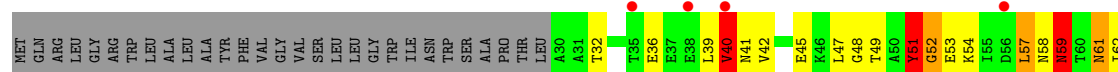
• Molecule 14: photosystem II PsbT protein



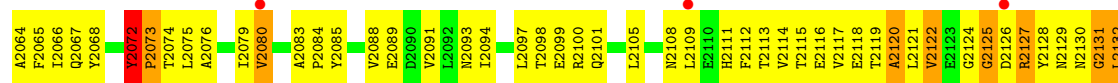
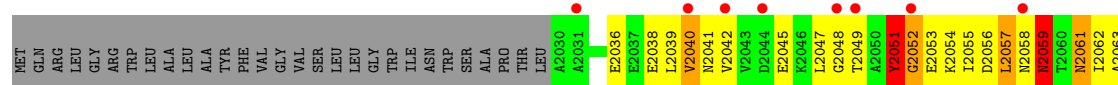
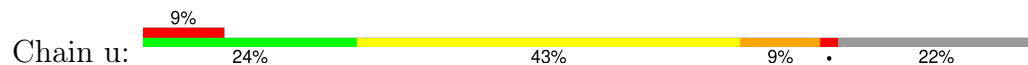
• Molecule 14: photosystem II PsbT protein



• Molecule 15: Photosystem II 12 kDa extrinsic protein

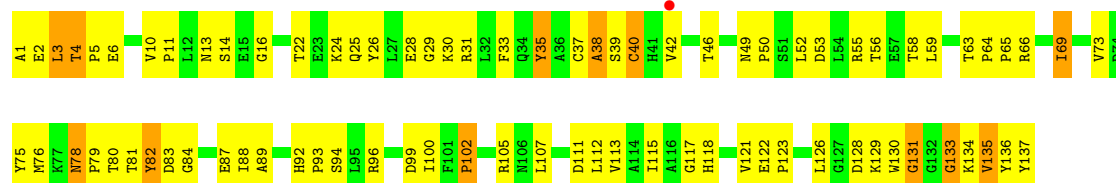
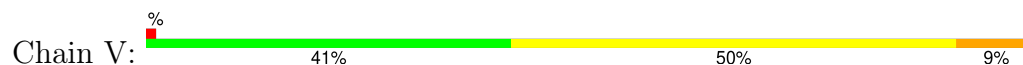


• Molecule 15: Photosystem II 12 kDa extrinsic protein

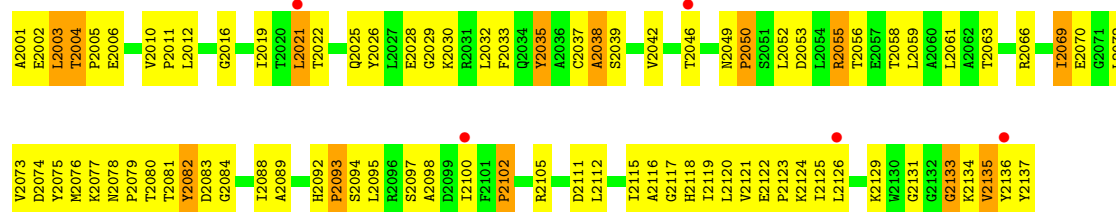


Y2133
K2134

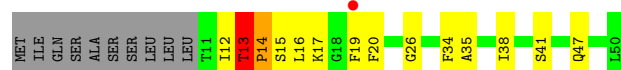
• Molecule 16: Cytochrome c-550



• Molecule 16: Cytochrome c-550



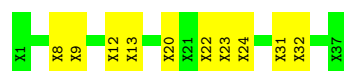
• Molecule 17: photosystem II PsbX protein



• Molecule 17: photosystem II PsbX protein



• Molecule 18: Photosystem II PsbN protein

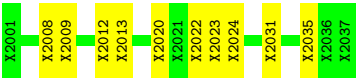


• Molecule 18: Photosystem II PsbN protein

Chain n:

73%

27%



• Molecule 19: Photosystem II reaction center Z protein

Chain Z:

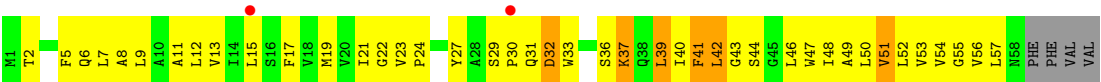
3%

26%

58%

10%

6%



• Molecule 19: Photosystem II reaction center Z protein

Chain z:

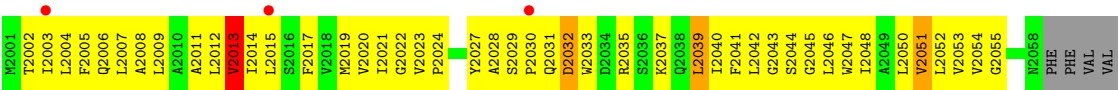
5%

21%

66%

5%

6%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	134.99Å 228.85Å 309.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.50 20.00 – 3.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-3.50) 85.2 (20.00-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 3.49Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.296 , 0.342 0.309 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	118.3	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 80.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	45945	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.90% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: BCT, PL9, LMT, BCR, HEC, CLA, PHO, OEC, FE

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	0.87	5/2702 (0.2%)	1.28	43/3685 (1.2%)
1	a	0.76	1/2701 (0.0%)	1.27	40/3685 (1.1%)
2	B	0.72	0/3870	1.23	48/5271 (0.9%)
2	b	0.71	0/3870	1.23	53/5271 (1.0%)
3	C	0.74	1/3361 (0.0%)	1.26	45/4579 (1.0%)
3	c	0.69	0/3361	1.24	39/4579 (0.9%)
4	D	0.75	1/2797 (0.0%)	1.26	30/3813 (0.8%)
4	d	0.74	0/2797	1.27	36/3813 (0.9%)
5	E	0.73	0/643	1.26	8/876 (0.9%)
5	e	0.77	1/643 (0.2%)	1.26	9/876 (1.0%)
6	F	0.90	1/278 (0.4%)	1.26	4/379 (1.1%)
6	f	0.88	2/278 (0.7%)	1.30	7/379 (1.8%)
7	H	0.75	0/419	1.29	6/570 (1.1%)
7	h	0.73	0/419	1.23	6/570 (1.1%)
8	I	0.70	0/319	1.08	3/429 (0.7%)
8	i	0.68	0/319	1.07	2/429 (0.5%)
9	J	0.74	0/278	1.34	7/376 (1.9%)
9	j	0.73	0/278	1.38	8/376 (2.1%)
10	K	0.81	0/303	1.27	3/416 (0.7%)
10	k	0.77	0/303	1.25	4/416 (1.0%)
11	L	0.85	0/311	1.20	3/422 (0.7%)
11	l	0.90	0/311	1.18	3/422 (0.7%)
12	M	0.85	0/237	1.21	1/324 (0.3%)
12	m	0.87	0/237	1.18	1/324 (0.3%)
13	O	0.80	0/1919	1.44	38/2601 (1.5%)
13	o	0.80	0/1919	1.44	40/2601 (1.5%)
14	T	0.81	0/274	1.34	8/370 (2.2%)
14	t	0.84	0/274	1.30	4/370 (1.1%)
15	U	0.84	1/838 (0.1%)	1.23	5/1137 (0.4%)
15	u	0.75	0/838	1.21	7/1137 (0.6%)
16	V	0.77	1/1085 (0.1%)	1.09	4/1473 (0.3%)
16	v	0.66	0/1085	1.08	4/1473 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	X	0.67	0/299	1.12	3/403 (0.7%)
17	x	0.70	0/299	1.18	2/403 (0.5%)
19	Z	0.68	0/451	1.10	0/617
19	z	0.67	0/451	1.05	1/617 (0.2%)
All	All	0.76	14/40767 (0.0%)	1.26	525/55482 (0.9%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	1
2	b	0	1
11	l	0	1
13	O	0	1
15	U	0	2
All	All	0	7

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	183	MET	SD-CE	-10.50	1.53	1.79
1	A	328	MET	SD-CE	-7.79	1.60	1.79
1	A	172	MET	SD-CE	-6.34	1.63	1.79
16	V	113	VAL	CA-CB	-5.88	1.47	1.54
1	A	290	ILE	CA-CB	-5.87	1.47	1.54

The worst 5 of 525 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	O	193	THR	N-CA-C	13.08	125.47	108.34
13	o	2193	THR	N-CA-C	11.98	125.75	108.86
14	T	2	GLU	N-CA-C	-10.92	99.16	111.71
4	D	334	GLN	CA-C-N	10.88	131.25	119.28
4	D	334	GLN	C-N-CA	10.88	131.25	119.28

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	246	TYR	Sidechain
2	B	273	TYR	Sidechain
13	O	240	TYR	Sidechain
15	U	133	TYR	Sidechain
15	U	51	TYR	Sidechain

5.2 Too-close contacts

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	2617	0	2514	468	0
1	a	2616	0	2514	493	0
2	B	3739	0	3613	491	0
2	b	3739	0	3613	494	0
3	C	3253	0	3192	553	0
3	c	3253	0	3192	519	0
4	D	2702	0	2605	428	0
4	d	2702	0	2605	467	0
5	E	624	0	613	98	0
5	e	624	0	613	91	0
6	F	269	0	277	45	0
6	f	269	0	277	46	0
7	H	409	0	424	52	0
7	h	409	0	424	57	0
8	I	312	0	329	29	0
8	i	312	0	326	35	0
9	J	272	0	279	45	0
9	j	272	0	279	42	0
10	K	293	0	308	59	0
10	k	293	0	305	63	0
11	L	304	0	316	50	0
11	l	304	0	313	64	0
12	M	234	0	255	43	0
12	m	234	0	252	45	0
13	O	1888	0	1867	297	6
13	o	1888	0	1864	297	0
14	T	265	0	275	42	0
14	t	265	0	272	36	0
15	U	827	0	819	125	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	u	827	0	819	117	0
16	V	1064	0	1075	131	0
16	v	1064	0	1070	117	0
17	X	296	0	328	13	0
17	x	296	0	328	16	0
18	N	186	0	40	10	0
18	n	186	0	40	10	6
19	Z	442	0	480	64	0
19	z	442	0	477	65	0
20	A	1	0	0	0	0
20	a	1	0	0	0	0
21	A	4	0	0	0	0
21	D	4	0	0	0	0
21	a	4	0	0	0	0
21	d	4	0	0	0	0
22	A	9	0	0	1	0
22	a	9	0	0	0	0
23	A	260	0	288	22	0
23	B	1040	0	1152	113	0
23	C	910	0	1008	100	0
23	D	130	0	144	16	0
23	a	195	0	216	20	0
23	b	1040	0	1152	109	0
23	c	910	0	1008	104	0
23	d	195	0	216	30	0
24	A	64	0	74	5	0
24	D	64	0	74	7	0
24	a	64	0	74	5	0
24	d	64	0	74	10	0
25	A	45	0	61	8	0
25	D	45	0	61	6	0
25	a	45	0	61	11	0
25	d	45	0	61	8	0
26	B	35	0	46	0	0
26	d	35	0	46	5	0
27	B	80	0	112	18	0
27	C	80	0	112	23	0
27	F	40	0	56	3	0
27	J	40	0	56	2	0
27	K	40	0	56	13	0
27	b	80	0	112	19	0
27	c	80	0	112	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	d	40	0	56	2	0
27	j	40	0	56	2	0
27	k	40	0	56	16	0
28	E	43	0	32	17	0
28	V	43	0	32	9	0
28	e	43	0	32	15	0
28	v	43	0	31	1	0
All	All	45945	0	45919	5461	6

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 59.

The worst 5 of 5461 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)
28:V:138:HEC:C2B	28:V:138:HEC:CMB	1.74	1.58
28:V:138:HEC:C2C	28:V:138:HEC:CMC	1.75	1.57
16:V:37:CYS:SG	28:V:138:HEC:HAB	1.57	1.44
5:E:12:ILE:CG2	5:E:18:TYR:HB2	1.44	1.43
5:e:2012:ILE:CG2	5:e:2018:TYR:HB2	1.46	1.42

The worst 5 of 6 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:246:ALA:C	18:n:2035:UNK:O[2_555]	1.76	0.44
13:O:246:ALA:N	18:n:2035:UNK:O[2_555]	1.97	0.23
13:O:246:ALA:O	18:n:2035:UNK:O[2_555]	2.07	0.13
13:O:246:ALA:O	18:n:2035:UNK:CB[2_555]	2.15	0.05
13:O:246:ALA:N	18:n:2035:UNK:C[2_555]	2.17	0.03

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	331/344 (96%)	251 (76%)	58 (18%)	22 (7%)	1	11
1	a	331/344 (96%)	253 (76%)	56 (17%)	22 (7%)	1	11
2	B	474/510 (93%)	367 (77%)	84 (18%)	23 (5%)	1	16
2	b	474/510 (93%)	367 (77%)	83 (18%)	24 (5%)	1	15
3	C	419/473 (89%)	326 (78%)	60 (14%)	33 (8%)	1	8
3	c	419/473 (89%)	326 (78%)	62 (15%)	31 (7%)	1	9
4	D	337/352 (96%)	274 (81%)	49 (14%)	14 (4%)	2	19
4	d	337/352 (96%)	270 (80%)	51 (15%)	16 (5%)	2	17
5	E	74/84 (88%)	62 (84%)	10 (14%)	2 (3%)	4	27
5	e	74/84 (88%)	57 (77%)	14 (19%)	3 (4%)	2	19
6	F	31/45 (69%)	23 (74%)	5 (16%)	3 (10%)	0	6
6	f	31/45 (69%)	22 (71%)	6 (19%)	3 (10%)	0	6
7	H	51/66 (77%)	35 (69%)	13 (26%)	3 (6%)	1	12
7	h	51/66 (77%)	35 (69%)	13 (26%)	3 (6%)	1	12
8	I	36/38 (95%)	25 (69%)	10 (28%)	1 (3%)	4	26
8	i	36/38 (95%)	27 (75%)	7 (19%)	2 (6%)	1	13
9	J	36/40 (90%)	32 (89%)	3 (8%)	1 (3%)	4	26
9	j	36/40 (90%)	30 (83%)	4 (11%)	2 (6%)	1	13
10	K	35/37 (95%)	27 (77%)	2 (6%)	6 (17%)	0	2
10	k	35/37 (95%)	26 (74%)	3 (9%)	6 (17%)	0	2
11	L	35/37 (95%)	28 (80%)	3 (9%)	4 (11%)	0	5
11	l	35/37 (95%)	27 (77%)	5 (14%)	3 (9%)	0	7
12	M	28/36 (78%)	22 (79%)	5 (18%)	1 (4%)	2	22
12	m	28/36 (78%)	22 (79%)	4 (14%)	2 (7%)	1	10
13	O	244/246 (99%)	180 (74%)	44 (18%)	20 (8%)	0	8
13	o	244/246 (99%)	179 (73%)	45 (18%)	20 (8%)	0	8
14	T	29/32 (91%)	23 (79%)	3 (10%)	3 (10%)	0	5
14	t	29/32 (91%)	22 (76%)	5 (17%)	2 (7%)	1	10
15	U	103/134 (77%)	78 (76%)	14 (14%)	11 (11%)	0	5
15	u	103/134 (77%)	81 (79%)	11 (11%)	11 (11%)	0	5
16	V	135/137 (98%)	111 (82%)	16 (12%)	8 (6%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	v	135/137 (98%)	106 (78%)	22 (16%)	7 (5%)	1	14
17	X	38/50 (76%)	36 (95%)	1 (3%)	1 (3%)	4	27
17	x	38/50 (76%)	35 (92%)	2 (5%)	1 (3%)	4	27
19	Z	56/62 (90%)	39 (70%)	15 (27%)	2 (4%)	2	22
19	z	56/62 (90%)	40 (71%)	13 (23%)	3 (5%)	1	14
All	All	4984/5446 (92%)	3864 (78%)	801 (16%)	319 (6%)	1	11

5 of 319 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	90	GLY
1	A	228	THR
1	A	242	GLU
1	A	308	ASP
2	B	88	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	270/280 (96%)	247 (92%)	23 (8%)	10	34
1	a	270/280 (96%)	246 (91%)	24 (9%)	9	32
2	B	377/407 (93%)	357 (95%)	20 (5%)	20	47
2	b	377/407 (93%)	356 (94%)	21 (6%)	19	46
3	C	326/374 (87%)	306 (94%)	20 (6%)	17	43
3	c	326/374 (87%)	304 (93%)	22 (7%)	15	41
4	D	275/283 (97%)	256 (93%)	19 (7%)	14	39
4	d	275/283 (97%)	253 (92%)	22 (8%)	11	35
5	E	68/73 (93%)	65 (96%)	3 (4%)	25	51
5	e	68/73 (93%)	64 (94%)	4 (6%)	18	44
6	F	27/39 (69%)	25 (93%)	2 (7%)	13	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	f	27/39 (69%)	26 (96%)	1 (4%)	30	56
7	H	44/55 (80%)	42 (96%)	2 (4%)	24	50
7	h	44/55 (80%)	40 (91%)	4 (9%)	9	32
8	I	35/35 (100%)	31 (89%)	4 (11%)	5	24
8	i	35/35 (100%)	32 (91%)	3 (9%)	10	33
9	J	26/28 (93%)	25 (96%)	1 (4%)	29	55
9	j	26/28 (93%)	26 (100%)	0	100	100
10	K	30/30 (100%)	27 (90%)	3 (10%)	7	28
10	k	30/30 (100%)	28 (93%)	2 (7%)	15	41
11	L	35/35 (100%)	31 (89%)	4 (11%)	5	24
11	l	35/35 (100%)	31 (89%)	4 (11%)	5	24
12	M	27/33 (82%)	24 (89%)	3 (11%)	6	25
12	m	27/33 (82%)	26 (96%)	1 (4%)	30	56
13	O	208/208 (100%)	185 (89%)	23 (11%)	6	25
13	o	208/208 (100%)	190 (91%)	18 (9%)	9	33
14	T	28/29 (97%)	27 (96%)	1 (4%)	31	57
14	t	28/29 (97%)	26 (93%)	2 (7%)	13	38
15	U	89/112 (80%)	85 (96%)	4 (4%)	24	50
15	u	89/112 (80%)	85 (96%)	4 (4%)	24	50
16	V	117/117 (100%)	111 (95%)	6 (5%)	21	48
16	v	117/117 (100%)	112 (96%)	5 (4%)	26	51
17	X	33/42 (79%)	30 (91%)	3 (9%)	9	32
17	x	33/42 (79%)	29 (88%)	4 (12%)	5	22
19	Z	48/52 (92%)	43 (90%)	5 (10%)	7	27
19	z	48/52 (92%)	45 (94%)	3 (6%)	16	42
All	All	4126/4464 (92%)	3836 (93%)	290 (7%)	14	39

5 of 290 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	d	2279	LEU
17	x	2047	GLN
5	e	2053	SER

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Mol	Chain	Res	Type
13	o	2068	THR
11	L	4	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 116 such sidechains are listed below:

Mol	Chain	Res	Type
13	O	236	GLN
13	o	2236	GLN
1	a	2322	ASN
13	o	2155	ASN
6	f	2043	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 108 ligands modelled in this entry, 2 are monoatomic - leaving 106 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	$\# Z > 2$
23	CLA	A	350	-	69,73,73	1.33	5 (7%)	82,113,113	1.78	12 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
21	BCT	a	2346	22	3,3,3	1.80	1 (33%)	2,3,3	1.34	0
26	LMT	B	526	-	36,36,36	1.35	4 (11%)	47,47,47	1.93	8 (17%)
23	CLA	b	2521	2	69,73,73	1.38	9 (13%)	82,113,113	1.67	8 (9%)
27	BCR	C	489	-	41,41,41	1.78	7 (17%)	56,56,56	2.00	16 (28%)
23	CLA	B	527	-	69,73,73	1.54	12 (17%)	82,113,113	1.96	12 (14%)
23	CLA	D	356	4	69,73,73	1.35	13 (18%)	82,113,113	1.93	10 (12%)
23	CLA	c	2479	3	69,73,73	1.34	8 (11%)	82,113,113	2.17	17 (20%)
24	PHO	d	2356	-	58,69,69	1.65	9 (15%)	55,99,99	2.29	17 (30%)
24	PHO	a	2350	-	58,69,69	1.80	10 (17%)	55,99,99	2.07	16 (29%)
27	BCR	K	50	-	41,41,41	1.97	14 (34%)	56,56,56	1.95	17 (30%)
23	CLA	C	483	3	69,73,73	1.39	11 (15%)	82,113,113	2.11	13 (15%)
23	CLA	B	523	2	69,73,73	1.31	7 (10%)	82,113,113	2.05	11 (13%)
27	BCR	c	2488	-	41,41,41	2.00	9 (21%)	56,56,56	2.01	19 (33%)
23	CLA	d	2355	-	69,73,73	1.27	7 (10%)	82,113,113	2.11	13 (15%)
23	CLA	b	2522	2	69,73,73	1.31	9 (13%)	82,113,113	1.90	12 (14%)
27	BCR	b	2527	-	41,41,41	1.92	7 (17%)	56,56,56	2.24	20 (35%)
23	CLA	c	2477	3	69,73,73	1.46	8 (11%)	82,113,113	2.15	14 (17%)
23	CLA	C	486	3	69,73,73	1.39	8 (11%)	82,113,113	1.90	13 (15%)
23	CLA	C	477	3	69,73,73	1.47	10 (14%)	82,113,113	2.16	14 (17%)
23	CLA	B	518	2	69,73,73	1.31	5 (7%)	82,113,113	2.02	12 (14%)
23	CLA	C	480	3	69,73,73	1.26	6 (8%)	82,113,113	1.85	10 (12%)
23	CLA	D	354	4	69,73,73	1.38	9 (13%)	82,113,113	1.94	11 (13%)
23	CLA	A	348	1	69,73,73	1.34	9 (13%)	82,113,113	1.84	14 (17%)
23	CLA	b	2516	2	69,73,73	1.63	13 (18%)	82,113,113	1.94	13 (15%)
23	CLA	b	2517	2	69,73,73	1.28	9 (13%)	82,113,113	1.92	11 (13%)
27	BCR	d	2360	-	41,41,41	2.00	7 (17%)	56,56,56	2.50	21 (37%)
23	CLA	c	2482	3	69,73,73	1.45	10 (14%)	82,113,113	1.90	11 (13%)
23	CLA	B	524	-	69,73,73	1.28	8 (11%)	82,113,113	2.11	11 (13%)
28	HEC	v	2138	16	50,50,50	2.85	26 (52%)	68,82,82	2.38	26 (38%)
23	CLA	C	481	3	69,73,73	1.26	7 (10%)	82,113,113	2.11	10 (12%)
27	BCR	b	2528	-	41,41,41	2.09	10 (24%)	56,56,56	2.25	22 (39%)
23	CLA	B	514	-	69,73,73	1.45	10 (14%)	82,113,113	1.96	13 (15%)
23	CLA	B	519	2	69,73,73	1.55	13 (18%)	82,113,113	2.36	13 (15%)
23	CLA	b	2520	2	69,73,73	1.46	11 (15%)	82,113,113	2.41	13 (15%)
26	LMT	d	2359	-	36,36,36	1.36	4 (11%)	47,47,47	1.93	7 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	CLA	b	2519	2	69,73,73	1.49	12 (17%)	82,113,113	2.27	11 (13%)
27	BCR	j	2053	-	41,41,41	2.19	8 (19%)	56,56,56	2.15	21 (37%)
23	CLA	C	487	-	69,73,73	1.58	12 (17%)	82,113,113	1.90	14 (17%)
23	CLA	B	513	2	69,73,73	1.41	10 (14%)	82,113,113	2.23	15 (18%)
23	CLA	A	349	-	69,73,73	1.30	7 (10%)	82,113,113	2.19	13 (15%)
23	CLA	c	2474	3	69,73,73	1.27	8 (11%)	82,113,113	1.97	10 (12%)
23	CLA	a	2349	-	69,73,73	1.31	5 (7%)	82,113,113	1.74	12 (14%)
27	BCR	B	528	-	41,41,41	2.03	7 (17%)	56,56,56	2.23	21 (37%)
23	CLA	C	485	-	69,73,73	1.29	8 (11%)	82,113,113	1.87	13 (15%)
23	CLA	b	2512	2	69,73,73	1.30	9 (13%)	82,113,113	2.04	11 (13%)
23	CLA	B	516	2	69,73,73	1.59	11 (15%)	82,113,113	1.94	13 (15%)
23	CLA	C	482	3	69,73,73	1.43	9 (13%)	82,113,113	1.98	10 (12%)
27	BCR	C	488	-	41,41,41	1.82	9 (21%)	56,56,56	2.02	18 (32%)
23	CLA	c	2475	-	69,73,73	1.60	12 (17%)	82,113,113	1.89	9 (10%)
25	PL9	A	353	-	45,45,55	2.32	19 (42%)	56,57,69	2.18	17 (30%)
23	CLA	B	520	2	69,73,73	1.44	10 (14%)	82,113,113	2.38	12 (14%)
23	CLA	c	2485	-	69,73,73	1.36	8 (11%)	82,113,113	1.91	12 (14%)
27	BCR	J	53	-	41,41,41	1.94	6 (14%)	56,56,56	2.14	21 (37%)
23	CLA	B	521	2	69,73,73	1.35	10 (14%)	82,113,113	1.68	10 (12%)
21	BCT	A	346	22	3,3,3	1.14	0	2,3,3	0.80	0
23	CLA	c	2483	3	69,73,73	1.38	9 (13%)	82,113,113	2.08	12 (14%)
23	CLA	B	525	2	69,73,73	1.35	9 (13%)	82,113,113	1.93	10 (12%)
23	CLA	c	2484	3	69,73,73	1.39	10 (14%)	82,113,113	1.89	11 (13%)
23	CLA	C	474	3	69,73,73	1.26	7 (10%)	82,113,113	2.01	13 (15%)
23	CLA	b	2515	2	69,73,73	1.36	10 (14%)	82,113,113	1.95	14 (17%)
23	CLA	b	2525	2	69,73,73	1.38	9 (13%)	82,113,113	1.97	10 (12%)
23	CLA	B	511	2	69,73,73	1.44	14 (20%)	82,113,113	2.15	14 (17%)
23	CLA	c	2480	3	69,73,73	1.27	6 (8%)	82,113,113	1.87	9 (10%)
21	BCT	D	353	20	3,3,3	2.10	1 (33%)	2,3,3	0.22	0
25	PL9	d	2358	-	45,45,55	2.37	19 (42%)	56,57,69	1.75	12 (21%)
23	CLA	a	2348	1	69,73,73	1.36	9 (13%)	82,113,113	1.81	13 (15%)
22	OEC	a	2347	1,3,21	0,13,13	-	-	-	-	-
23	CLA	c	2486	3	69,73,73	1.40	7 (10%)	82,113,113	1.94	15 (18%)
24	PHO	A	351	-	58,69,69	1.62	9 (15%)	55,99,99	2.03	15 (27%)
23	CLA	B	517	2	69,73,73	1.29	7 (10%)	82,113,113	1.96	11 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	BCR	F	48	-	41,41,41	2.03	7 (17%)	56,56,56	2.55	22 (39%)
23	CLA	C	478	3	69,73,73	1.35	7 (10%)	82,113,113	2.01	13 (15%)
27	BCR	c	2489	-	41,41,41	1.97	8 (19%)	56,56,56	2.02	18 (32%)
23	CLA	b	2526	-	69,73,73	1.49	11 (15%)	82,113,113	1.98	13 (15%)
23	CLA	B	515	2	69,73,73	1.37	6 (8%)	82,113,113	1.94	15 (18%)
23	CLA	c	2476	3	69,73,73	1.38	11 (15%)	82,113,113	1.87	11 (13%)
22	OEC	A	347	1,3,21	0,13,13	-	-	-	-	-
23	CLA	B	522	2	69,73,73	1.31	8 (11%)	82,113,113	1.91	12 (14%)
23	CLA	C	484	3	69,73,73	1.48	13 (18%)	82,113,113	1.87	12 (14%)
23	CLA	b	2524	-	69,73,73	1.26	9 (13%)	82,113,113	2.11	12 (14%)
23	CLA	d	2354	4	69,73,73	1.37	8 (11%)	82,113,113	1.96	11 (13%)
23	CLA	b	2513	2	69,73,73	1.39	10 (14%)	82,113,113	2.23	16 (19%)
23	CLA	C	479	3	69,73,73	1.31	8 (11%)	82,113,113	2.12	17 (20%)
23	CLA	c	2481	3	69,73,73	1.28	9 (13%)	82,113,113	2.11	13 (15%)
23	CLA	c	2478	3	69,73,73	1.33	6 (8%)	82,113,113	2.03	14 (17%)
23	CLA	b	2518	2	69,73,73	1.37	10 (14%)	82,113,113	1.99	10 (12%)
28	HEC	e	2084	6,5	50,50,50	2.34	21 (42%)	68,82,82	1.32	10 (14%)
23	CLA	b	2514	-	69,73,73	1.47	11 (15%)	82,113,113	1.97	13 (15%)
23	CLA	b	2511	2	69,73,73	1.44	12 (17%)	82,113,113	2.14	13 (15%)
27	BCR	k	2050	-	41,41,41	2.02	15 (36%)	56,56,56	1.92	17 (30%)
23	CLA	C	475	-	69,73,73	1.61	12 (17%)	82,113,113	1.96	11 (13%)
23	CLA	b	2523	2	69,73,73	1.34	10 (14%)	82,113,113	2.04	11 (13%)
28	HEC	E	84	6,5	50,50,50	2.27	15 (30%)	68,82,82	1.43	13 (19%)
23	CLA	a	2351	1	69,73,73	1.39	10 (14%)	82,113,113	1.93	12 (14%)
23	CLA	d	2357	4	69,73,73	1.39	9 (13%)	82,113,113	1.93	10 (12%)
25	PL9	a	2352	-	45,45,55	2.32	18 (40%)	56,57,69	2.21	17 (30%)
24	PHO	D	355	-	58,69,69	1.67	8 (13%)	55,99,99	2.30	18 (32%)
23	CLA	C	476	3	69,73,73	1.31	7 (10%)	82,113,113	1.92	12 (14%)
28	HEC	V	138	16	50,50,50	5.90	37 (74%)	68,82,82	2.46	27 (39%)
23	CLA	B	512	2	69,73,73	1.33	9 (13%)	82,113,113	1.98	8 (9%)
25	PL9	D	357	-	45,45,55	2.32	18 (40%)	56,57,69	1.75	12 (21%)
27	BCR	B	529	-	41,41,41	2.12	8 (19%)	56,56,56	2.32	21 (37%)
23	CLA	c	2487	-	69,73,73	1.59	11 (15%)	82,113,113	1.86	15 (18%)
23	CLA	A	352	1	69,73,73	1.36	10 (14%)	82,113,113	1.93	13 (15%)
21	BCT	d	2353	20	3,3,3	1.94	1 (33%)	2,3,3	0.13	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	CLA	A	350	-	-	7/39/115/115	-
26	LMT	B	526	-	-	8/21/61/61	0/2/2/2
23	CLA	b	2521	2	-	6/39/115/115	-
27	BCR	C	489	-	-	2/29/63/63	0/2/2/2
23	CLA	B	527	-	-	15/39/115/115	-
23	CLA	D	356	4	-	6/39/115/115	-
23	CLA	c	2479	3	-	11/39/115/115	-
24	PHO	d	2356	-	-	11/37/103/103	0/5/6/6
24	PHO	a	2350	-	-	9/37/103/103	0/5/6/6
27	BCR	K	50	-	-	3/29/63/63	0/2/2/2
23	CLA	C	483	3	-	12/39/115/115	-
23	CLA	B	523	2	-	10/39/115/115	-
27	BCR	c	2488	-	-	5/29/63/63	0/2/2/2
23	CLA	d	2355	-	-	14/39/115/115	-
23	CLA	b	2522	2	-	17/39/115/115	-
27	BCR	b	2527	-	-	5/29/63/63	0/2/2/2
23	CLA	c	2477	3	-	17/39/115/115	-
23	CLA	C	486	3	-	7/39/115/115	-
23	CLA	C	477	3	-	17/39/115/115	-
23	CLA	B	518	2	-	12/39/115/115	-
23	CLA	C	480	3	-	16/39/115/115	-
23	CLA	D	354	4	-	8/39/115/115	-
23	CLA	A	348	1	-	12/39/115/115	-
23	CLA	b	2516	2	-	6/39/115/115	-
23	CLA	b	2517	2	-	15/39/115/115	-
27	BCR	d	2360	-	-	4/29/63/63	0/2/2/2
23	CLA	c	2482	3	-	12/39/115/115	-
28	HEC	v	2138	16	1/1/3/7	6/14/54/54	-
23	CLA	B	524	-	-	15/39/115/115	-
23	CLA	C	481	3	-	9/39/115/115	-
27	BCR	b	2528	-	-	6/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	CLA	B	514	-	-	16/39/115/115	-
23	CLA	B	519	2	-	8/39/115/115	-
23	CLA	b	2520	2	-	7/39/115/115	-
26	LMT	d	2359	-	-	8/21/61/61	0/2/2/2
23	CLA	b	2519	2	-	8/39/115/115	-
27	BCR	j	2053	-	-	4/29/63/63	0/2/2/2
23	CLA	C	487	-	-	15/39/115/115	-
23	CLA	B	513	2	-	14/39/115/115	-
23	CLA	A	349	-	-	14/39/115/115	-
23	CLA	c	2474	3	-	13/39/115/115	-
23	CLA	a	2349	-	-	6/39/115/115	-
27	BCR	B	528	-	-	5/29/63/63	0/2/2/2
23	CLA	C	485	-	-	14/39/115/115	-
23	CLA	b	2512	2	-	10/39/115/115	-
23	CLA	B	516	2	-	6/39/115/115	-
23	CLA	C	482	3	-	11/39/115/115	-
27	BCR	C	488	-	-	6/29/63/63	0/2/2/2
23	CLA	c	2475	-	-	12/39/115/115	-
25	PL9	A	353	-	-	10/41/61/73	0/1/1/1
23	CLA	B	520	2	-	5/39/115/115	-
23	CLA	c	2485	-	-	14/39/115/115	-
27	BCR	J	53	-	-	4/29/63/63	0/2/2/2
23	CLA	B	521	2	-	6/39/115/115	-
23	CLA	c	2483	3	-	12/39/115/115	-
23	CLA	B	525	2	-	14/39/115/115	-
23	CLA	c	2484	3	-	17/39/115/115	-
23	CLA	C	474	3	-	13/39/115/115	-
23	CLA	b	2515	2	-	17/39/115/115	-
23	CLA	b	2525	2	-	13/39/115/115	-
23	CLA	B	511	2	-	16/39/115/115	-
23	CLA	c	2480	3	-	16/39/115/115	-
25	PL9	d	2358	-	-	12/41/61/73	0/1/1/1
23	CLA	a	2348	1	-	12/39/115/115	-
22	OEC	a	2347	1,3,21	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	CLA	c	2486	3	-	7/39/115/115	-
24	PHO	A	351	-	-	9/37/103/103	0/5/6/6
23	CLA	B	517	2	-	15/39/115/115	-
27	BCR	F	48	-	-	3/29/63/63	0/2/2/2
23	CLA	C	478	3	-	14/39/115/115	-
27	BCR	c	2489	-	-	2/29/63/63	0/2/2/2
23	CLA	b	2526	-	-	15/39/115/115	-
23	CLA	B	515	2	-	17/39/115/115	-
23	CLA	c	2476	3	-	12/39/115/115	-
22	OEC	A	347	1,3,21	-	-	0/6/5/5
23	CLA	B	522	2	-	16/39/115/115	-
23	CLA	C	484	3	-	16/39/115/115	-
23	CLA	b	2524	-	-	15/39/115/115	-
23	CLA	d	2354	4	-	8/39/115/115	-
23	CLA	b	2513	2	-	13/39/115/115	-
23	CLA	C	479	3	-	11/39/115/115	-
23	CLA	c	2481	3	-	8/39/115/115	-
23	CLA	c	2478	3	-	14/39/115/115	-
23	CLA	b	2518	2	-	12/39/115/115	-
28	HEC	e	2084	6,5	1/1/3/7	2/14/54/54	-
23	CLA	b	2514	-	-	16/39/115/115	-
23	CLA	b	2511	2	-	16/39/115/115	-
27	BCR	k	2050	-	-	3/29/63/63	0/2/2/2
23	CLA	C	475	-	-	11/39/115/115	-
23	CLA	b	2523	2	-	10/39/115/115	-
28	HEC	E	84	6,5	1/1/3/7	2/14/54/54	-
23	CLA	a	2351	1	-	9/39/115/115	-
23	CLA	d	2357	4	-	6/39/115/115	-
25	PL9	a	2352	-	-	10/41/61/73	0/1/1/1
24	PHO	D	355	-	-	13/37/103/103	0/5/6/6
23	CLA	C	476	3	-	12/39/115/115	-
28	HEC	V	138	16	1/1/3/7	4/14/54/54	-
23	CLA	B	512	2	-	10/39/115/115	-
25	PL9	D	357	-	-	12/41/61/73	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	BCR	B	529	-	-	6/29/63/63	0/2/2/2
23	CLA	c	2487	-	-	14/39/115/115	-
23	CLA	A	352	1	-	9/39/115/115	-

The worst 5 of 1004 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	V	138	HEC	CMC-C2C	12.23	1.75	1.50
28	V	138	HEC	CMB-C2B	11.74	1.74	1.50
28	V	138	HEC	C1D-ND	10.84	1.58	1.40
28	V	138	HEC	CHA-C1A	10.42	1.58	1.38
28	V	138	HEC	C4B-NB	10.23	1.57	1.40

The worst 5 of 1364 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	b	2513	CLA	C4A-NA-C1A	14.75	113.41	106.68
23	B	513	CLA	C4A-NA-C1A	14.60	113.34	106.68
23	c	2479	CLA	C4A-NA-C1A	14.27	113.19	106.68
23	B	511	CLA	C4A-NA-C1A	14.15	113.13	106.68
23	B	519	CLA	C4A-NA-C1A	13.99	113.06	106.68

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
28	E	84	HEC	NA
28	V	138	HEC	NA
28	e	2084	HEC	NA
28	v	2138	HEC	NA

5 of 1033 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	A	348	CLA	C2-C1-O2A-CGA
23	A	349	CLA	C2B-C3B-CAB-CBB
23	A	349	CLA	C4B-C3B-CAB-CBB
23	A	352	CLA	C2B-C3B-CAB-CBB
23	A	352	CLA	C4B-C3B-CAB-CBB

There are no ring outliers.

100 monomers are involved in 707 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	A	350	CLA	6	0
23	b	2521	CLA	11	0
27	C	489	BCR	11	0
23	B	527	CLA	5	0
23	D	356	CLA	8	0
23	c	2479	CLA	12	0
24	d	2356	PHO	10	0
24	a	2350	PHO	5	0
27	K	50	BCR	13	0
23	C	483	CLA	9	0
23	B	523	CLA	7	0
27	c	2488	BCR	12	0
23	d	2355	CLA	6	0
23	b	2522	CLA	13	0
27	b	2527	BCR	4	0
23	c	2477	CLA	8	0
23	C	486	CLA	17	0
23	C	477	CLA	7	0
23	B	518	CLA	16	0
23	C	480	CLA	6	0
23	D	354	CLA	8	0
23	A	348	CLA	13	0
23	b	2516	CLA	7	0
23	b	2517	CLA	3	0
27	d	2360	BCR	2	0
23	c	2482	CLA	4	0
23	B	524	CLA	25	0
28	v	2138	HEC	1	0
23	C	481	CLA	4	0
27	b	2528	BCR	15	0
23	B	514	CLA	4	0
23	B	519	CLA	6	0
23	b	2520	CLA	9	0
26	d	2359	LMT	5	0
23	b	2519	CLA	7	0
27	j	2053	BCR	2	0
23	C	487	CLA	20	0
23	B	513	CLA	6	0
23	A	349	CLA	2	0
23	c	2474	CLA	8	0
23	a	2349	CLA	9	0
27	B	528	BCR	4	0
23	C	485	CLA	10	0

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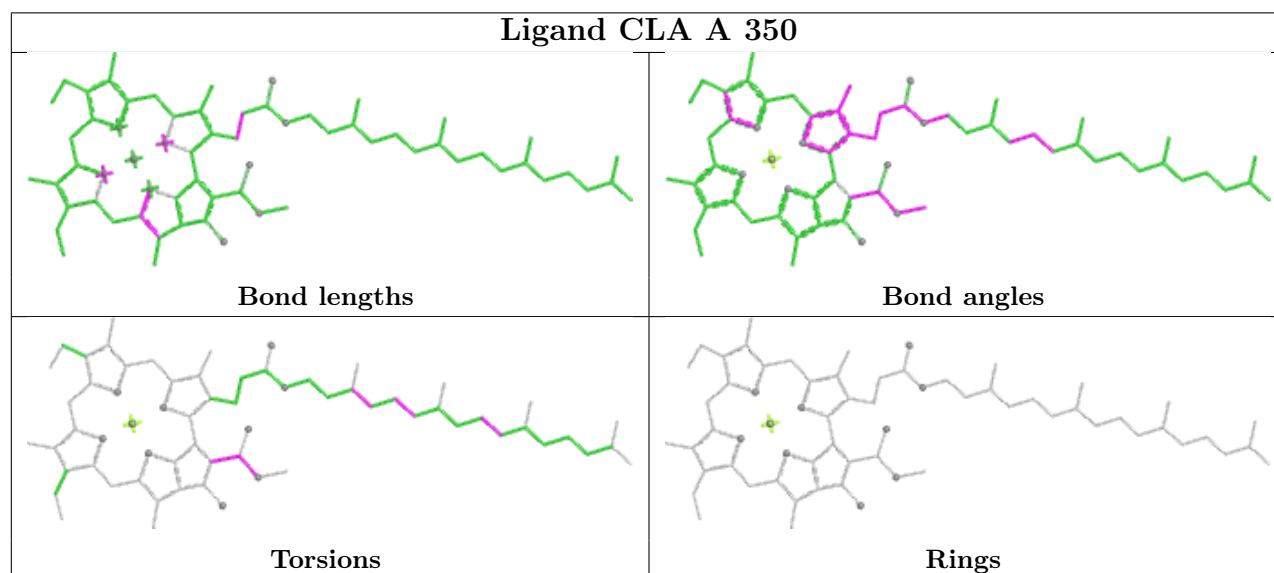
Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	b	2512	CLA	5	0
23	B	516	CLA	6	0
23	C	482	CLA	4	0
27	C	488	BCR	12	0
23	c	2475	CLA	3	0
25	A	353	PL9	8	0
23	B	520	CLA	10	0
23	c	2485	CLA	8	0
27	J	53	BCR	2	0
23	B	521	CLA	10	0
23	c	2483	CLA	8	0
23	B	525	CLA	9	0
23	c	2484	CLA	2	0
23	C	474	CLA	10	0
23	b	2515	CLA	6	0
23	b	2525	CLA	9	0
23	B	511	CLA	4	0
23	c	2480	CLA	4	0
25	d	2358	PL9	8	0
23	a	2348	CLA	9	0
23	c	2486	CLA	23	0
24	A	351	PHO	5	0
23	B	517	CLA	3	0
27	F	48	BCR	3	0
23	C	478	CLA	6	0
27	c	2489	BCR	10	0
23	b	2526	CLA	5	0
23	B	515	CLA	6	0
23	c	2476	CLA	5	0
22	A	347	OEC	1	0
23	B	522	CLA	14	0
23	C	484	CLA	2	0
23	b	2524	CLA	23	0
23	d	2354	CLA	10	0
23	b	2513	CLA	6	0
23	C	479	CLA	11	0
23	c	2481	CLA	8	0
23	c	2478	CLA	6	0
23	b	2518	CLA	15	0
28	e	2084	HEC	15	0
23	b	2514	CLA	3	0
23	b	2511	CLA	4	0

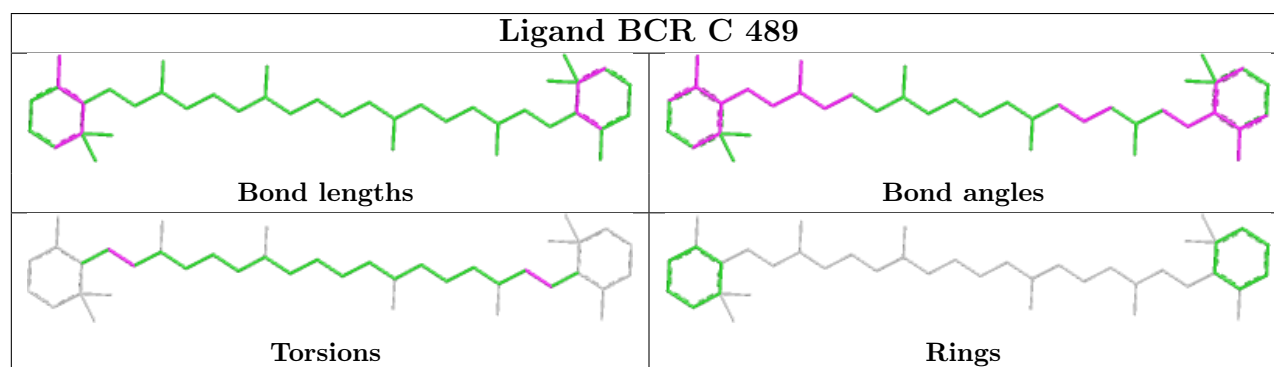
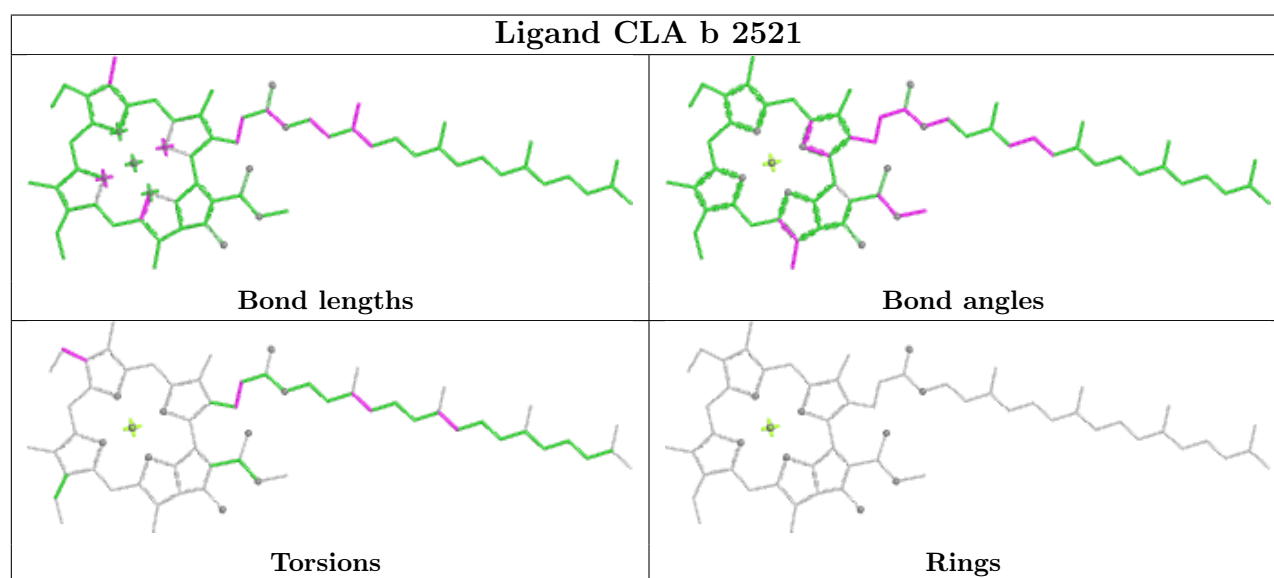
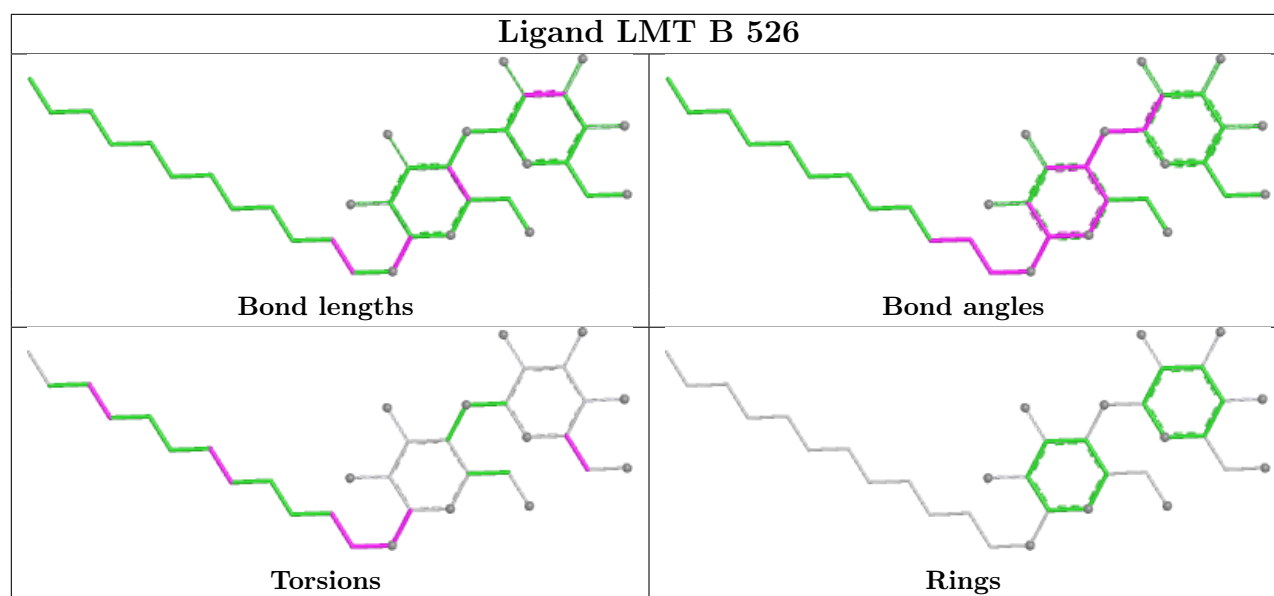
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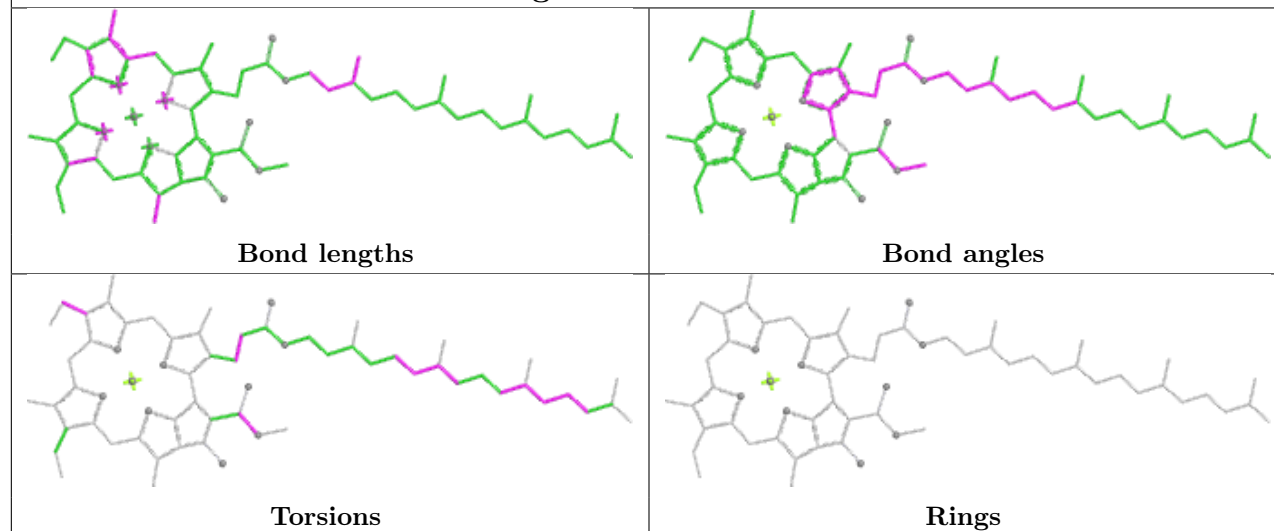
Mol	Chain	Res	Type	Clashes	Symm-Clashes
27	k	2050	BCR	16	0
23	C	475	CLA	5	0
23	b	2523	CLA	8	0
28	E	84	HEC	17	0
23	a	2351	CLA	2	0
23	d	2357	CLA	14	0
25	a	2352	PL9	11	0
24	D	355	PHO	7	0
23	C	476	CLA	4	0
28	V	138	HEC	9	0
23	B	512	CLA	7	0
25	D	357	PL9	6	0
27	B	529	BCR	14	0
23	c	2487	CLA	19	0
23	A	352	CLA	1	0

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

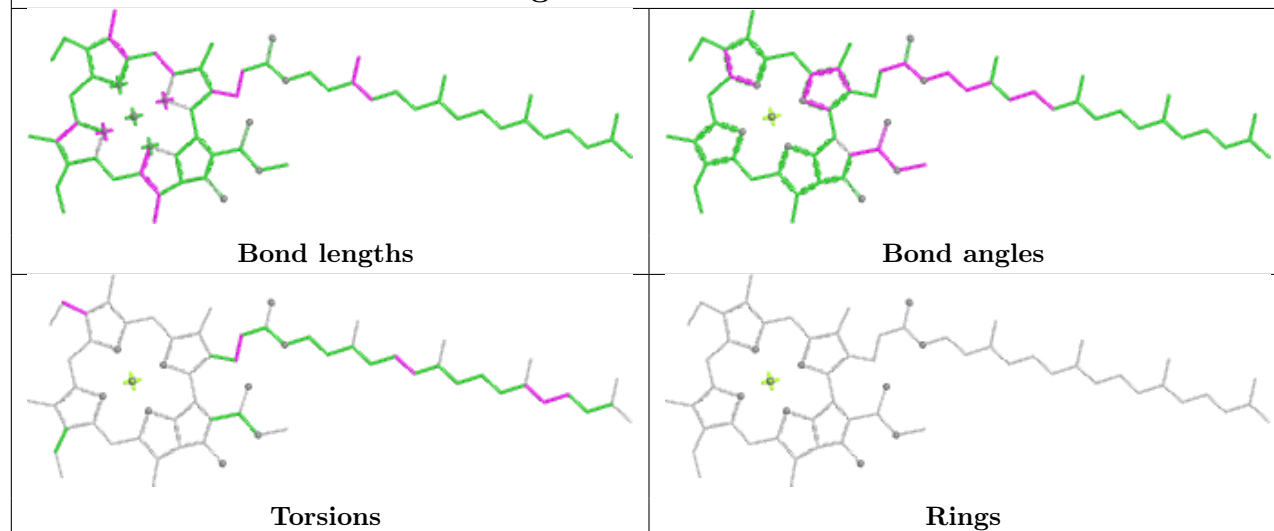




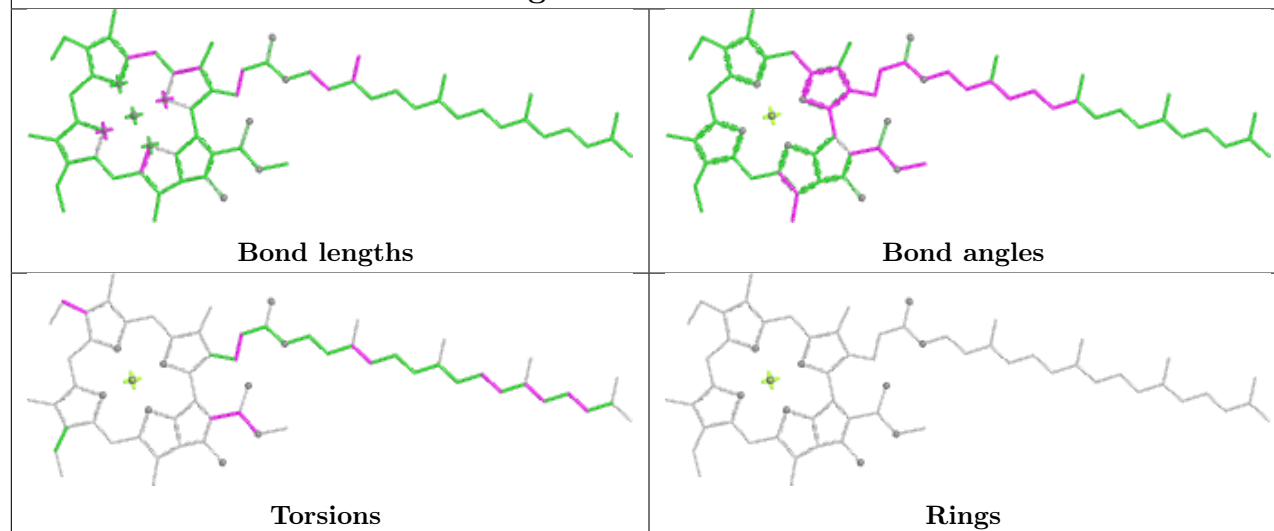
Ligand CLA B 527

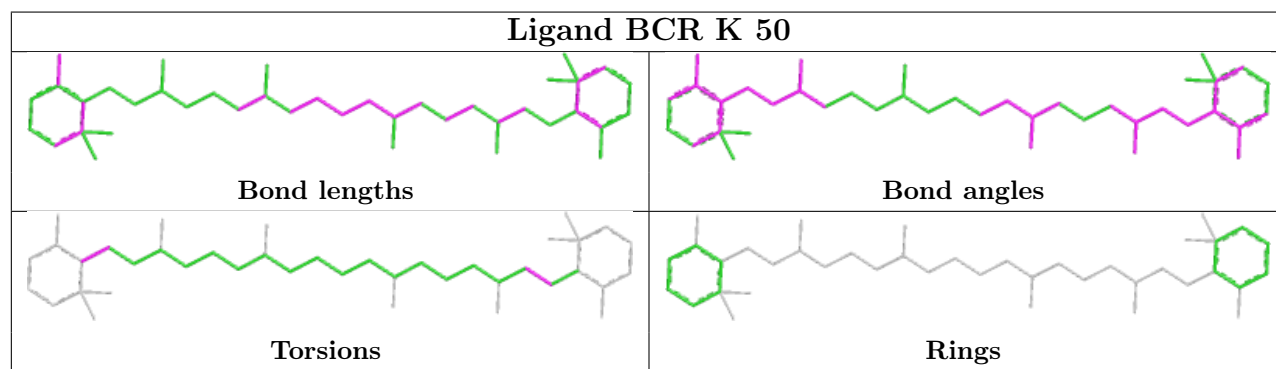
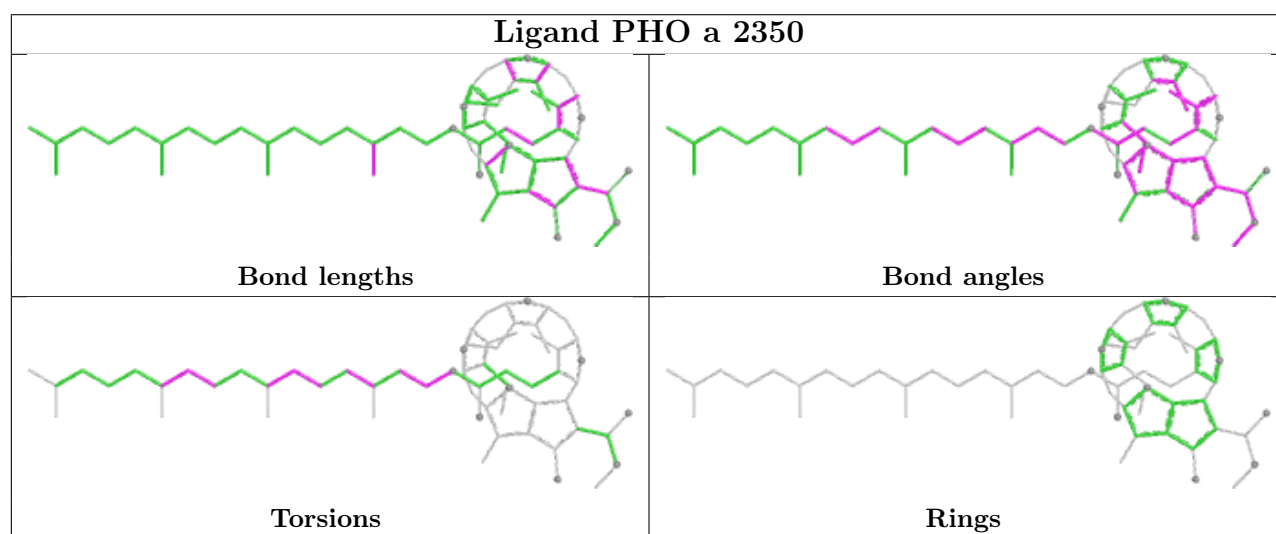
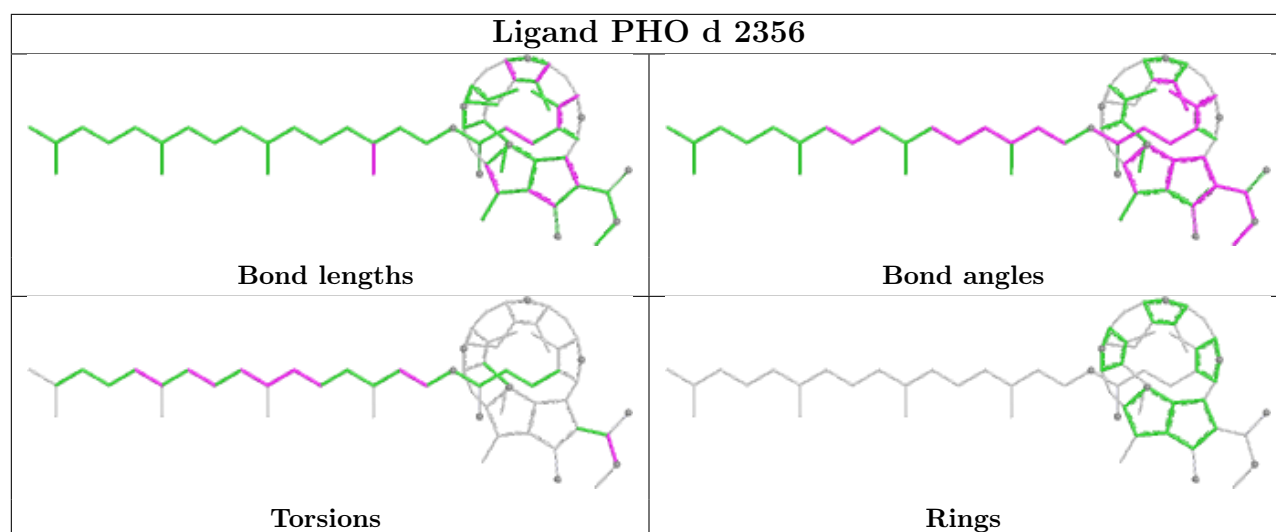


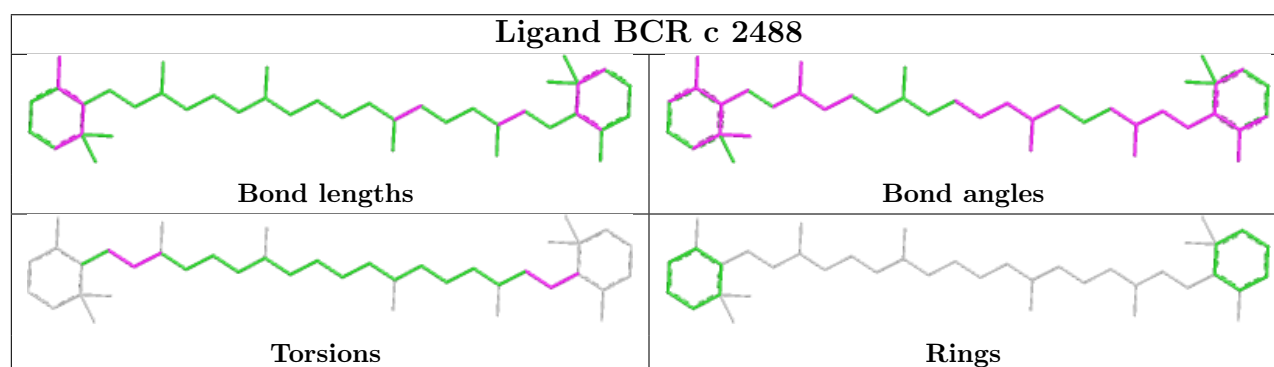
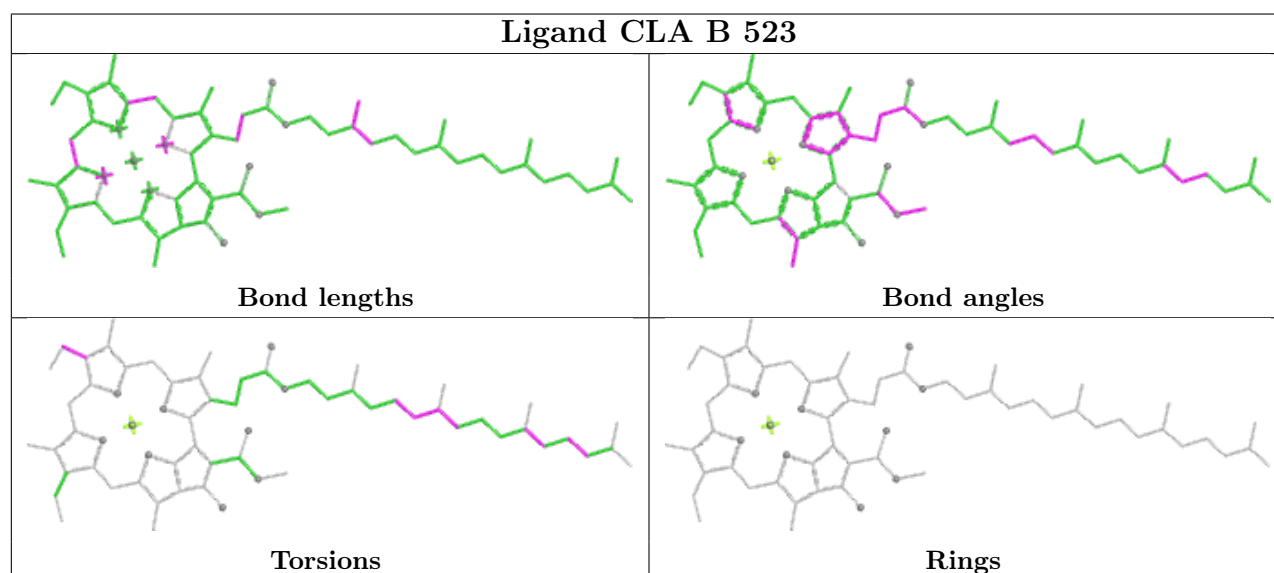
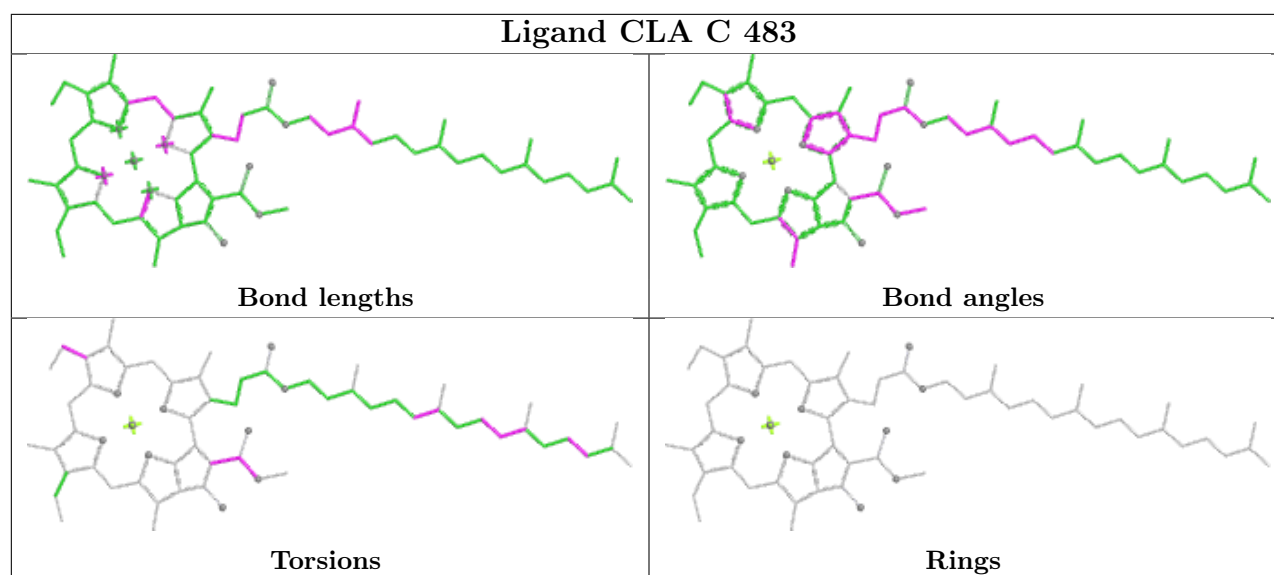
Ligand CLA D 356

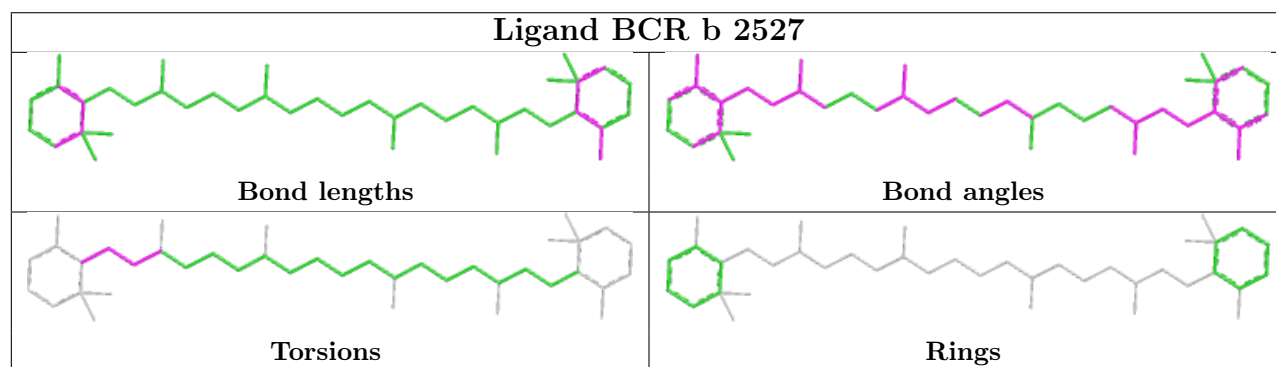
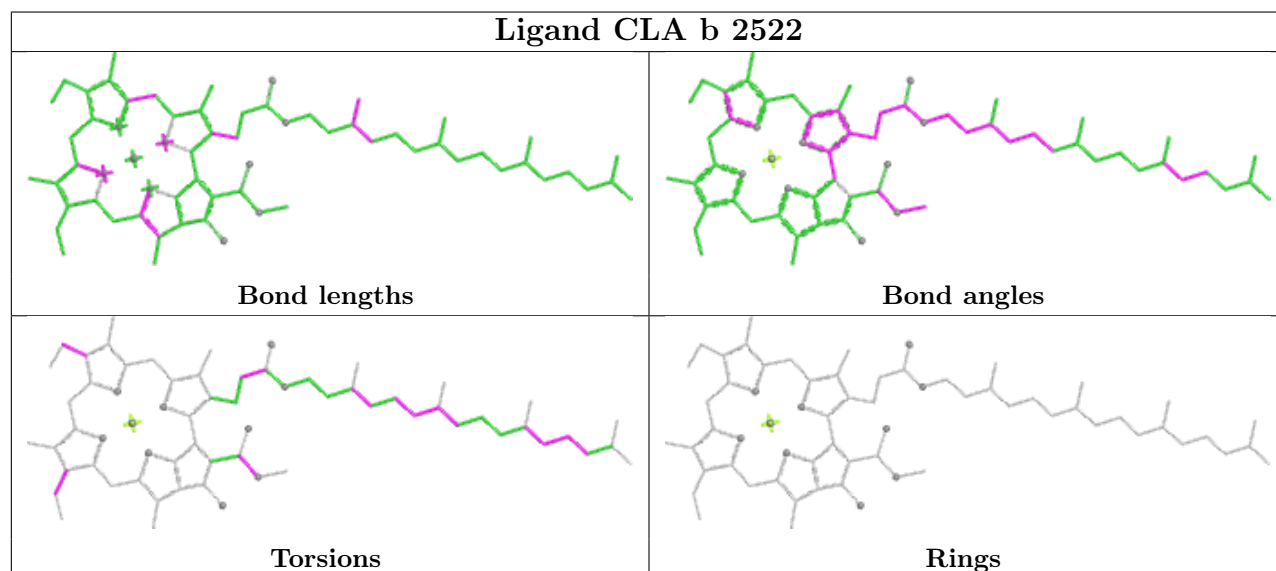
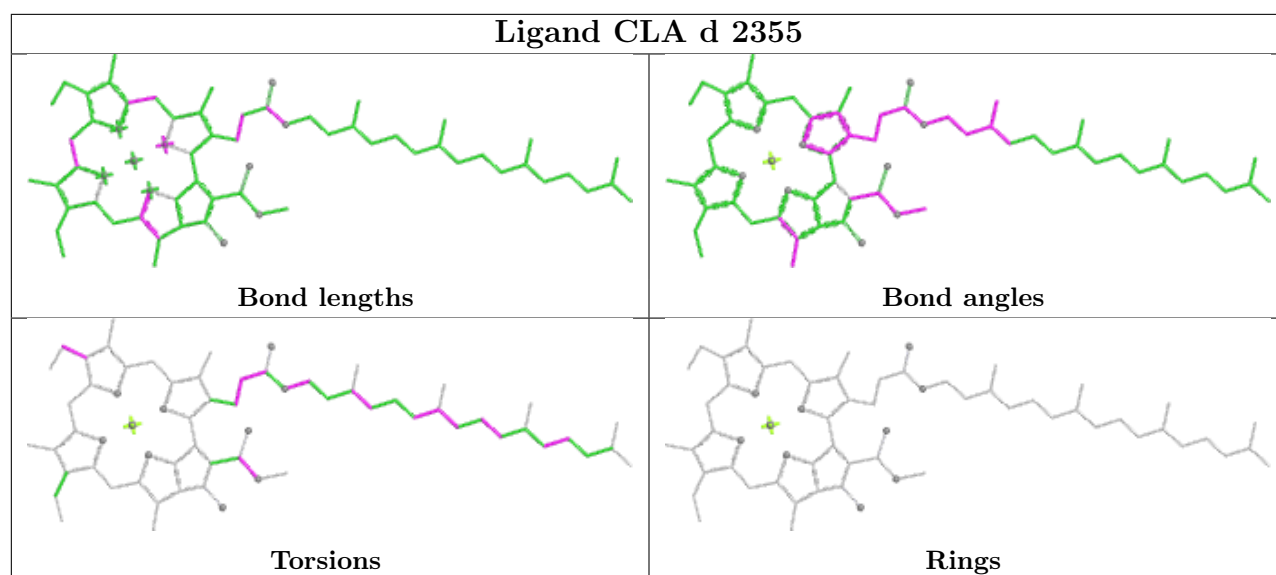


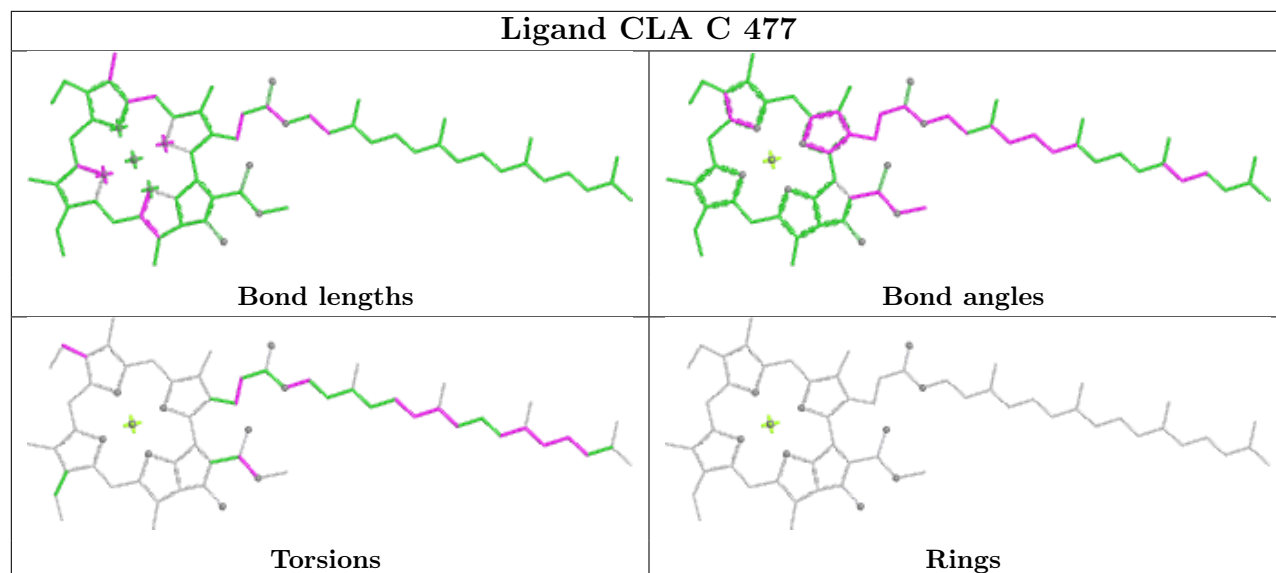
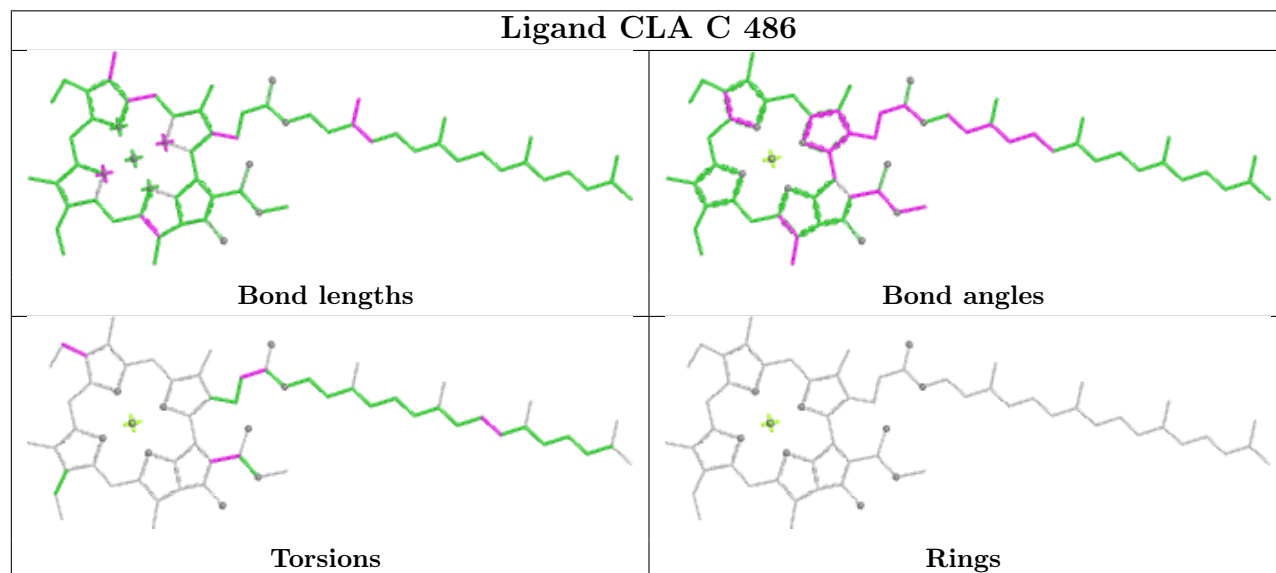
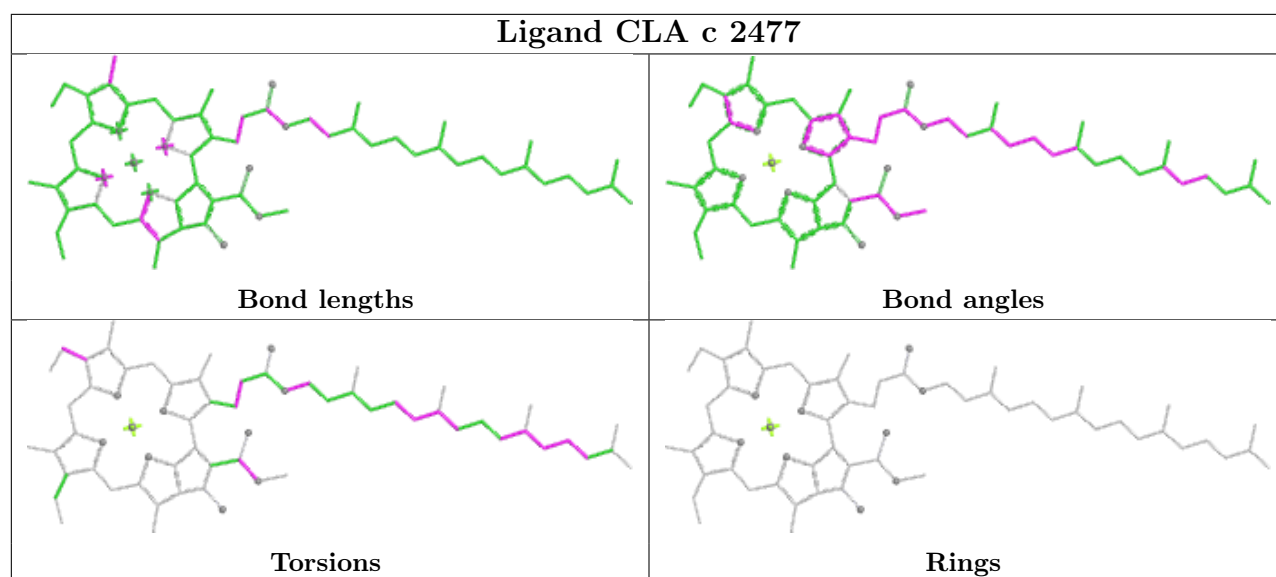
Ligand CLA c 2479

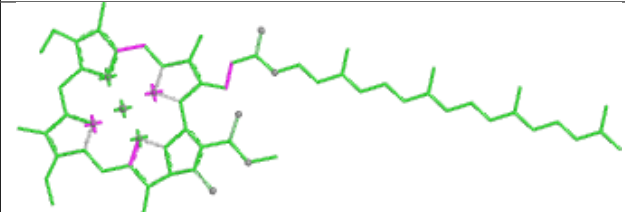
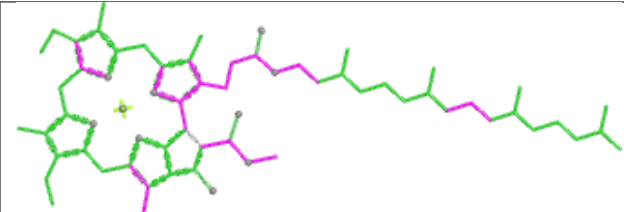
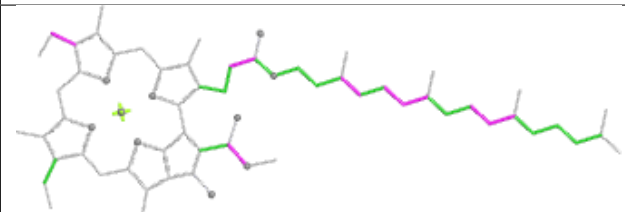
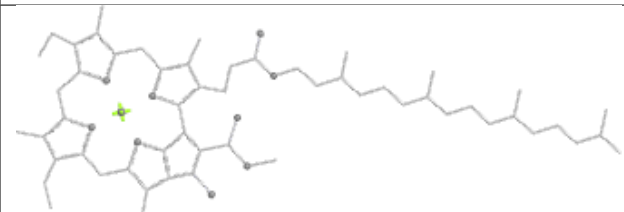


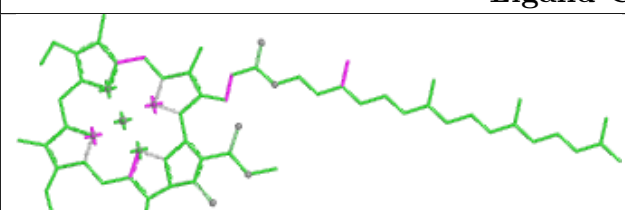
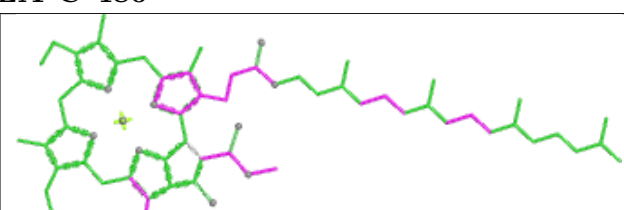
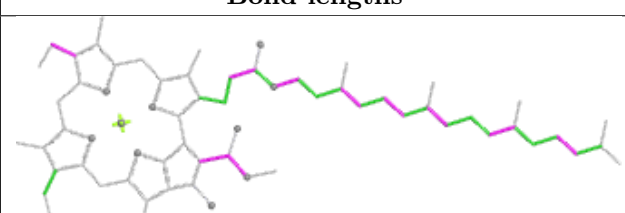
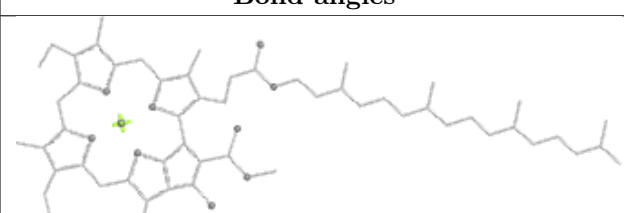


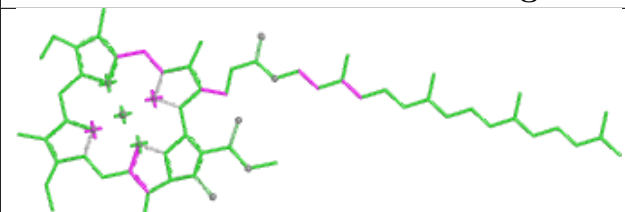
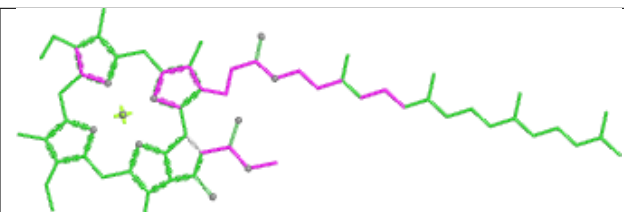
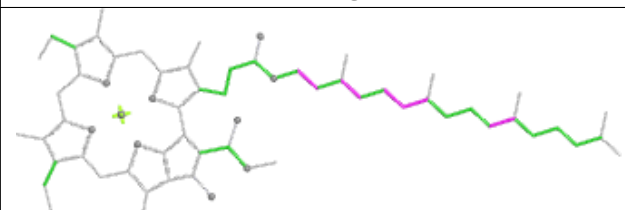
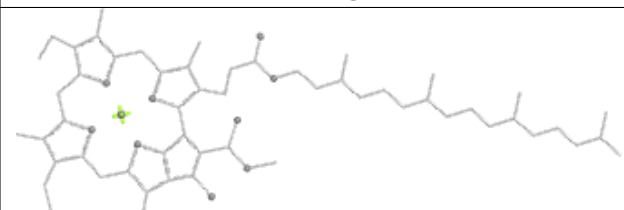


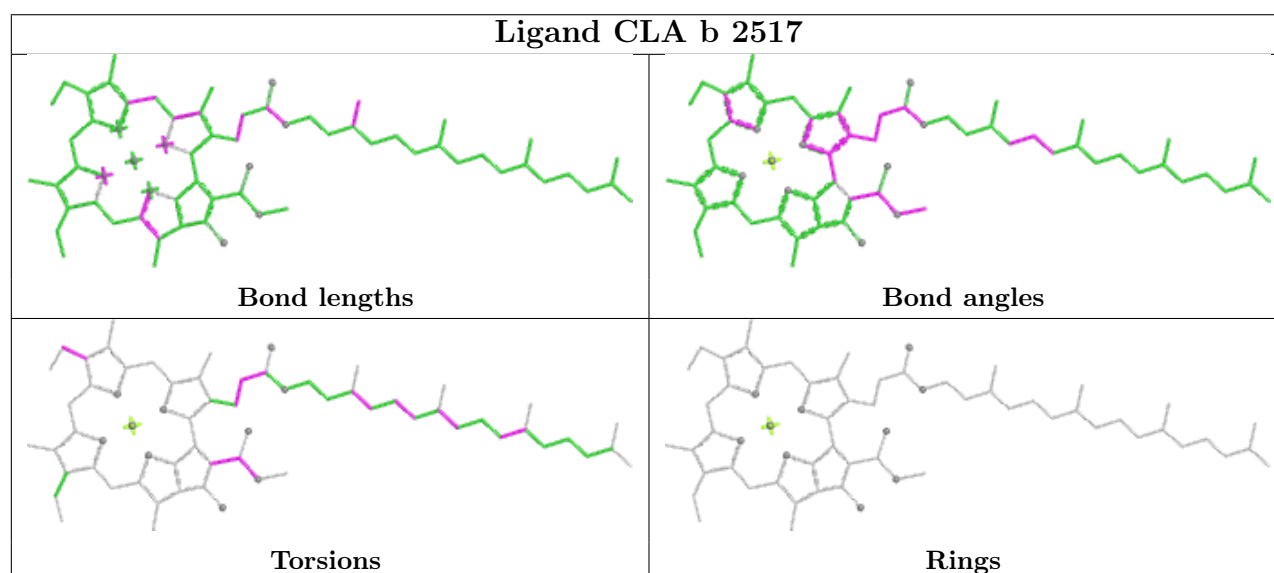
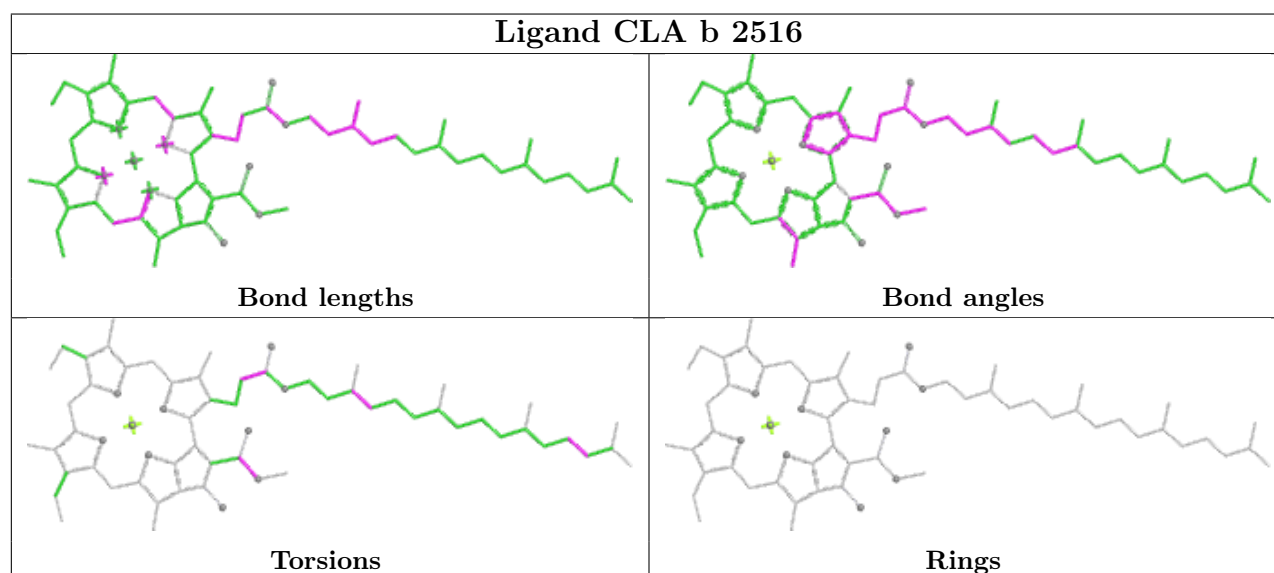
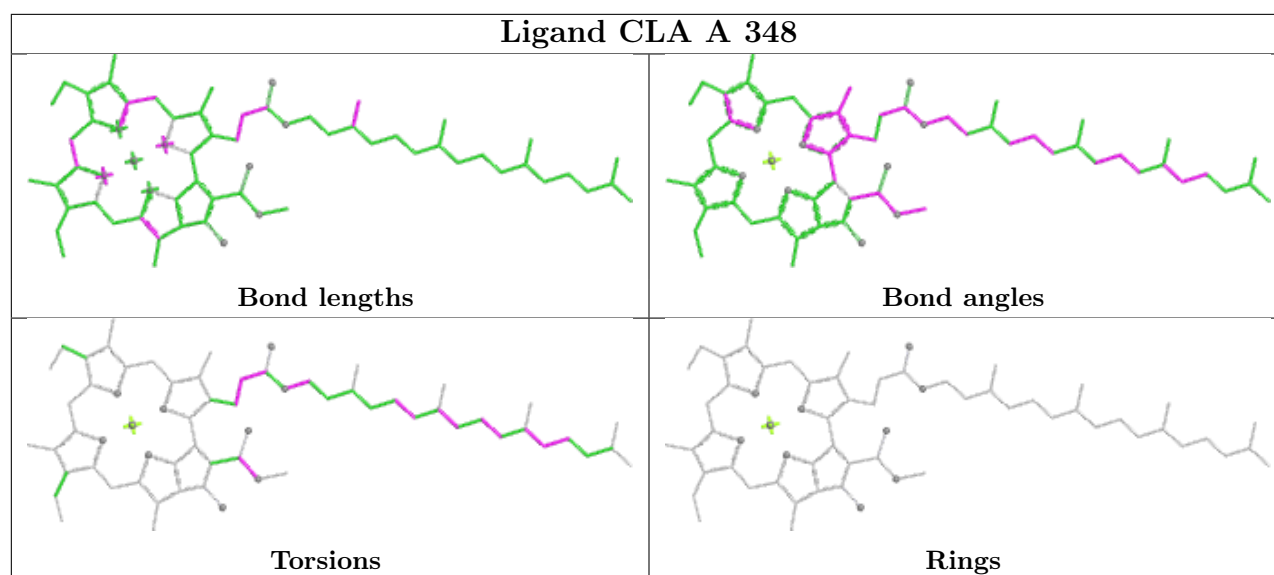


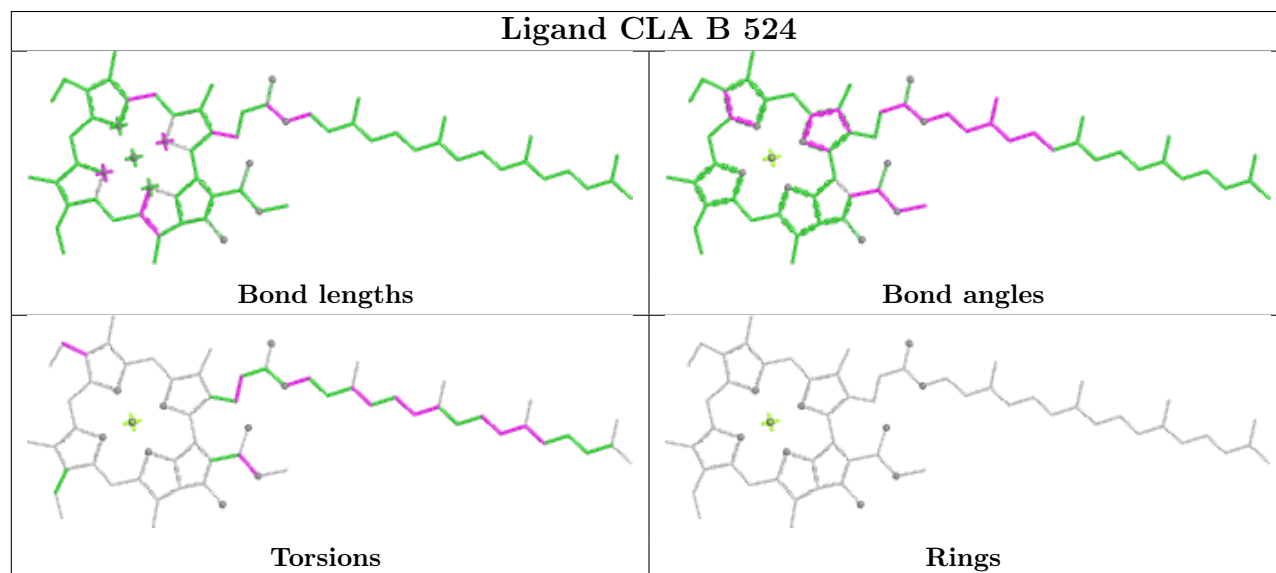
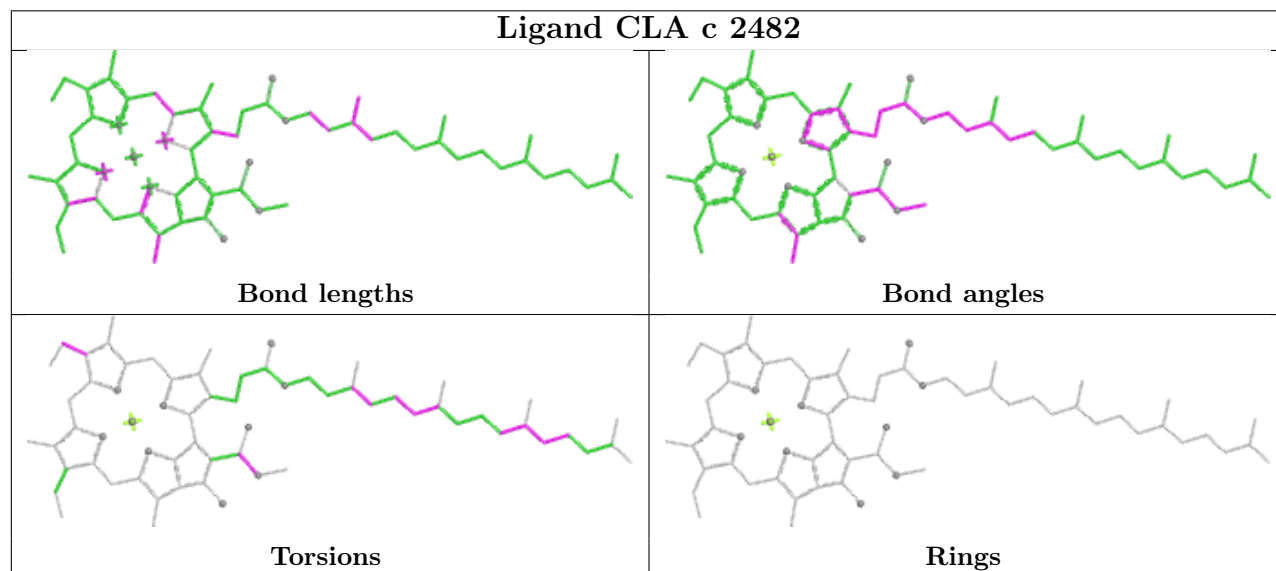
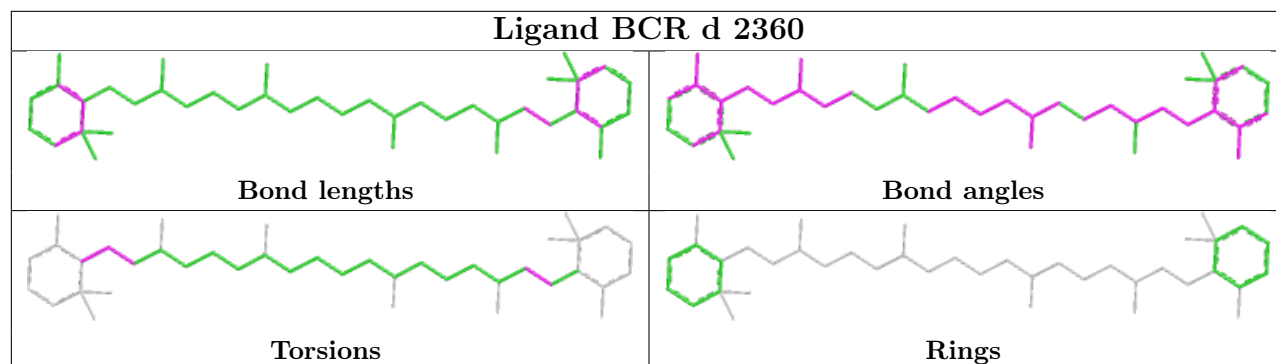


Ligand CLA B 518	
	
Bond lengths	Bond angles
	
Torsions	Rings

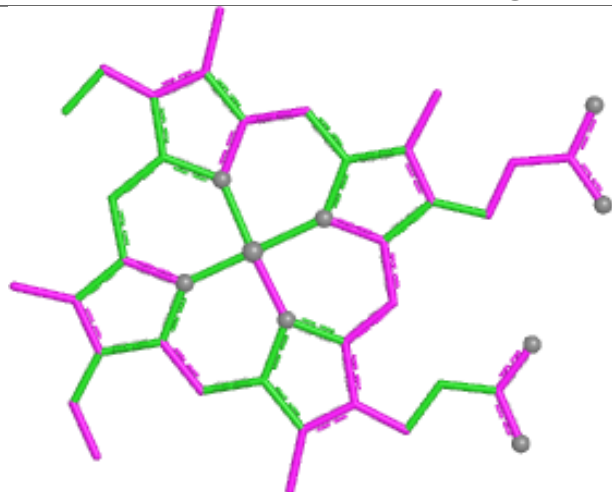
Ligand CLA C 480	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA D 354	
	
Bond lengths	Bond angles
	
Torsions	Rings

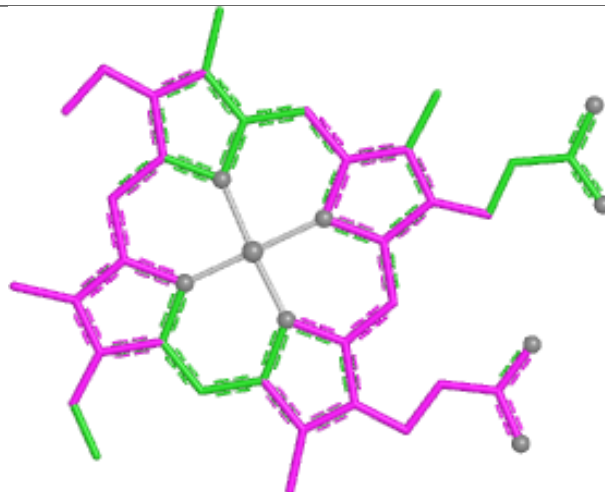




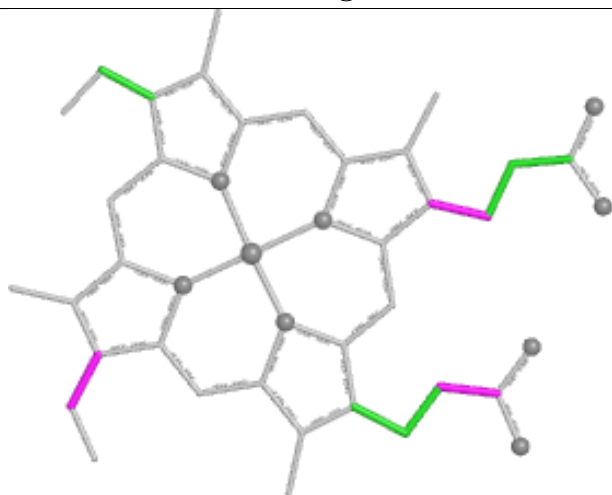
Ligand HEC v 2138



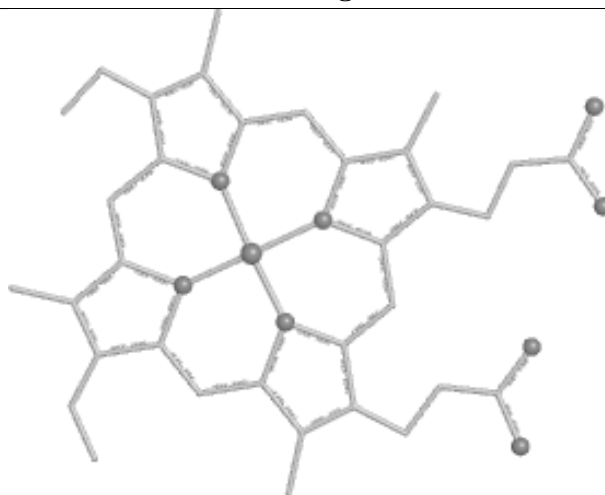
Bond lengths



Bond angles

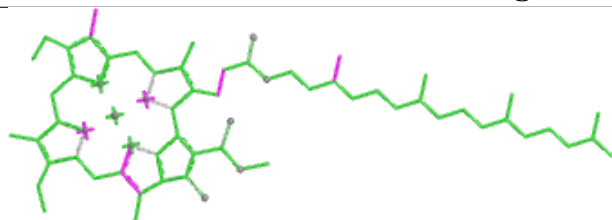


Torsions

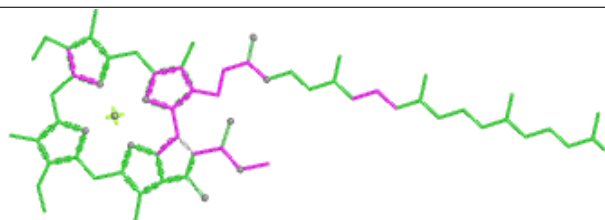


Rings

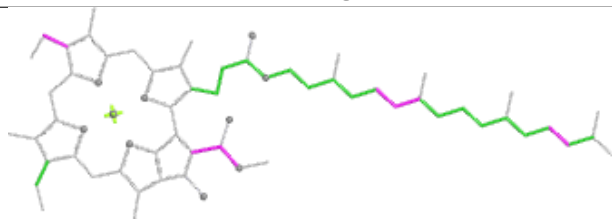
Ligand CLA C 481



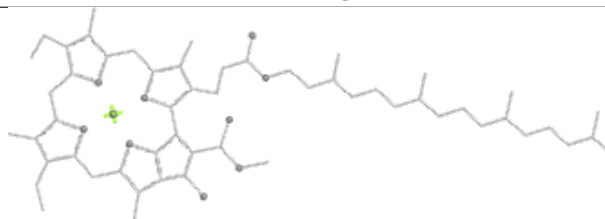
Bond lengths



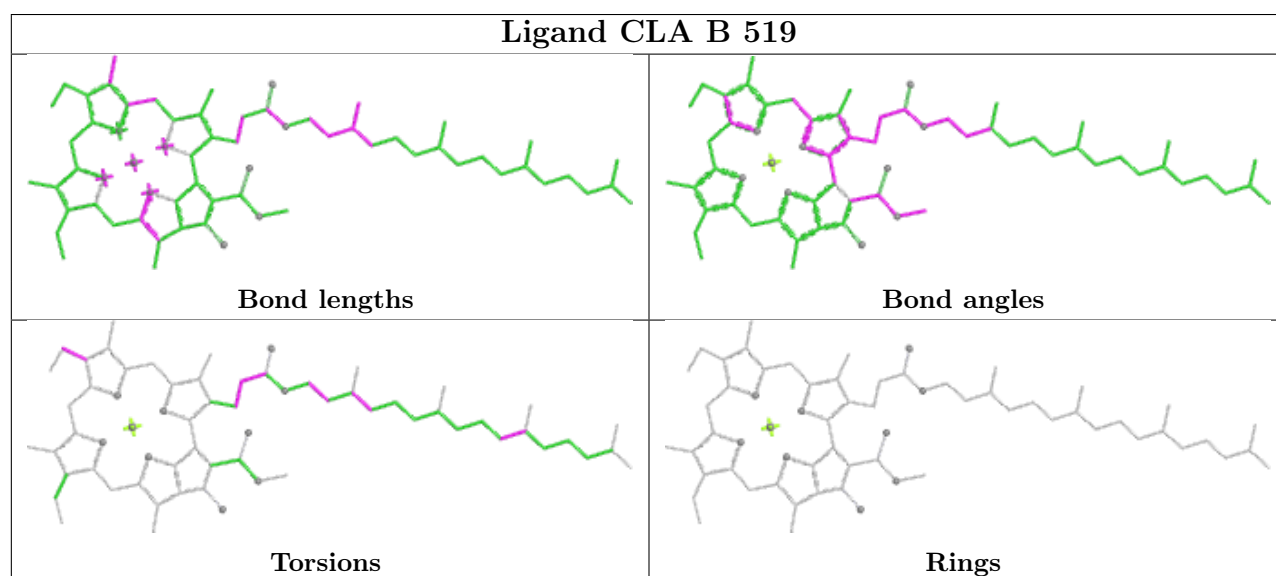
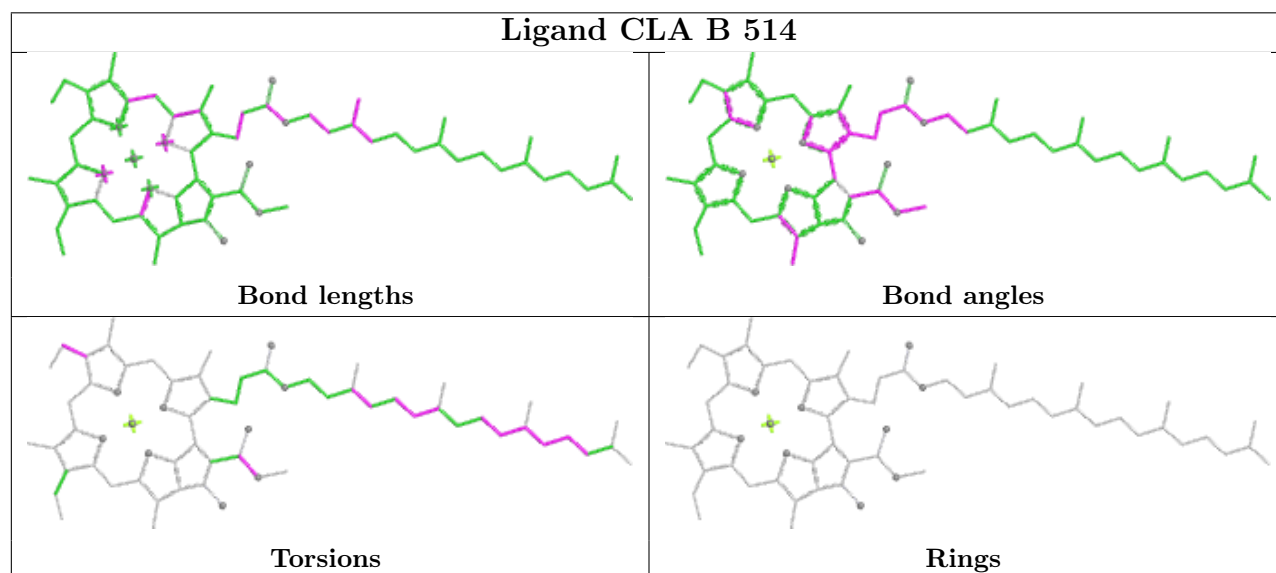
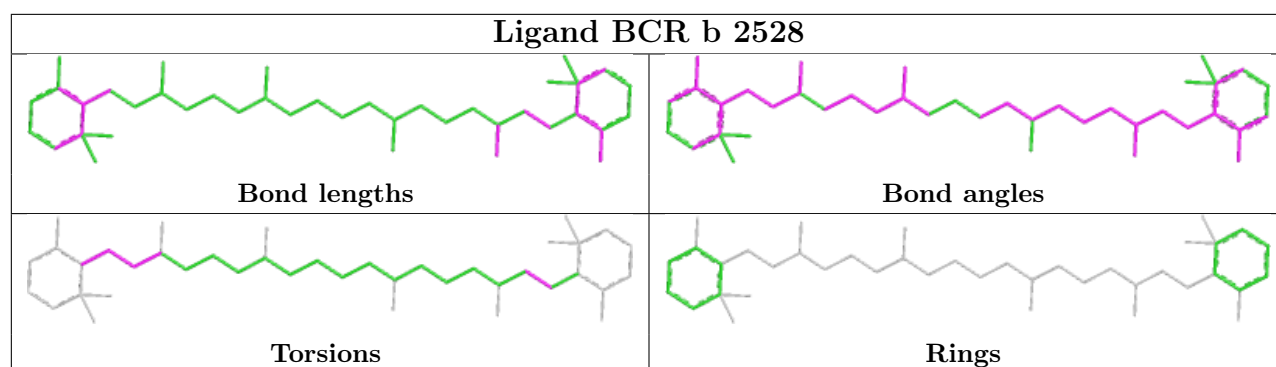
Bond angles

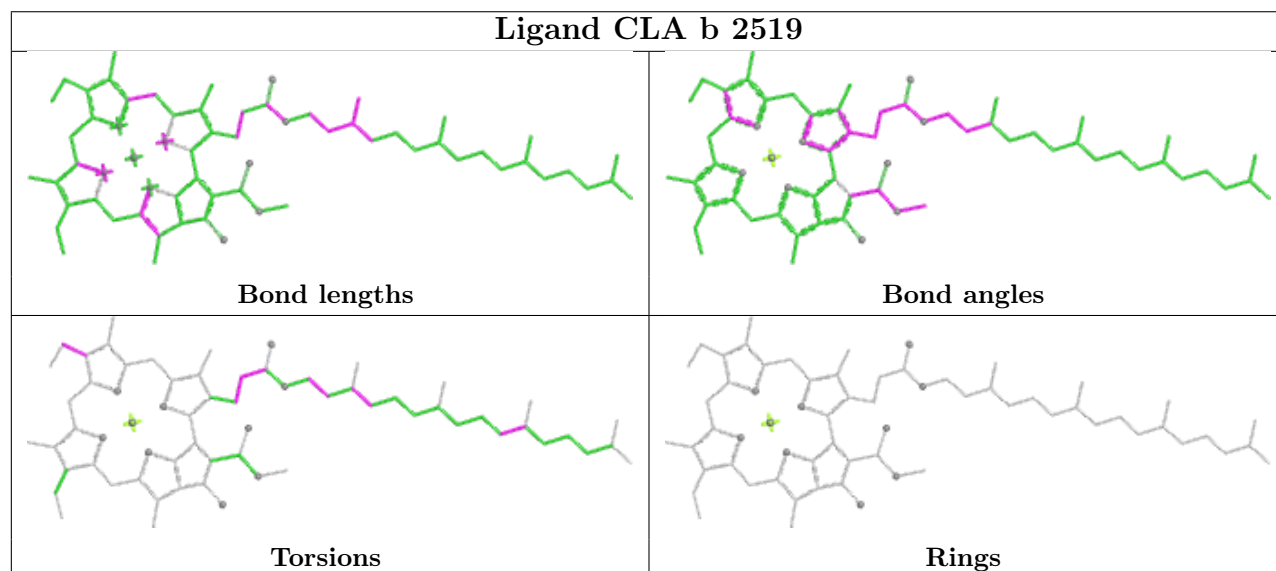
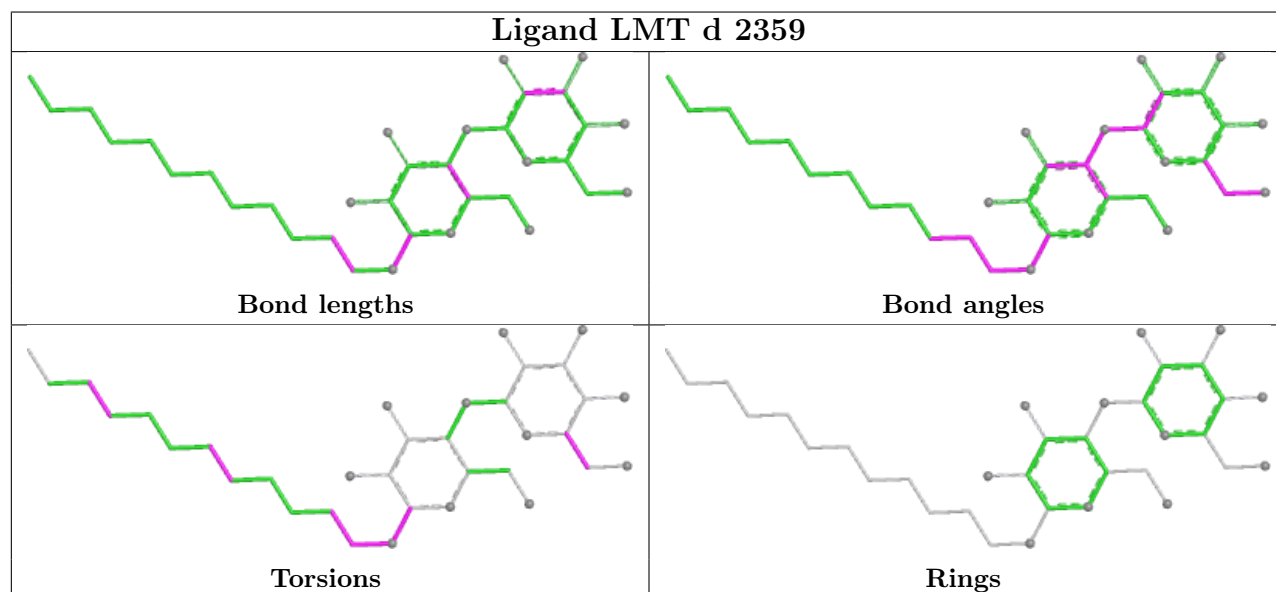
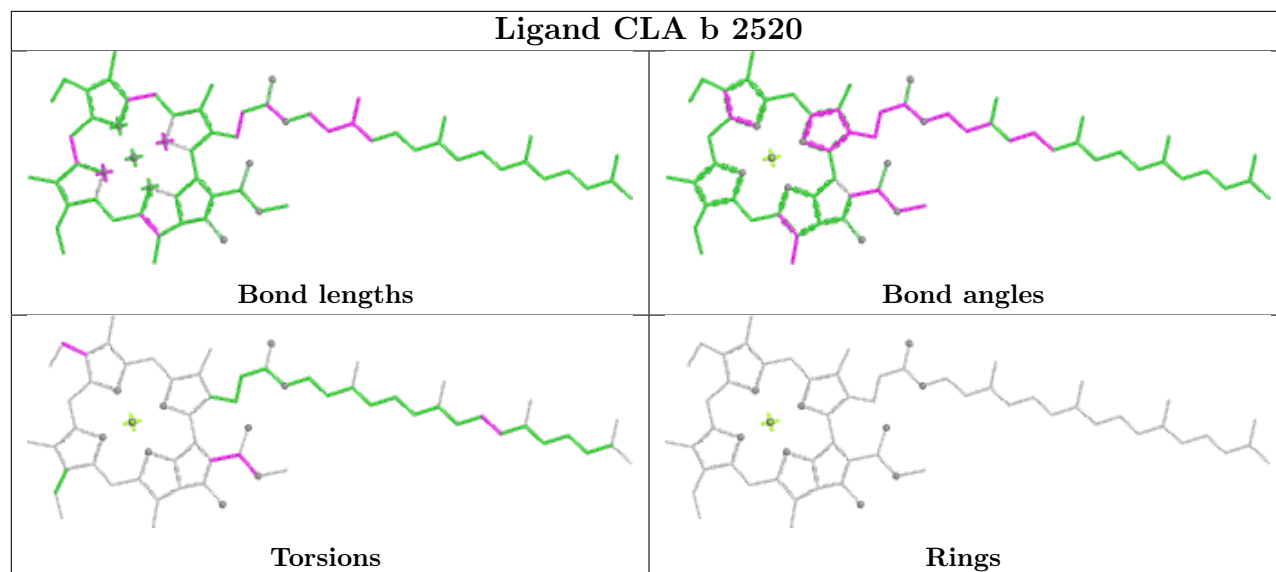


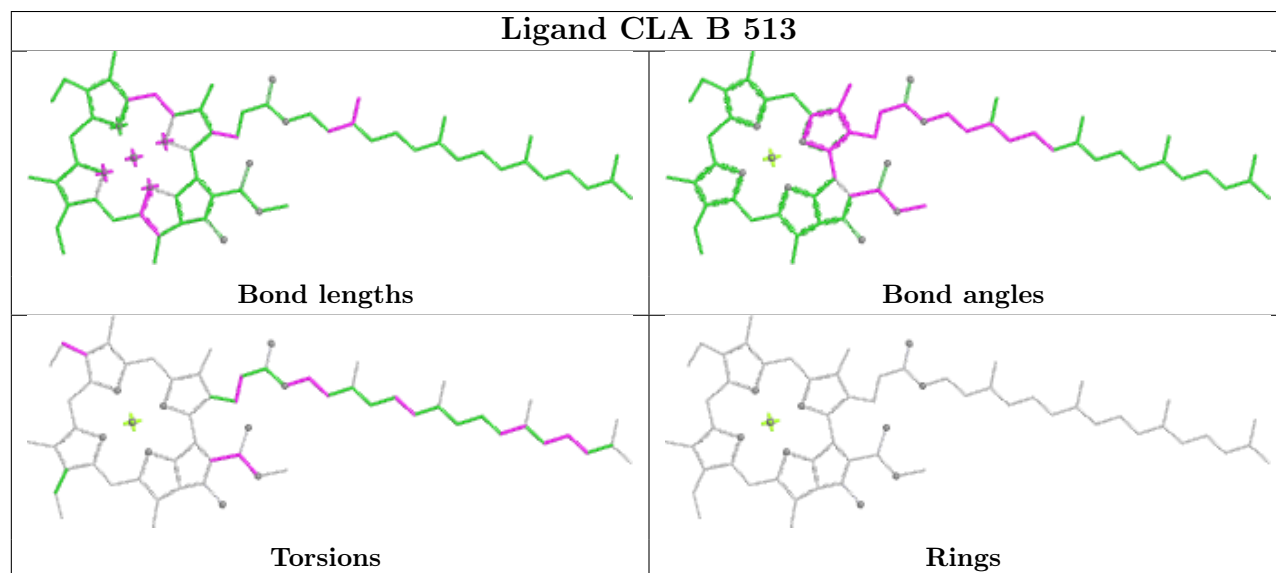
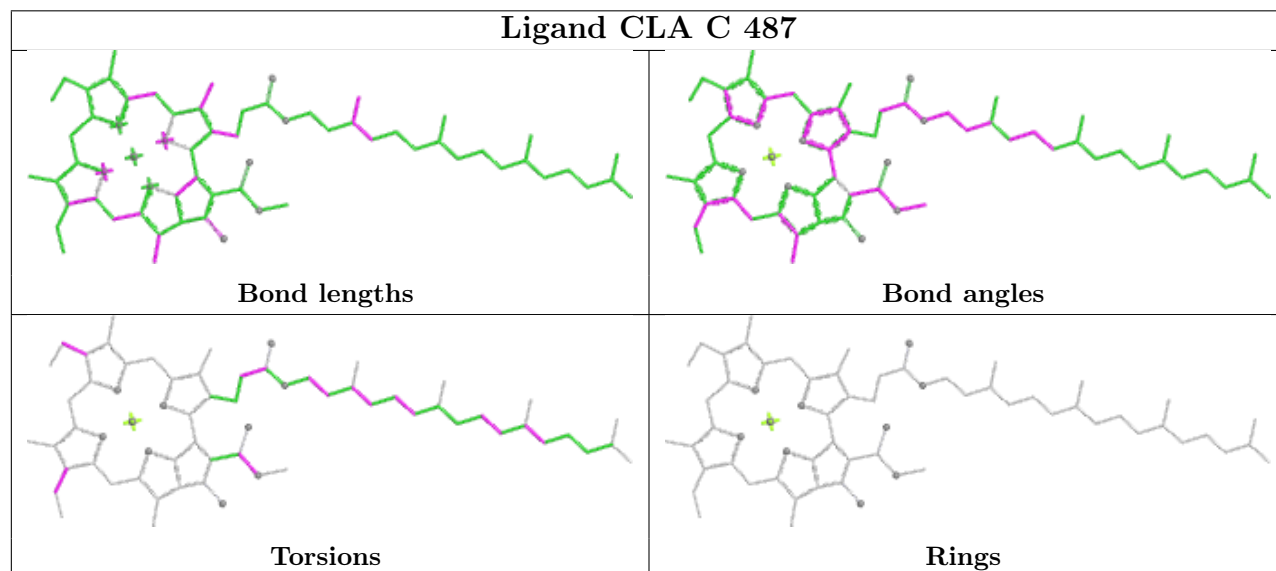
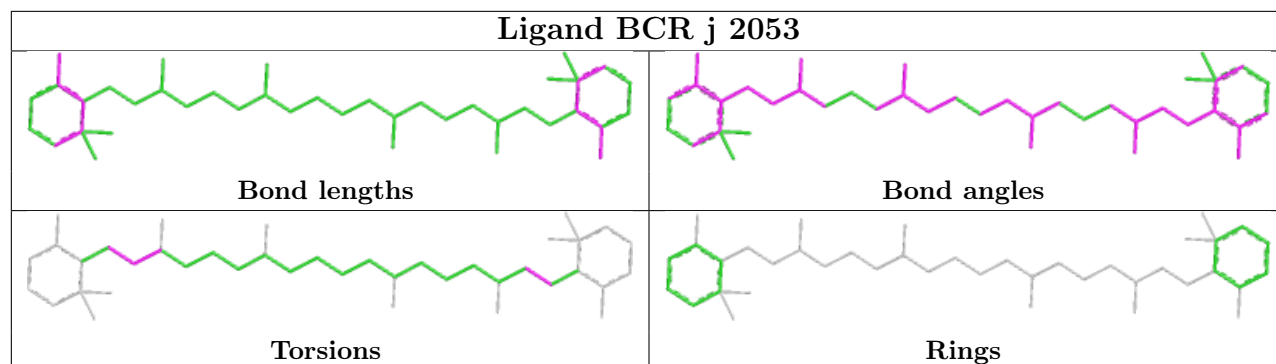
Torsions

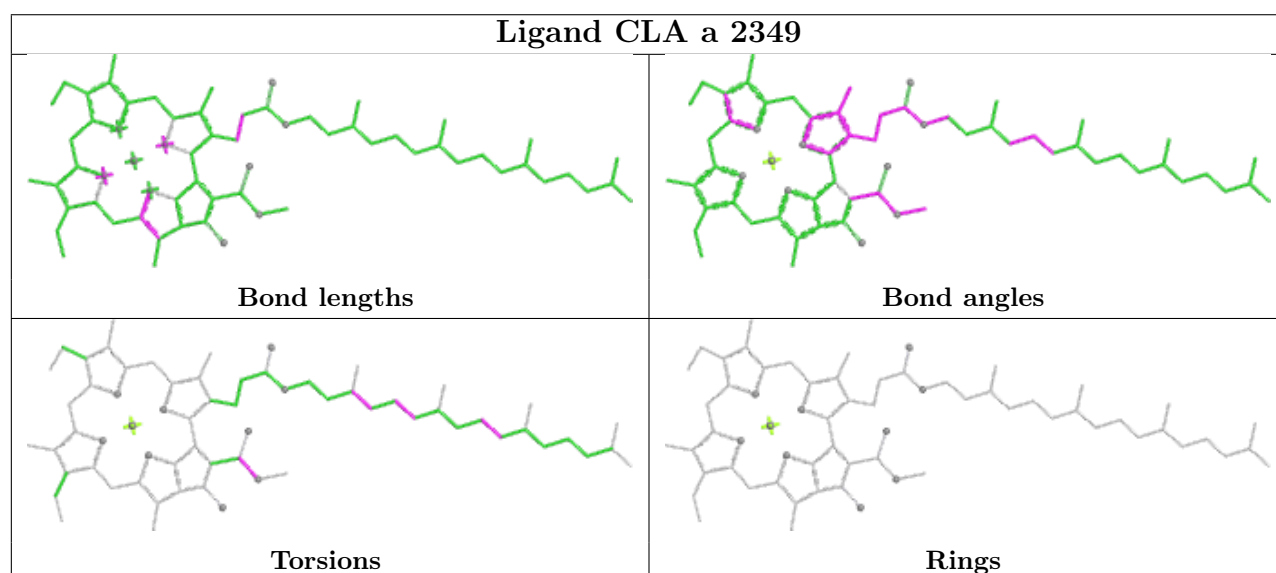
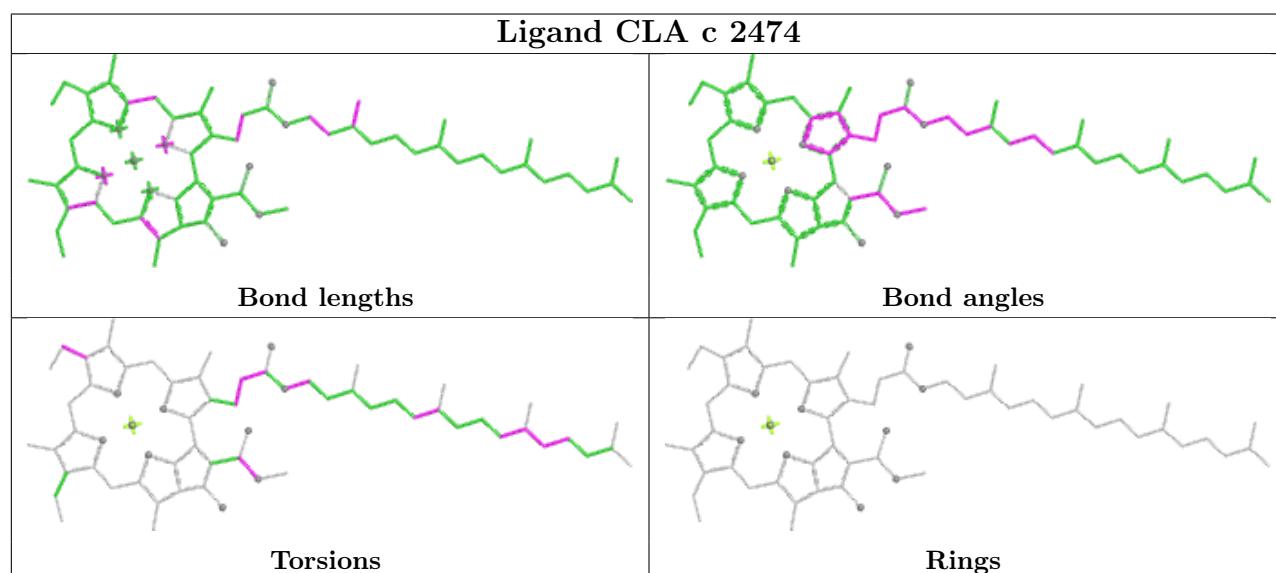
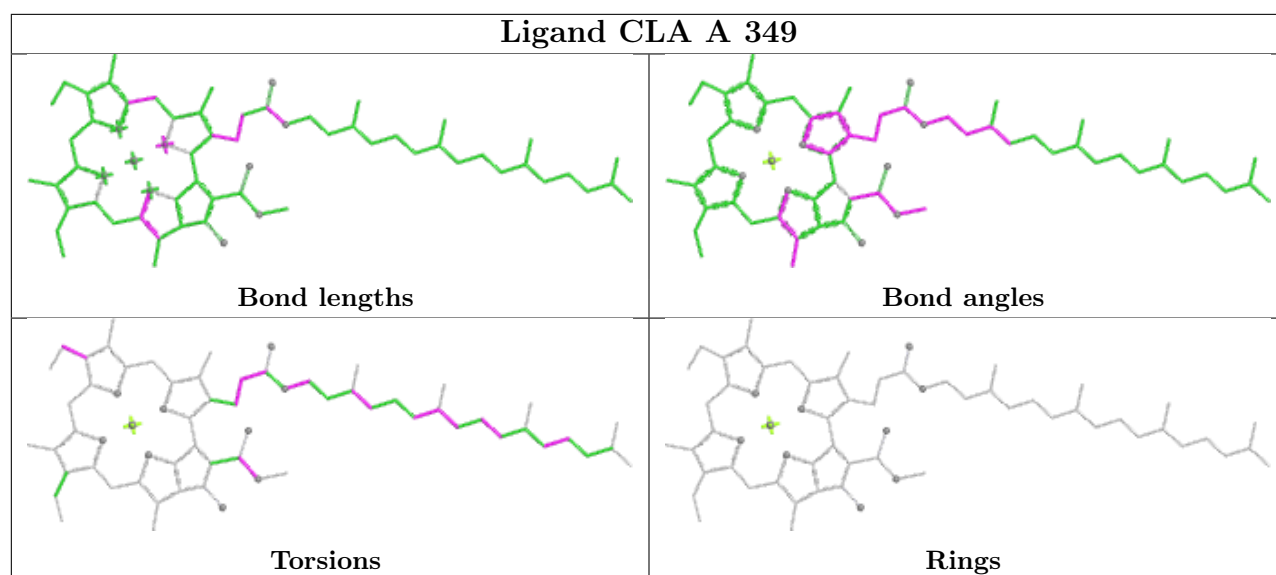


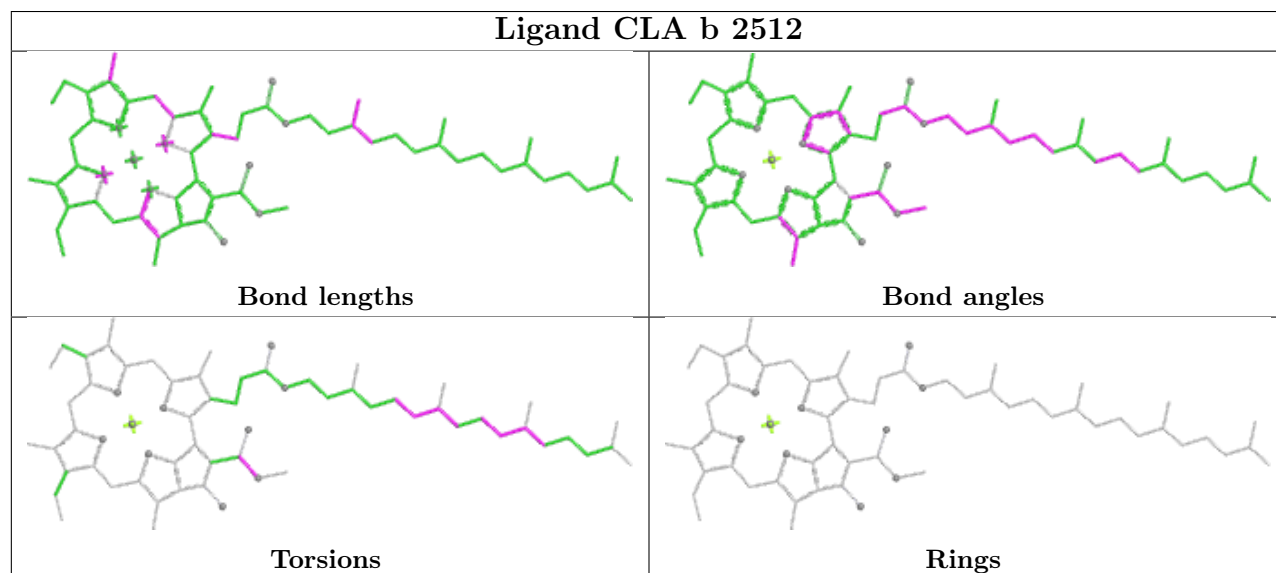
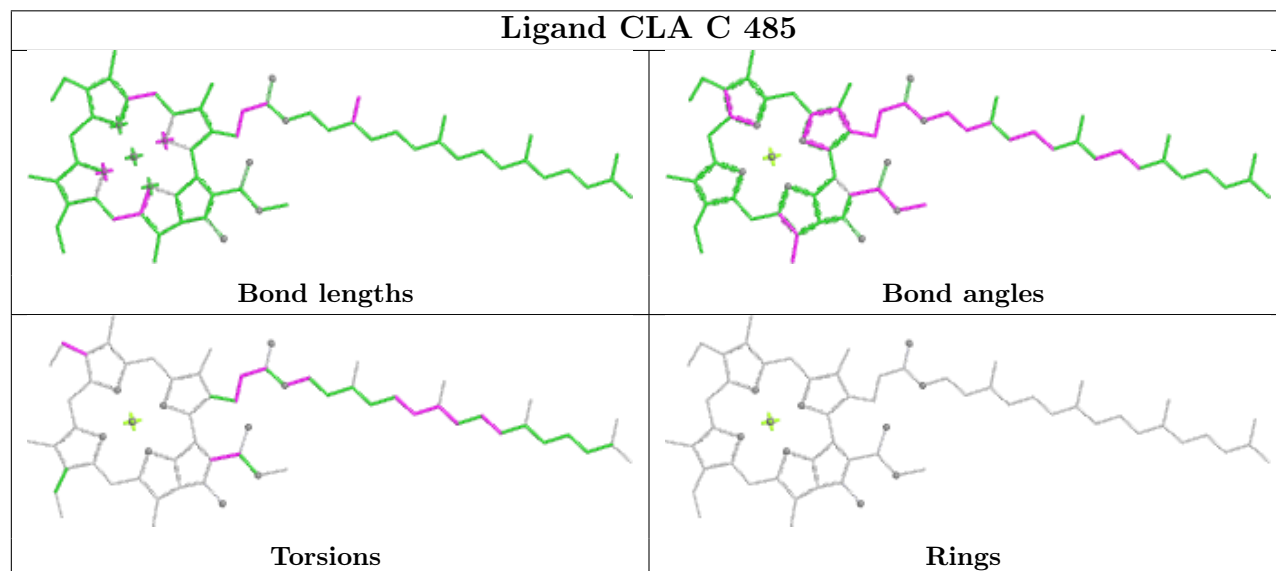
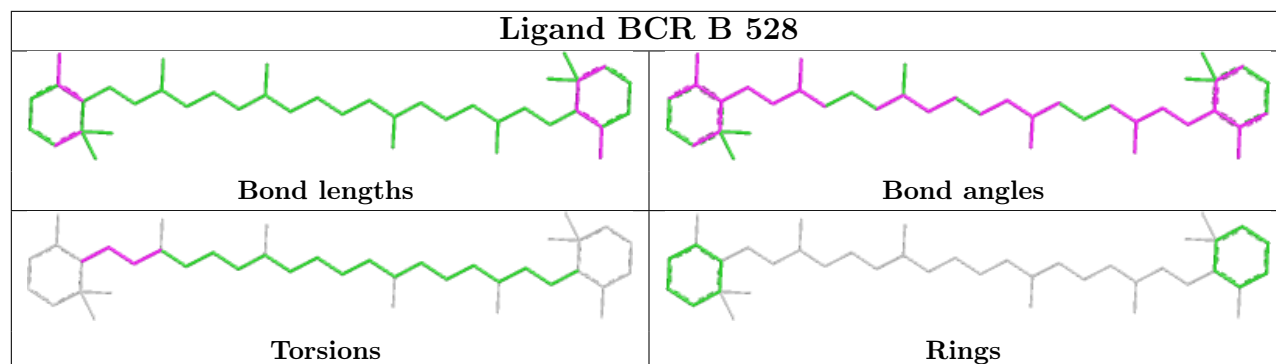
Rings

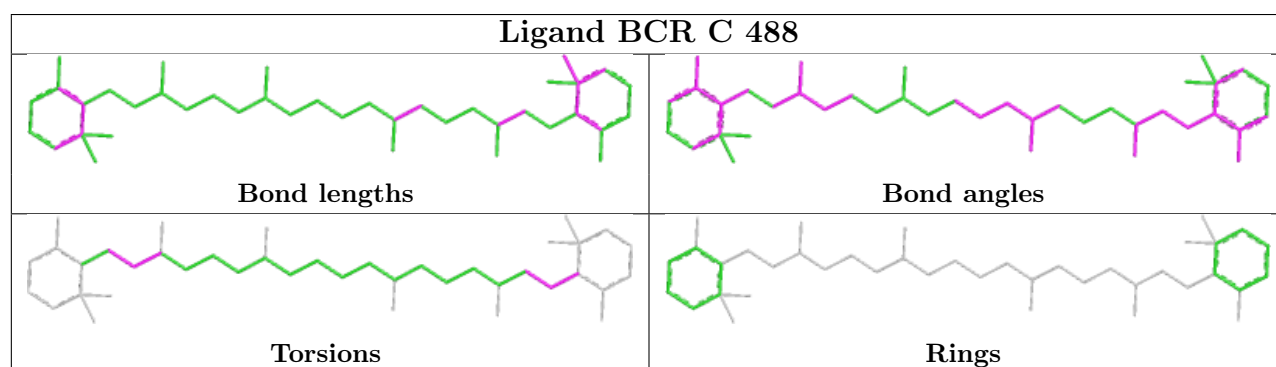
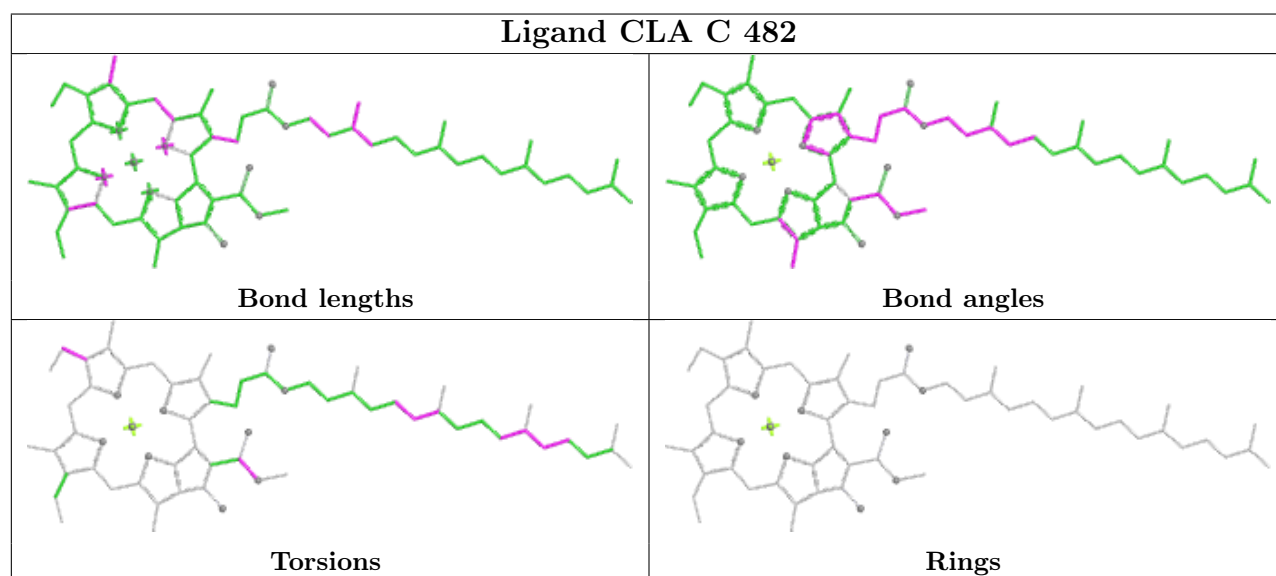
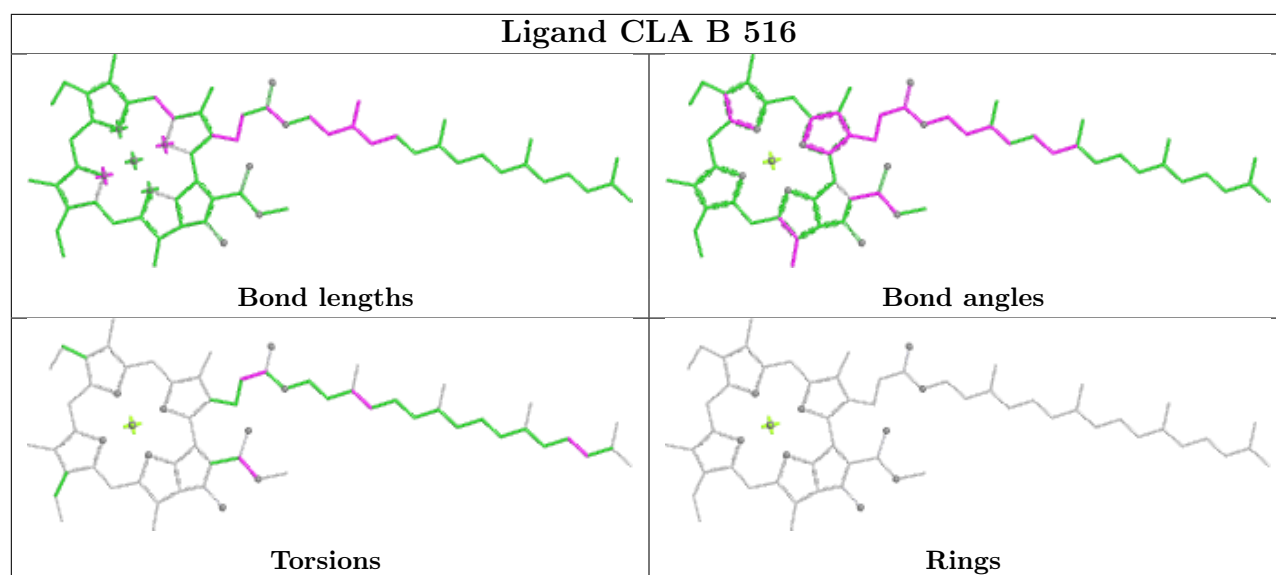


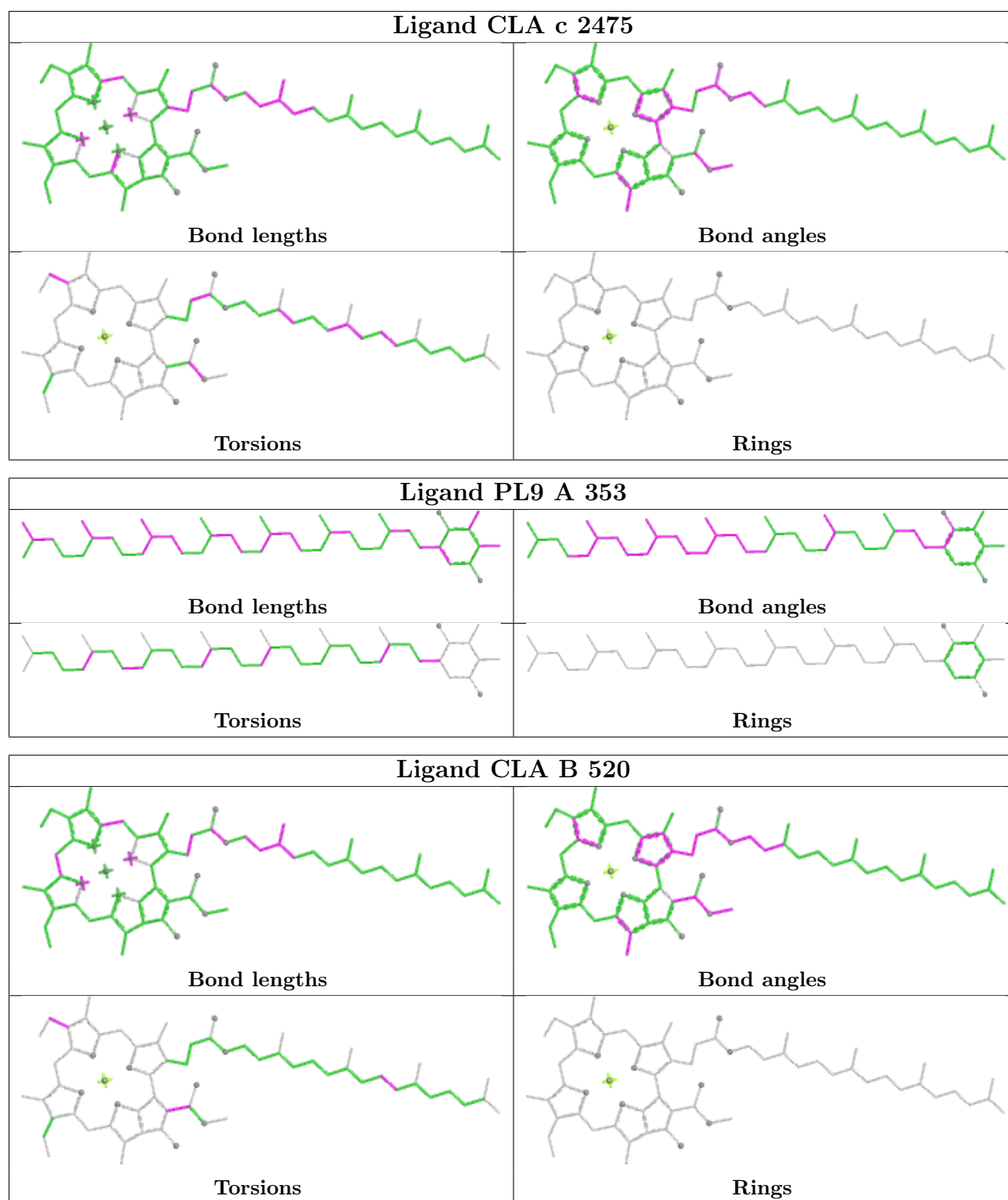


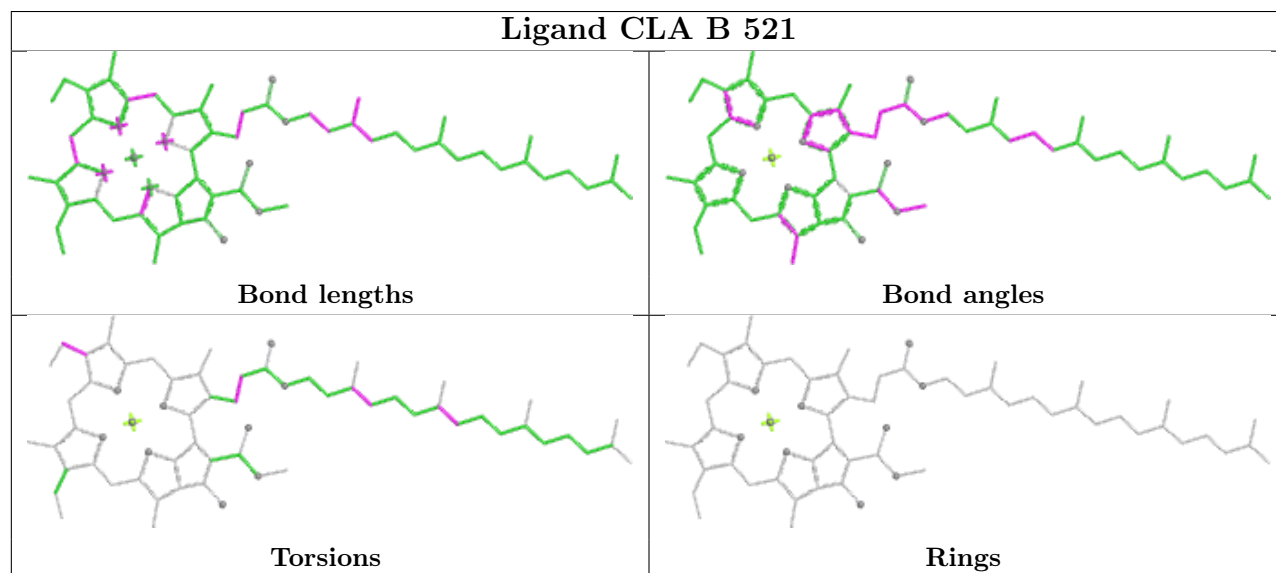
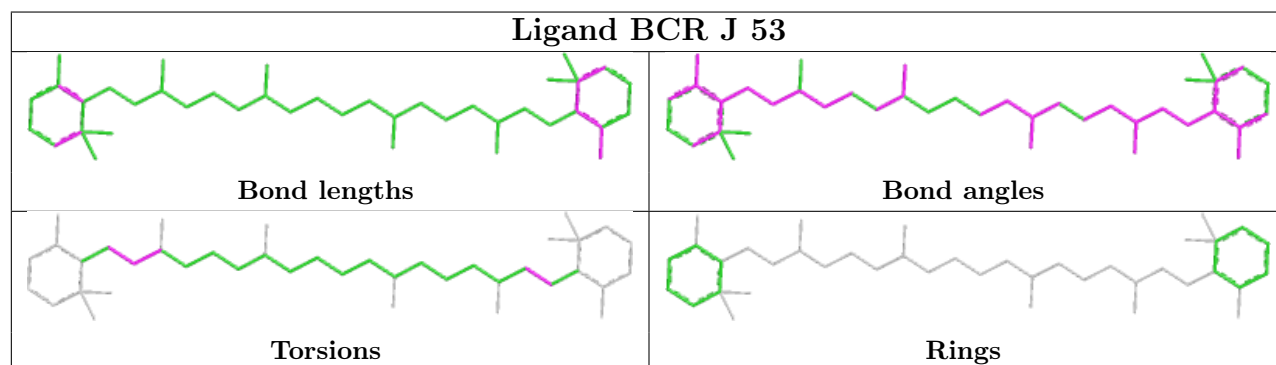
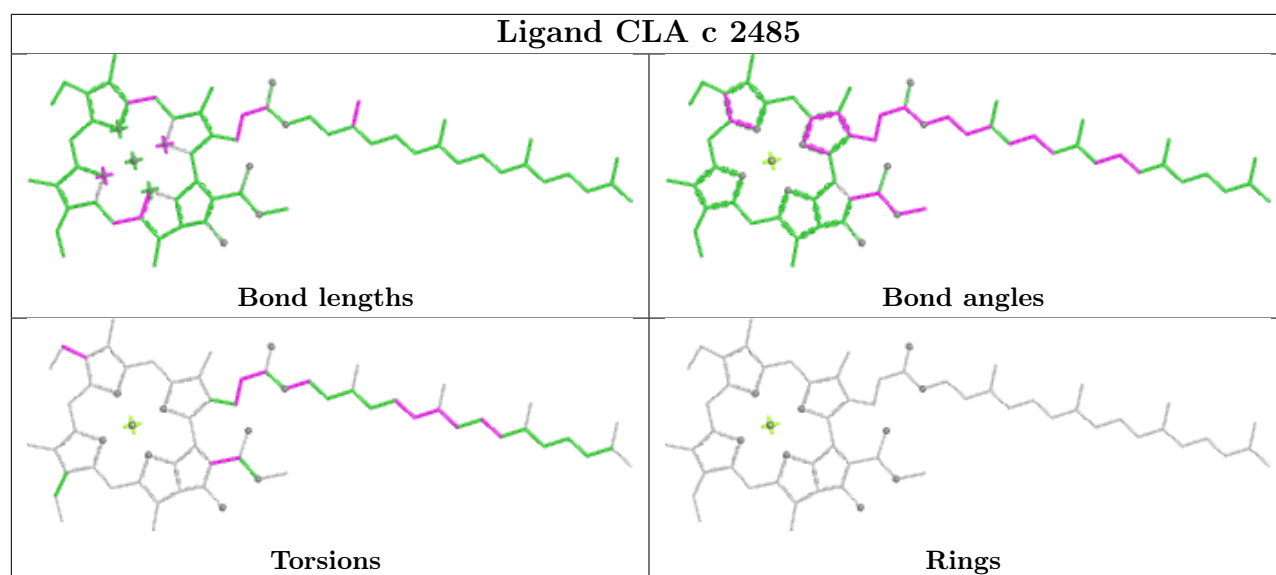


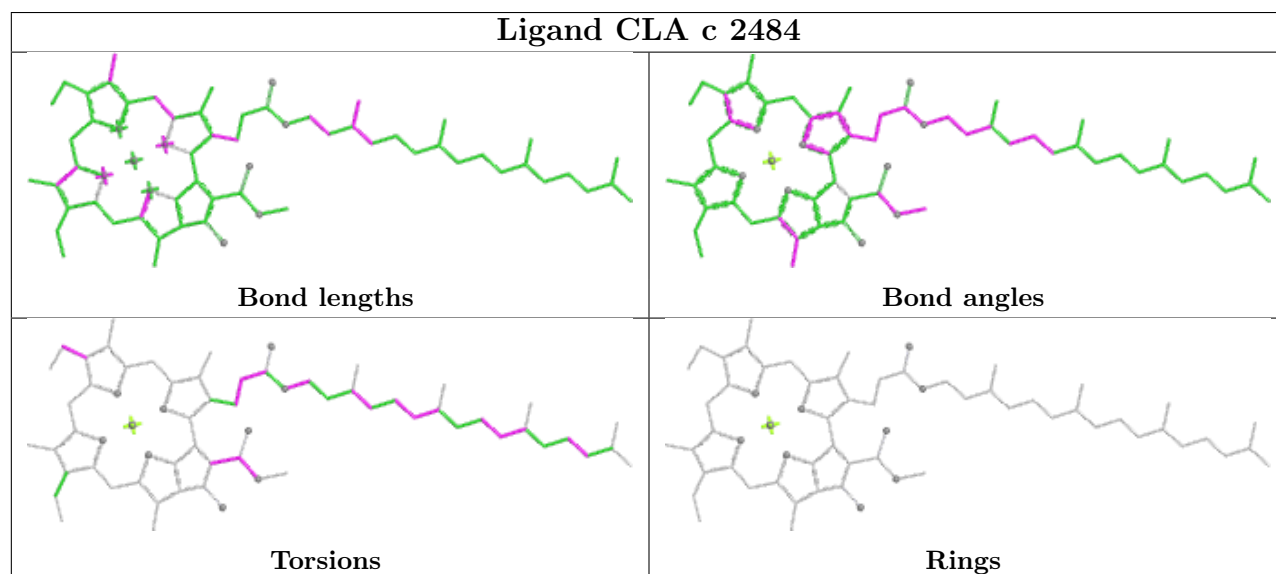
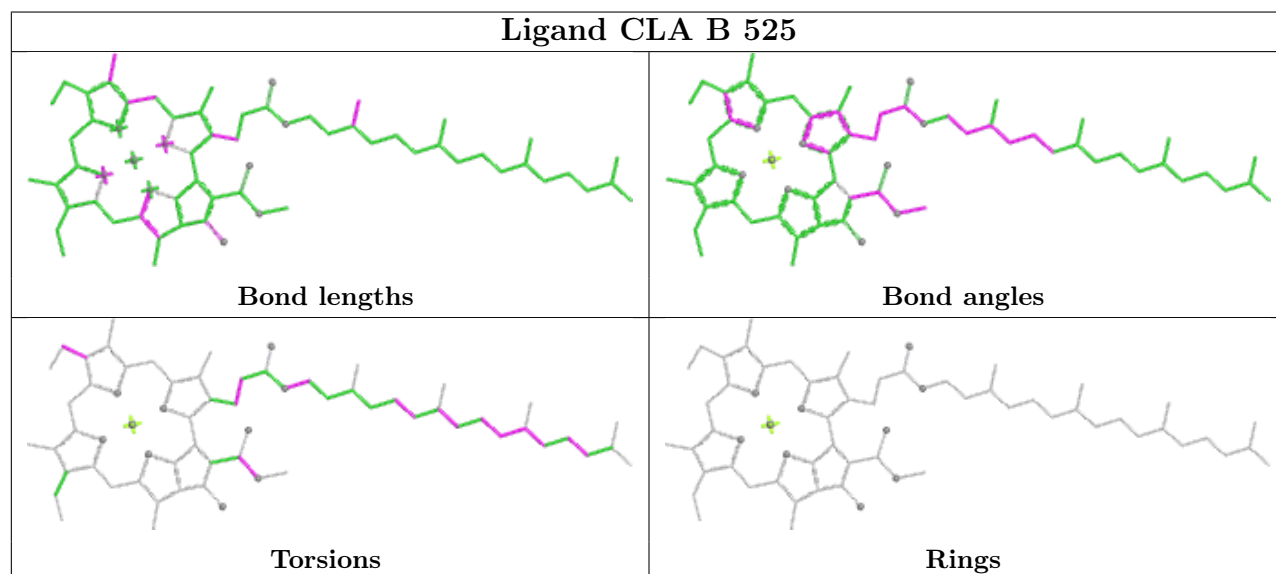
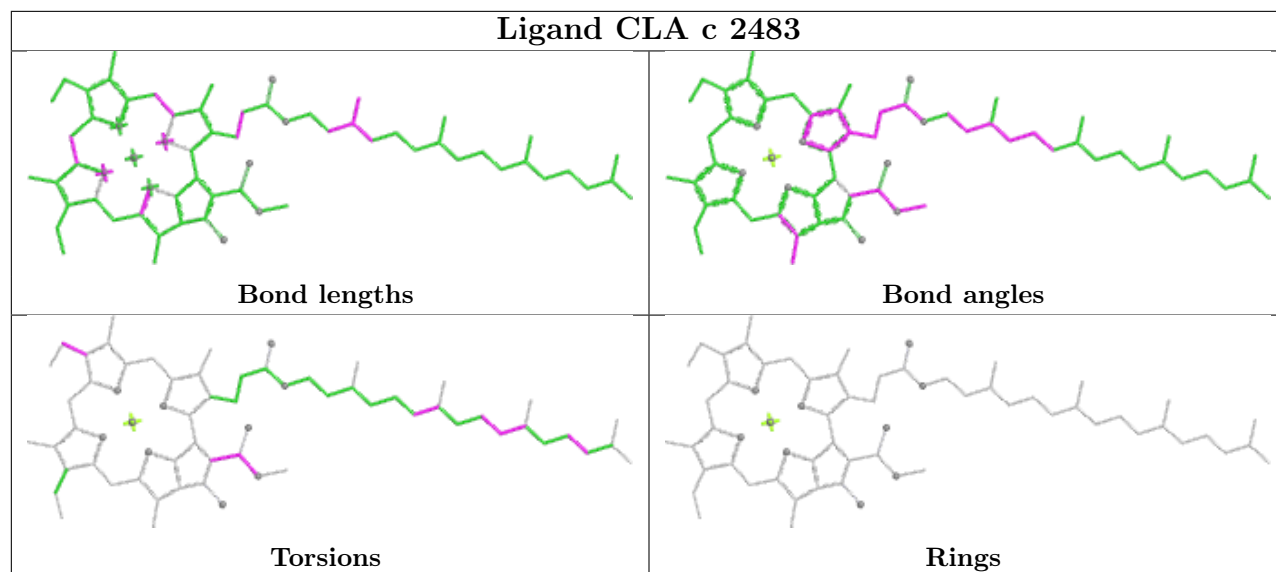


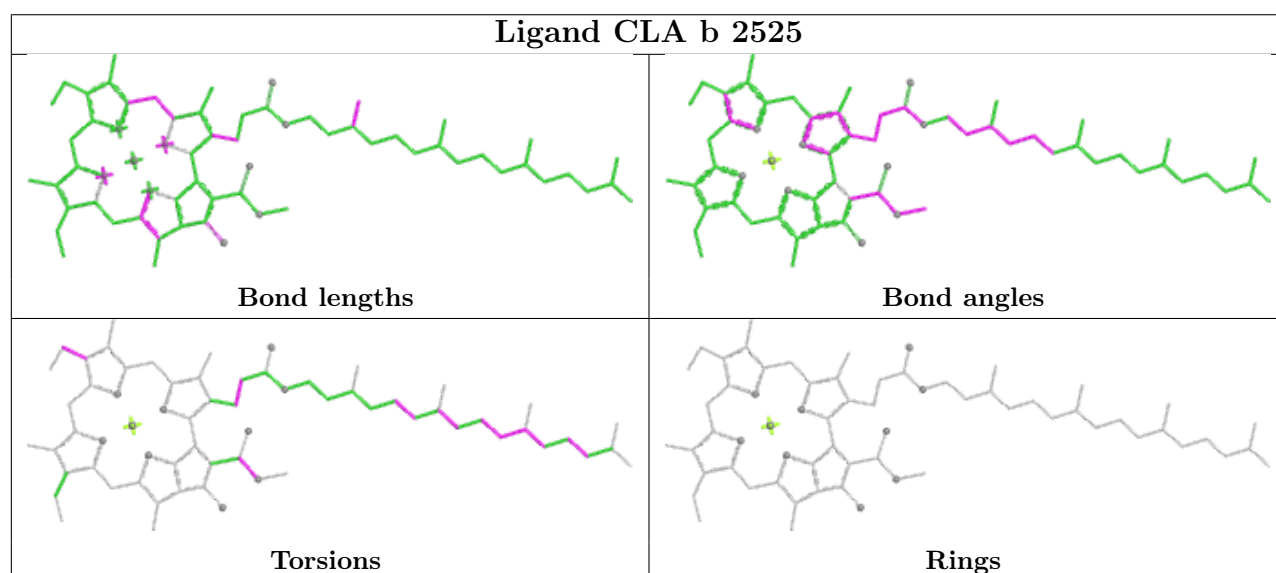
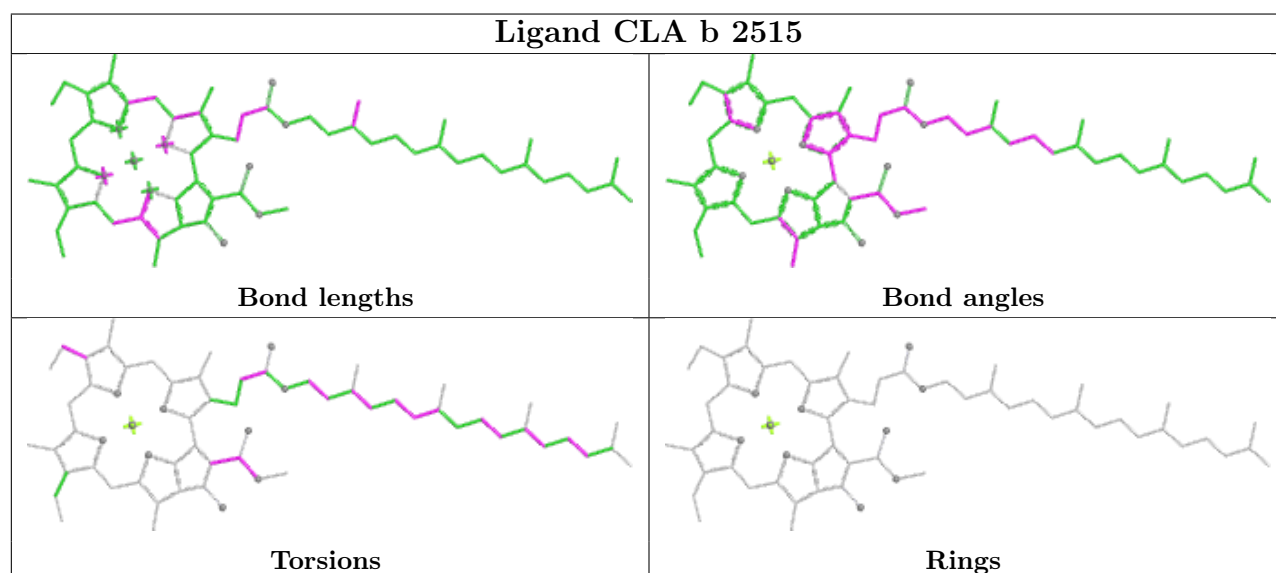
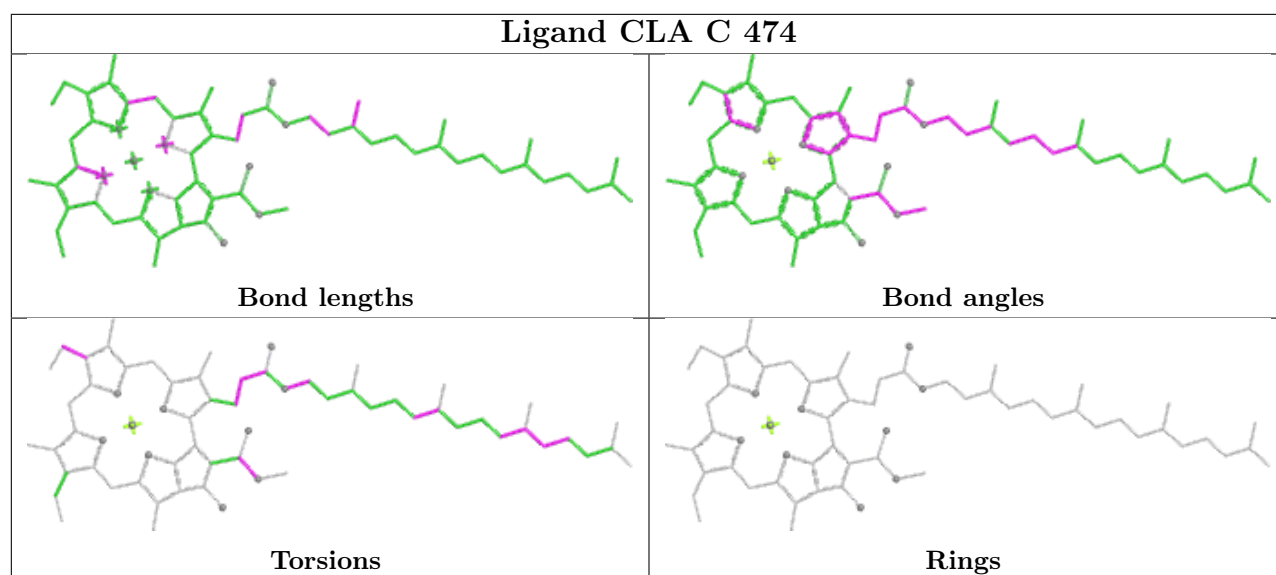


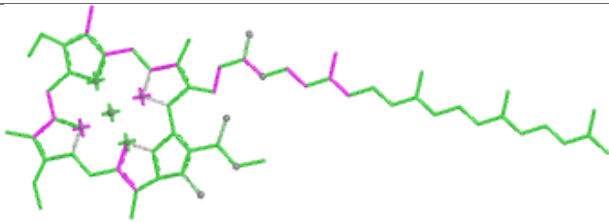
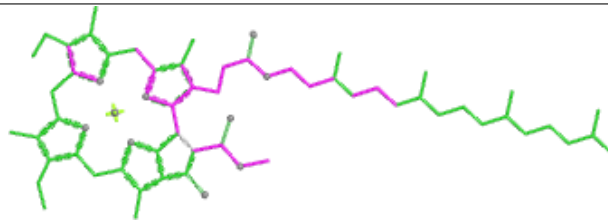
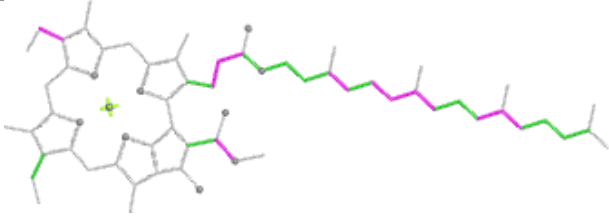
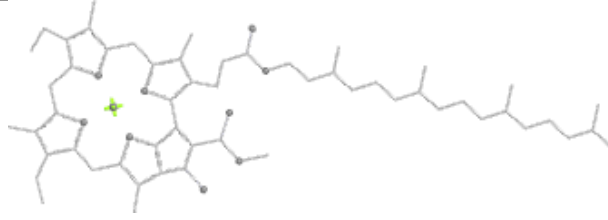


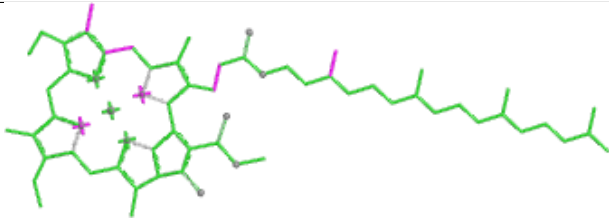
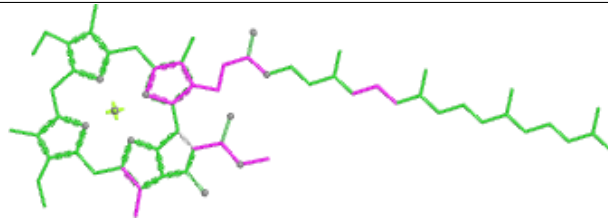
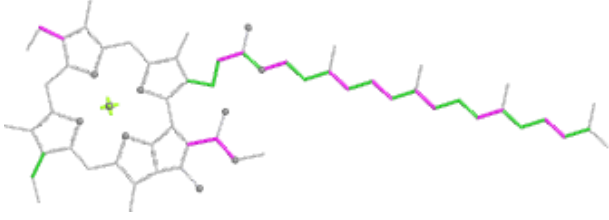
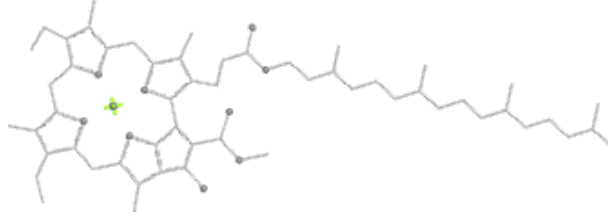


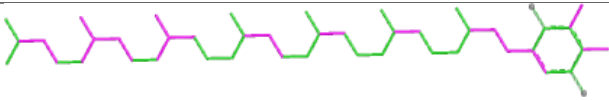
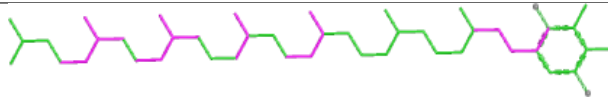
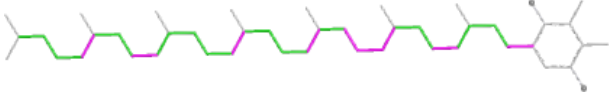
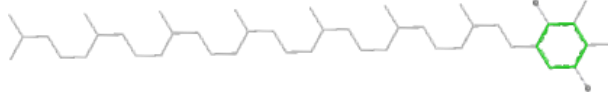


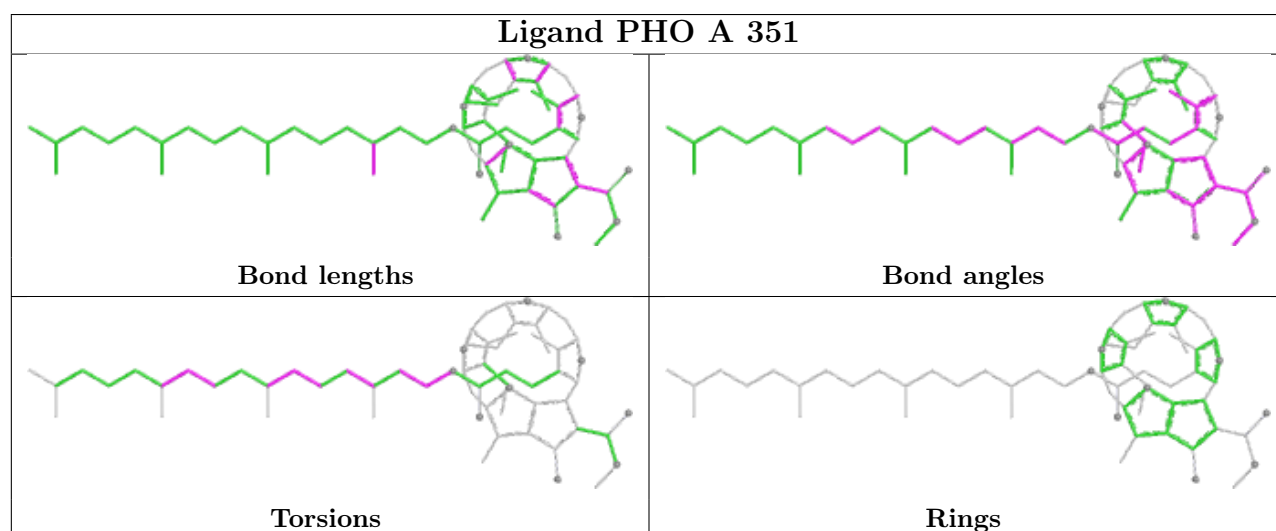
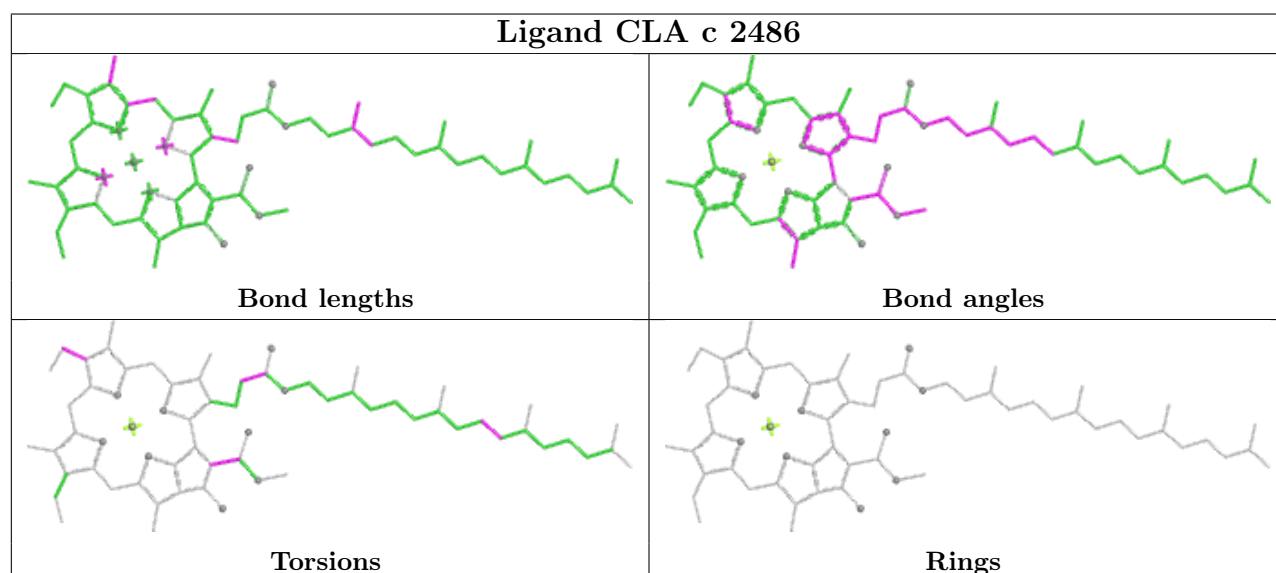
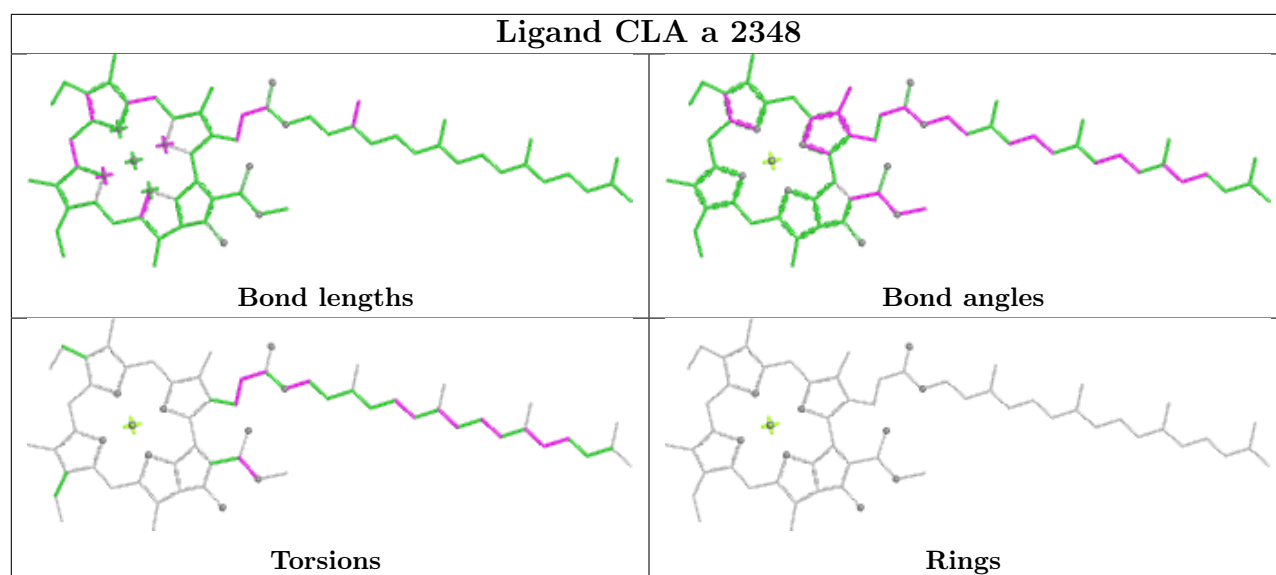


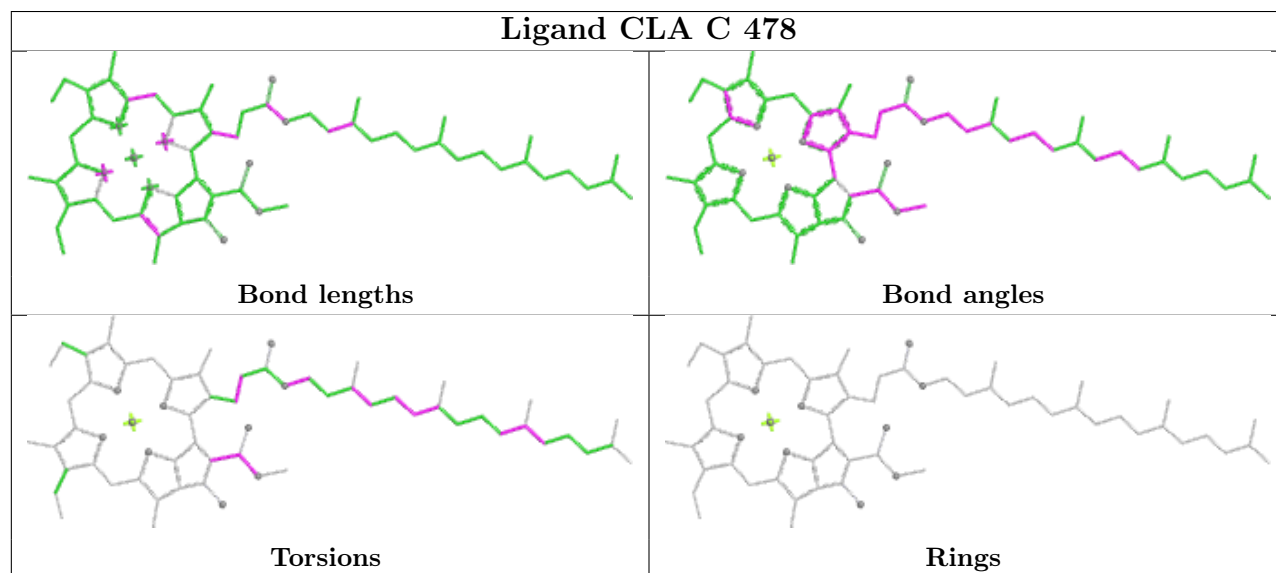
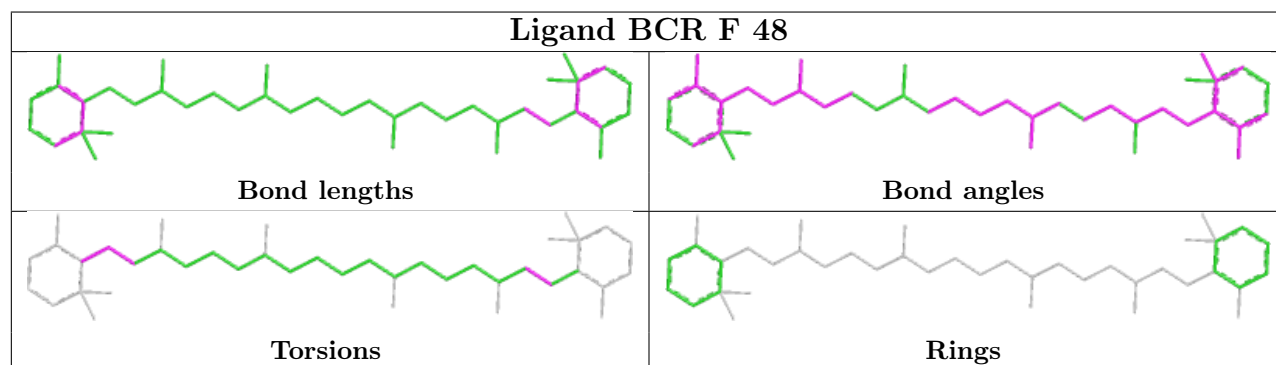
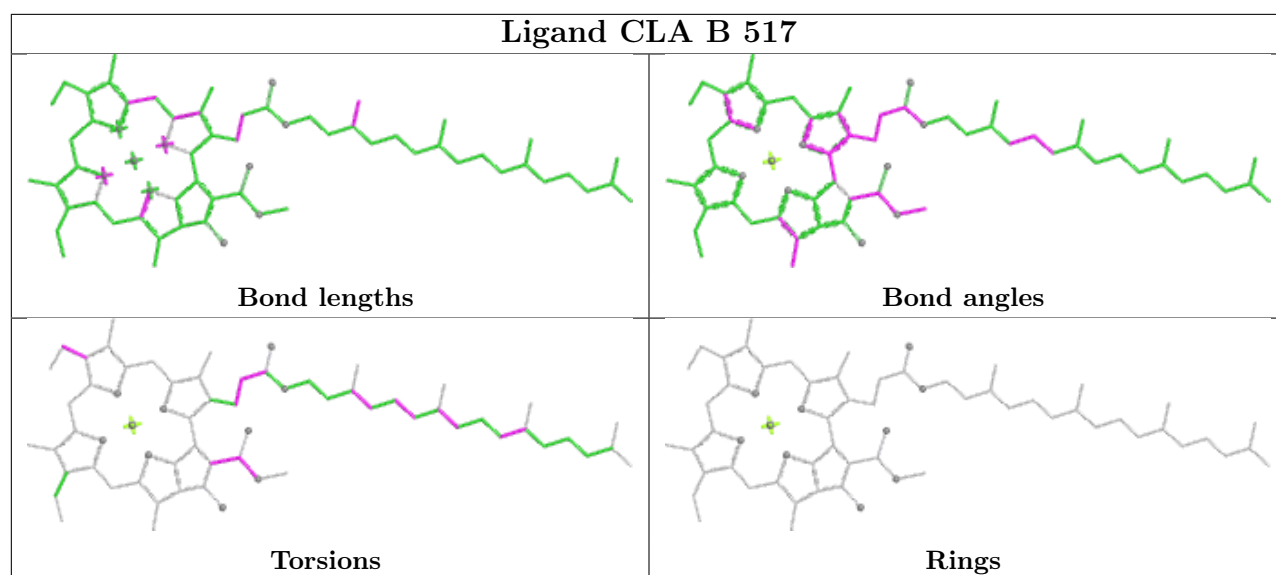


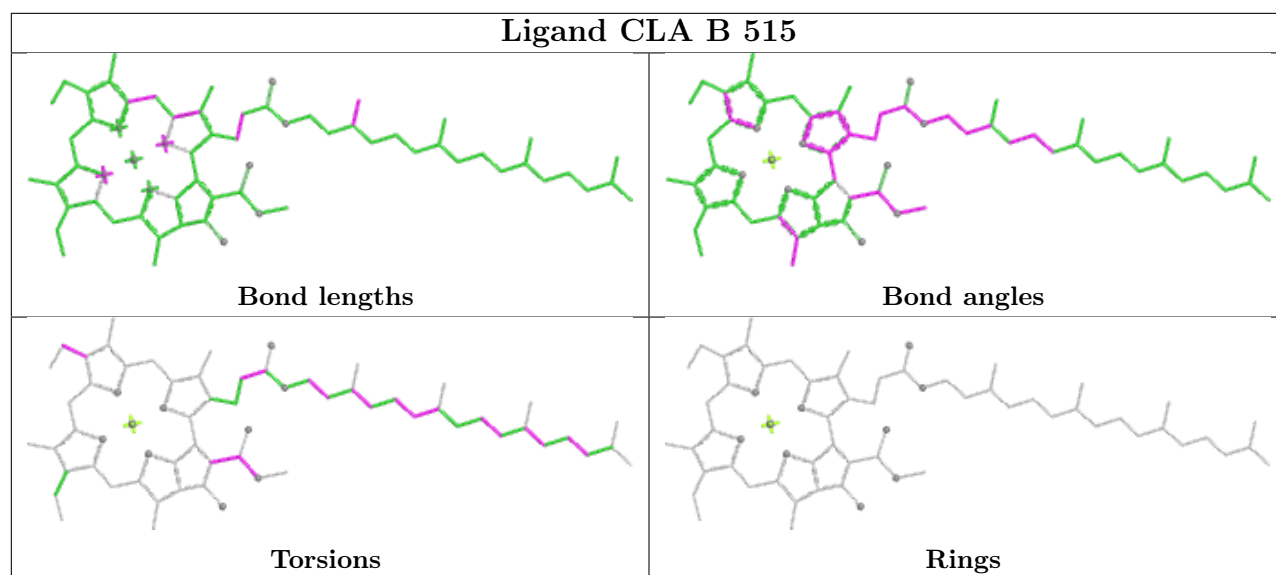
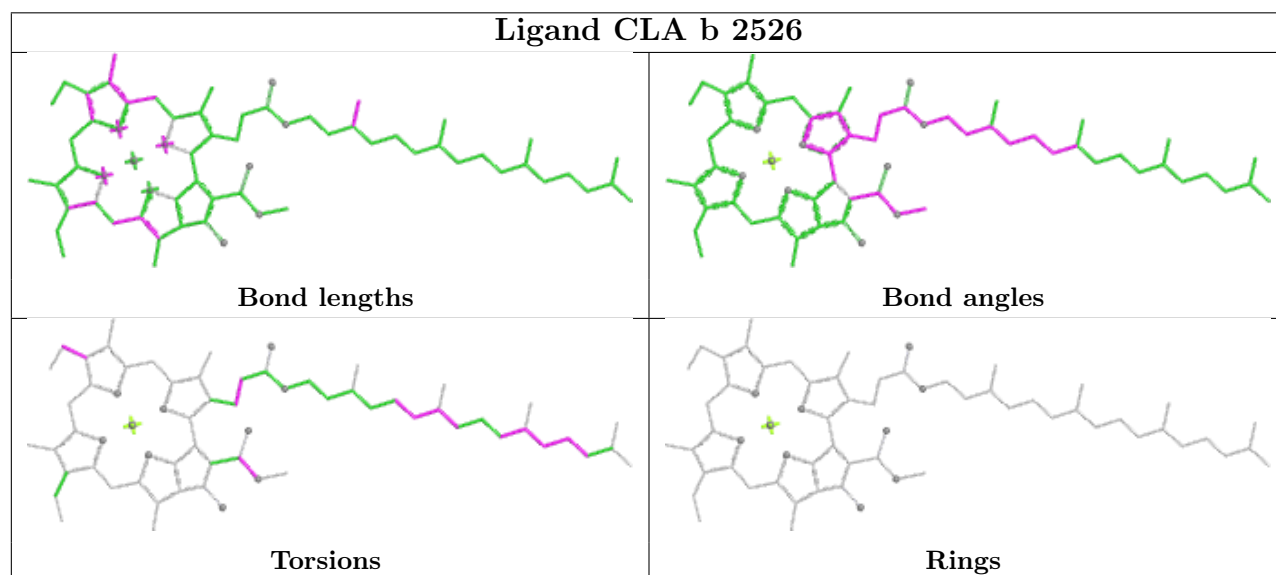
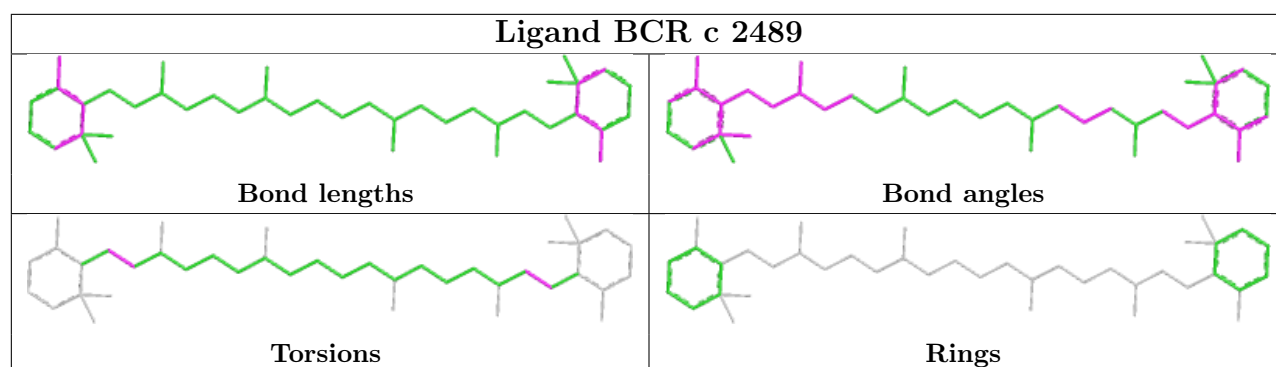
Ligand CLA B 511	
	
Bond lengths	Bond angles
	
Torsions	Rings

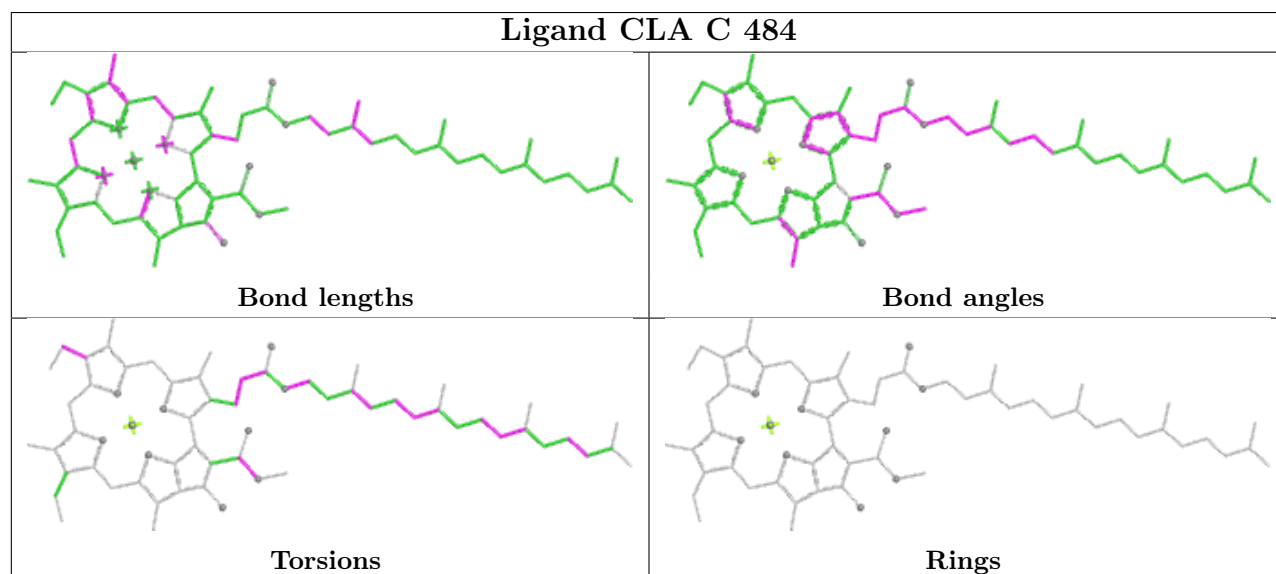
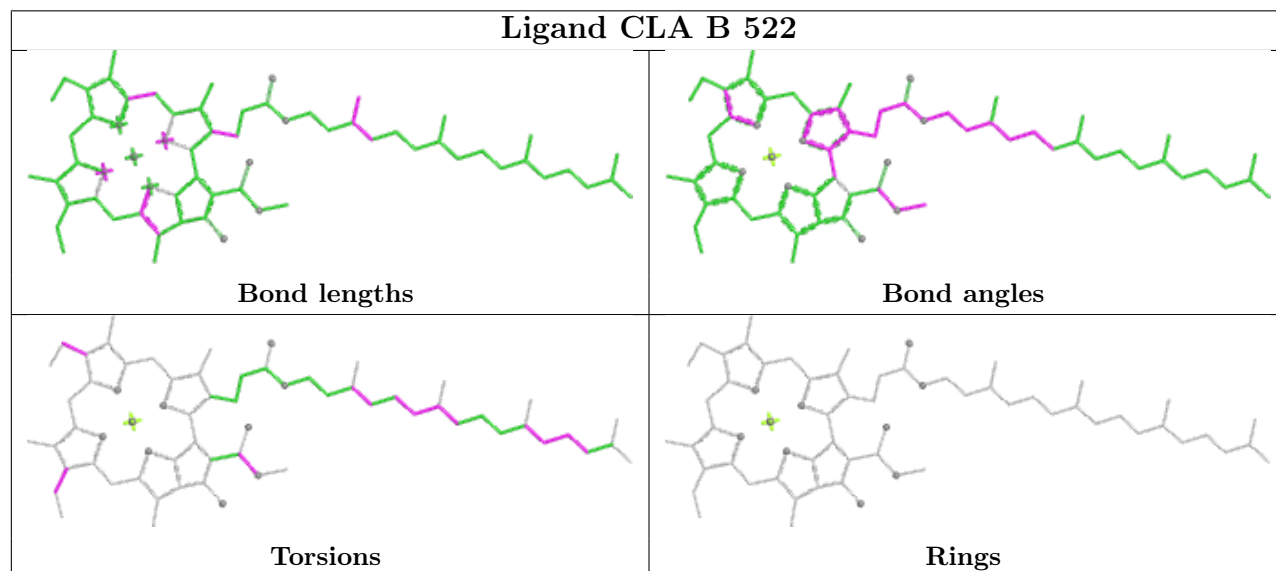
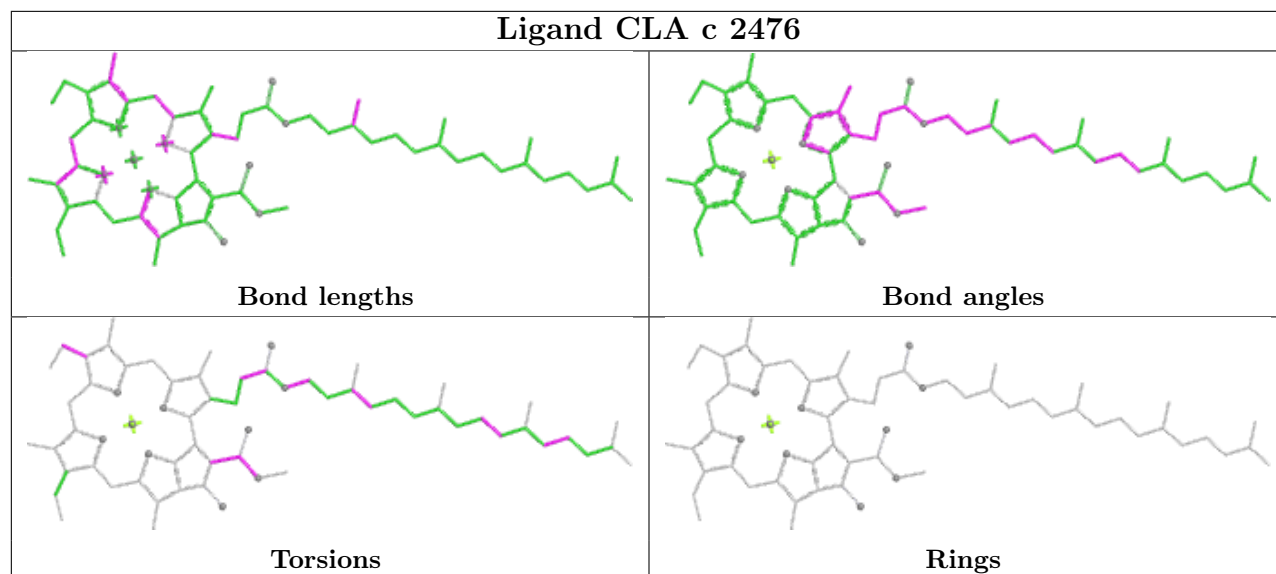
Ligand CLA c 2480	
	
Bond lengths	Bond angles
	
Torsions	Rings

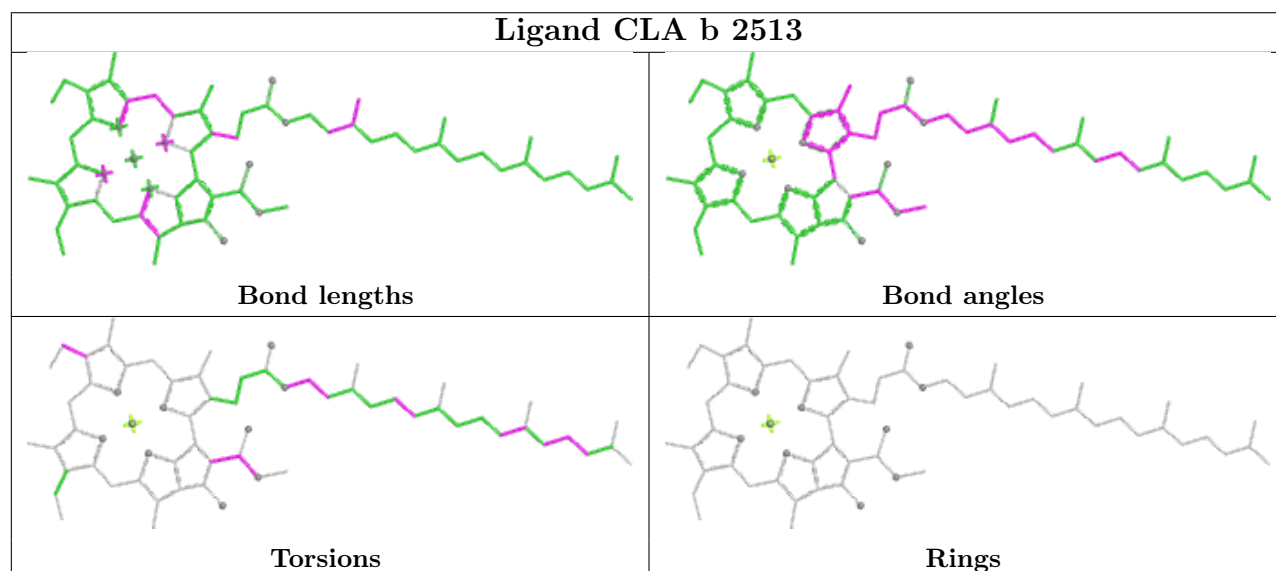
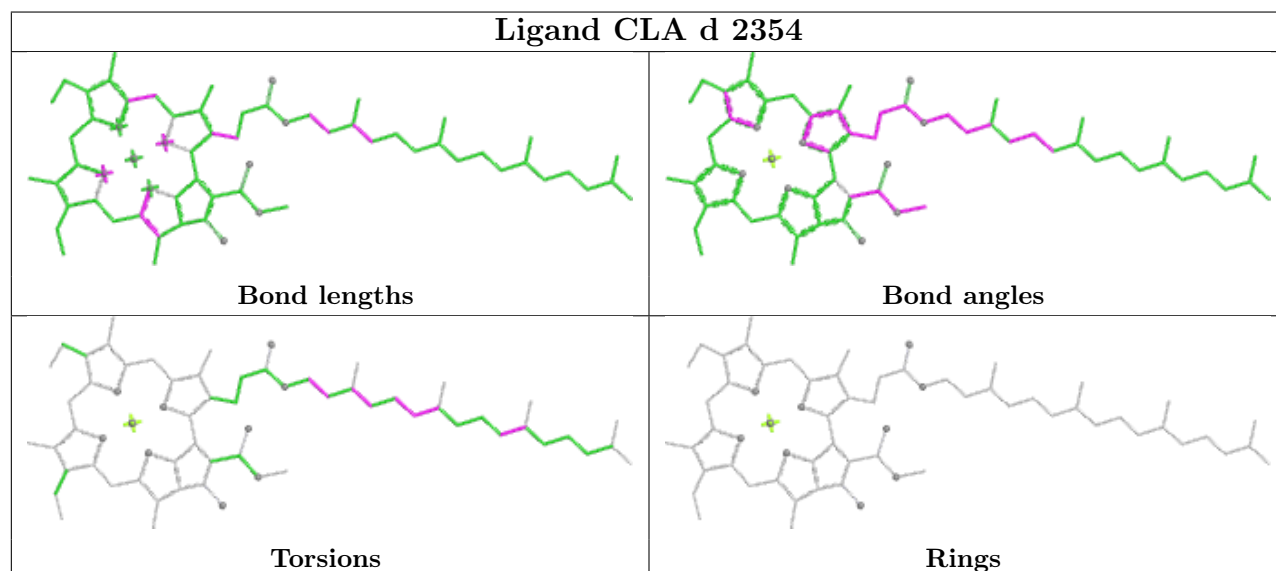
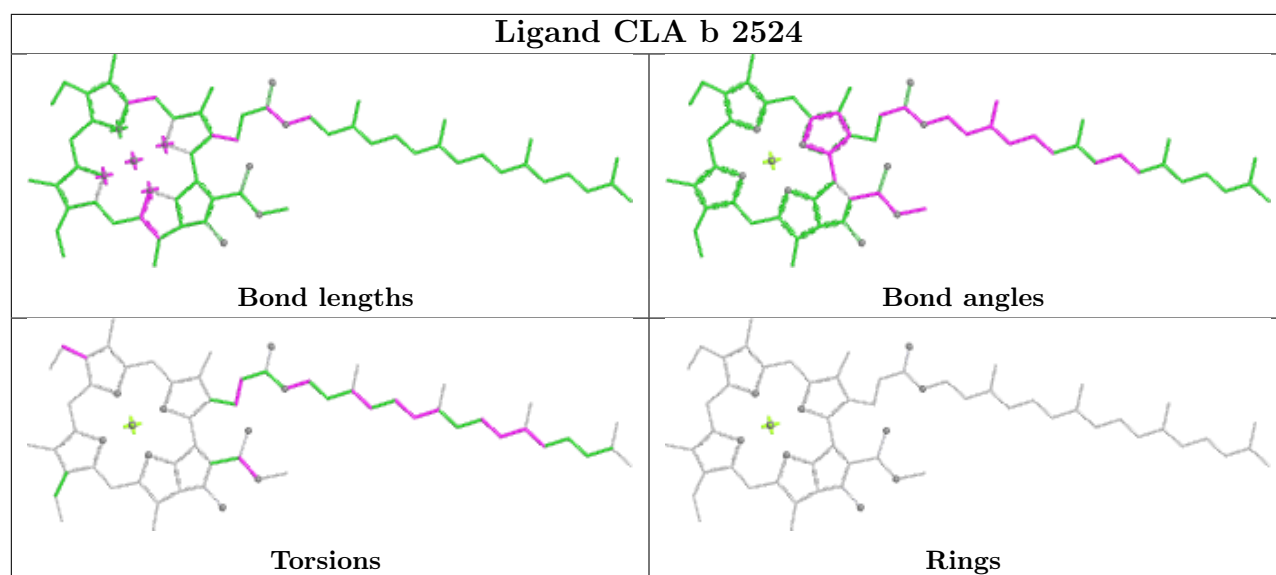
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Bond lengths	Bond angles
	
Torsions	Rings

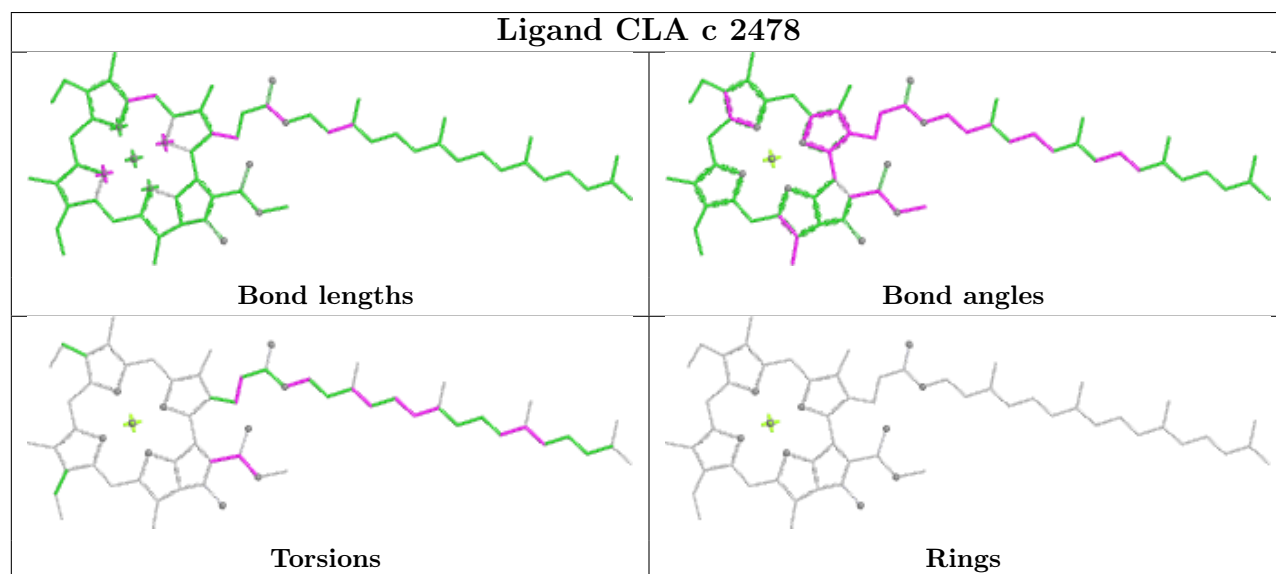
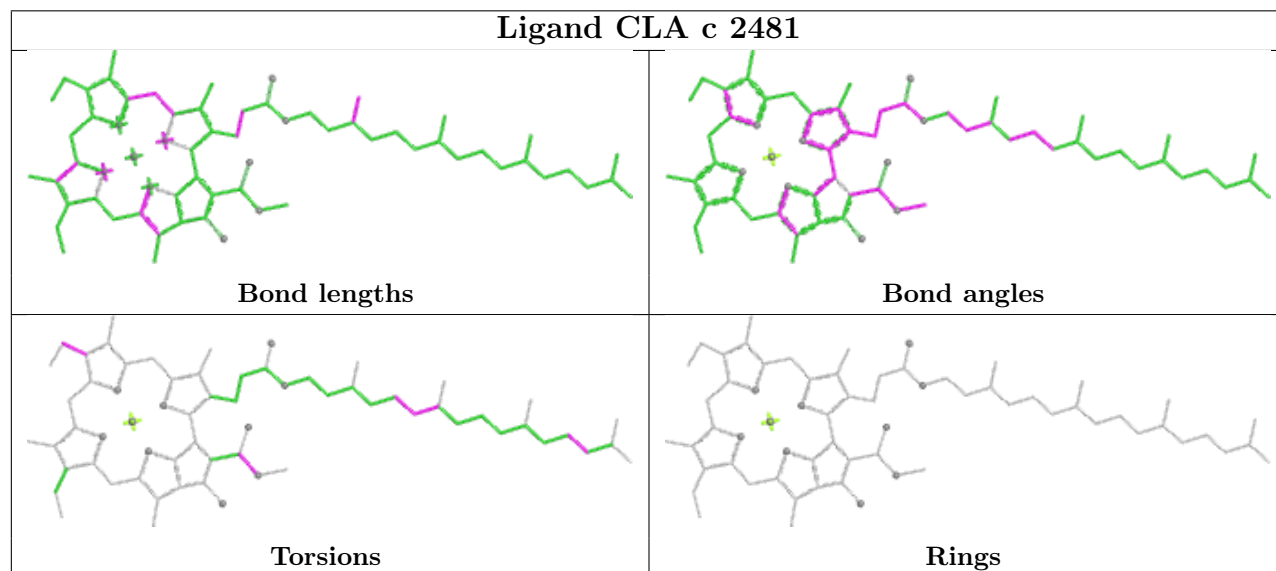
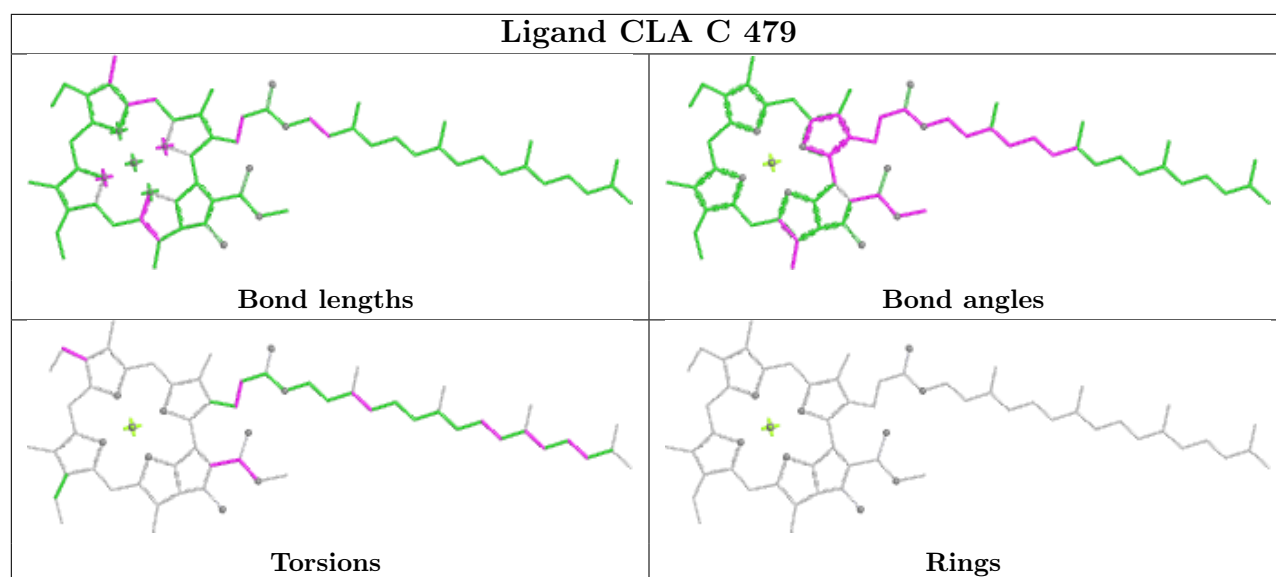


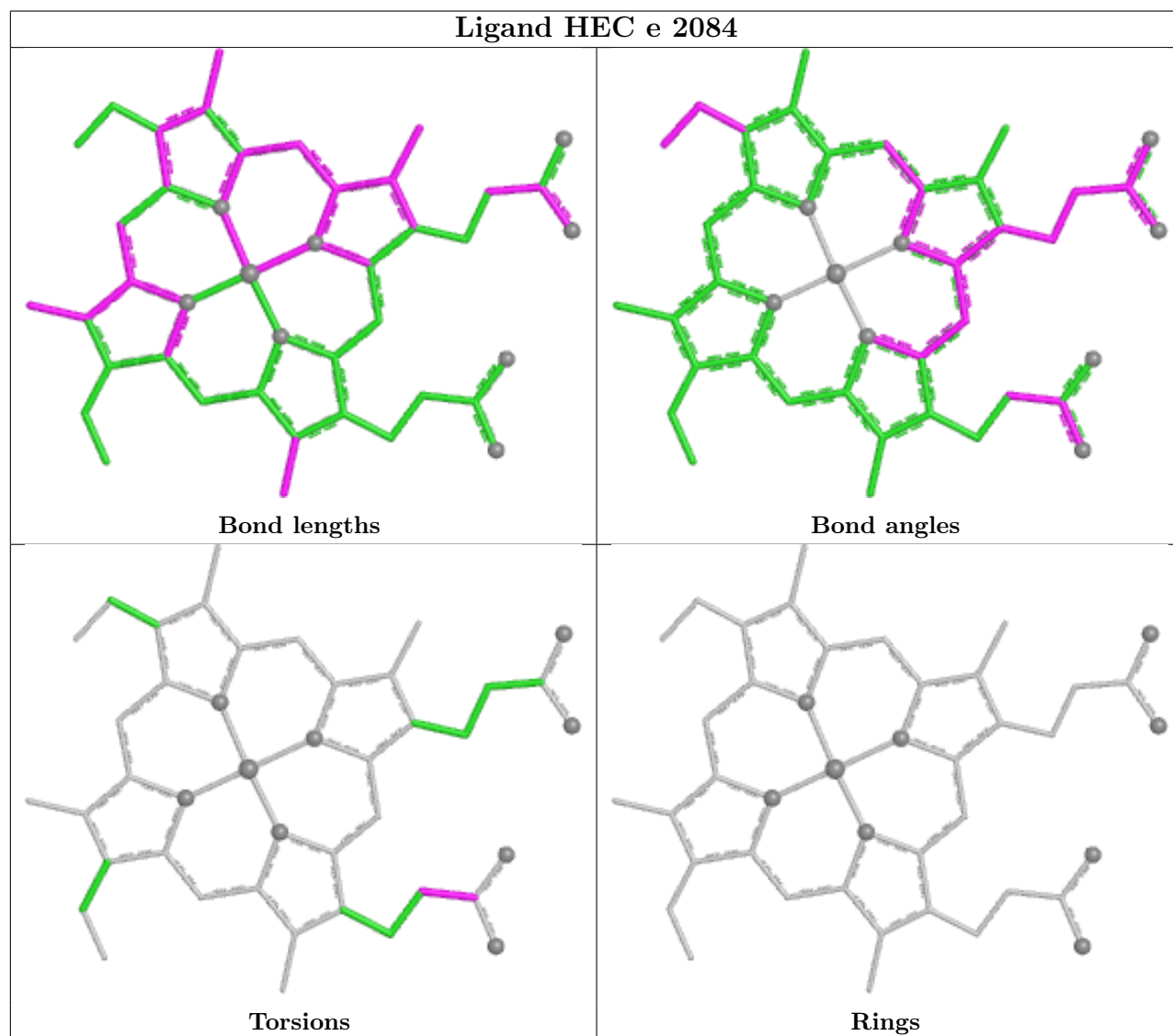
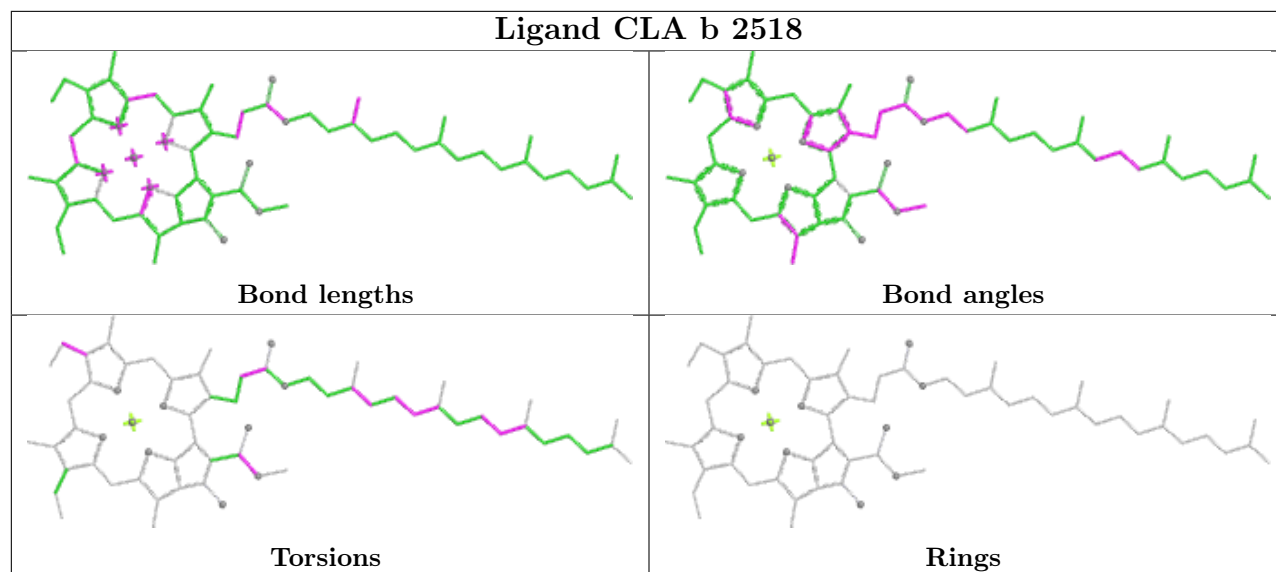


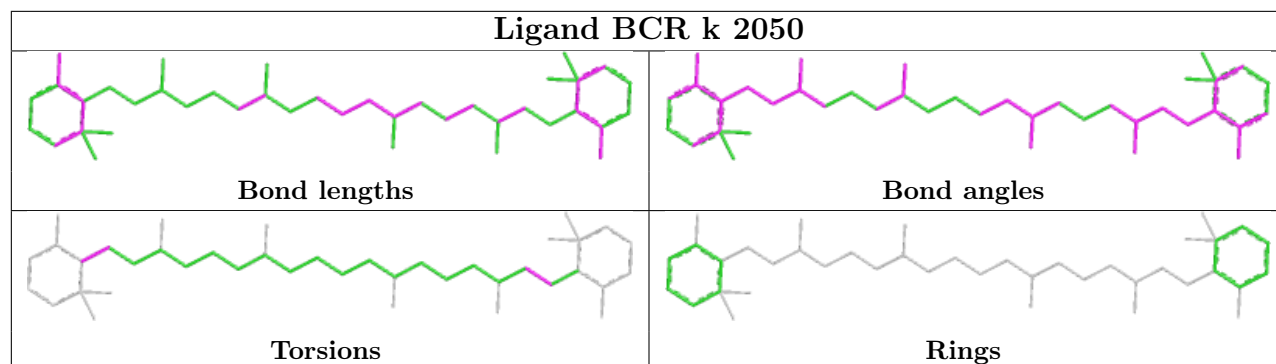
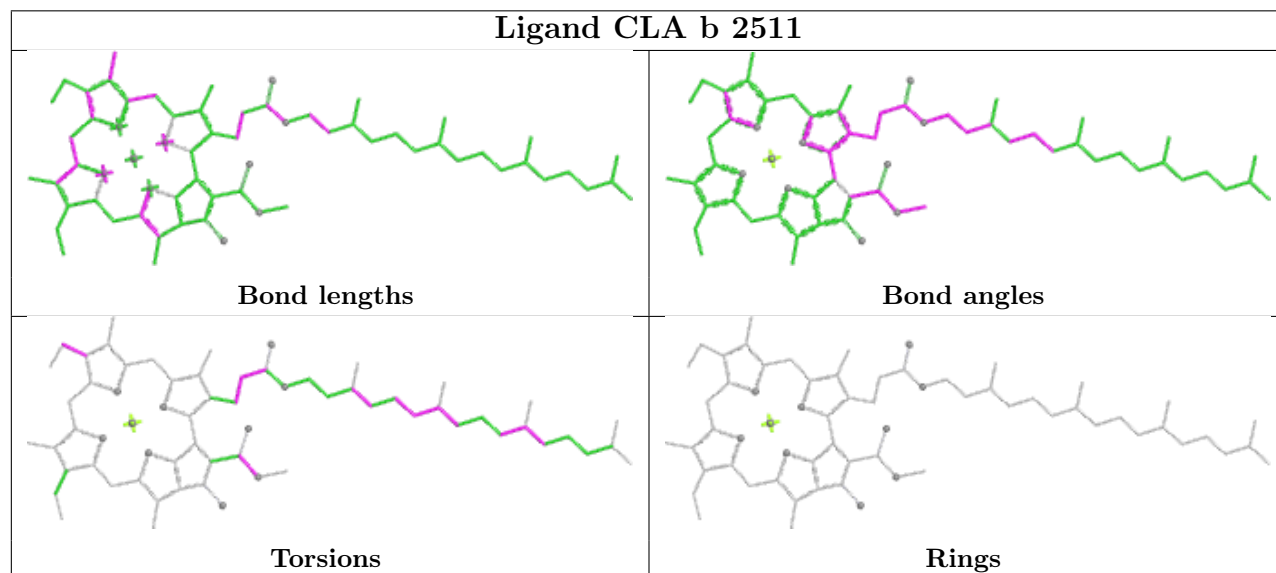
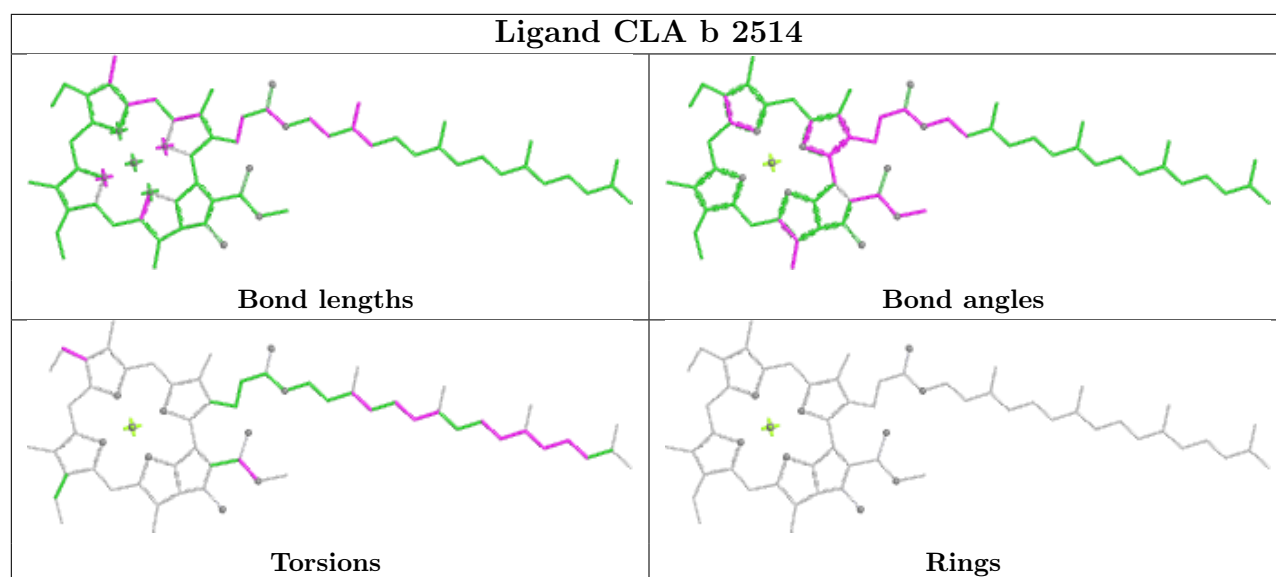


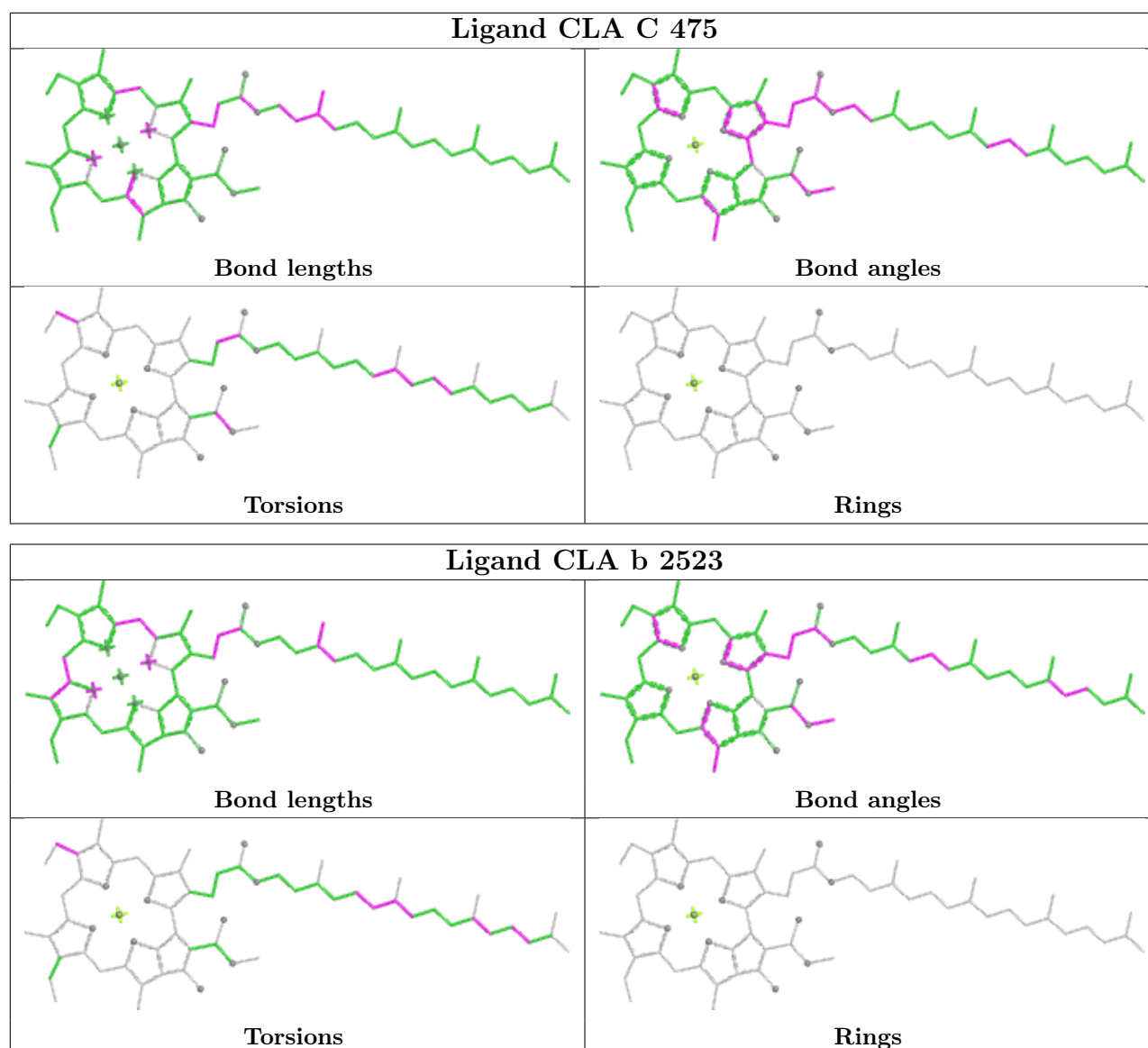




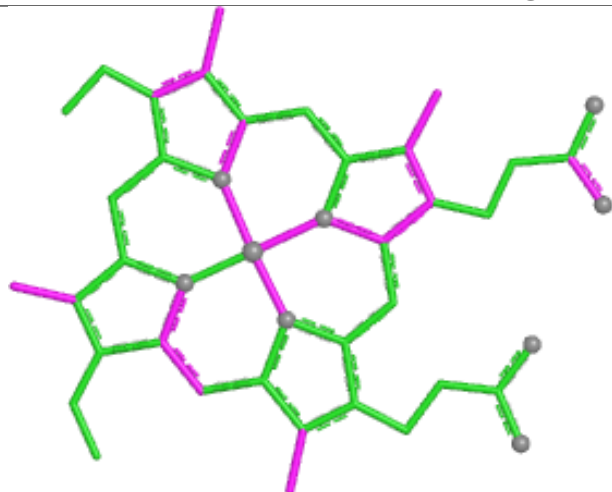




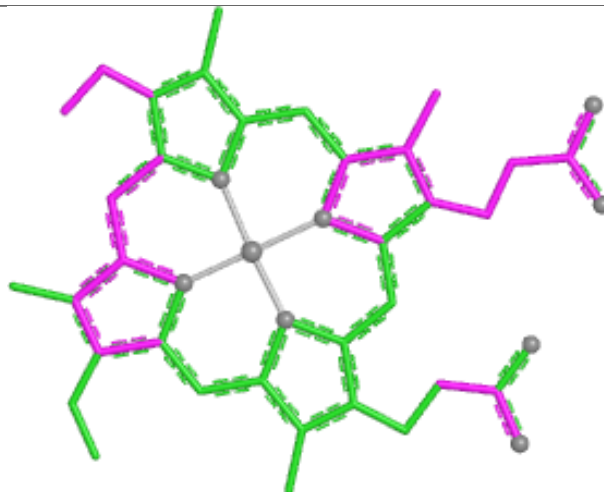




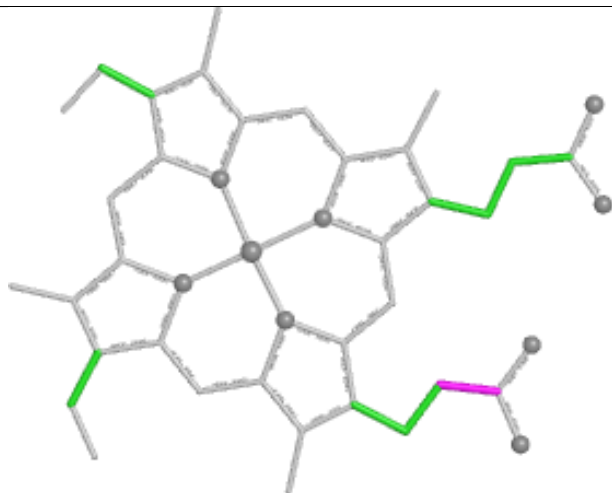
Ligand HEC E 84



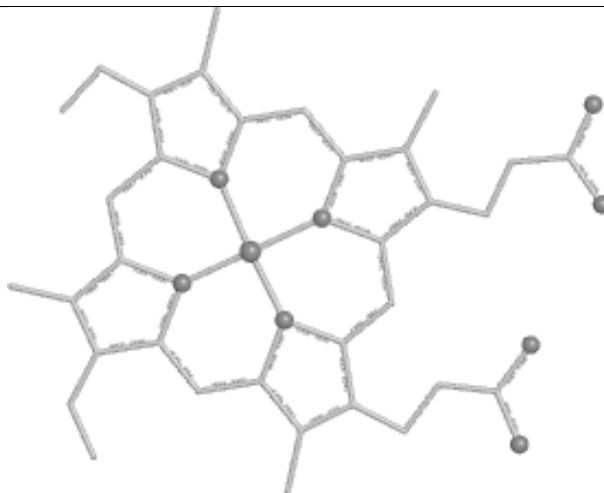
Bond lengths



Bond angles

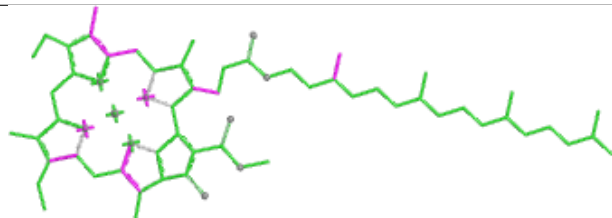


Torsions

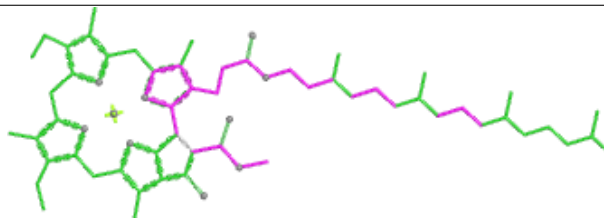


Rings

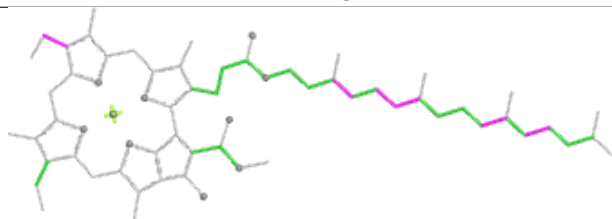
Ligand CLA a 2351



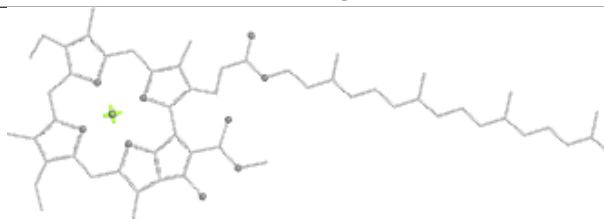
Bond lengths



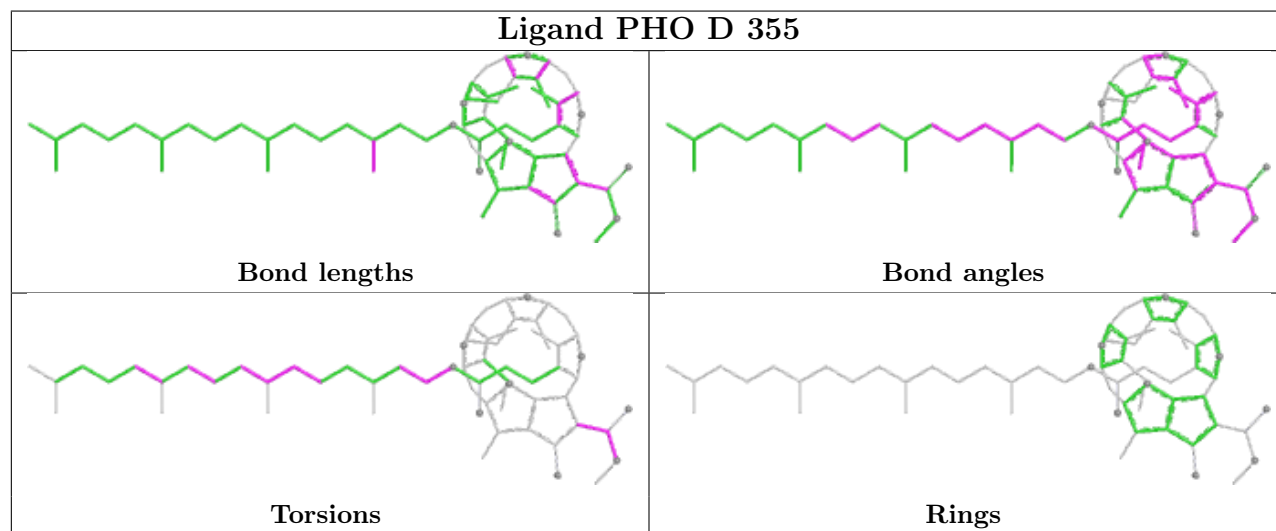
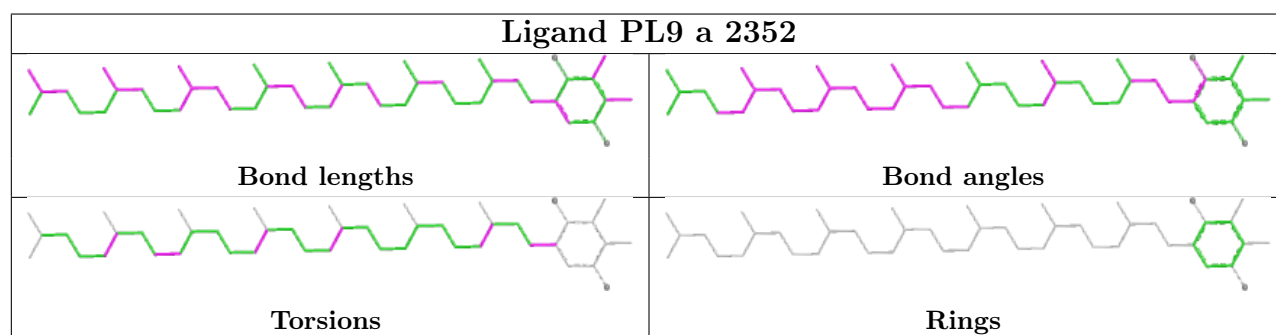
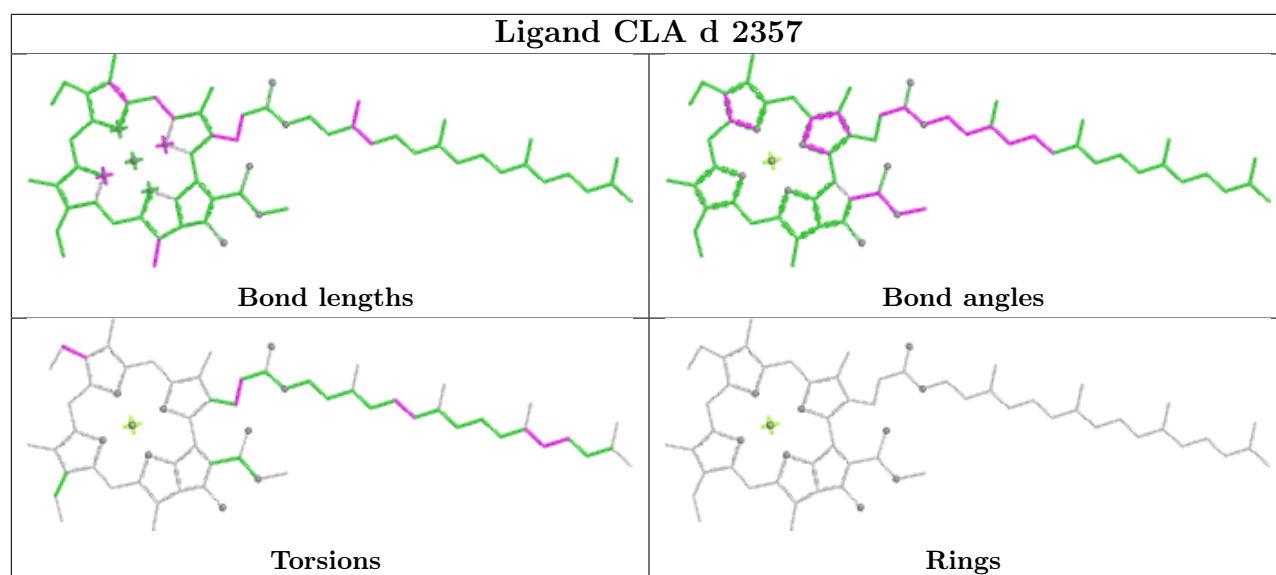
Bond angles



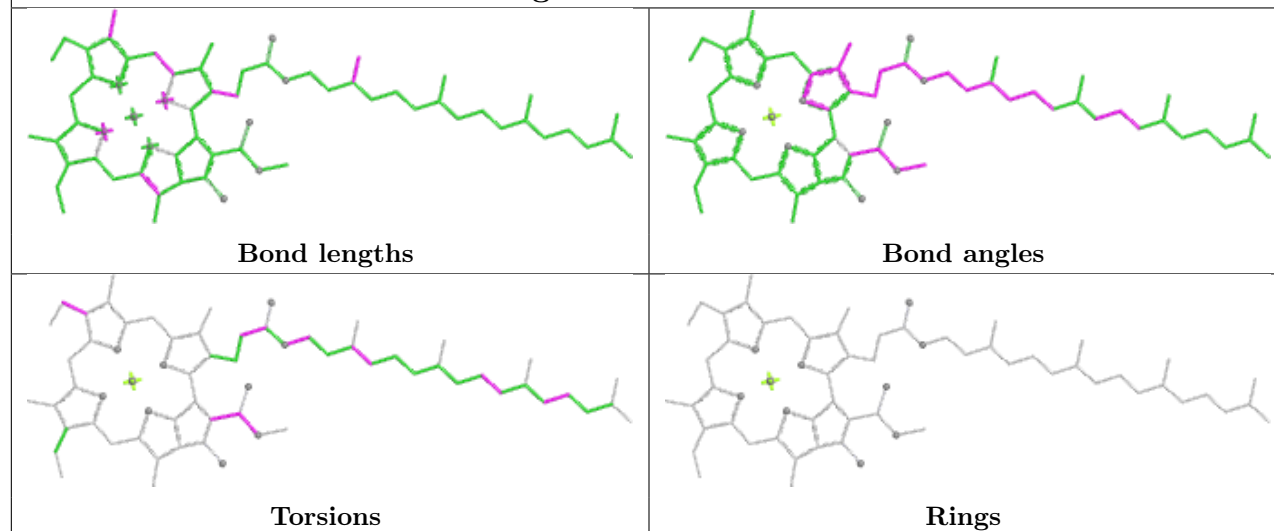
Torsions



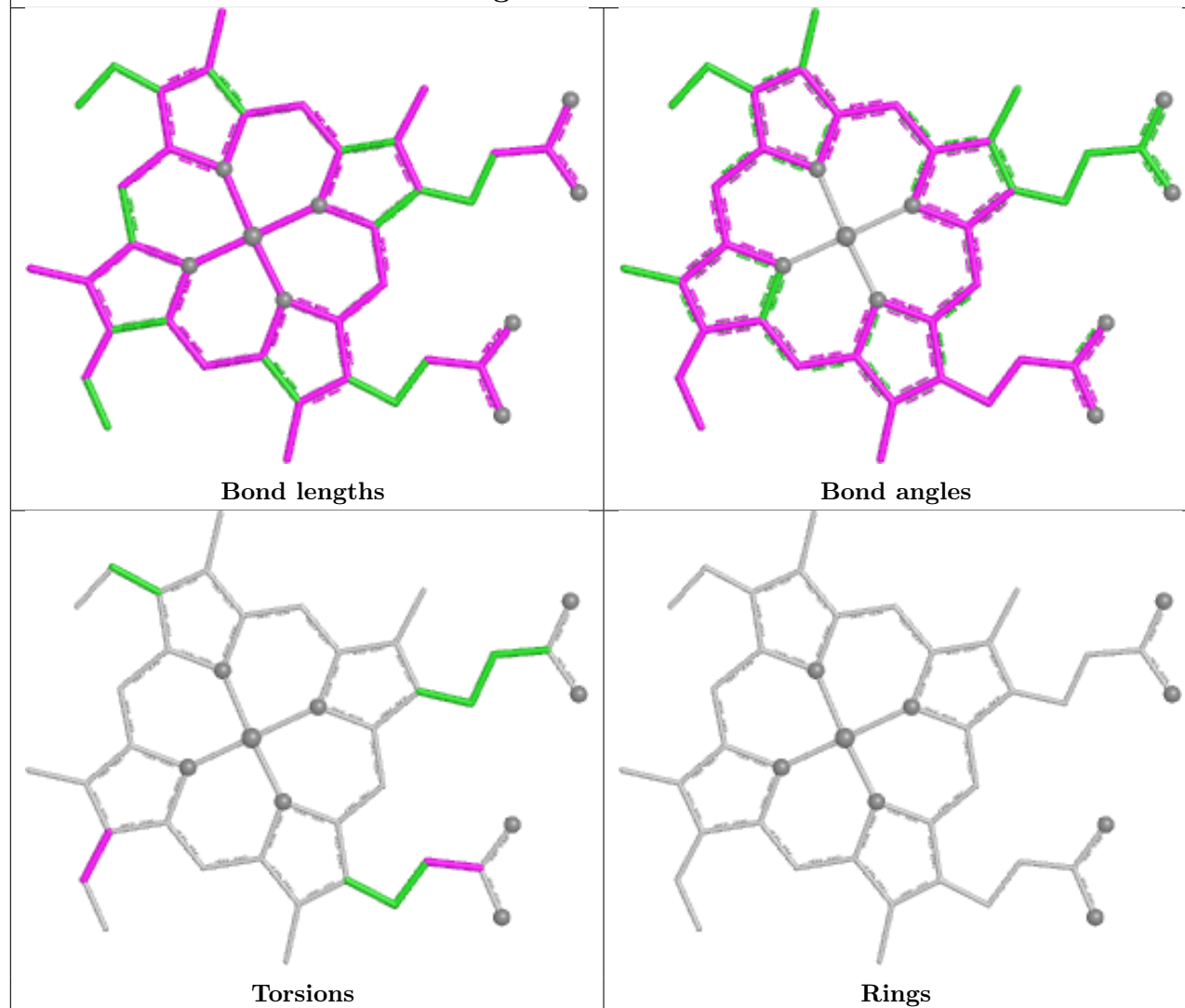
Rings

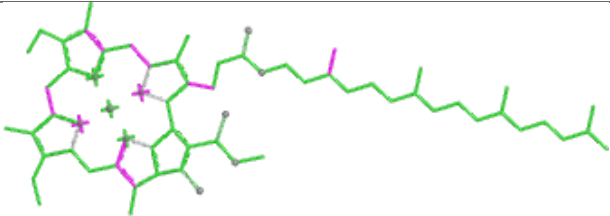
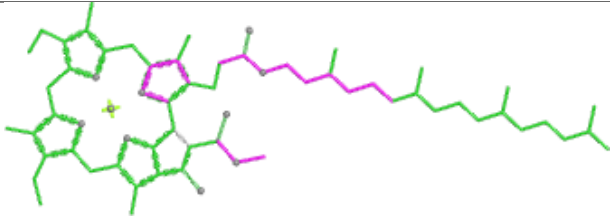
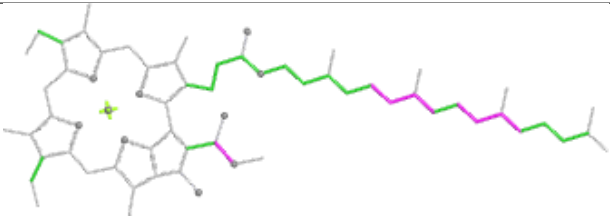
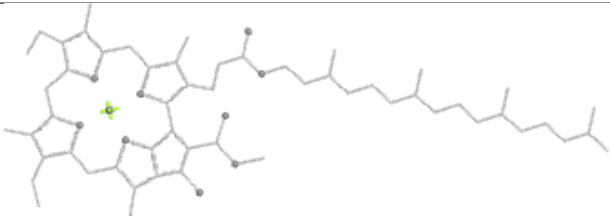
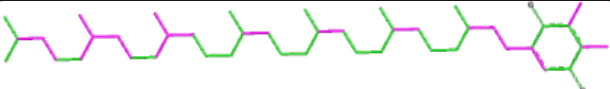
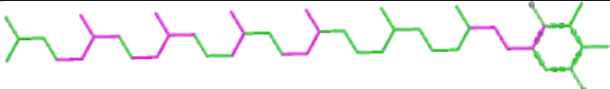
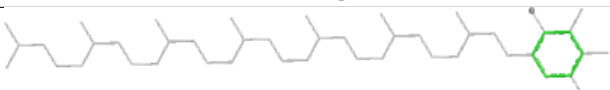
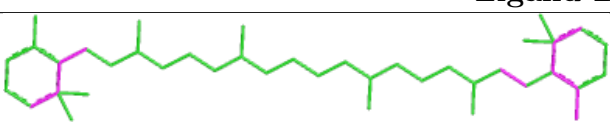
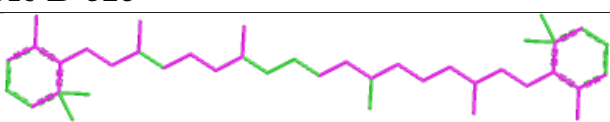
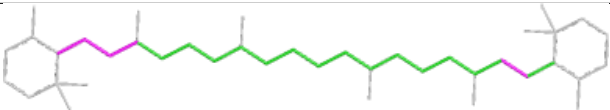
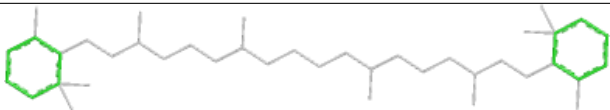


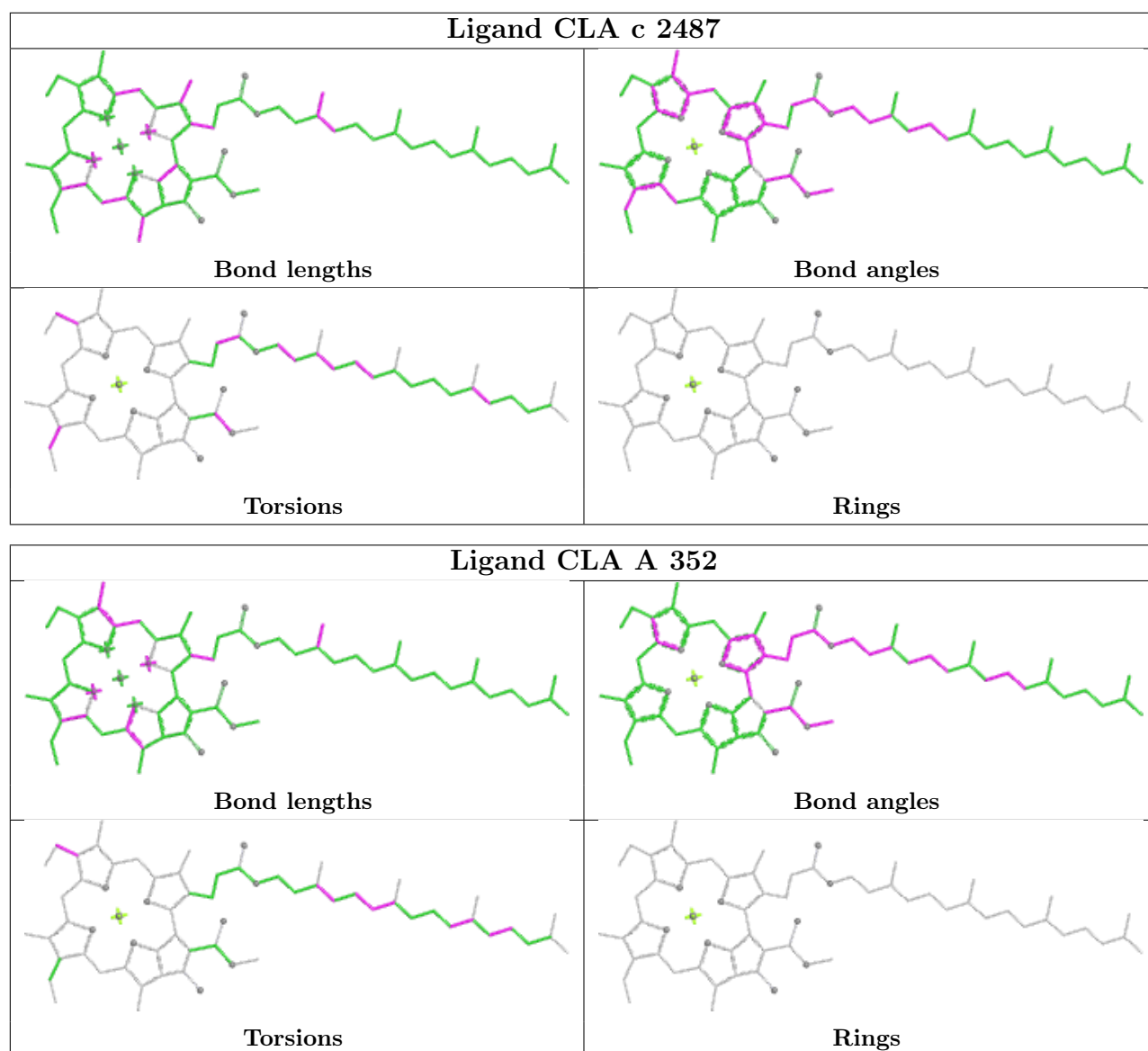
Ligand CLA C 476



Ligand HEC V 138



Ligand CLA B 512	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand PL9 D 357	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand BCR B 529	
 Bond lengths	 Bond angles
 Torsions	 Rings



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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	333/344 (96%)	0.59	18 (5%)	31	18	33, 60, 91, 104	0
1	a	333/344 (96%)	0.56	20 (6%)	27	16	39, 63, 92, 105	0
2	B	476/510 (93%)	0.65	35 (7%)	20	13	39, 65, 89, 105	0
2	b	476/510 (93%)	0.59	23 (4%)	35	19	39, 65, 89, 106	0
3	C	421/473 (89%)	0.63	25 (5%)	28	16	34, 69, 89, 103	0
3	c	421/473 (89%)	0.70	30 (7%)	22	14	36, 71, 90, 107	0
4	D	339/352 (96%)	0.53	24 (7%)	22	14	22, 60, 92, 106	0
4	d	339/352 (96%)	0.52	20 (5%)	28	16	31, 62, 92, 106	0
5	E	76/84 (90%)	0.61	2 (2%)	57	33	55, 76, 94, 107	0
5	e	76/84 (90%)	0.88	8 (10%)	11	8	60, 79, 96, 107	0
6	F	33/45 (73%)	0.49	2 (6%)	27	16	49, 68, 92, 107	0
6	f	33/45 (73%)	0.59	2 (6%)	27	16	49, 70, 92, 101	0
7	H	53/66 (80%)	0.41	3 (5%)	29	17	46, 73, 104, 106	0
7	h	53/66 (80%)	0.45	2 (3%)	44	24	56, 74, 106, 109	0
8	I	38/38 (100%)	1.04	7 (18%)	3	4	60, 76, 100, 102	0
8	i	38/38 (100%)	0.66	5 (13%)	7	6	59, 76, 100, 104	0
9	J	38/40 (95%)	0.47	4 (10%)	11	8	60, 79, 99, 103	0
9	j	38/40 (95%)	0.85	1 (2%)	57	33	61, 82, 98, 107	0
10	K	37/37 (100%)	0.30	0	100	100	61, 71, 95, 95	0
10	k	37/37 (100%)	0.45	0	100	100	65, 73, 96, 97	0
11	L	37/37 (100%)	0.47	1 (2%)	56	33	39, 58, 101, 104	0
11	l	37/37 (100%)	0.52	2 (5%)	31	18	34, 61, 99, 101	0
12	M	30/36 (83%)	0.11	0	100	100	45, 56, 78, 88	0
12	m	30/36 (83%)	0.26	0	100	100	44, 56, 79, 88	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	O	246/246 (100%)	0.76	17 (6%) 23 14	41, 75, 100, 110	0
13	o	246/246 (100%)	0.80	18 (7%) 21 13	46, 75, 99, 107	0
14	T	31/32 (96%)	0.23	1 (3%) 50 29	27, 54, 86, 89	0
14	t	31/32 (96%)	0.18	1 (3%) 50 29	32, 53, 90, 93	0
15	U	105/134 (78%)	0.68	9 (8%) 16 11	41, 67, 91, 104	0
15	u	105/134 (78%)	0.68	12 (11%) 10 7	46, 68, 92, 103	0
16	V	137/137 (100%)	0.36	1 (0%) 84 63	42, 66, 80, 88	0
16	v	137/137 (100%)	0.47	5 (3%) 46 25	46, 70, 85, 90	0
17	X	40/50 (80%)	0.28	1 (2%) 58 35	67, 74, 102, 109	0
17	x	40/50 (80%)	0.26	2 (5%) 34 19	67, 77, 104, 108	0
18	N	0/37	-	-	-	-
18	n	0/37	-	-	-	-
19	Z	58/62 (93%)	0.43	2 (3%) 48 27	62, 80, 93, 102	0
19	z	58/62 (93%)	0.56	3 (5%) 33 19	70, 81, 94, 106	0
All	All	5056/5520 (91%)	0.59	306 (6%) 27 16	22, 68, 95, 110	0

The worst 5 of 306 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	b	2006	TYR	6.9
8	I	28	PRO	6.3
4	D	242	GLU	6.2
2	B	328	GLY	6.0
3	C	47	GLY	5.8

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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
23	CLA	C	487	65/65	0.49	0.24	87,101,114,118	0
23	CLA	c	2487	65/65	0.53	0.22	88,101,114,118	0
27	BCR	c	2489	40/40	0.53	0.20	85,90,100,100	0
26	LMT	d	2359	35/35	0.55	0.26	73,82,91,92	0
27	BCR	j	2053	40/40	0.56	0.14	71,87,100,101	0
27	BCR	k	2050	40/40	0.57	0.25	80,85,97,101	0
27	BCR	B	529	40/40	0.59	0.23	76,93,105,106	0
27	BCR	J	53	40/40	0.63	0.15	70,88,100,100	0
27	BCR	K	50	40/40	0.65	0.22	79,85,96,101	0
27	BCR	C	489	40/40	0.66	0.24	85,90,100,100	0
25	PL9	D	357	45/55	0.66	0.24	71,80,86,88	0
25	PL9	d	2358	45/55	0.67	0.22	70,80,87,89	0
23	CLA	c	2475	65/65	0.67	0.19	66,80,97,102	0
27	BCR	b	2528	40/40	0.67	0.23	77,92,105,106	0
23	CLA	B	527	65/65	0.68	0.16	84,89,106,109	0
23	CLA	b	2526	65/65	0.70	0.16	82,89,106,110	0
23	CLA	C	482	65/65	0.71	0.17	71,80,97,98	0
23	CLA	c	2486	65/65	0.71	0.22	79,84,92,94	0
27	BCR	d	2360	40/40	0.72	0.21	67,79,91,93	0
23	CLA	d	2357	65/65	0.72	0.21	68,77,91,95	0
23	CLA	c	2484	65/65	0.72	0.17	77,87,101,102	0
27	BCR	c	2488	40/40	0.73	0.23	76,84,93,96	0
23	CLA	b	2511	65/65	0.75	0.20	58,81,92,97	0
23	CLA	B	511	65/65	0.75	0.21	58,81,92,97	0
25	PL9	a	2352	45/55	0.75	0.15	77,85,90,91	0
25	PL9	A	353	45/55	0.76	0.16	77,86,91,92	0
23	CLA	B	523	65/65	0.76	0.18	60,64,94,109	0
23	CLA	C	484	65/65	0.76	0.16	76,87,101,102	0
26	LMT	B	526	35/35	0.77	0.21	72,82,90,91	0
23	CLA	c	2482	65/65	0.77	0.15	72,81,97,98	0
23	CLA	C	477	65/65	0.77	0.17	71,79,97,100	0
23	CLA	b	2525	65/65	0.77	0.17	73,80,89,91	0
21	BCT	d	2353	4/4	0.78	0.13	66,68,69,69	0
21	BCT	A	346	4/4	0.78	0.14	70,70,71,74	0
23	CLA	c	2480	65/65	0.78	0.17	65,80,82,87	0
23	CLA	c	2474	65/65	0.79	0.17	70,76,88,89	0
23	CLA	b	2517	65/65	0.79	0.17	64,71,80,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	CLA	B	520	65/65	0.79	0.15	63,68,79,79	0
23	CLA	A	352	65/65	0.79	0.18	48,65,101,102	0
23	CLA	b	2523	65/65	0.80	0.16	59,64,94,108	0
23	CLA	c	2477	65/65	0.80	0.16	73,79,98,101	0
23	CLA	B	514	65/65	0.80	0.17	60,67,79,82	0
27	BCR	B	528	40/40	0.80	0.19	63,79,85,87	0
23	CLA	C	483	65/65	0.80	0.14	67,73,101,106	0
23	CLA	c	2483	65/65	0.80	0.16	68,74,100,106	0
23	CLA	B	525	65/65	0.80	0.16	72,80,89,92	0
23	CLA	C	474	65/65	0.81	0.17	69,76,87,89	0
23	CLA	b	2513	65/65	0.81	0.18	45,57,102,106	0
23	CLA	C	485	65/65	0.81	0.18	64,75,91,95	0
27	BCR	b	2527	40/40	0.81	0.15	64,78,84,86	0
23	CLA	B	519	65/65	0.81	0.15	58,67,90,91	0
23	CLA	a	2349	65/65	0.82	0.14	36,54,93,95	0
23	CLA	c	2479	65/65	0.82	0.16	57,76,80,84	0
23	CLA	a	2351	65/65	0.82	0.16	50,66,101,102	0
23	CLA	c	2481	65/65	0.82	0.15	55,60,85,89	0
23	CLA	b	2520	65/65	0.82	0.14	61,68,78,79	0
23	CLA	B	516	65/65	0.82	0.16	44,55,92,93	0
23	CLA	c	2476	65/65	0.82	0.16	50,64,75,78	0
23	CLA	B	515	65/65	0.83	0.16	45,66,84,87	0
23	CLA	c	2485	65/65	0.83	0.17	61,75,90,94	0
23	CLA	b	2514	65/65	0.83	0.17	59,67,79,82	0
23	CLA	b	2516	65/65	0.83	0.14	42,54,93,94	0
21	BCT	a	2346	4/4	0.83	0.14	71,72,73,76	0
24	PHO	a	2350	64/64	0.83	0.18	56,66,81,82	0
23	CLA	D	356	65/65	0.83	0.15	69,77,90,95	0
23	CLA	b	2521	65/65	0.83	0.18	67,71,80,82	0
27	BCR	C	488	40/40	0.84	0.23	75,83,92,95	0
23	CLA	C	486	65/65	0.84	0.18	78,84,91,95	0
27	BCR	F	48	40/40	0.84	0.15	66,80,91,92	0
23	CLA	C	475	65/65	0.84	0.17	66,80,97,103	0
24	PHO	D	355	64/64	0.84	0.16	62,69,103,111	0
23	CLA	B	524	65/65	0.84	0.17	56,68,75,88	0
23	CLA	B	521	65/65	0.85	0.16	67,72,80,81	0
23	CLA	b	2522	65/65	0.85	0.15	69,75,87,88	0
23	CLA	C	476	65/65	0.85	0.15	49,62,75,78	0
24	PHO	d	2356	64/64	0.85	0.16	62,70,103,111	0
28	HEC	e	2084	43/43	0.85	0.23	75,79,100,108	0
23	CLA	b	2519	65/65	0.86	0.13	60,66,90,91	0
23	CLA	B	512	65/65	0.86	0.13	37,50,63,67	0

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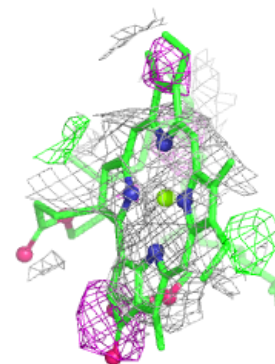
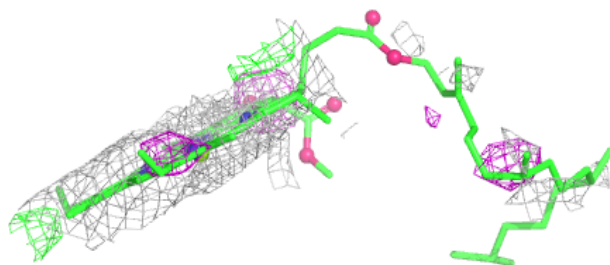
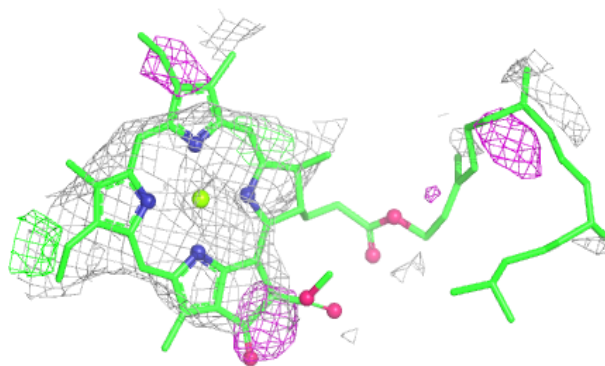
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	CLA	C	481	65/65	0.86	0.16	54,60,84,88	0
23	CLA	B	522	65/65	0.86	0.16	71,75,87,88	0
23	CLA	B	518	65/65	0.86	0.15	51,61,86,89	0
23	CLA	c	2478	65/65	0.87	0.19	55,66,87,92	0
23	CLA	C	480	65/65	0.87	0.16	64,79,82,87	0
23	CLA	B	517	65/65	0.87	0.16	65,71,79,89	0
23	CLA	b	2515	65/65	0.87	0.15	43,66,84,87	0
23	CLA	A	350	65/65	0.87	0.15	36,52,92,95	0
23	CLA	C	478	65/65	0.87	0.18	55,65,87,91	0
23	CLA	b	2524	65/65	0.87	0.17	56,68,76,89	0
23	CLA	b	2518	65/65	0.88	0.18	53,60,86,88	0
23	CLA	b	2512	65/65	0.88	0.13	34,50,63,66	0
23	CLA	A	348	65/65	0.88	0.14	44,50,65,70	0
23	CLA	d	2354	65/65	0.88	0.12	40,47,75,80	0
23	CLA	B	513	65/65	0.88	0.16	46,57,102,106	0
24	PHO	A	351	64/64	0.88	0.15	55,65,80,82	0
23	CLA	d	2355	65/65	0.89	0.14	19,32,75,86	0
23	CLA	a	2348	65/65	0.89	0.14	44,50,65,69	0
23	CLA	D	354	65/65	0.89	0.14	42,46,76,81	0
23	CLA	C	479	65/65	0.90	0.14	57,76,80,83	0
21	BCT	D	353	4/4	0.90	0.12	66,66,69,69	0
23	CLA	A	349	65/65	0.91	0.12	19,31,76,86	0
28	HEC	E	84	43/43	0.93	0.18	64,79,100,108	0
28	HEC	V	138	43/43	0.94	0.17	44,49,56,57	0
22	OEC	A	347	9/9	0.94	0.06	66,69,73,74	0
28	HEC	v	2138	43/43	0.94	0.12	40,50,55,57	0
22	OEC	a	2347	9/9	0.95	0.06	68,70,74,75	0
20	FE	a	2345	1/1	0.98	0.03	67,67,67,67	0
20	FE	A	345	1/1	0.99	0.04	58,58,58,58	0

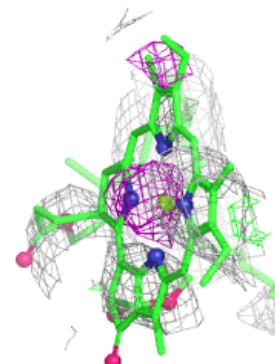
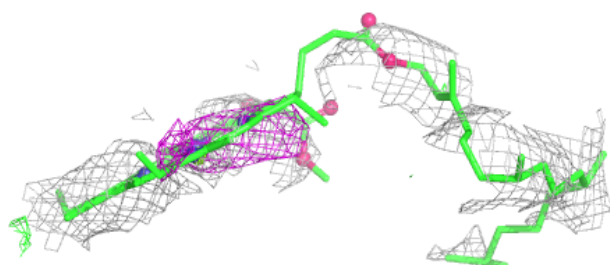
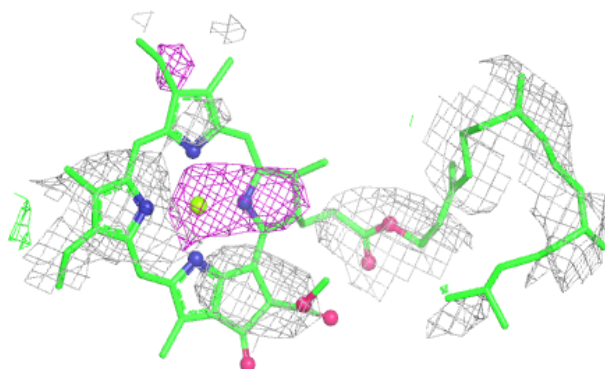
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around CLA C 487:

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

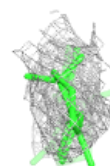
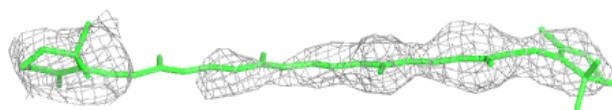
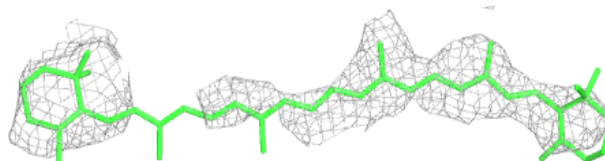
**Electron density around CLA c 2487:**

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

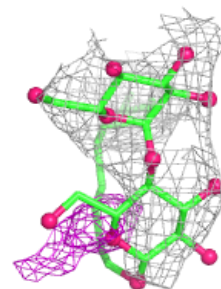
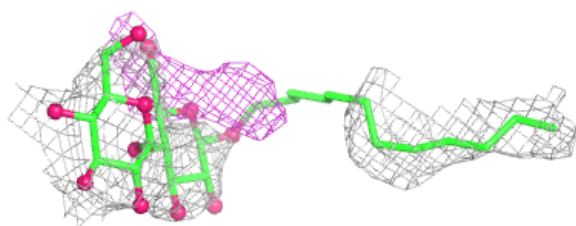
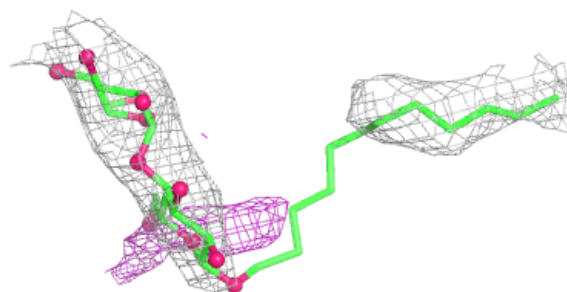


Electron density around BCR c 2489:

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

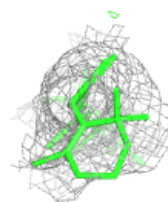
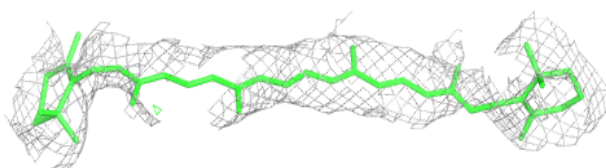
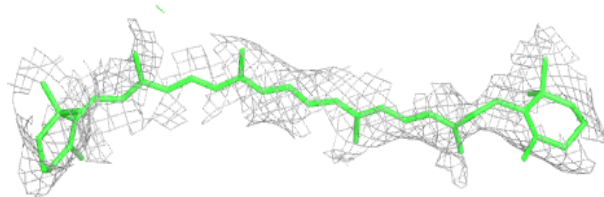
**Electron density around LMT d 2359:**

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

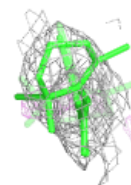
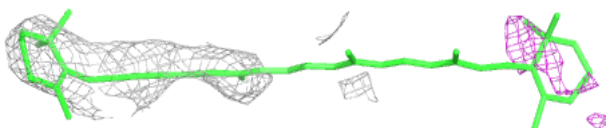
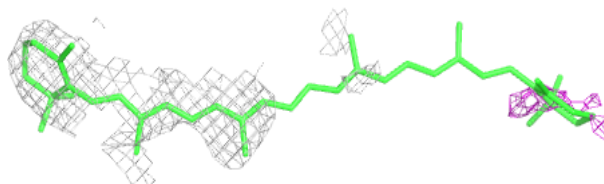


Electron density around BCR j 2053:

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

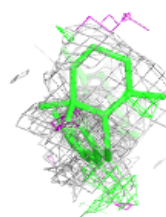
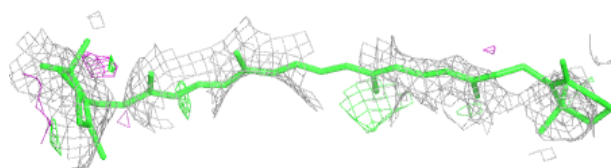
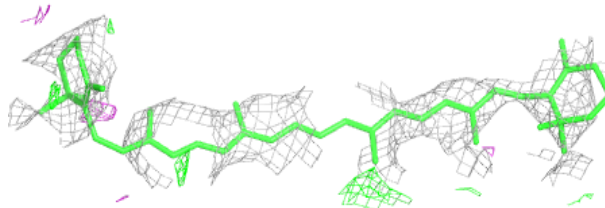
**Electron density around BCR k 2050:**

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

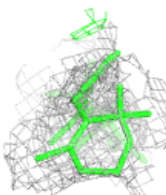
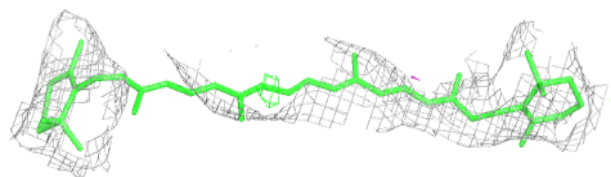
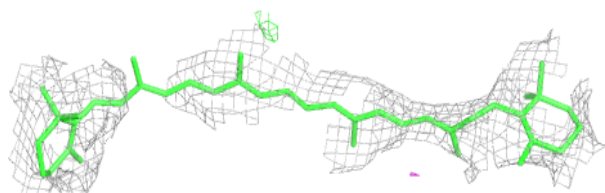


Electron density around BCR B 529:

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

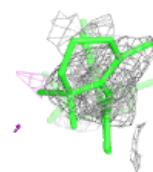
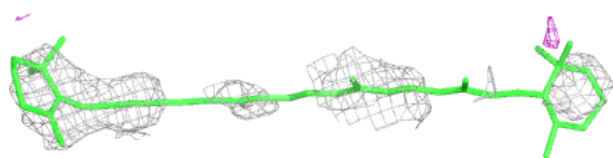
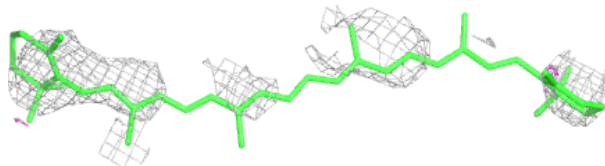
**Electron density around BCR J 53:**

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

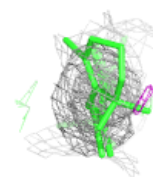
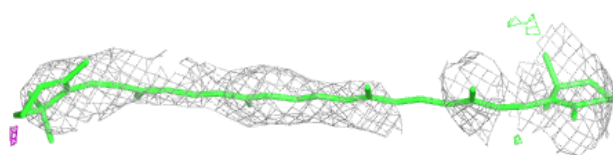
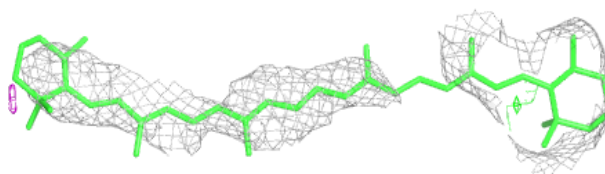


Electron density around BCR K 50:

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

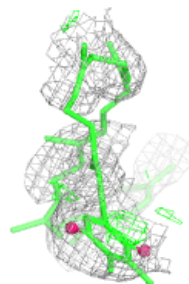
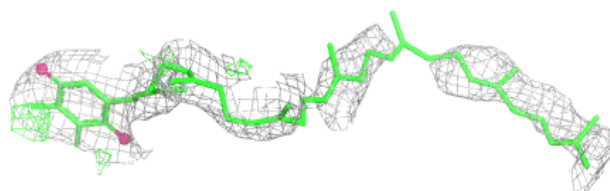
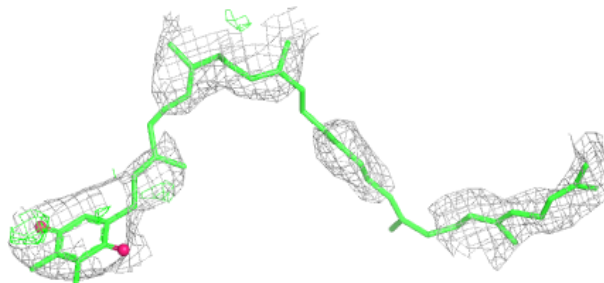
**Electron density around BCR C 489:**

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

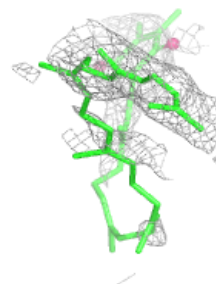
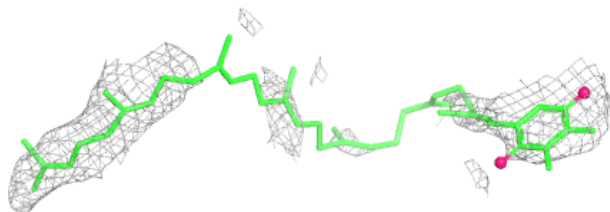


Electron density around PL9 D 357:

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

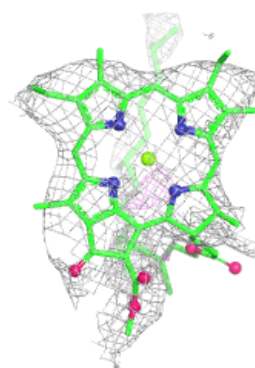
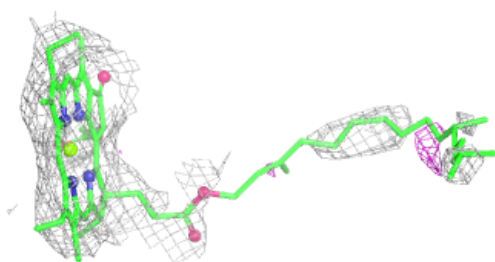
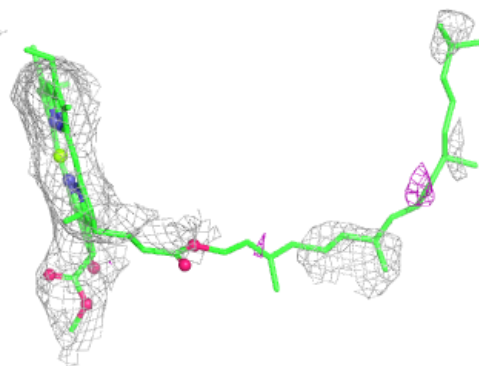
**Electron density around PL9 d 2358:**

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

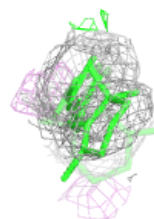
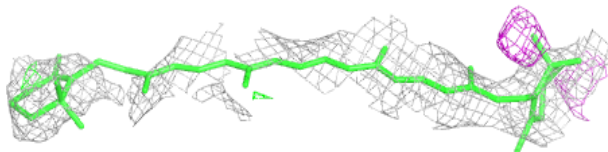
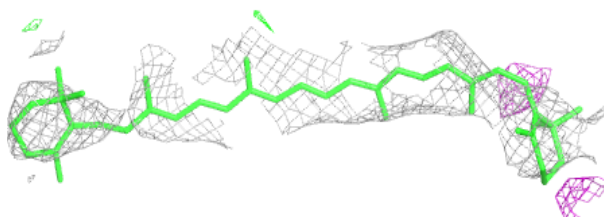


Electron density around CLA c 2475:

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

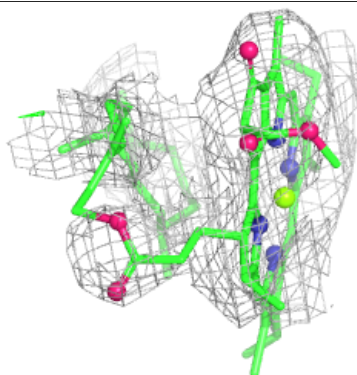
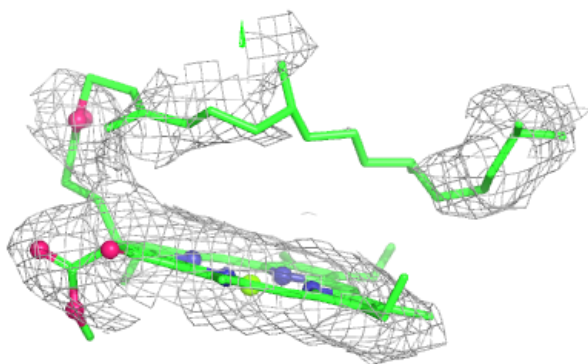
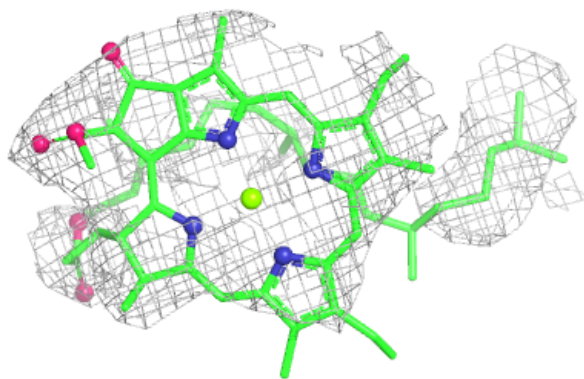
**Electron density around BCR b 2528:**

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

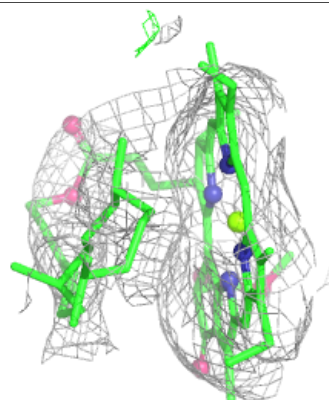
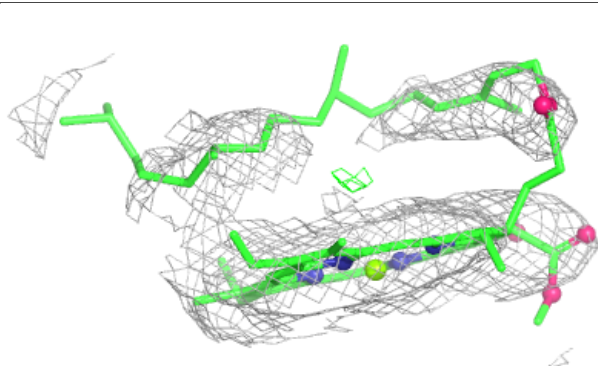
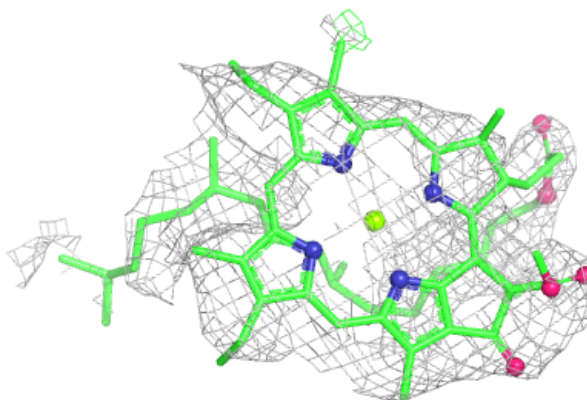


Electron density around CLA B 527:

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

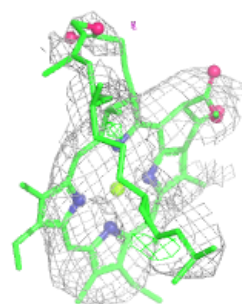
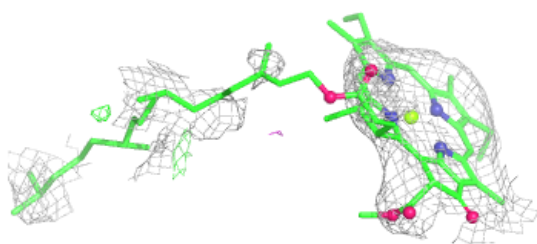
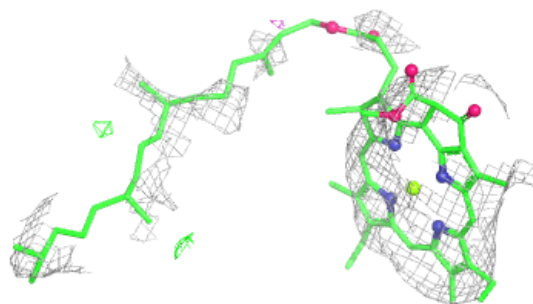
**Electron density around CLA b 2526:**

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

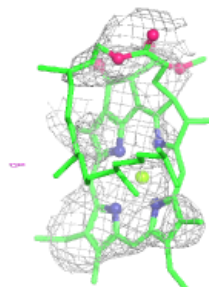
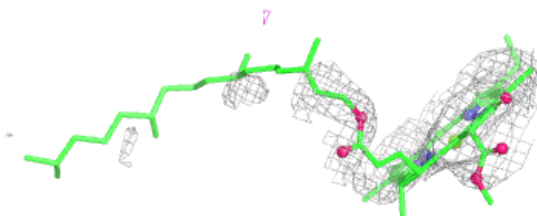


Electron density around CLA C 482:

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

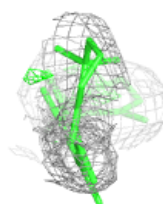
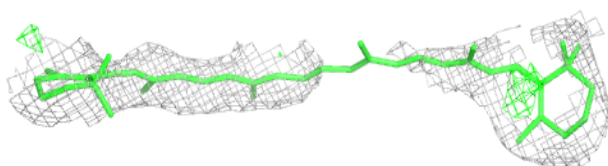
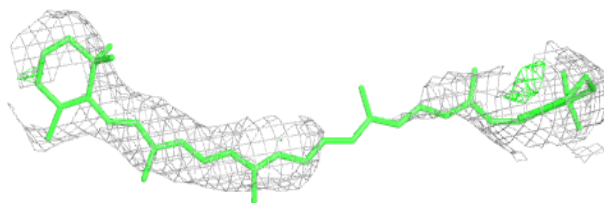
**Electron density around CLA c 2486:**

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

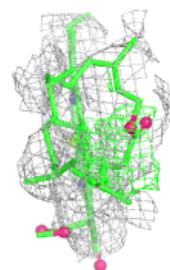
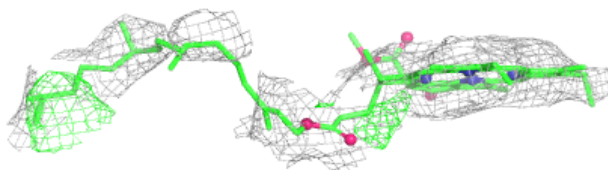
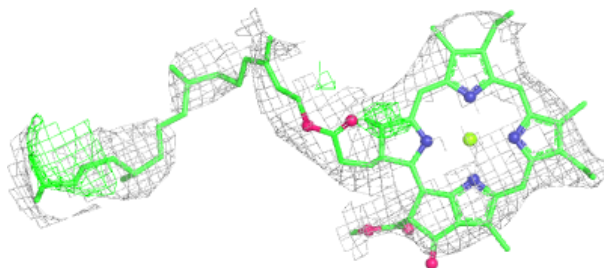


Electron density around BCR d 2360:

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

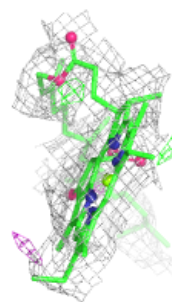
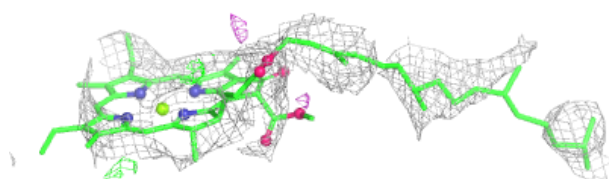
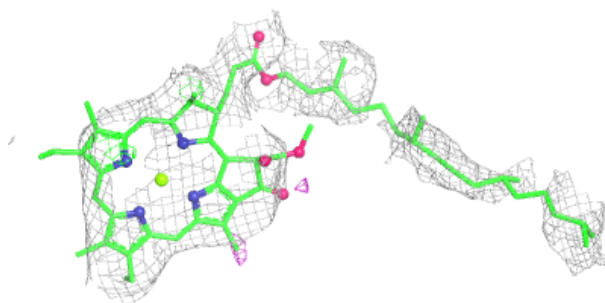
**Electron density around CLA d 2357:**

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

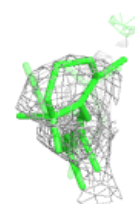
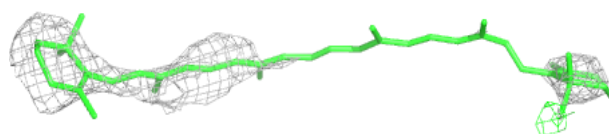
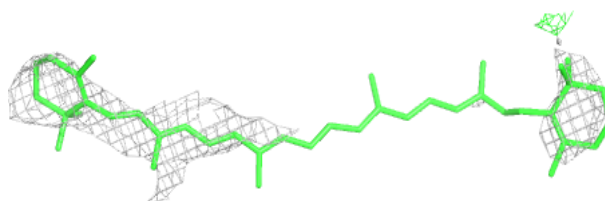


Electron density around CLA c 2484:

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

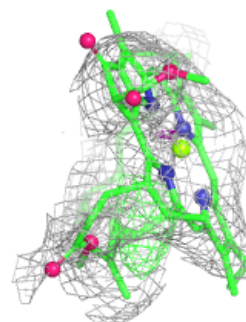
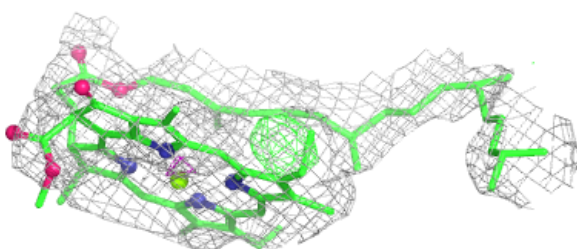
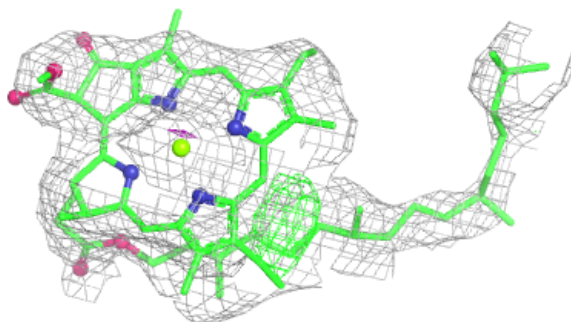
**Electron density around BCR c 2488:**

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

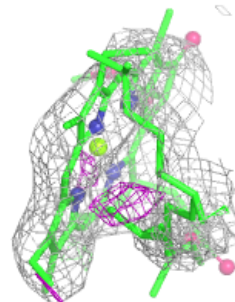
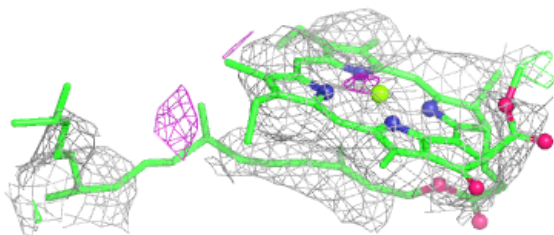
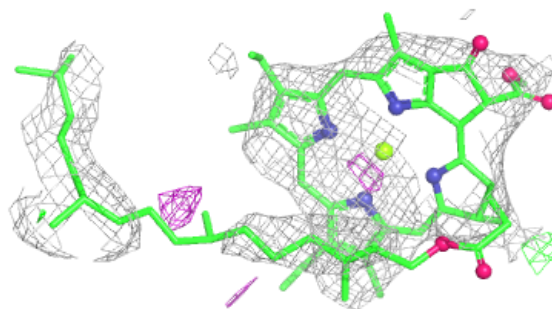


Electron density around CLA b 2511:

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

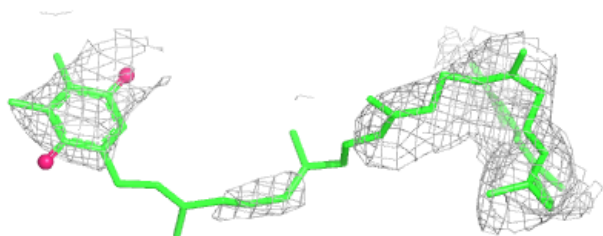
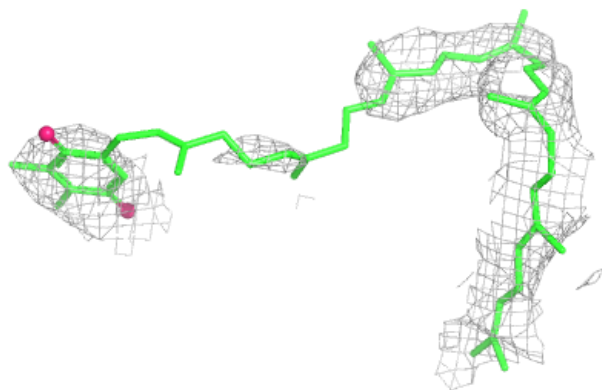
**Electron density around CLA B 511:**

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

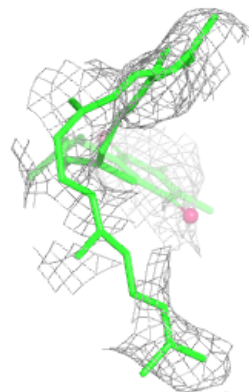
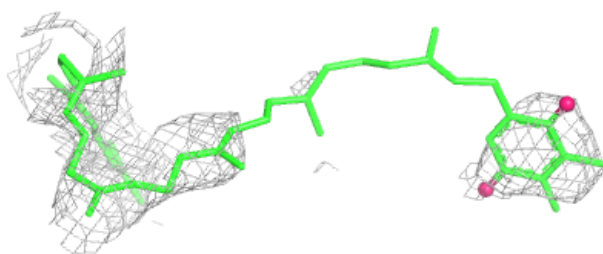
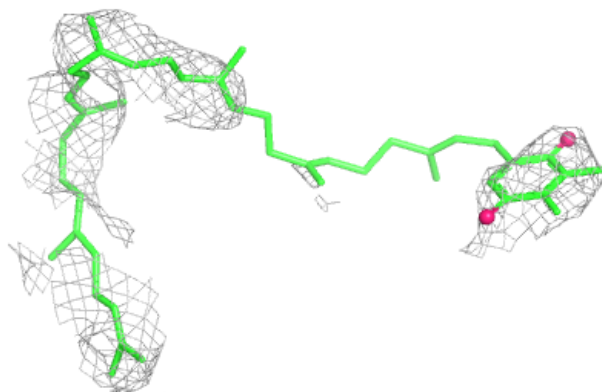


Electron density around PL9 a 2352:

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

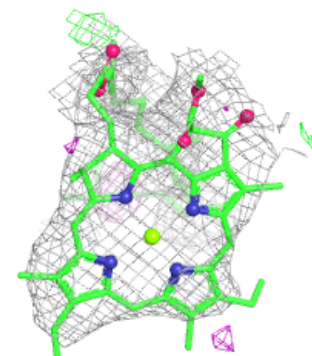
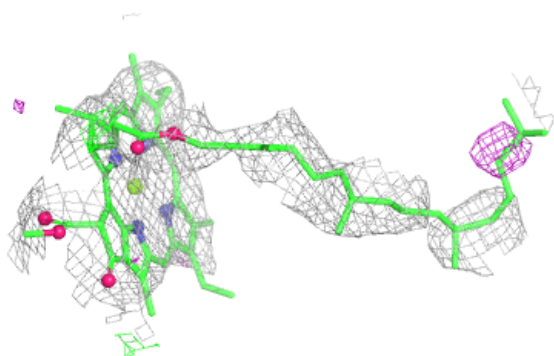
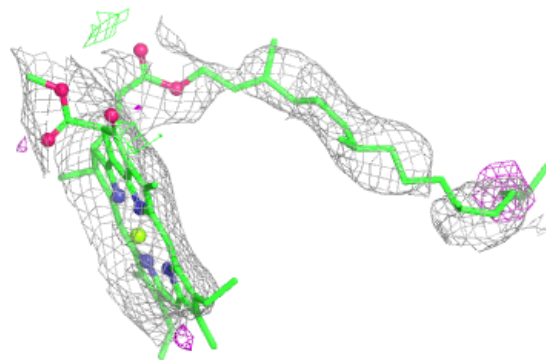
**Electron density around PL9 A 353:**

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

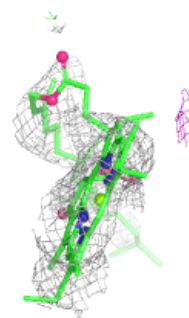
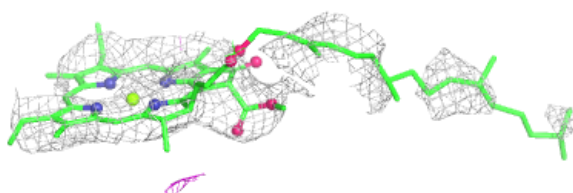
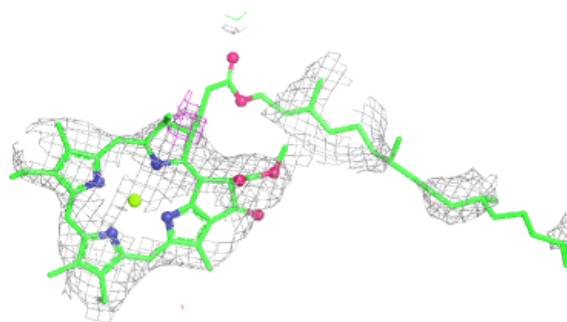


Electron density around CLA B 523:

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

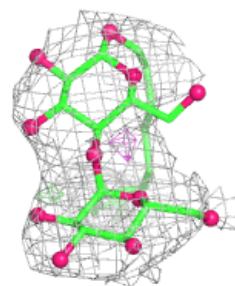
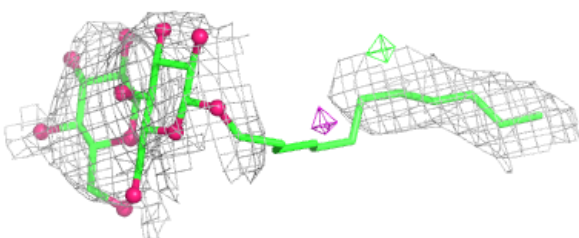
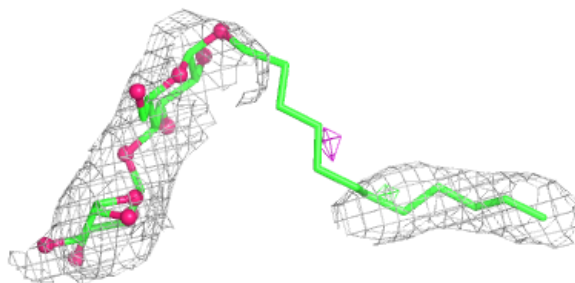
**Electron density around CLA C 484:**

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

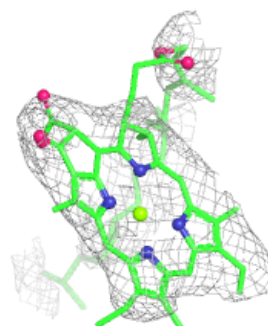
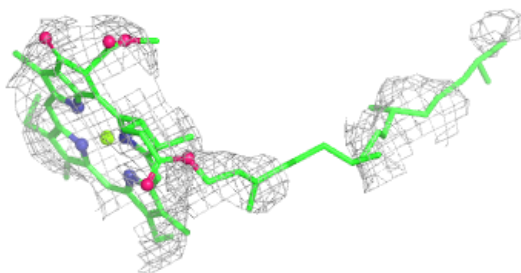
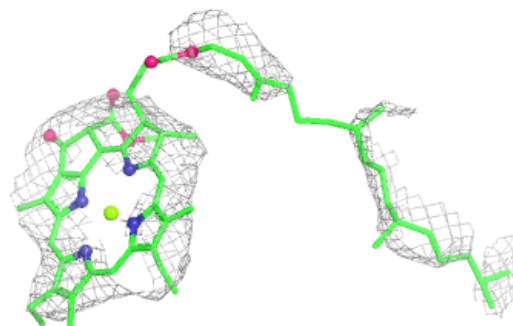


Electron density around LMT B 526:

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

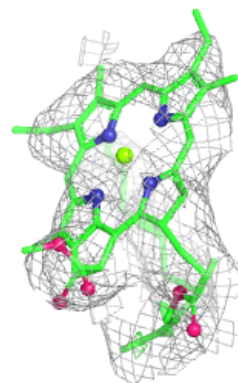
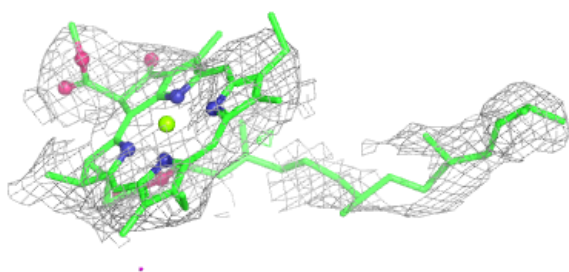
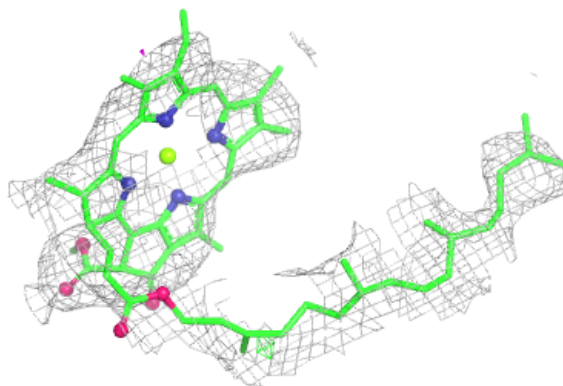
**Electron density around CLA c 2482:**

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



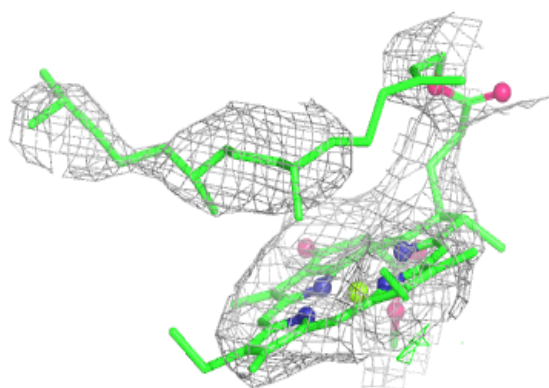
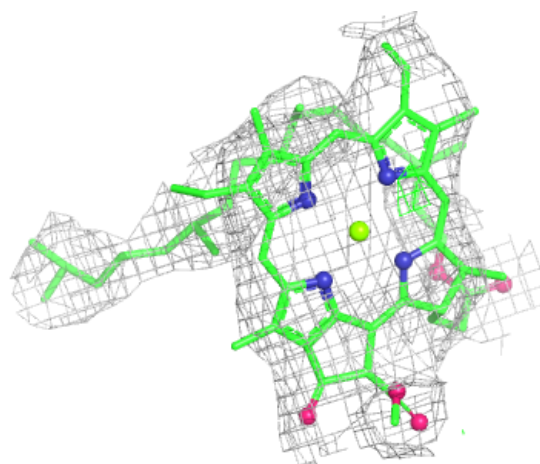
Electron density around CLA C 477:

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



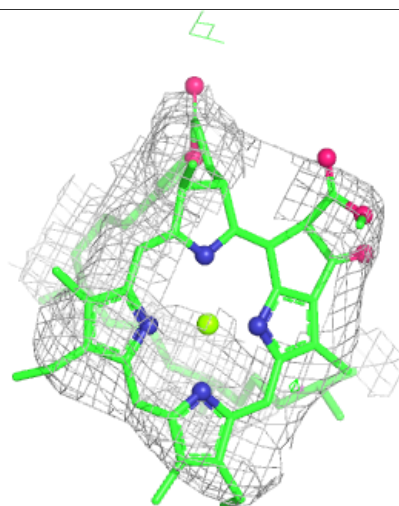
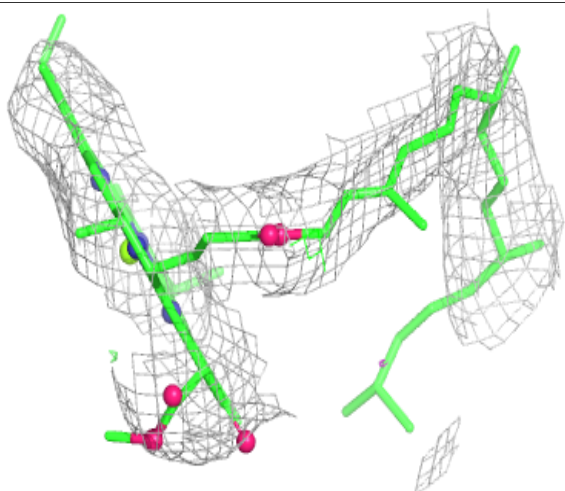
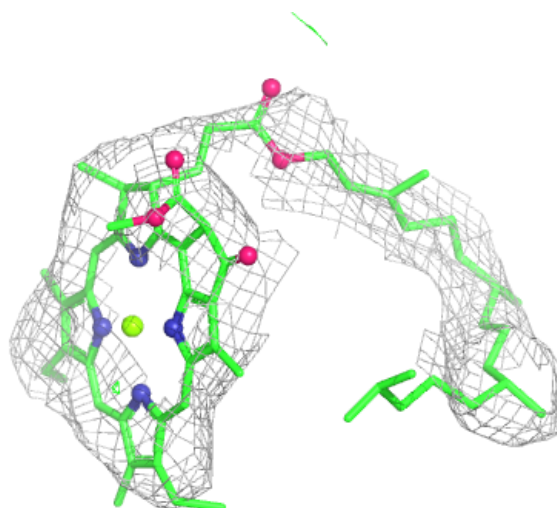
Electron density around CLA b 2525:

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



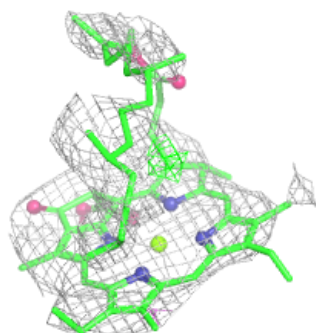
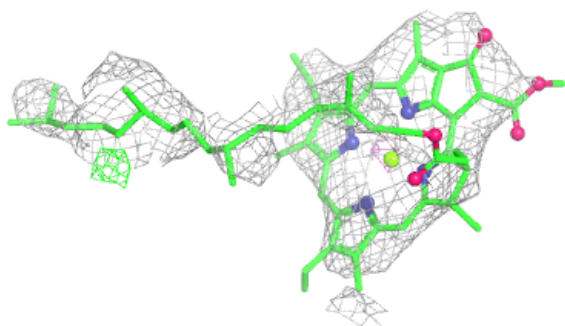
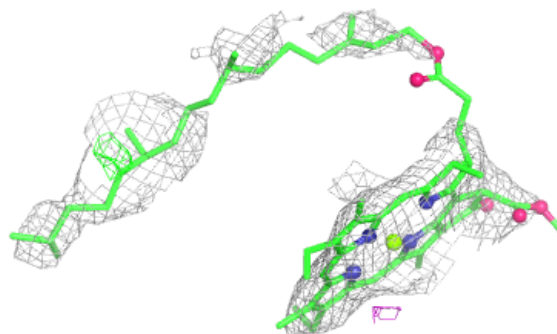
Electron density around CLA c 2480:

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

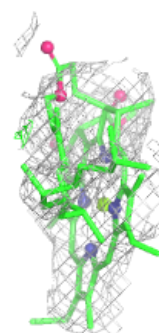
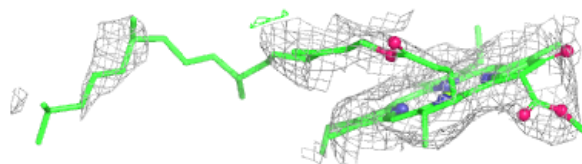
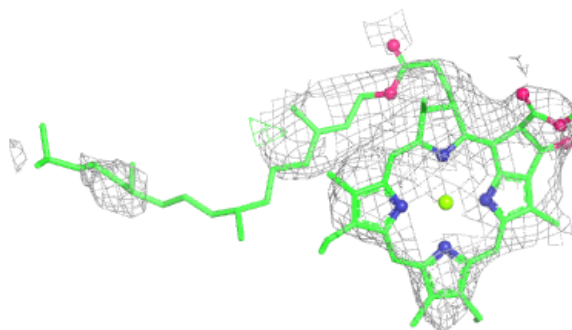


Electron density around CLA c 2474:

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

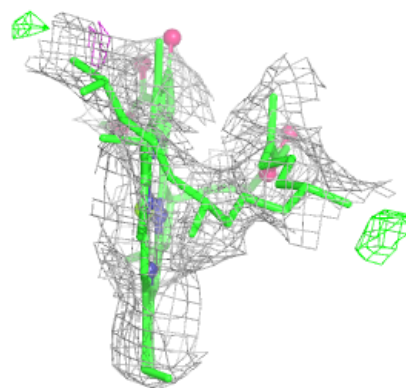
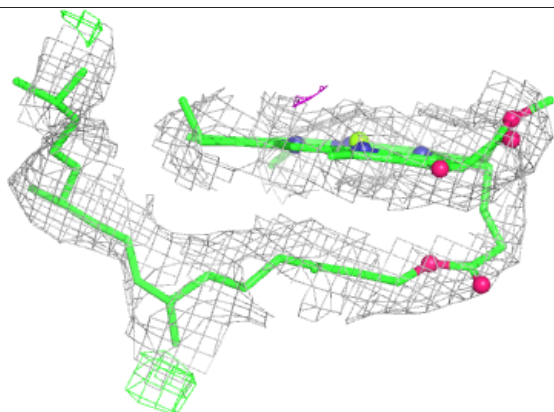
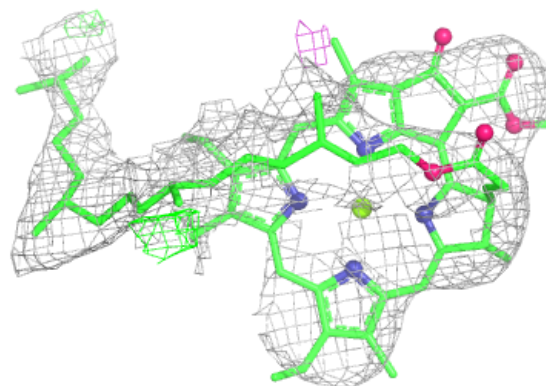
**Electron density around CLA b 2517:**

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

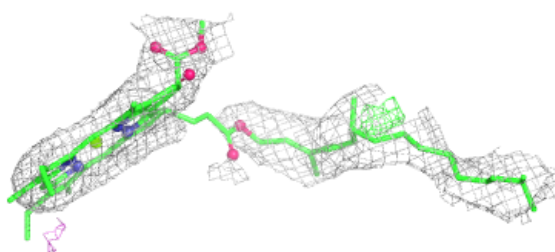
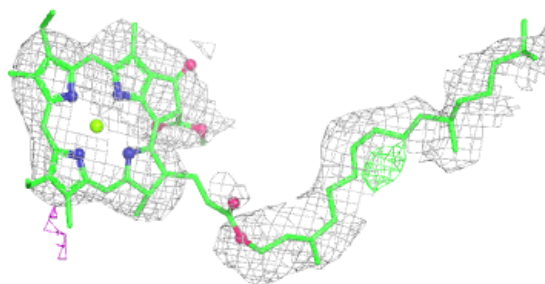


Electron density around CLA B 520:

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

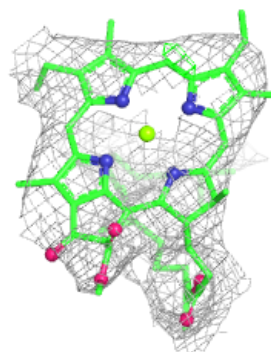
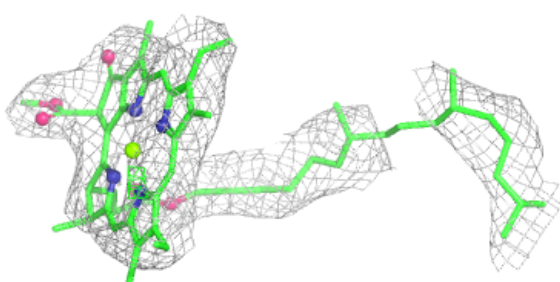
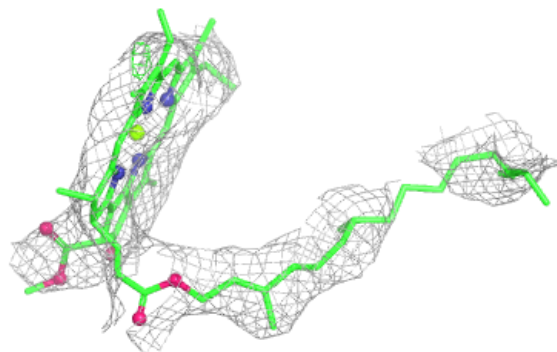
**Electron density around CLA A 352:**

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

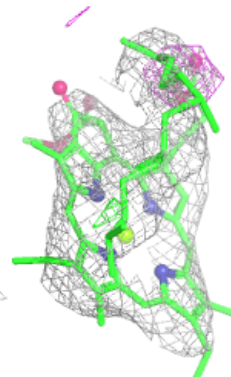
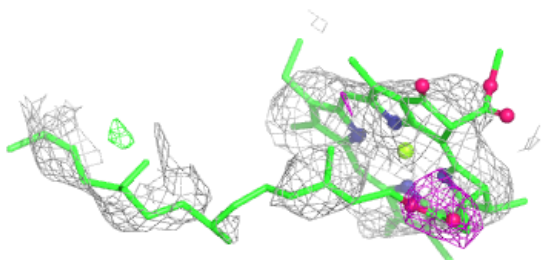
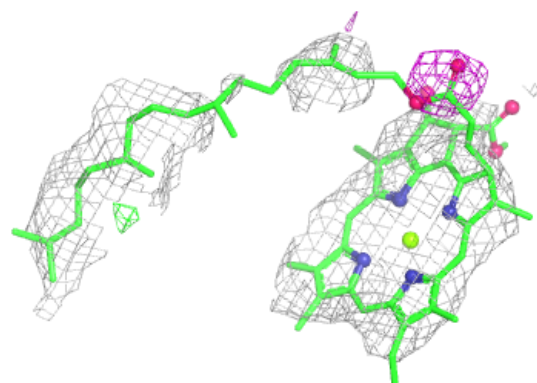


Electron density around CLA b 2523:

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

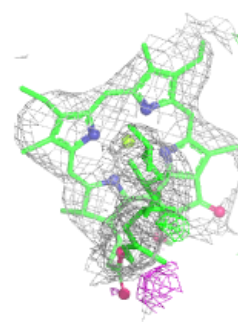
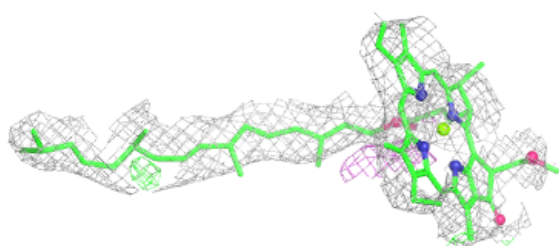
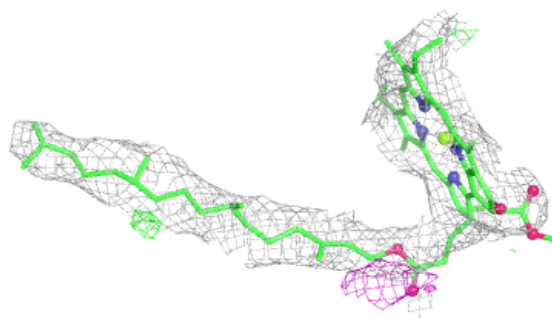
**Electron density around CLA c 2477:**

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

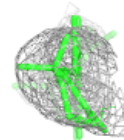
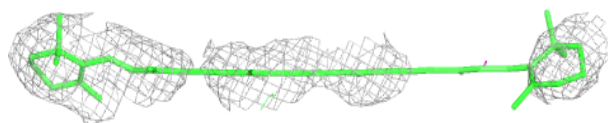
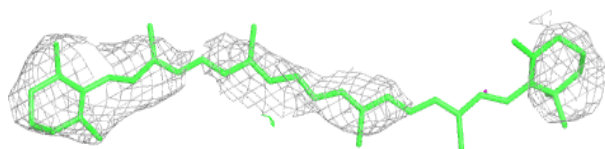


Electron density around CLA B 514:

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

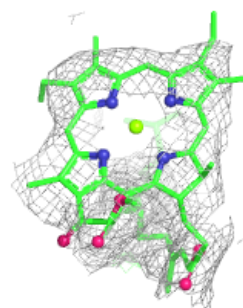
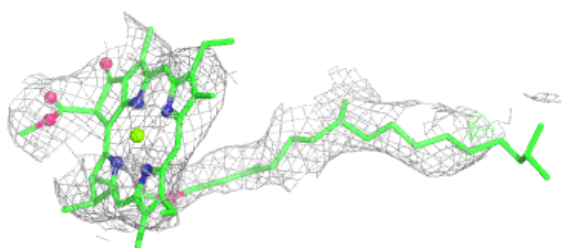
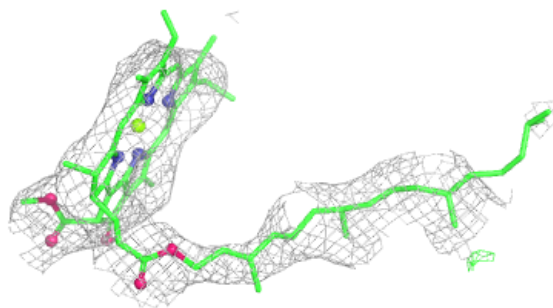
**Electron density around BCR B 528:**

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

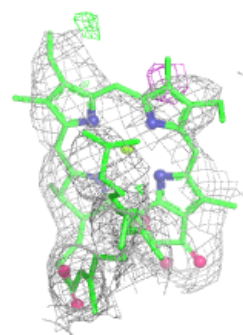
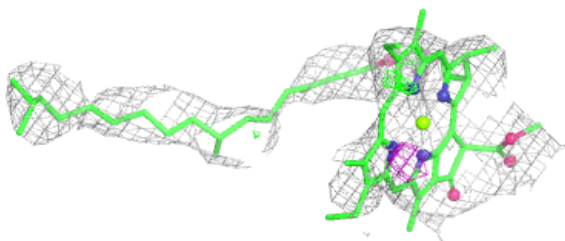
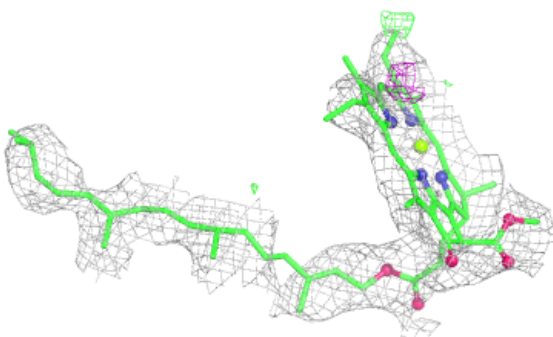


Electron density around CLA C 483:

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

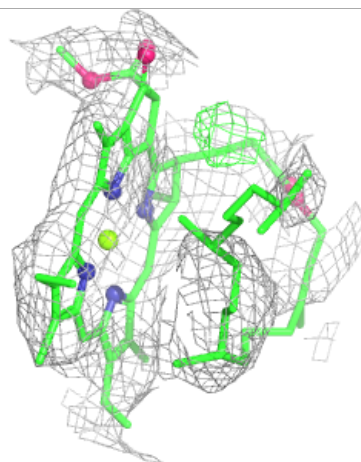
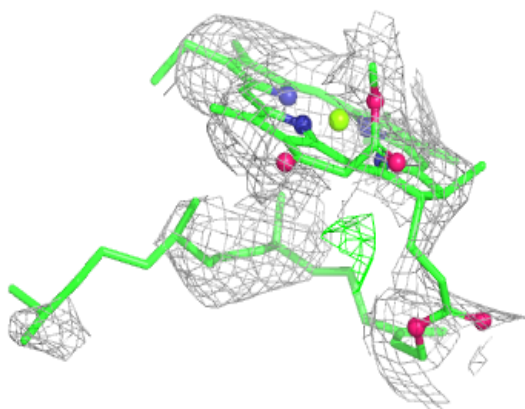
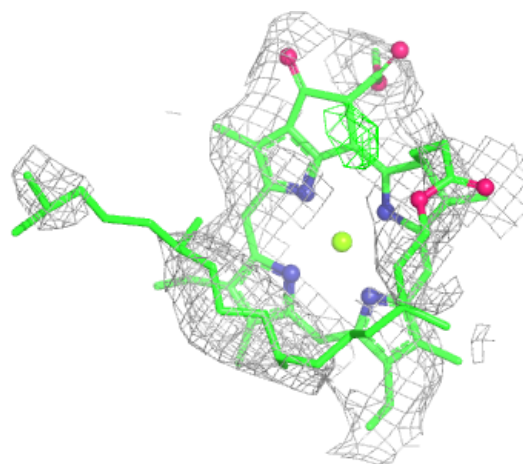
**Electron density around CLA c 2483:**

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



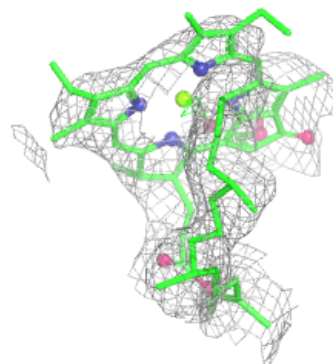
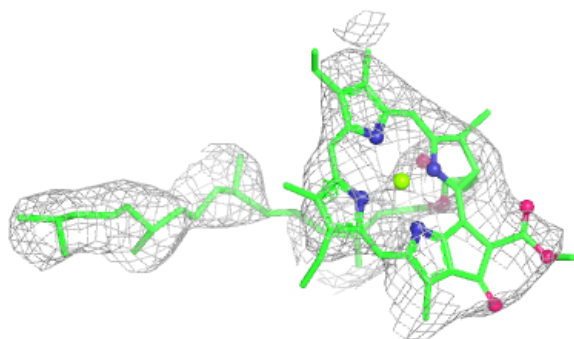
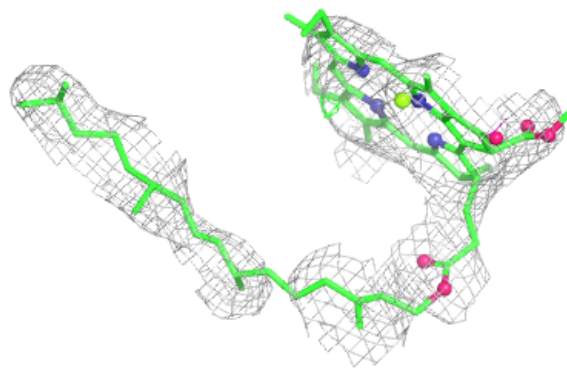
Electron density around CLA B 525:

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



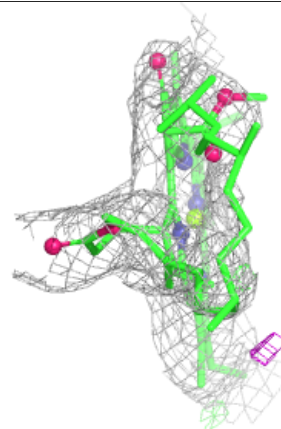
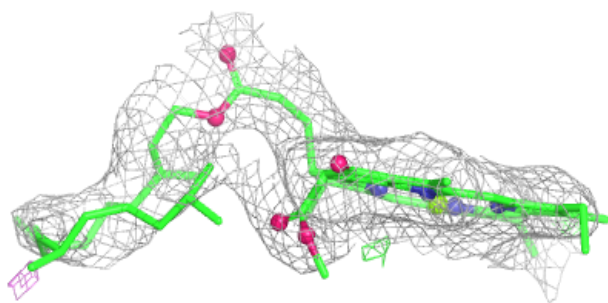
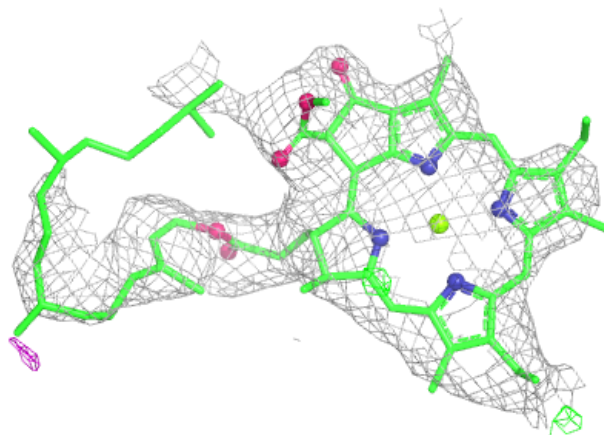
Electron density around CLA C 474:

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



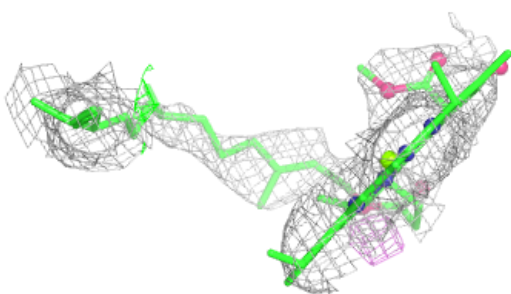
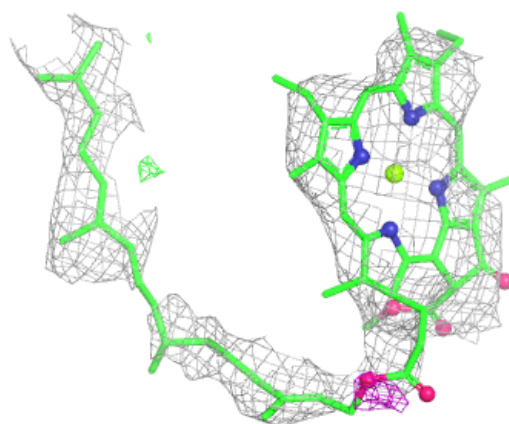
Electron density around CLA b 2513:

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

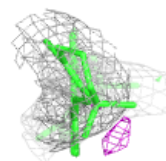
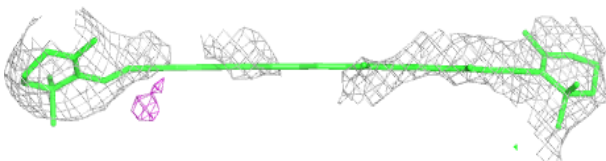
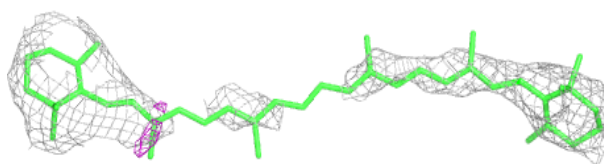


Electron density around CLA C 485:

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

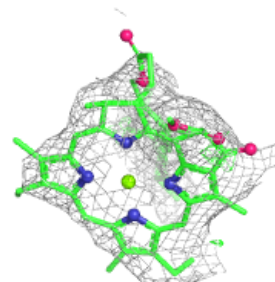
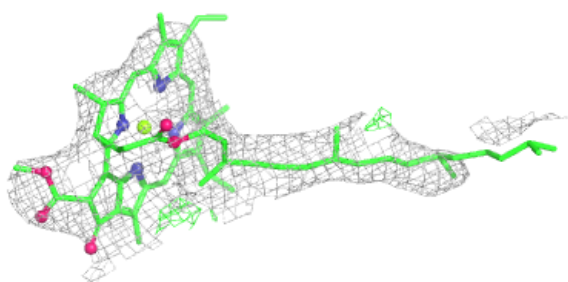
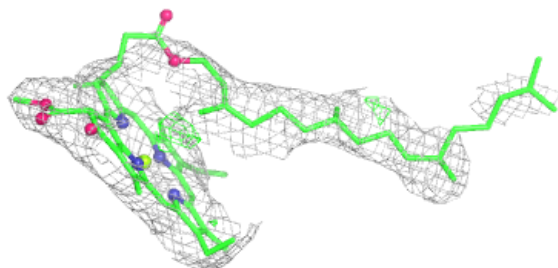
**Electron density around BCR b 2527:**

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

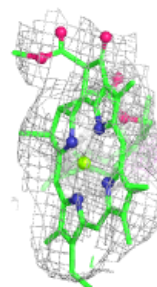
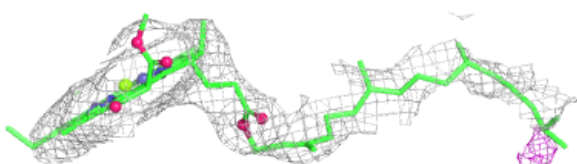
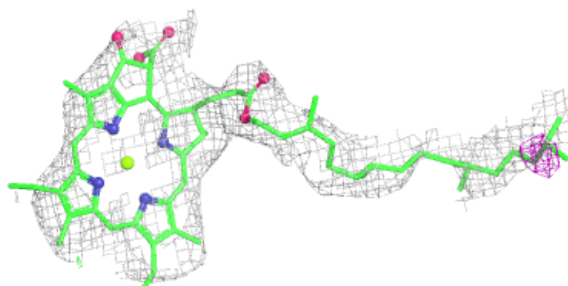


Electron density around CLA B 519:

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

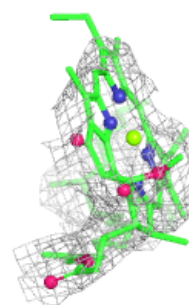
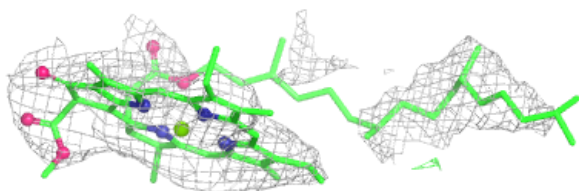
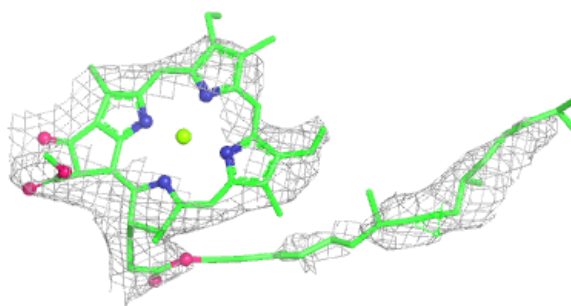
**Electron density around CLA a 2349:**

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

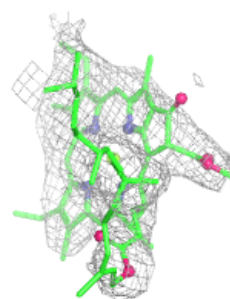
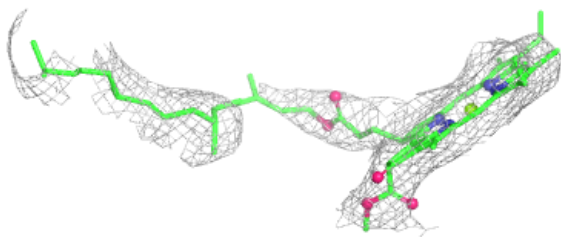
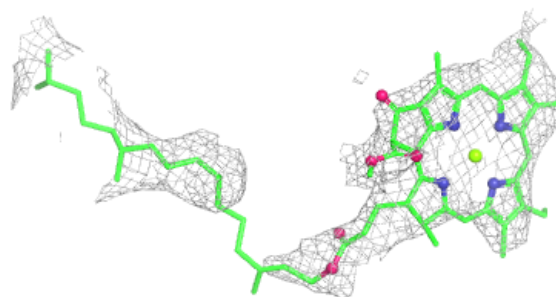


Electron density around CLA c 2479:

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

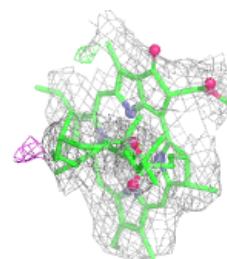
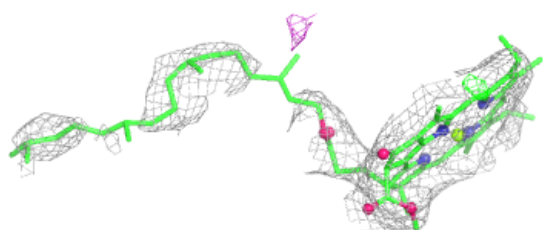
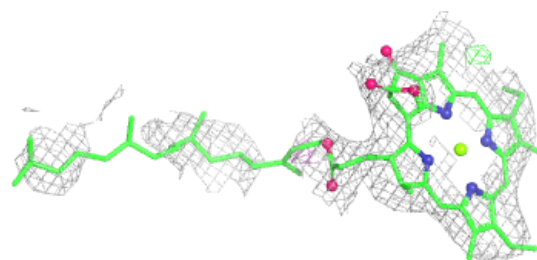
**Electron density around CLA a 2351:**

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

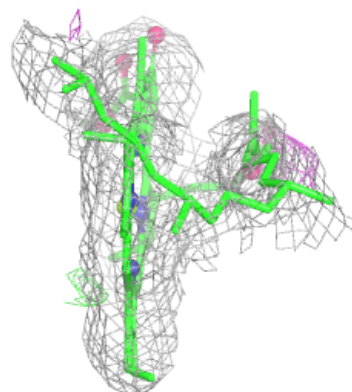
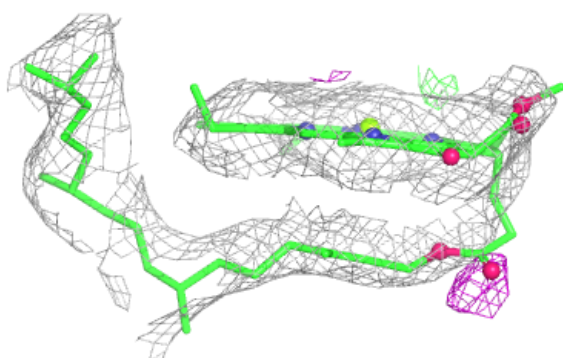
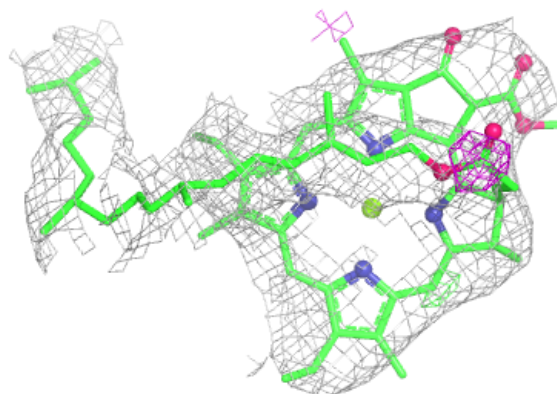


Electron density around CLA c 2481:

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

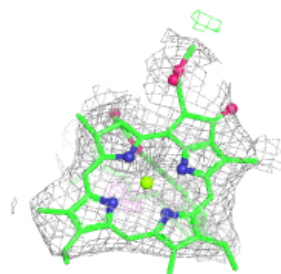
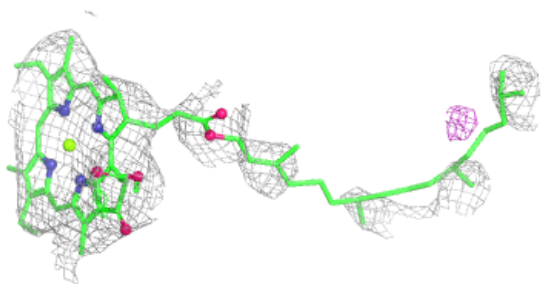
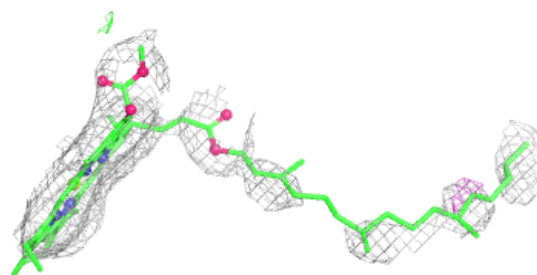
**Electron density around CLA b 2520:**

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



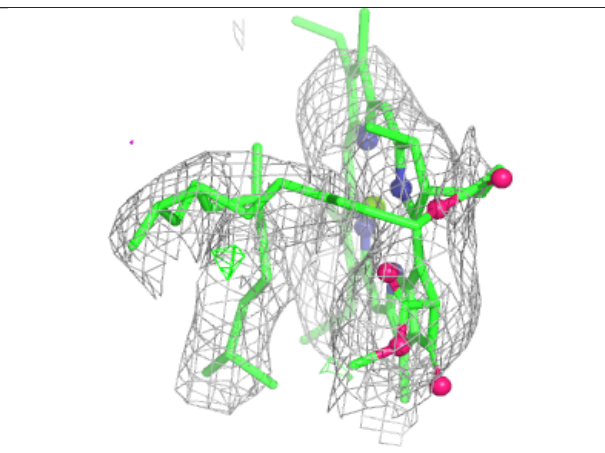
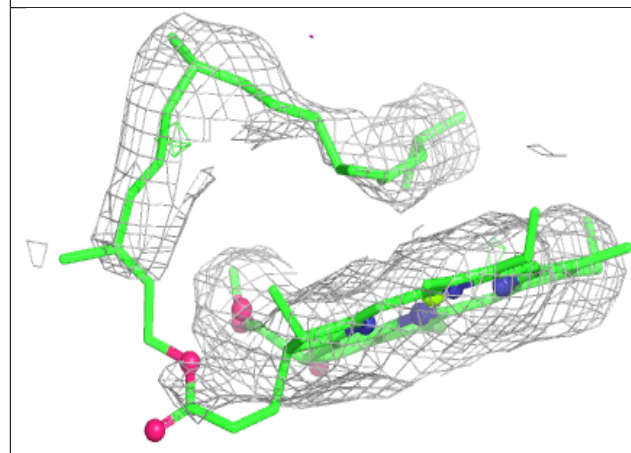
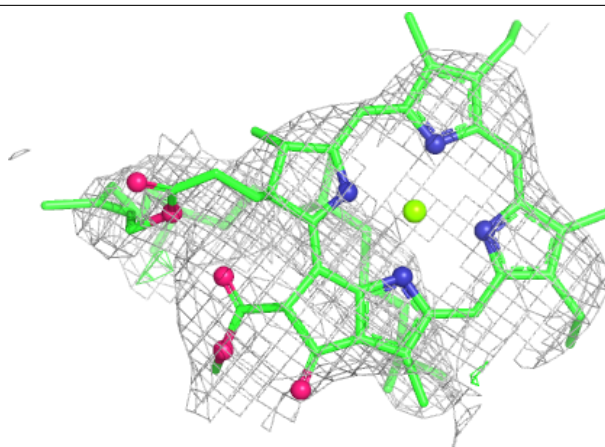
Electron density around CLA B 516:

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



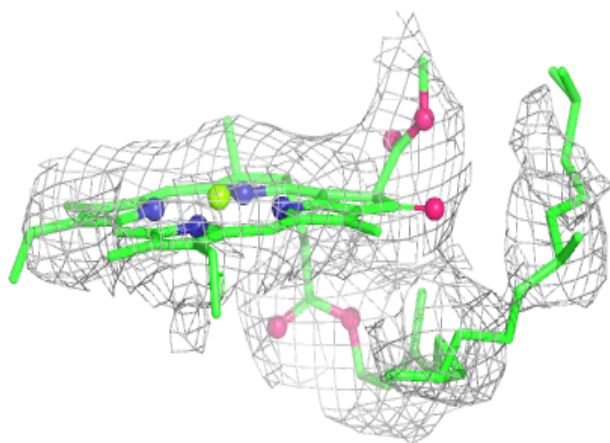
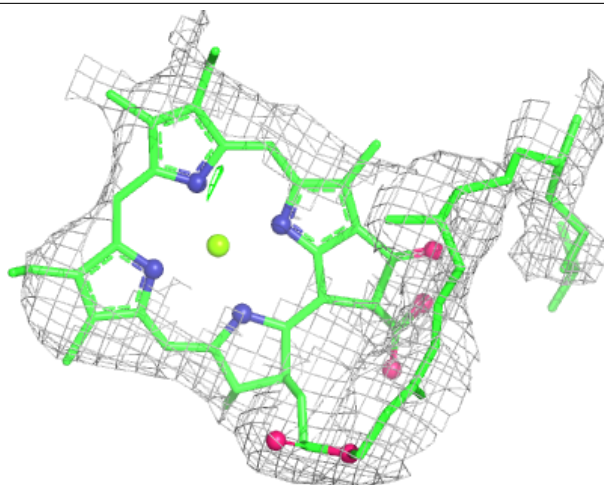
Electron density around CLA c 2476:

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



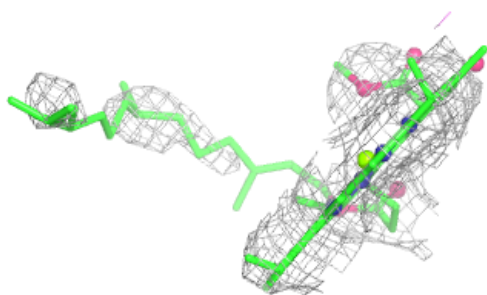
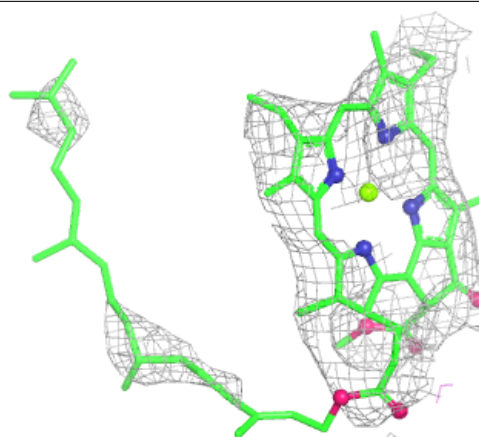
Electron density around CLA B 515:

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



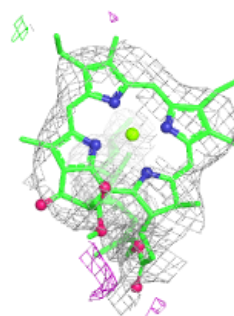
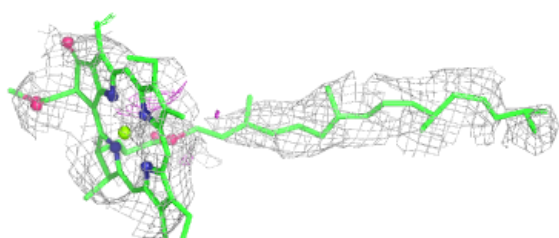
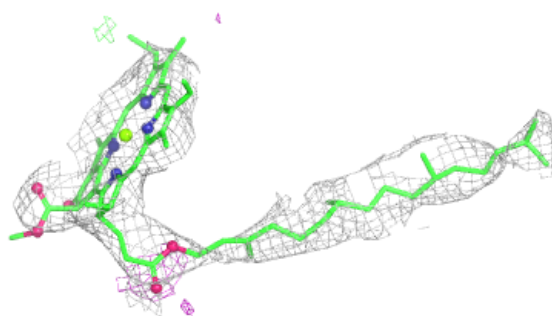
Electron density around CLA c 2485:

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

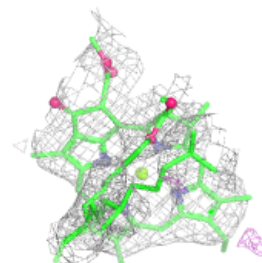
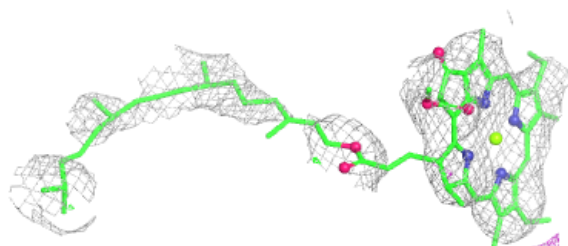
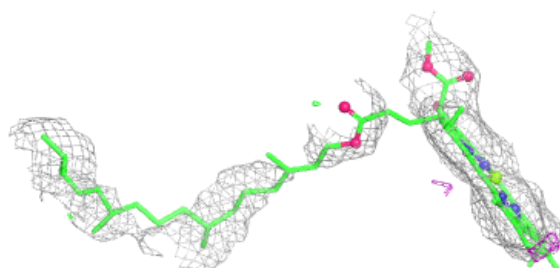


Electron density around CLA b 2514:

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

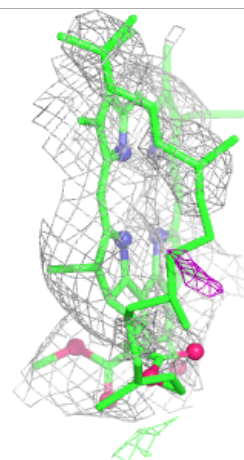
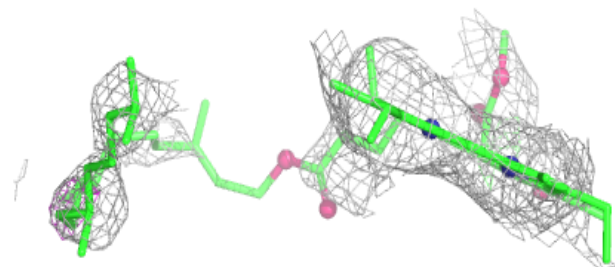
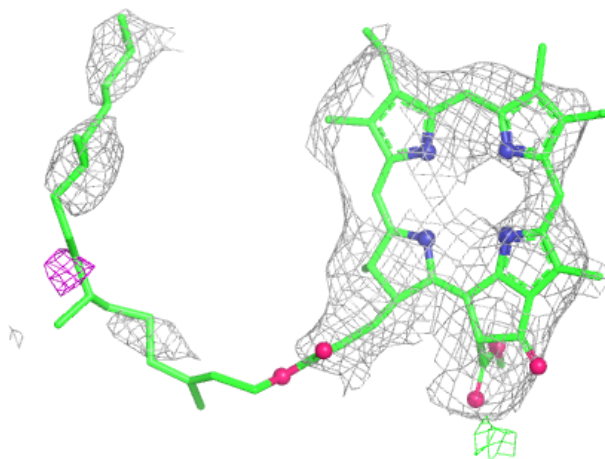
**Electron density around CLA b 2516:**

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



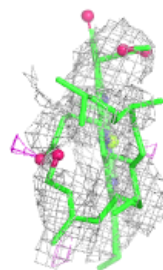
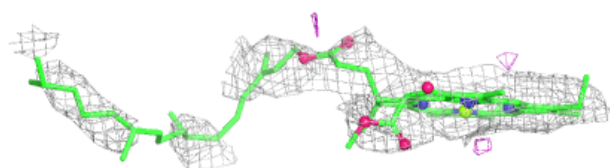
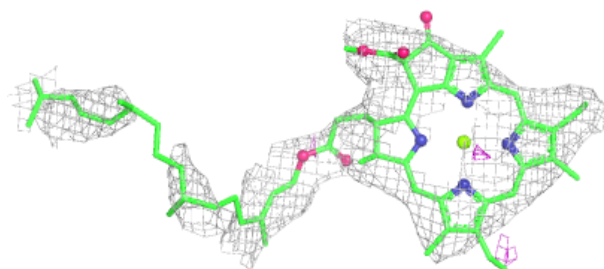
Electron density around PHO a 2350:

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

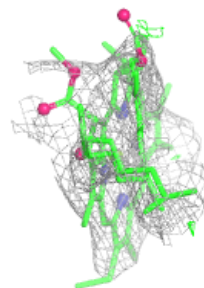
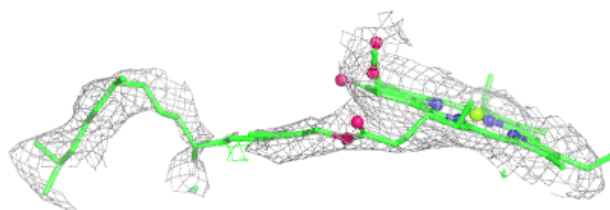
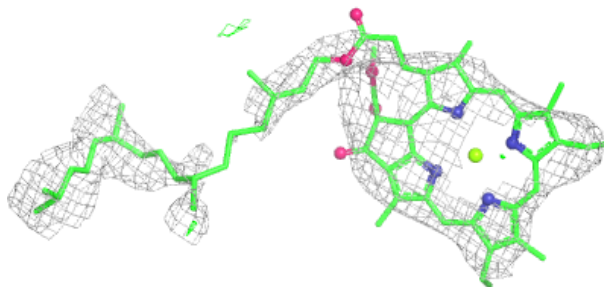


Electron density around CLA D 356:

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

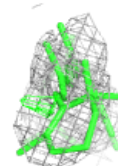
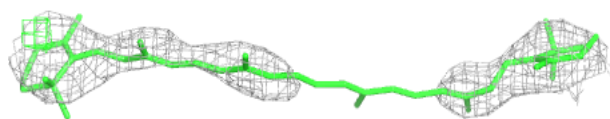
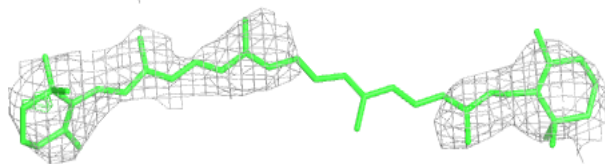
**Electron density around CLA b 2521:**

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

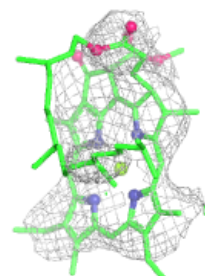
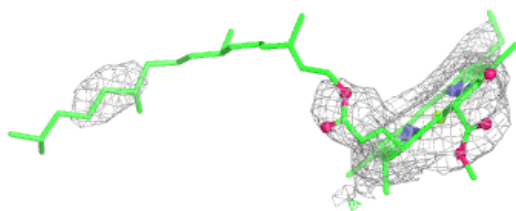
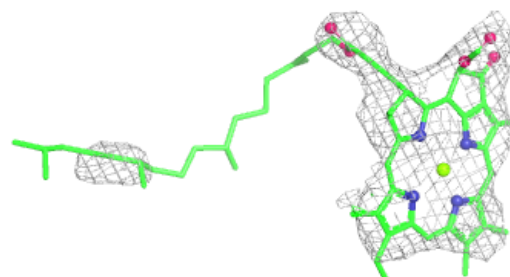


Electron density around BCR C 488:

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

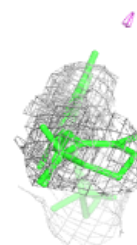
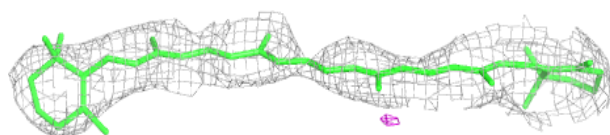
**Electron density around CLA C 486:**

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

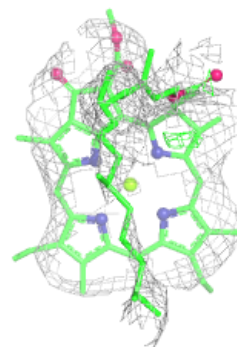
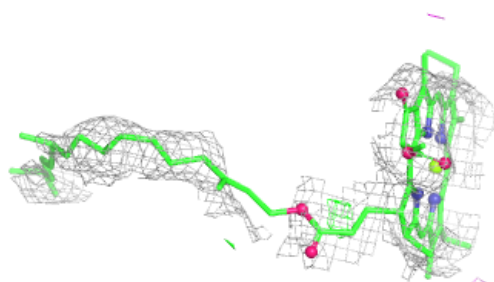


Electron density around BCR F 48:

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

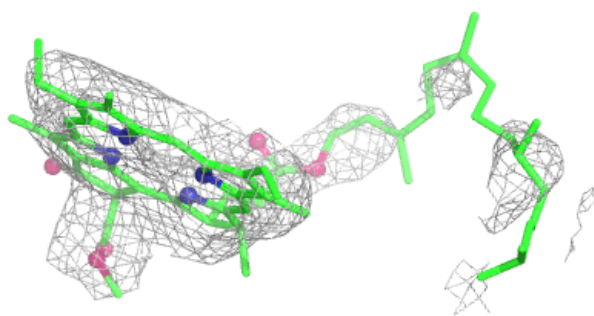
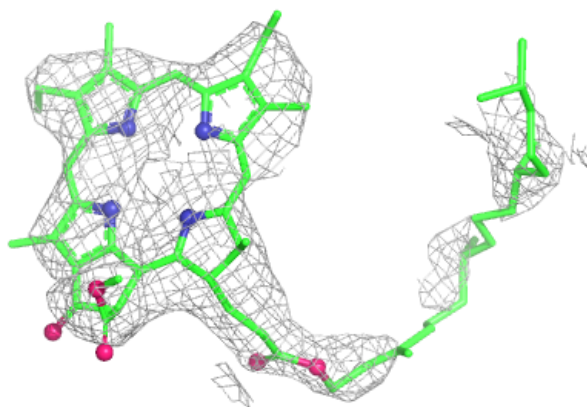
**Electron density around CLA C 475:**

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



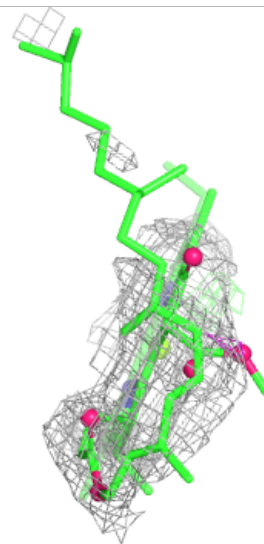
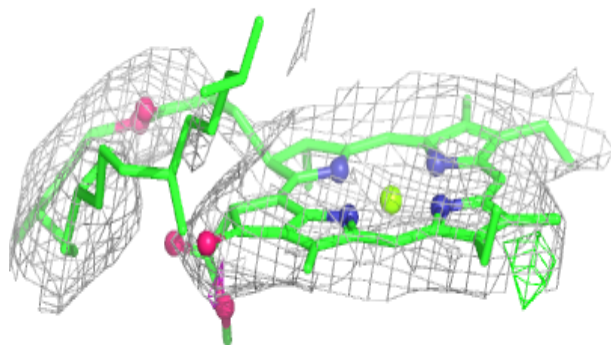
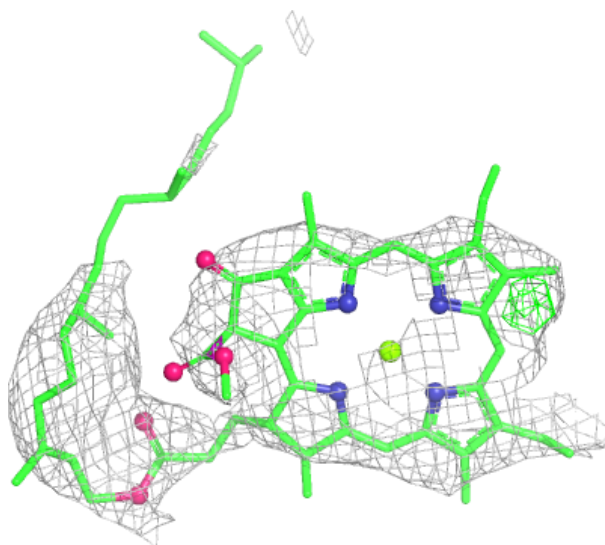
Electron density around PHO D 355:

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



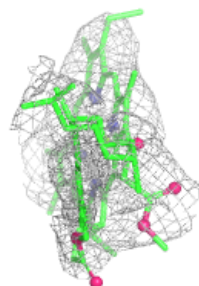
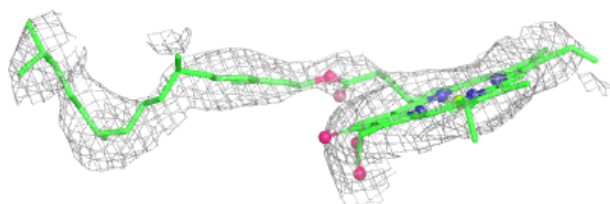
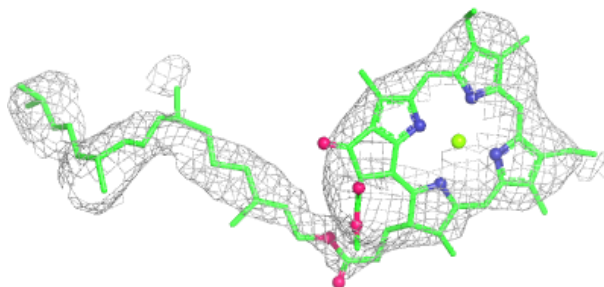
Electron density around CLA B 524:

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

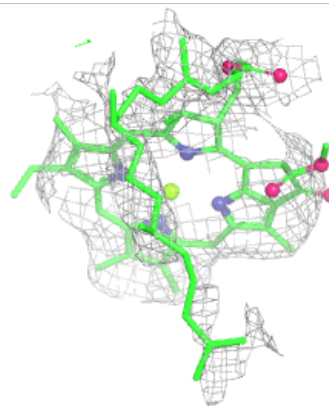
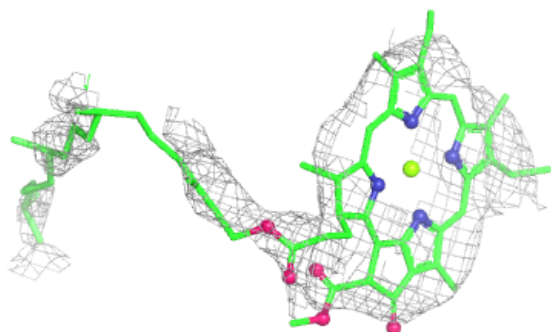
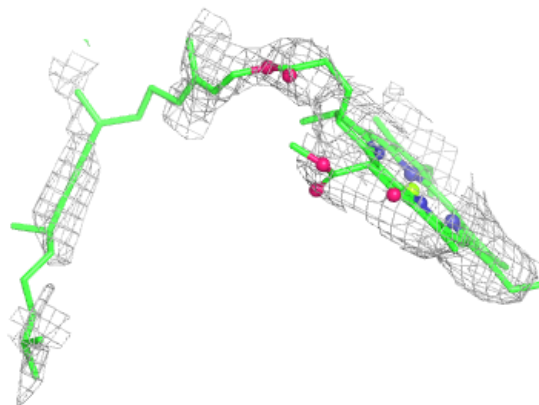


Electron density around CLA B 521:

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

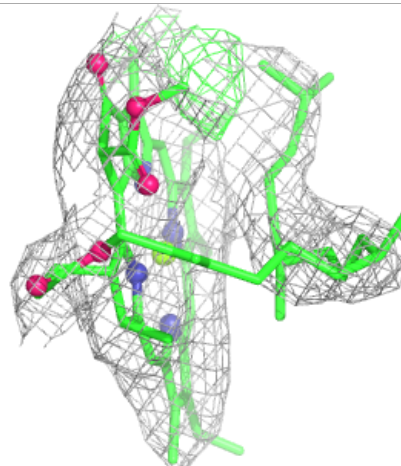
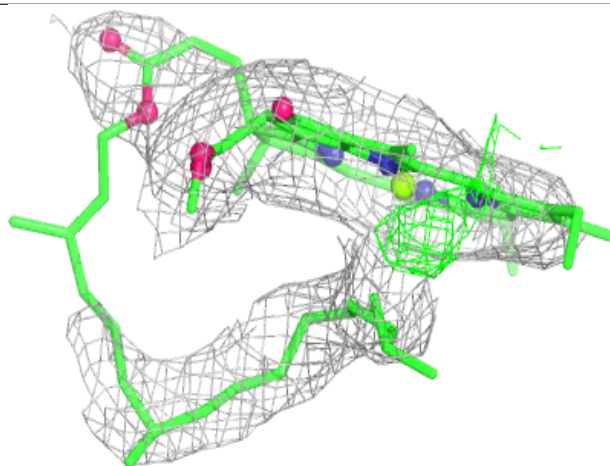
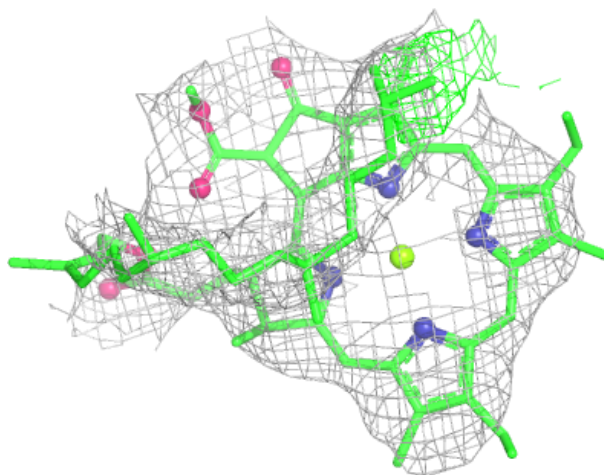
**Electron density around CLA b 2522:**

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



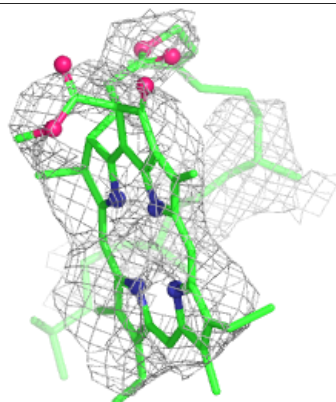
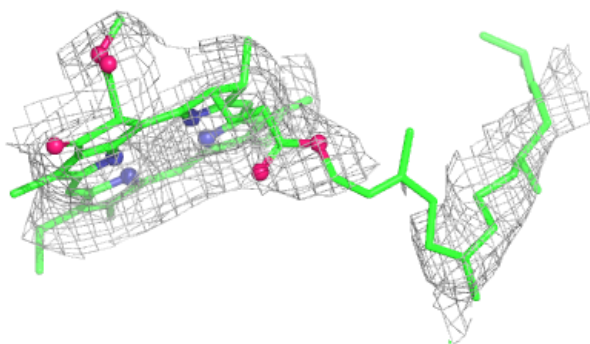
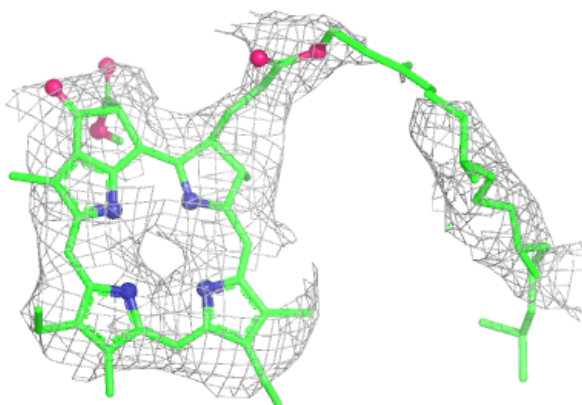
Electron density around CLA C 476:

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



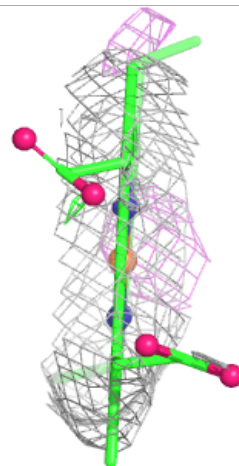
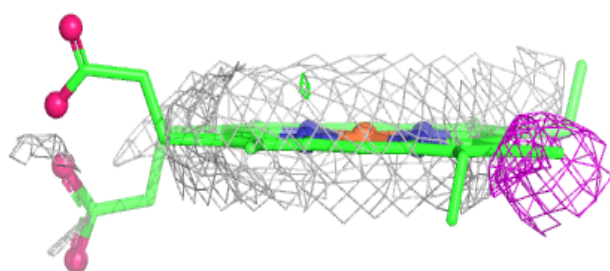
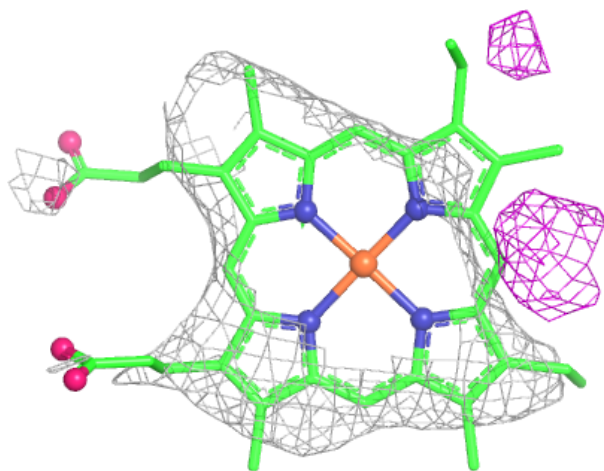
Electron density around PHO d 2356:

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



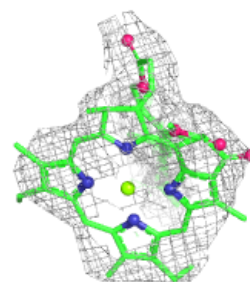
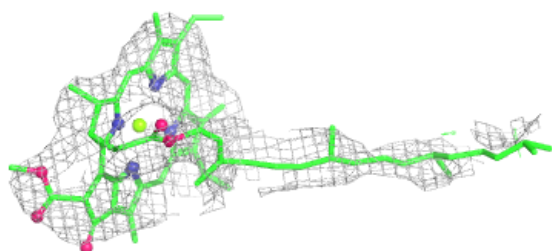
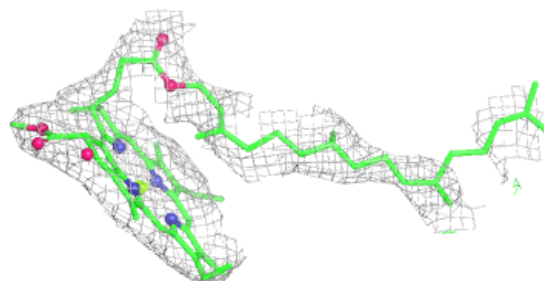
Electron density around HEC e 2084:

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



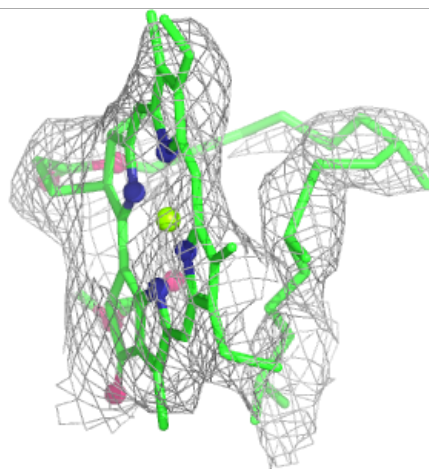
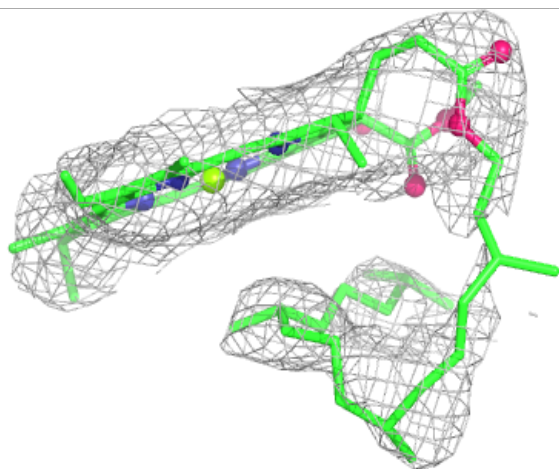
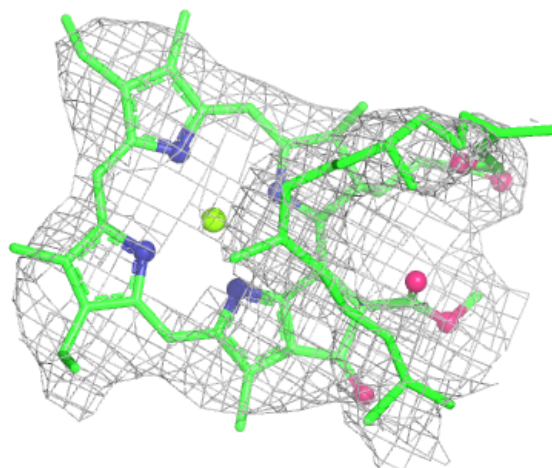
Electron density around CLA b 2519:

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



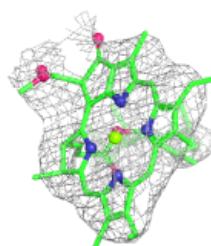
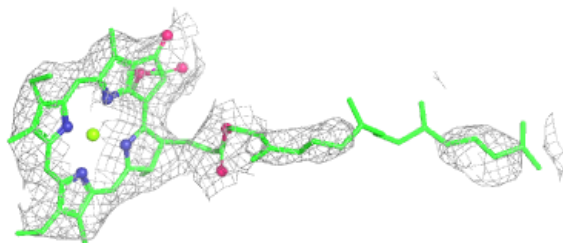
Electron density around CLA B 512:

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

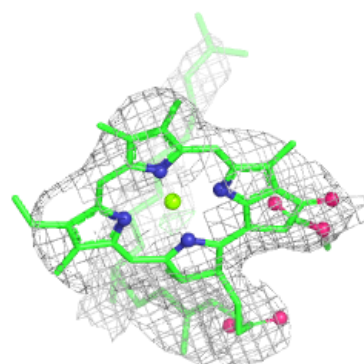
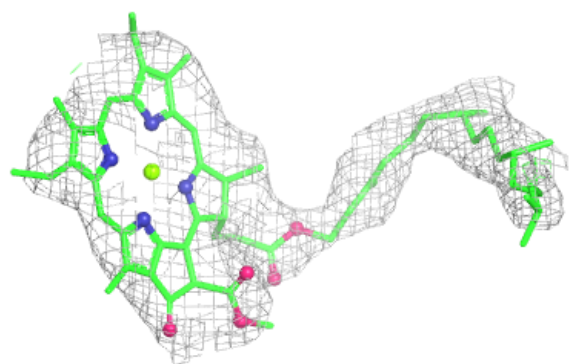
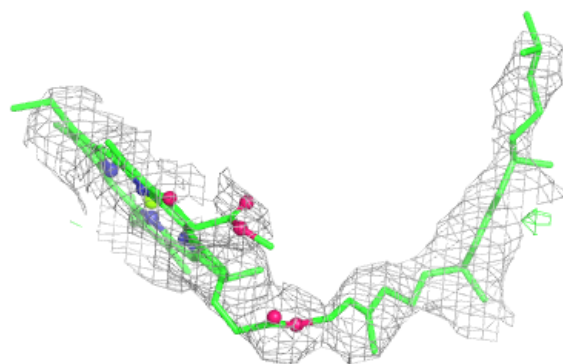


Electron density around CLA C 481:

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

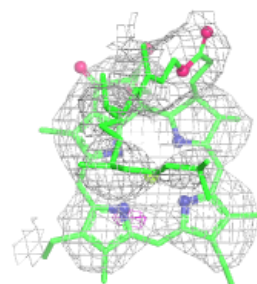
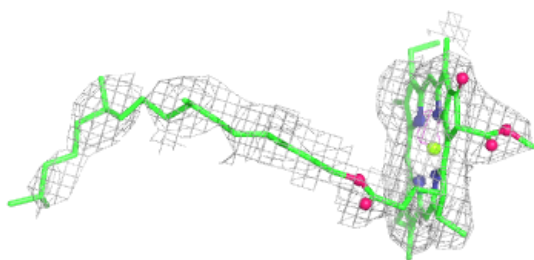
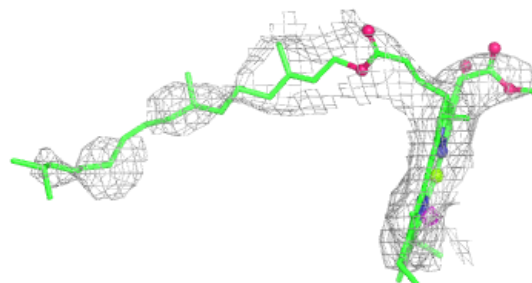
**Electron density around CLA B 522:**

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

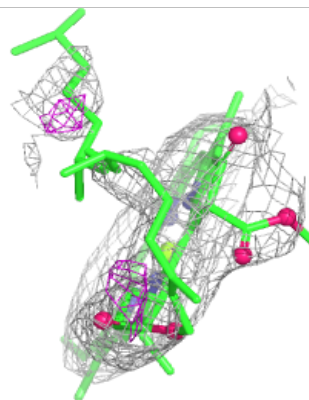
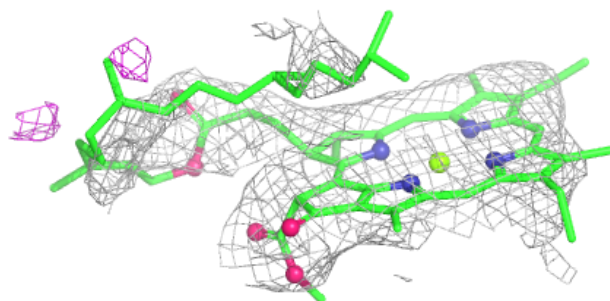
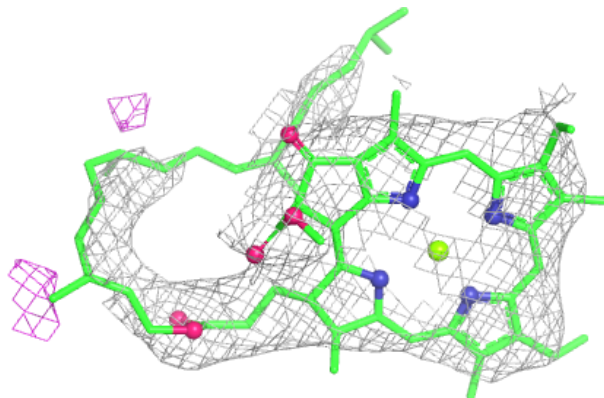


Electron density around CLA B 518:

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

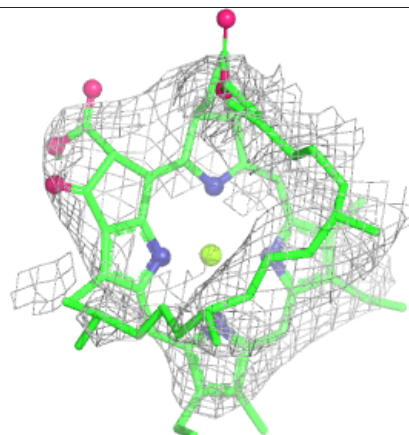
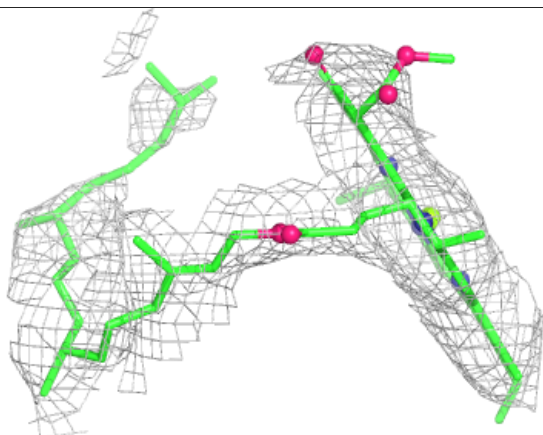
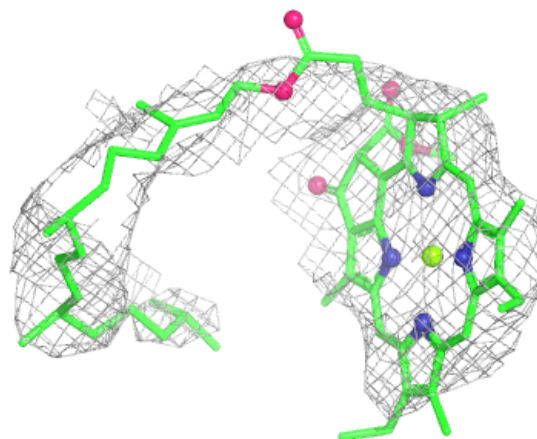
**Electron density around CLA c 2478:**

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



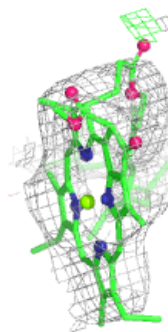
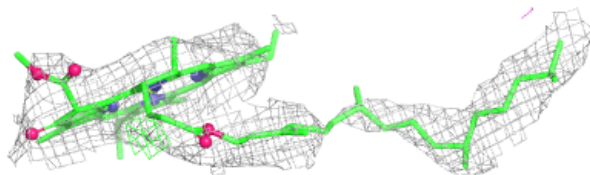
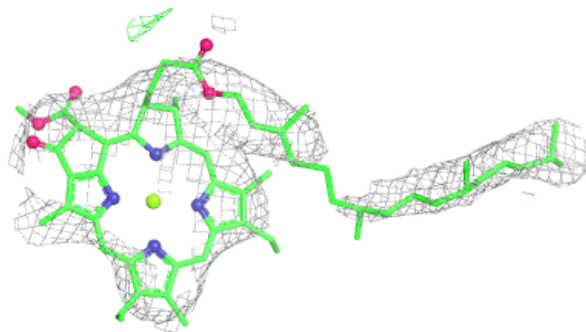
Electron density around CLA C 480:

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

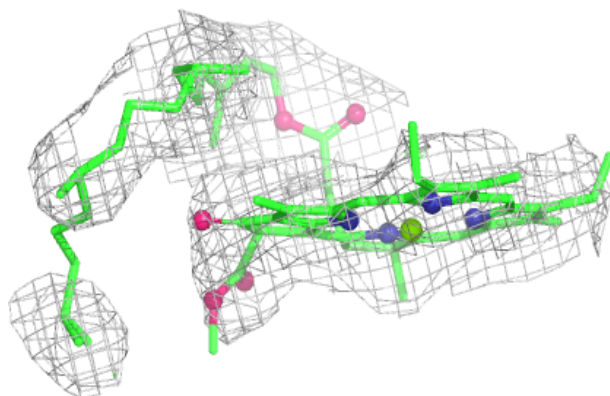
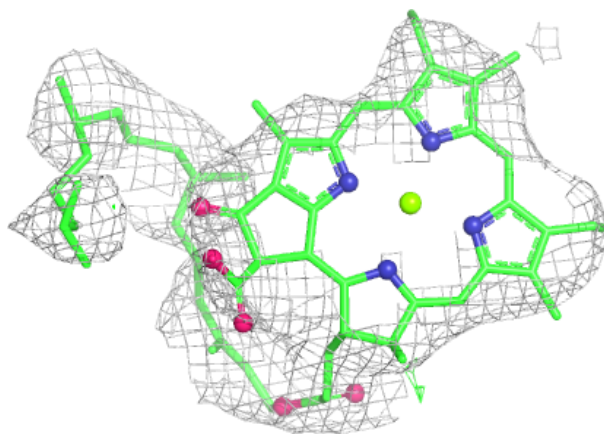


Electron density around CLA B 517:

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

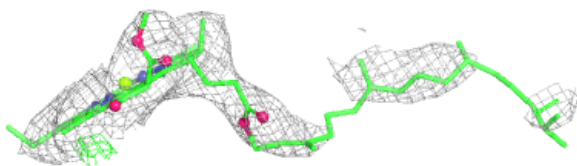
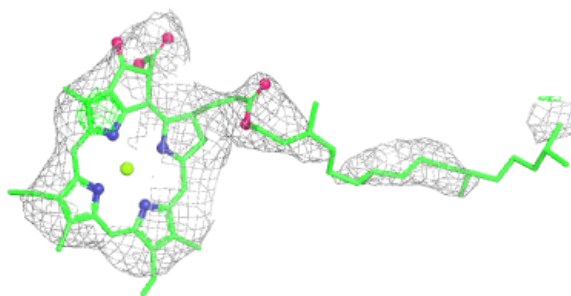
**Electron density around CLA b 2515:**

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



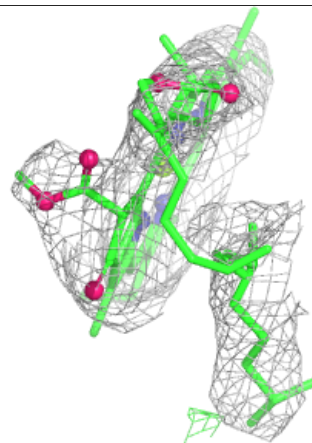
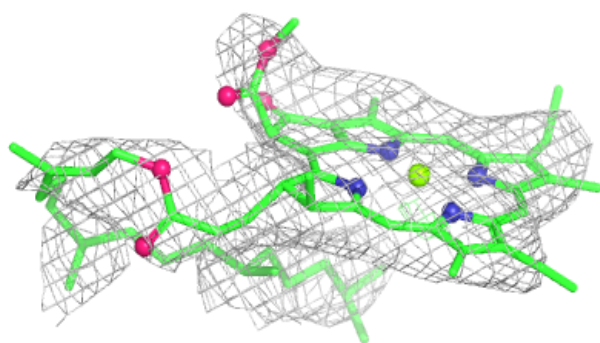
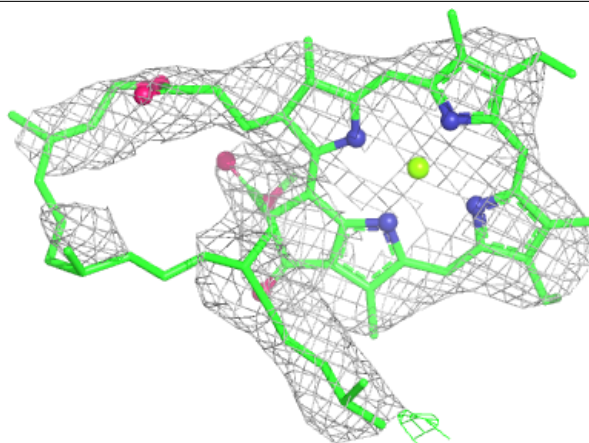
Electron density around CLA A 350:

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



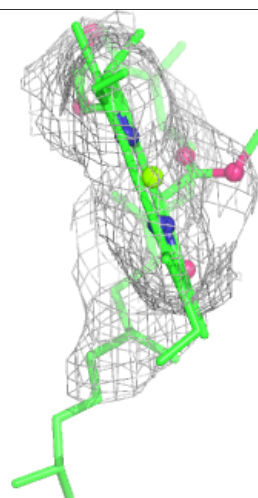
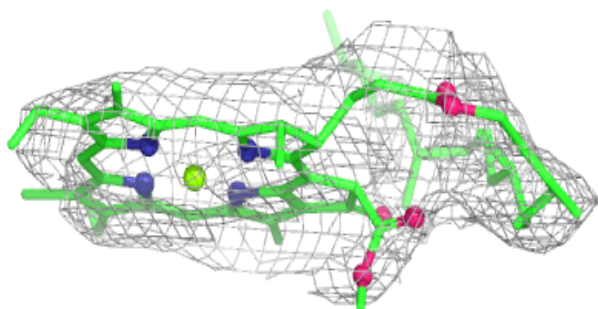
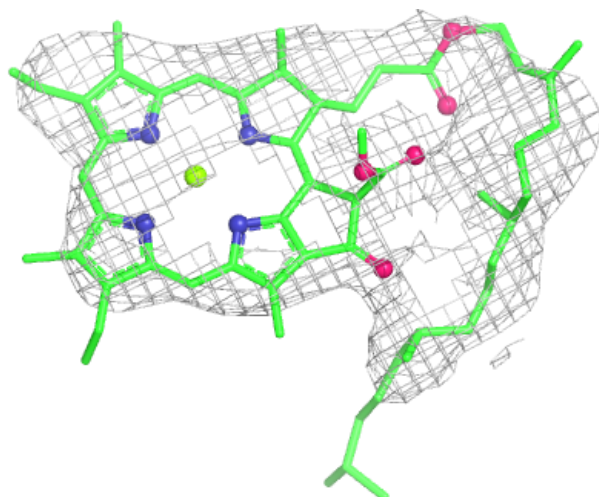
Electron density around CLA C 478:

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



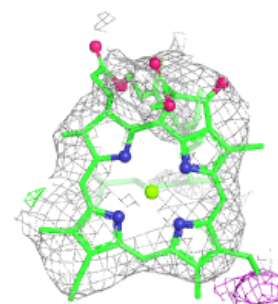
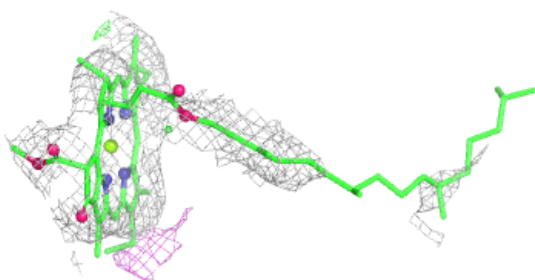
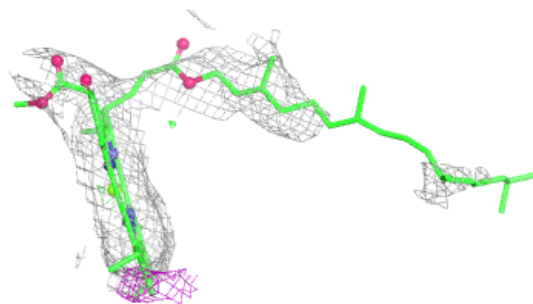
Electron density around CLA b 2524:

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



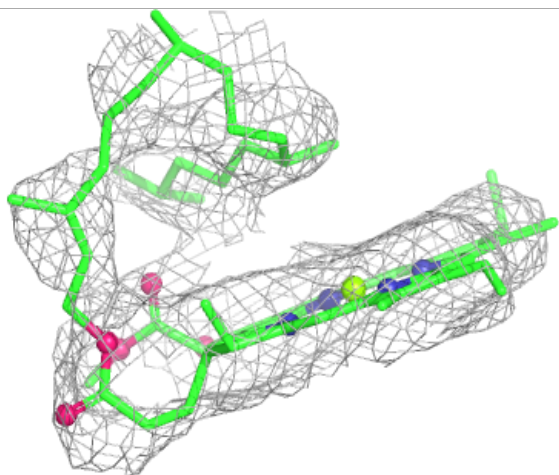
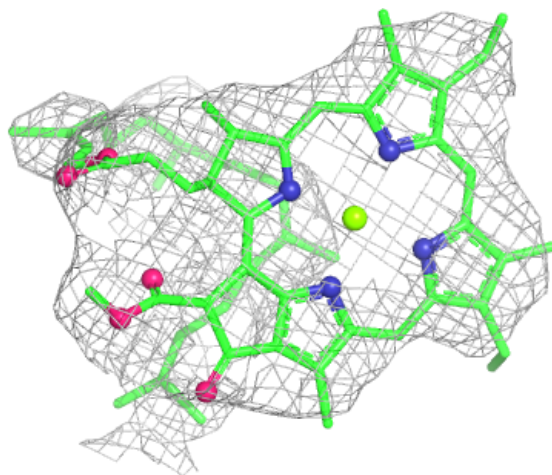
Electron density around CLA b 2518:

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



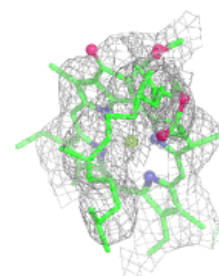
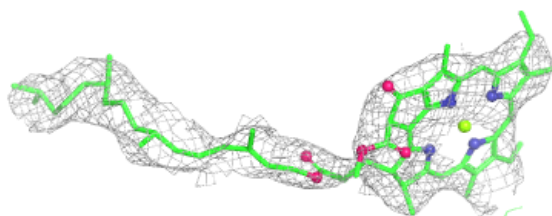
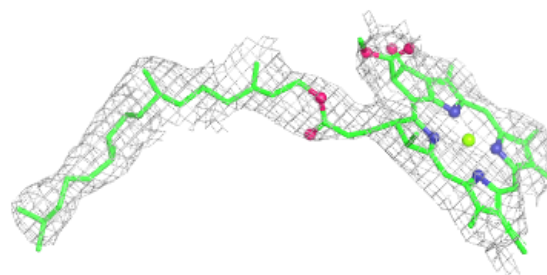
Electron density around CLA b 2512:

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

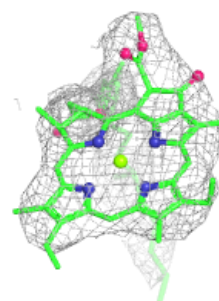
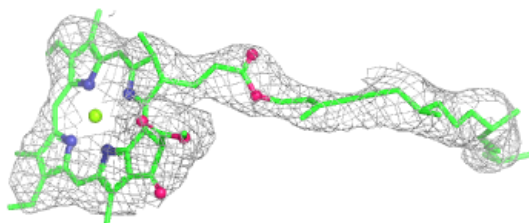
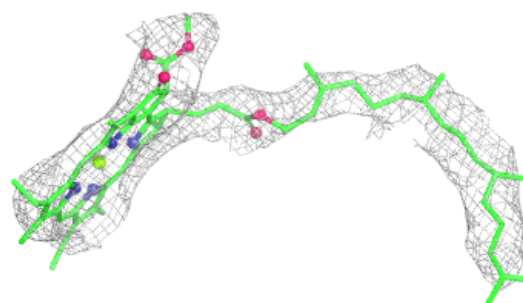


Electron density around CLA A 348:

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

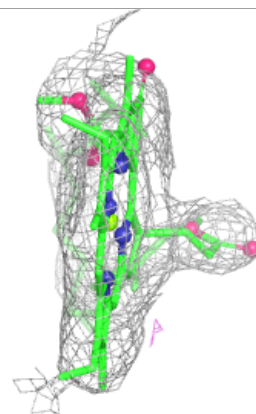
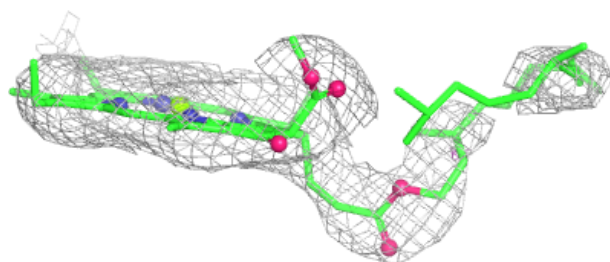
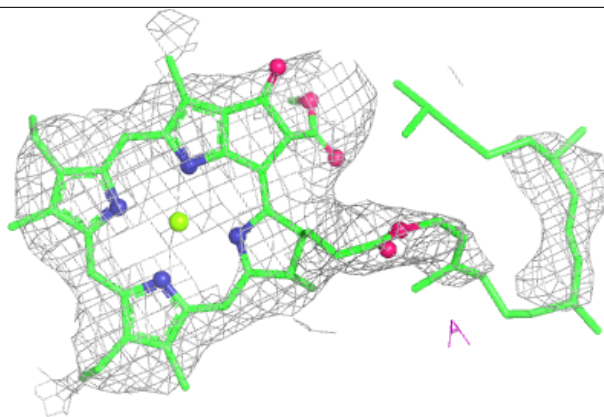
**Electron density around CLA d 2354:**

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

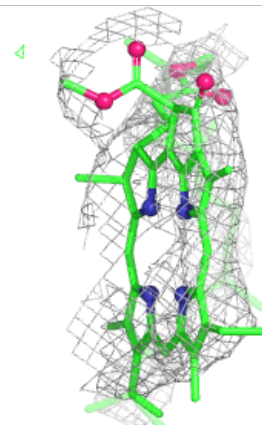
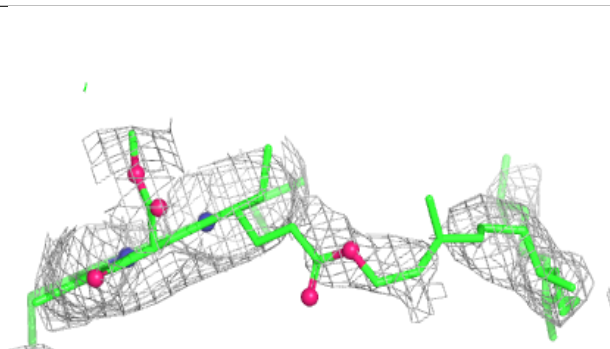
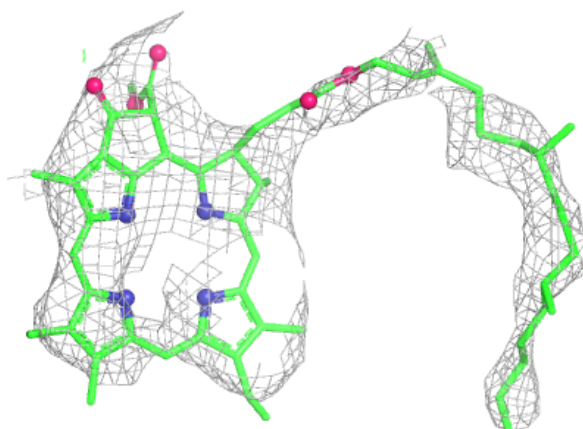


Electron density around CLA B 513:

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

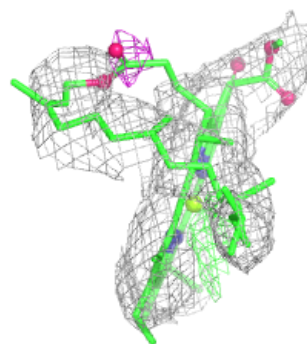
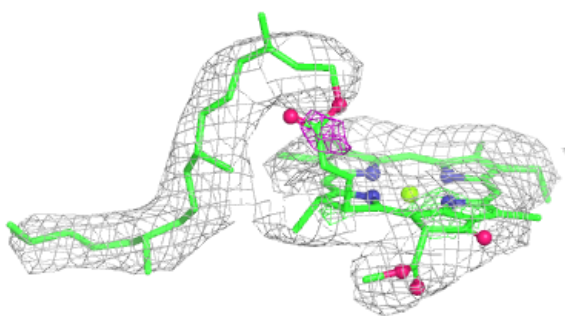
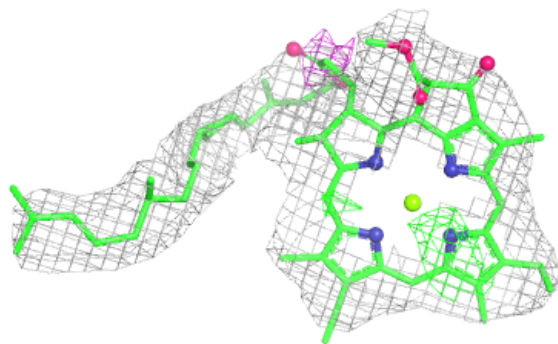
**Electron density around PHO A 351:**

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

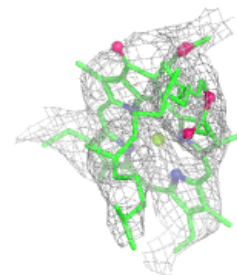
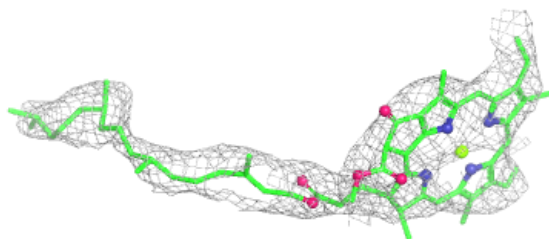
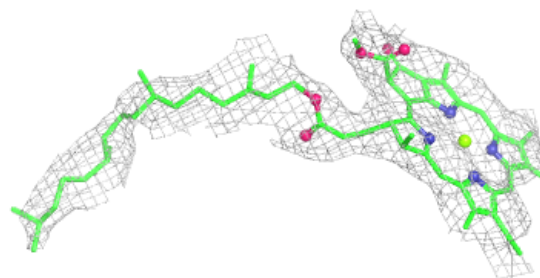


Electron density around CLA d 2355:

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

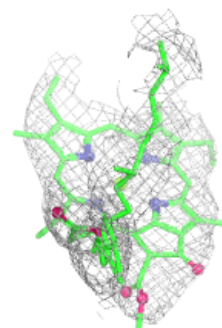
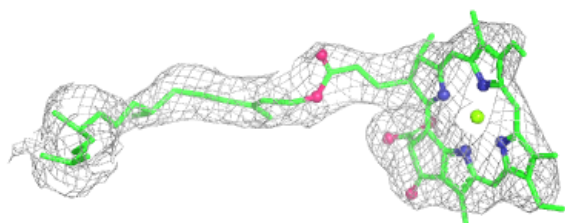
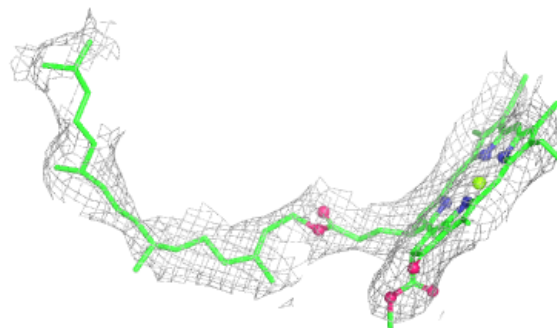
**Electron density around CLA a 2348:**

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

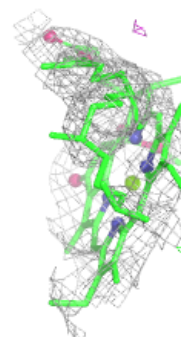
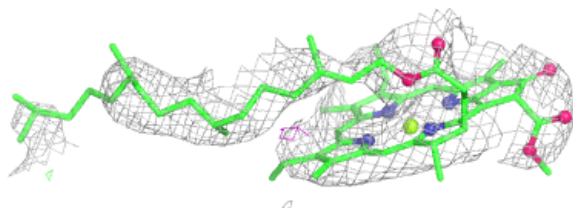
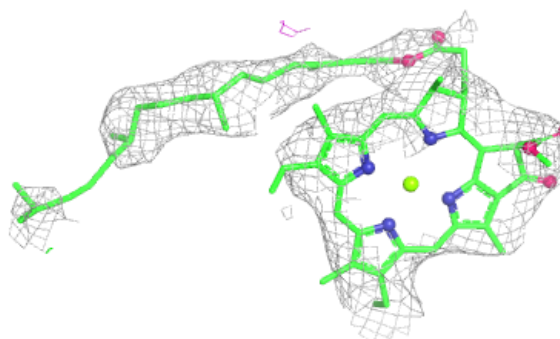


Electron density around CLA D 354:

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

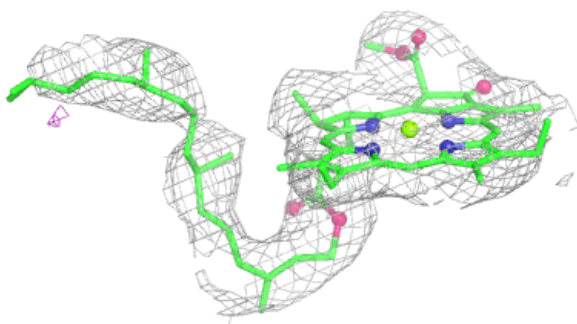
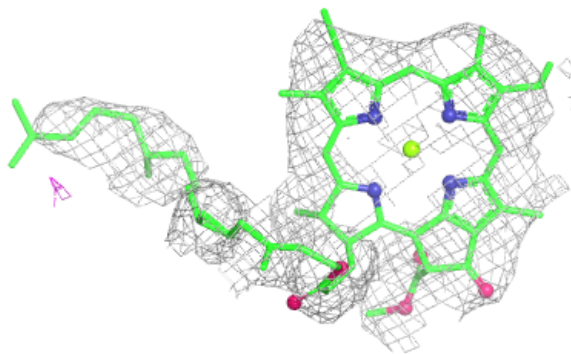
**Electron density around CLA C 479:**

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



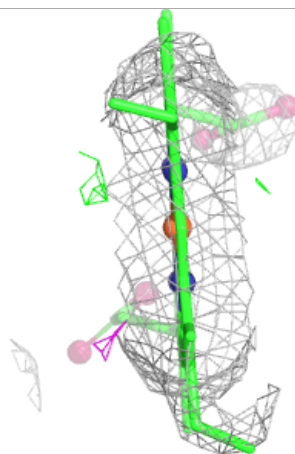
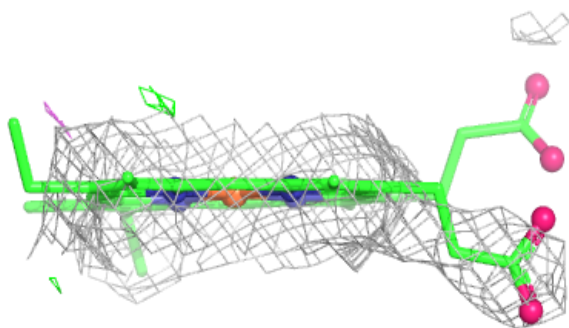
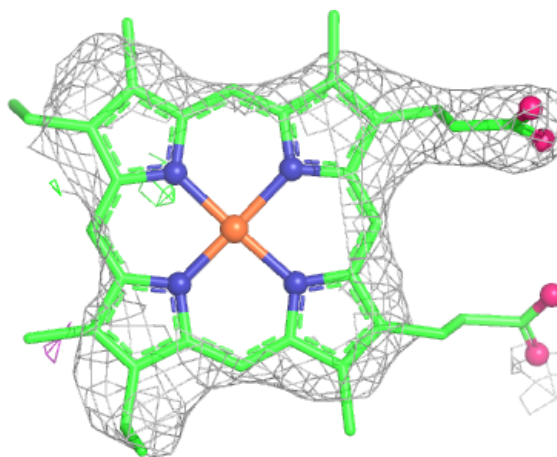
Electron density around CLA A 349:

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



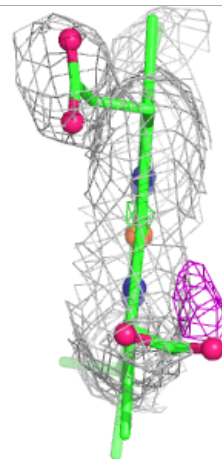
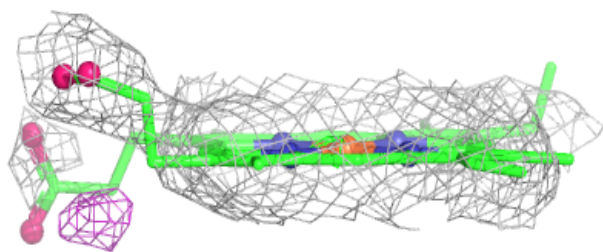
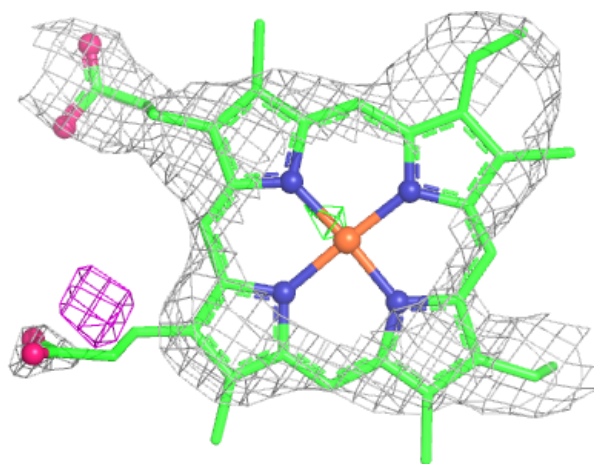
Electron density around HEC E 84:

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



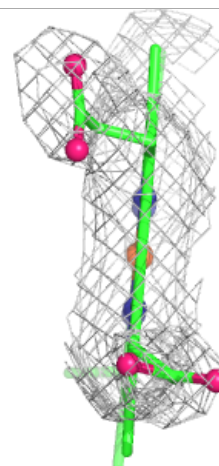
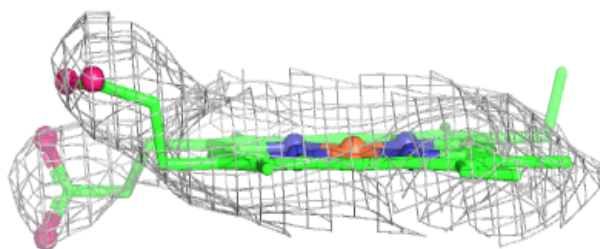
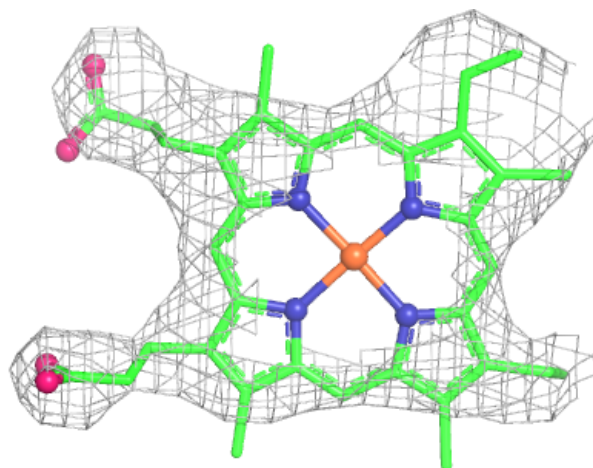
Electron density around HEC V 138:

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



Electron density around HEC v 2138:

$2mF_o-DF_c$ (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.