



wwPDB EM Validation Summary Report ⓘ

Aug 6, 2026 – 11:13 PM JST

PDB ID : 8ZEE / pdb_00008zee
EMDB ID : EMD-60026
Title : Cryo-EM structure of an intermediate-state PSII-PRF2' complex during the process of photosystem II repair
Authors : Li, A.; Liu, Z.
Deposited on : 2024-05-06
Resolution : 2.90 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>
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:

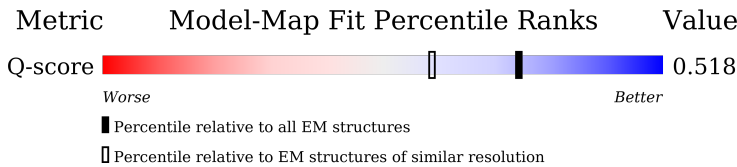
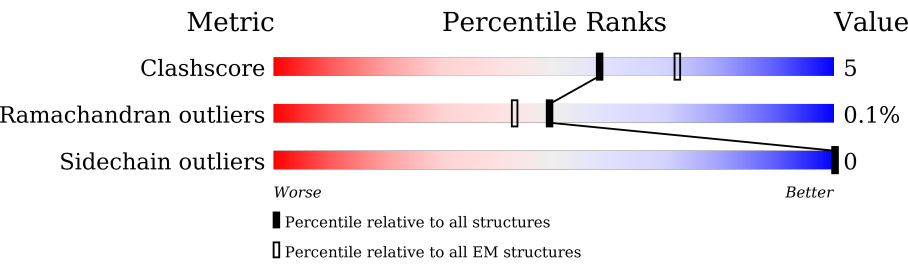
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.



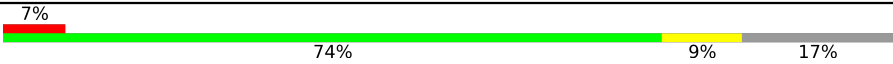
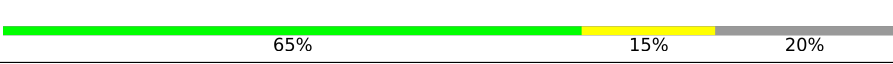
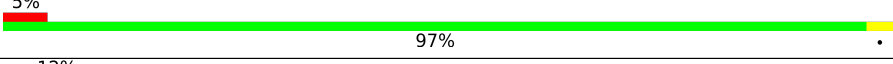
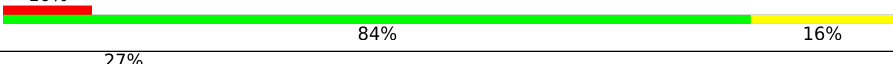
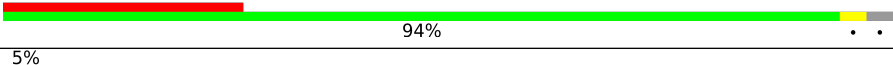
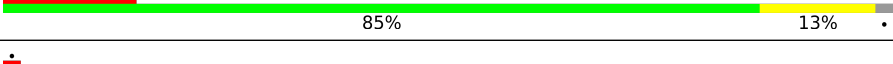
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13054 (2.40 - 3.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	508	5% 86% 8% 5%
2	D	352	5% 90% 9%
3	E	82	7% 83% 12% 5%
4	F	44	5% 59% 18% 23%

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Mol	Chain	Length	Quality of chain
5	H	88	
6	I	37	
7	K	46	
8	L	38	
9	M	34	
10	T	31	
11	V	33	
12	X	101	
13	Z	62	
14	C	461	
15	A	329	
16	1	99	

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 20218 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Photosystem II CP47 reaction center protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	482	Total	C	N	O	S	0	0
			3766	2469	629	656	12		

- Molecule 2 is a protein called Photosystem II D2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	351	Total	C	N	O	S	0	0
			2791	1841	459	479	12		

- Molecule 3 is a protein called Cytochrome b559 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	78	Total	C	N	O		0	0
			633	414	104	115			

- Molecule 4 is a protein called Cytochrome b559 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	34	Total	C	N	O	S	0	0
			277	190	45	41	1		

- Molecule 5 is a protein called Photosystem II reaction center protein H.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	73	Total	C	N	O	S	0	0
			561	372	84	103	2		

- Molecule 6 is a protein called Photosystem II reaction center protein I.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	35	Total	C	N	O	S	0	0
			283	193	43	45	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
7	K	37	Total	C	N	O	0	0
			297	209	43	45		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	38	Total	C	N	O	S	0	0
			314	210	51	52	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
9	M	31	Total	C	N	O	0	0
			239	163	33	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	T	31	Total	C	N	O	S	0	0
			256	177	38	39	2		

- Molecule 11 is a protein called Photosystem II reaction center protein Psb30.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	V	32	Total	C	N	O	0	0
			224	147	37	40		

- Molecule 12 is a protein called 4.1 kDa photosystem II subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	X	35	Total	C	N	O	0	0
			242	159	39	44		

- Molecule 13 is a protein called Photosystem II reaction center protein Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Z	61	Total	C	N	O	S	0	0
			458	314	68	75	1		

- Molecule 14 is a protein called Photosystem II CP43 reaction center protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	C	430	Total	C	N	O	S	0	0
			3368	2209	561	581	17		

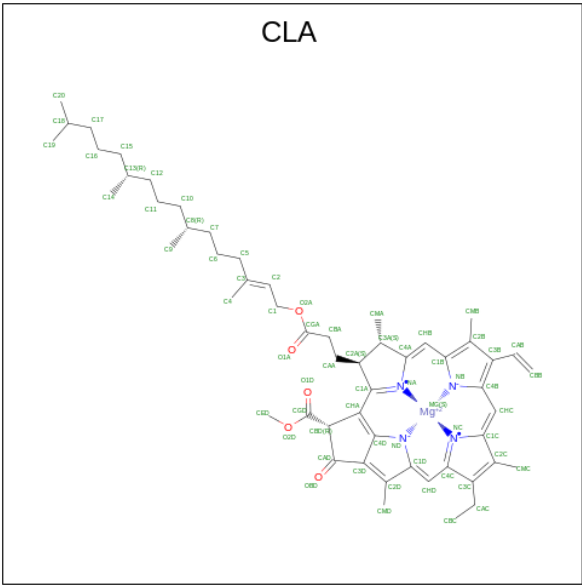
- Molecule 15 is a protein called Photosystem II protein D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	A	309	Total	C	N	O	S	0	0
			2418	1587	401	415	15		

- Molecule 16 is a protein called Chains: 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	1	44	Total	C	N	O	0	0
			313	204	51	58		

- Molecule 17 is CHLOROPHYLL A (CCD ID: CLA) (formula: C₅₅H₇₂MgN₄O₅) (labeled as "Ligand of Interest" by depositor).



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

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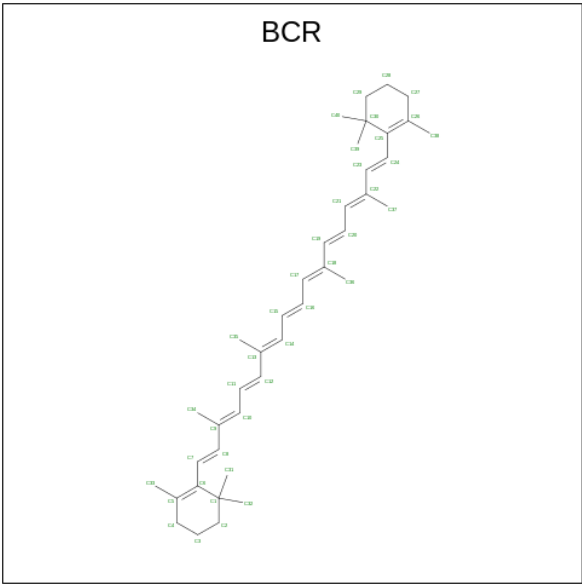
Mol	Chain	Residues	Atoms					AltConf
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17	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	B	1	Total 45	C 35	Mg 1	N 4	O 5	0
17	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	D	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	D	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	D	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	C	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	C	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	C	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	C	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	C	1	Total 65	C 55	Mg 1	N 4	O 5	0
17	C	1	Total 65	C 55	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
17	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
17	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
17	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
17	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
17	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
17	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
17	A	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
17	A	1	Total	C	Mg	N	O	0
			49	39	1	4	5	
17	A	1	Total	C	Mg	N	O	0
			60	50	1	4	5	

- Molecule 18 is BETA-CAROTENE (CCD ID: BCR) (formula: C₄₀H₅₆) (labeled as "Ligand of Interest" by depositor).



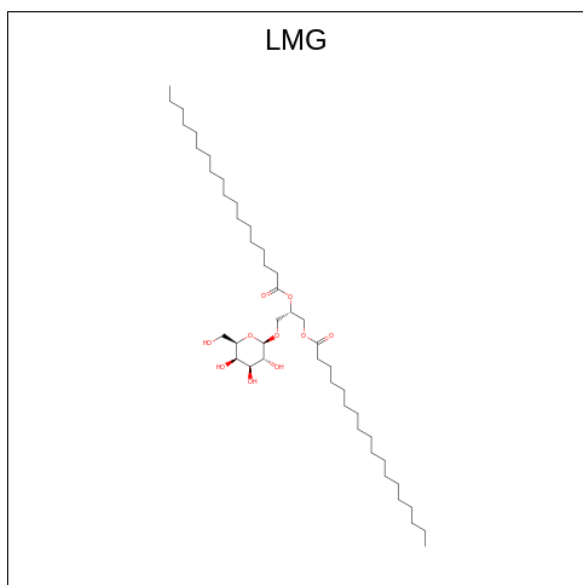
Mol	Chain	Residues	Atoms		AltConf
18	B	1	Total	C	0
			40	40	

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Mol	Chain	Residues	Atoms	AltConf
18	B	1	Total C 40 40	0
18	B	1	Total C 40 40	0
18	D	1	Total C 40 40	0
18	H	1	Total C 40 40	0
18	K	1	Total C 40 40	0
18	Z	1	Total C 40 40	0
18	C	1	Total C 40 40	0
18	C	1	Total C 40 40	0
18	A	1	Total C 40 40	0

- Molecule 19 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (CCD ID: LMG) (formula: $C_{45}H_{86}O_{10}$) (labeled as "Ligand of Interest" by depositor).



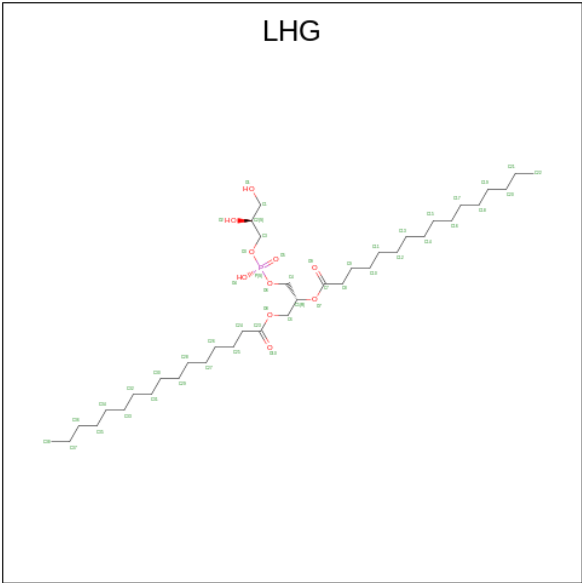
Mol	Chain	Residues	Atoms	AltConf
19	B	1	Total C O 46 36 10	0
19	D	1	Total C O 46 36 10	0

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Mol	Chain	Residues	Atoms			AltConf
19	H	1	Total	C	O	0
			48	38	10	
19	K	1	Total	C	O	0
			51	41	10	
19	C	1	Total	C	O	0
			49	39	10	
19	C	1	Total	C	O	0
			48	38	10	

- Molecule 20 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: C₃₈H₇₅O₁₀P) (labeled as "Ligand of Interest" by depositor).



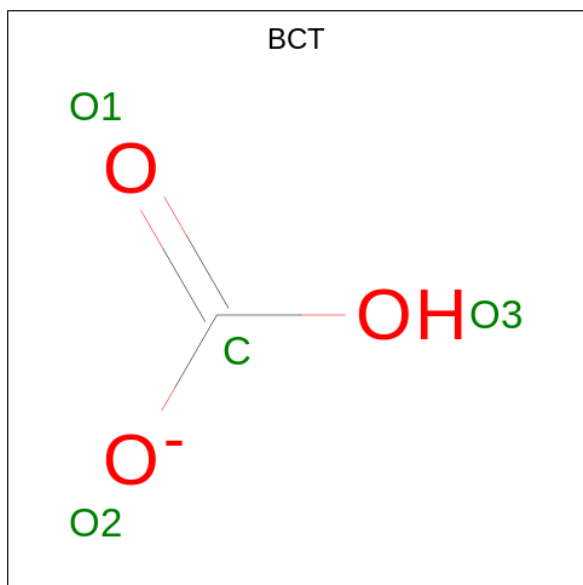
Mol	Chain	Residues	Atoms				AltConf
20	B	1	Total	C	O	P	0
			44	33	10	1	
20	B	1	Total	C	O	P	0
			47	36	10	1	
20	B	1	Total	C	O	P	0
			49	38	10	1	
20	D	1	Total	C	O	P	0
			49	38	10	1	
20	D	1	Total	C	O	P	0
			43	32	10	1	
20	D	1	Total	C	O	P	0
			49	38	10	1	
20	K	1	Total	C	O	P	0
			41	30	10	1	

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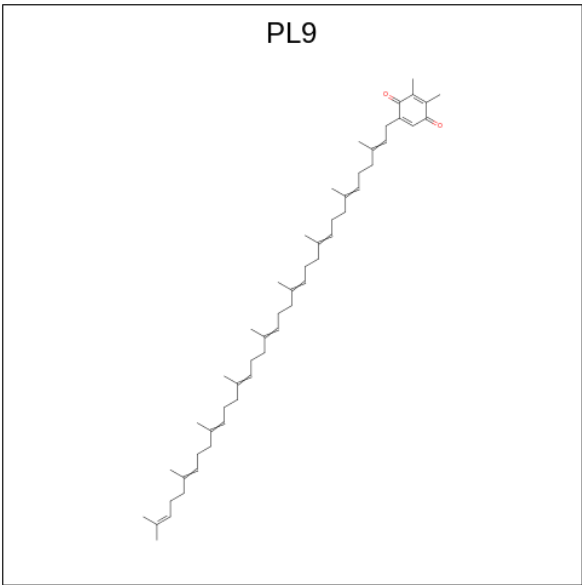
Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
20	L	1	49	38	10	1	0

- Molecule 21 is BICARBONATE ION (CCD ID: BCT) (formula: CHO_3) (labeled as "Ligand of Interest" by depositor).



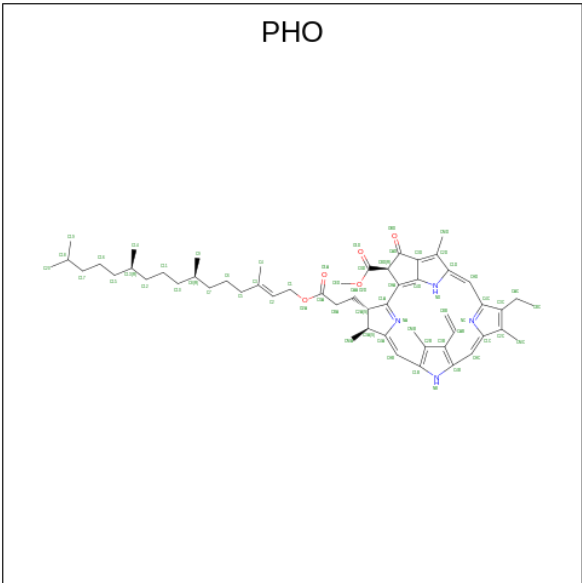
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
21	D	1	4	1	3	0

- Molecule 22 is 2,3-DIMETHYL-5-(3,7,11,15,19,23,27,31,35-NONAMETHYL-2,6,10,14,18,22,26,30,34-HEXATRIACONTANONAENYL-2,5-CYCLOHEXADIENE-1,4-DIONE-2,3-DIMETHYL-5-SOLANESYL-1,4-BENZOQUINONE (CCD ID: PL9) (formula: $\text{C}_{53}\text{H}_{80}\text{O}_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
22	D	1	Total	C	O	0
			55	53	2	

- Molecule 23 is PHEOPHYTIN A (CCD ID: PHO) (formula: C₅₅H₇₄N₄O₅) (labeled as "Ligand of Interest" by depositor).



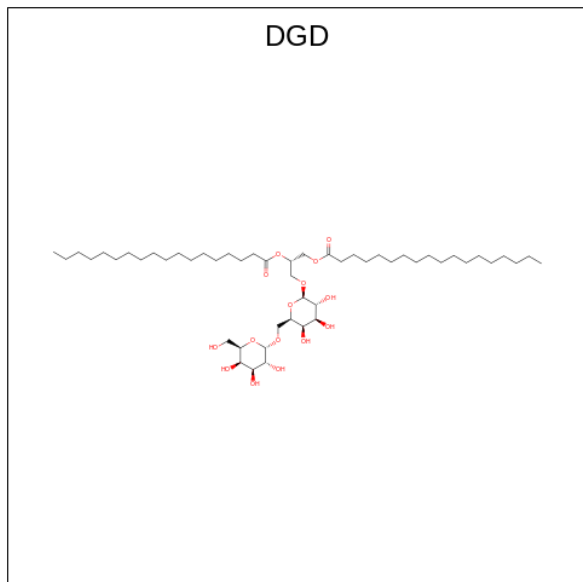
Mol	Chain	Residues	Atoms				AltConf
23	D	1	Total	C	N	O	0
			64	55	4	5	
23	D	1	Total	C	N	O	0
			64	55	4	5	

- # HEM

The chemical structure of VTQ (Vibrio toxin) is shown. It features a central core with a red 'OH' group. The structure is labeled with atom names (C1, C2, etc.) and includes a red 'OH' group. The molecule is complex, with multiple side chains and a central core. The red 'OH' group is located at the bottom left of the structure.

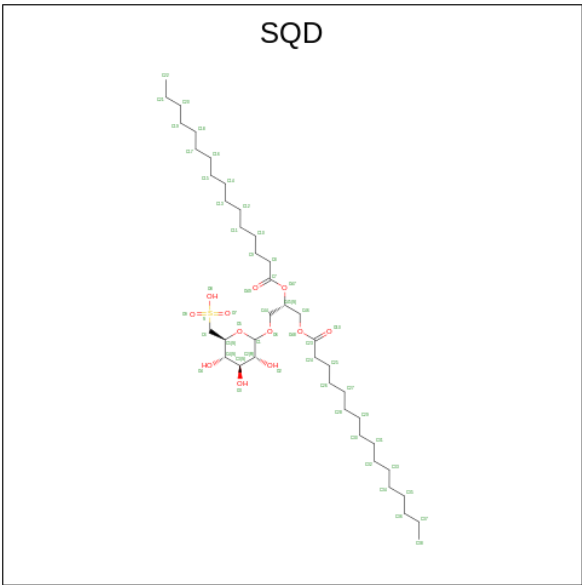


- Molecule 26 is DIGALACTOSYL DIACYL GLYCEROL (DGDG) (CCD ID: DGD) (formula: $C_{51}H_{96}O_{15}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
26	C	1	Total	C	O	0
			55	40	15	
26	C	1	Total	C	O	0
			57	42	15	
26	C	1	Total	C	O	0
			59	44	15	

- Molecule 27 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (CCD ID: SQD) (formula: $C_{41}H_{78}O_{12}S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	S	
27	C	1	51	38	12	1	0

- Molecule 28 is FE (II) ION (CCD ID: FE2) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

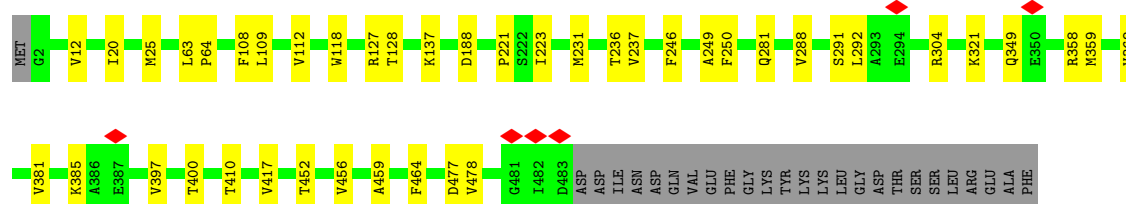
Mol	Chain	Residues	Atoms		AltConf
28	A	1	Total	Fe	0
			1	1	

3 Residue-property plots [i](#)

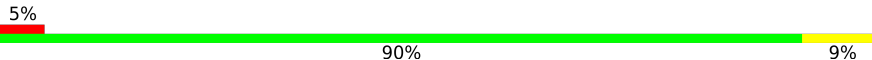
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Photosystem II CP47 reaction center protein

Chain B: 



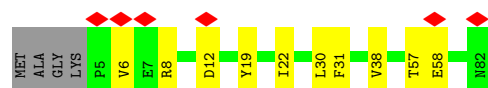
- Molecule 2: Photosystem II D2 protein

Chain D: 



- Molecule 3: Cytochrome b559 subunit alpha

Chain E: 

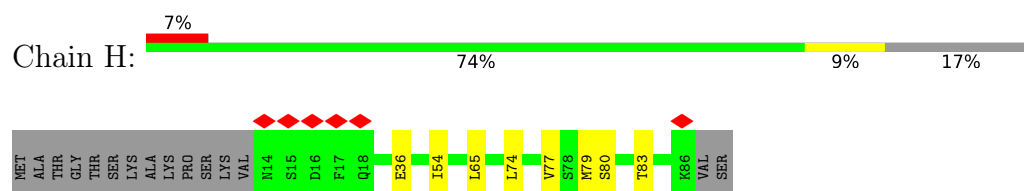


- Molecule 4: Cytochrome b559 subunit beta

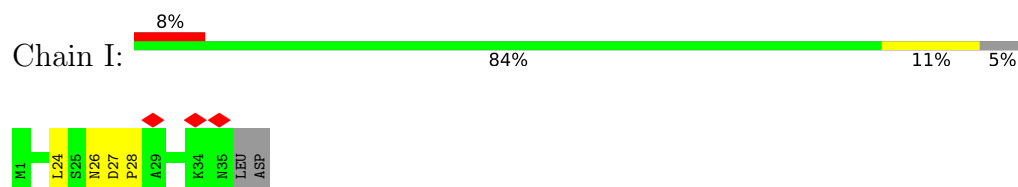
Chain F: 



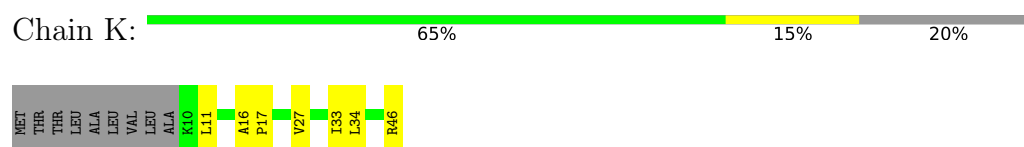
- Molecule 5: Photosystem II reaction center protein H



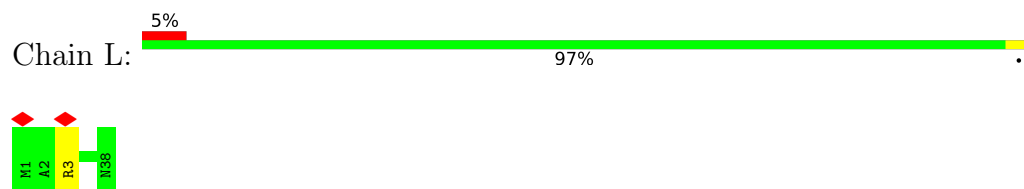
- Molecule 6: Photosystem II reaction center protein I



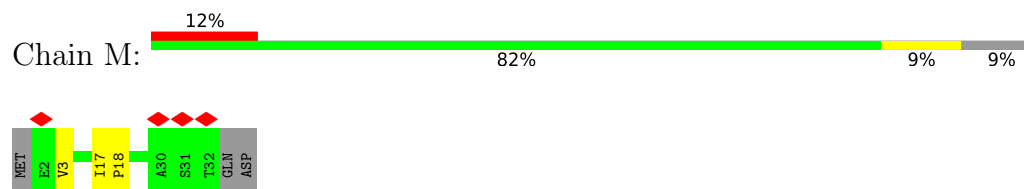
- Molecule 7: Photosystem II reaction center protein K



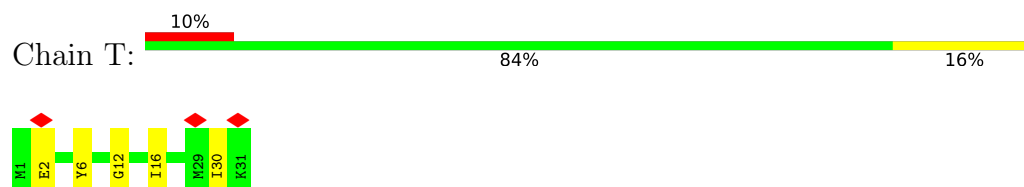
- Molecule 8: Photosystem II reaction center protein L



- Molecule 9: Photosystem II reaction center protein M

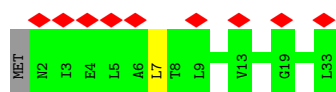


- Molecule 10: Photosystem II reaction center protein T

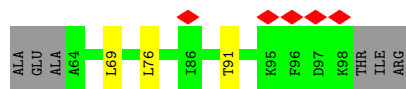
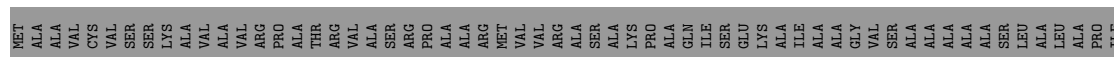


- Molecule 11: Photosystem II reaction center protein Psb30

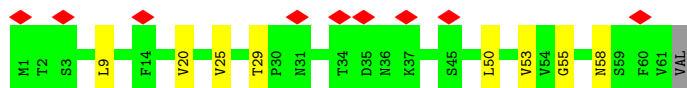
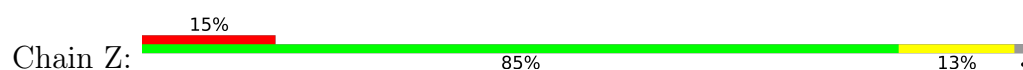




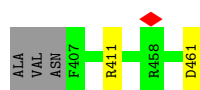
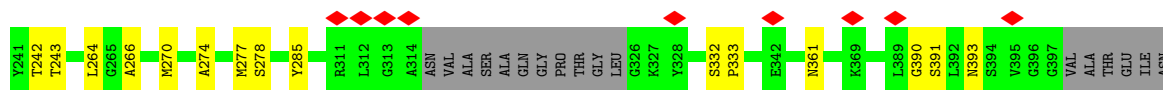
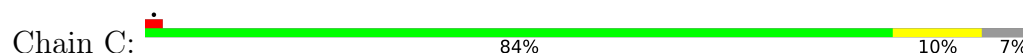
- Molecule 12: 4.1 kDa photosystem II subunit



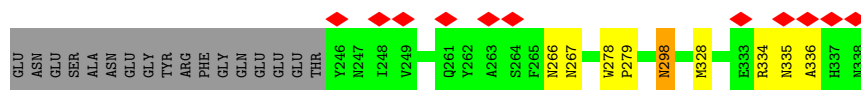
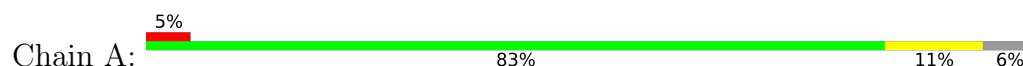
- Molecule 13: Photosystem II reaction center protein Z



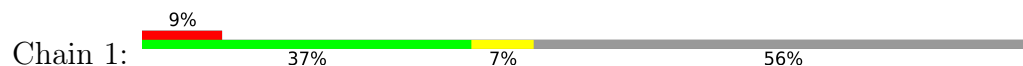
- Molecule 14: Photosystem II CP43 reaction center protein

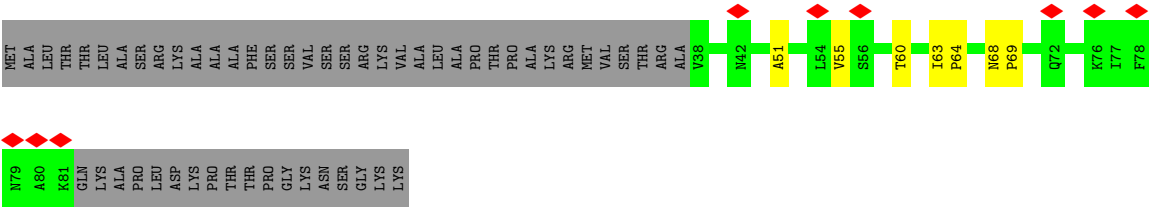


- Molecule 15: Photosystem II protein D1



- Molecule 16: Chains: 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	159928	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.215	Depositor
Minimum map value	-0.004	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.019	Depositor
Map size (Å)	280.80002, 280.80002, 280.80002	wwPDB
Map dimensions	208, 208, 208	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3500001, 1.3500001, 1.3500001	Depositor

5 Model quality

5.1 Standard geometry

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

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	B	0.13	0/3894	0.28	0/5302
2	D	0.13	0/2886	0.29	0/3937
3	E	0.12	0/652	0.31	0/890
4	F	0.13	0/286	0.26	0/389
5	H	0.10	0/573	0.26	0/783
6	I	0.16	0/291	0.31	0/394
7	K	0.10	0/309	0.29	0/425
8	L	0.14	0/322	0.23	0/437
9	M	0.07	0/243	0.20	0/333
10	T	0.14	0/263	0.21	0/354
11	V	0.07	0/224	0.18	0/307
12	X	0.10	0/244	0.20	0/330
13	Z	0.12	0/469	0.23	0/644
14	C	0.12	0/3486	0.28	0/4743
15	A	0.13	0/2495	0.32	0/3402
16	1	0.19	0/317	0.50	0/435
All	All	0.12	0/16954	0.29	0/23105

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	B	3766	0	3649	30	0
2	D	2791	0	2678	28	0
3	E	633	0	622	10	0
4	F	277	0	288	6	0
5	H	561	0	581	6	0
6	I	283	0	293	3	0
7	K	297	0	308	4	0
8	L	314	0	327	1	0
9	M	239	0	258	2	0
10	T	256	0	273	4	0
11	V	224	0	256	1	0
12	X	242	0	266	3	0
13	Z	458	0	490	7	0
14	C	3368	0	3240	37	0
15	A	2418	0	2349	25	0
16	1	313	0	331	8	0
17	A	174	0	170	0	0
17	B	1020	0	1113	8	0
17	C	845	0	936	16	0
17	D	195	0	216	4	0
18	A	40	0	56	2	0
18	B	120	0	168	3	0
18	C	80	0	112	11	0
18	D	40	0	56	0	0
18	H	40	0	56	5	0
18	K	40	0	56	1	0
18	Z	40	0	56	7	0
19	B	46	0	62	0	0
19	C	97	0	134	0	0
19	D	46	0	62	0	0
19	H	48	0	66	3	0
19	K	51	0	72	0	0
20	B	140	0	202	0	0
20	D	141	0	204	2	0
20	K	41	0	52	0	0
20	L	49	0	74	1	0
21	D	4	0	0	0	0
22	D	55	0	80	0	0
23	D	128	0	148	0	0
24	E	43	0	30	5	0
25	X	32	0	50	0	0
26	C	171	0	216	2	0
27	C	51	0	69	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	A	1	0	0	0	0
All	All	20218	0	20725	191	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 191 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)
24:E:101:HEM:HHC	24:E:101:HEM:HBB2	1.67	0.77
14:C:390:GLY:O	15:A:298:ASN:ND2	2.19	0.76
14:C:74:LEU:HD13	14:C:77:LEU:HD12	1.70	0.74
20:D:407:LHG:O5	15:A:140:ARG:NH2	2.22	0.73
18:C:616:BCR:H383	18:C:616:BCR:H23C	1.72	0.72

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	B	480/508 (94%)	470 (98%)	10 (2%)	0	100	100
2	D	349/352 (99%)	337 (97%)	12 (3%)	0	100	100
3	E	76/82 (93%)	72 (95%)	4 (5%)	0	100	100
4	F	32/44 (73%)	31 (97%)	1 (3%)	0	100	100
5	H	71/88 (81%)	68 (96%)	3 (4%)	0	100	100
6	I	33/37 (89%)	32 (97%)	1 (3%)	0	100	100
7	K	35/46 (76%)	34 (97%)	0	1 (3%)	3	15
8	L	36/38 (95%)	36 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	M	29/34 (85%)	28 (97%)	1 (3%)	0	100	100
10	T	29/31 (94%)	28 (97%)	1 (3%)	0	100	100
11	V	30/33 (91%)	30 (100%)	0	0	100	100
12	X	33/101 (33%)	33 (100%)	0	0	100	100
13	Z	59/62 (95%)	59 (100%)	0	0	100	100
14	C	424/461 (92%)	415 (98%)	9 (2%)	0	100	100
15	A	305/329 (93%)	290 (95%)	13 (4%)	2 (1%)	18	48
16	1	42/99 (42%)	42 (100%)	0	0	100	100
All	All	2063/2345 (88%)	2005 (97%)	55 (3%)	3 (0%)	49	77

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	A	298	ASN
15	A	335	ASN
7	K	11	LEU

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 PDB entries followed by that with respect to all EM entries.

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	B	384/407 (94%)	384 (100%)	0	100	100
2	D	280/281 (100%)	280 (100%)	0	100	100
3	E	69/71 (97%)	69 (100%)	0	100	100
4	F	28/37 (76%)	28 (100%)	0	100	100
5	H	63/75 (84%)	63 (100%)	0	100	100
6	I	32/34 (94%)	32 (100%)	0	100	100
7	K	31/38 (82%)	31 (100%)	0	100	100
8	L	35/35 (100%)	35 (100%)	0	100	100
9	M	27/30 (90%)	27 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	T	28/28 (100%)	28 (100%)	0	100	100
11	V	26/27 (96%)	26 (100%)	0	100	100
12	X	25/67 (37%)	25 (100%)	0	100	100
13	Z	51/52 (98%)	51 (100%)	0	100	100
14	C	338/362 (93%)	338 (100%)	0	100	100
15	A	251/268 (94%)	251 (100%)	0	100	100
16	1	32/75 (43%)	32 (100%)	0	100	100
All	All	1700/1887 (90%)	1700 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
8	L	9	GLN
15	A	108	ASN
16	1	71	GLN
15	A	322	ASN
5	H	18	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 70 ligands modelled in this entry, 1 is monoatomic - leaving 69 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	$\# Z > 2$
17	CLA	D	410	-	69,73,73	1.25	7 (10%)	83,113,113	1.11	7 (8%)
17	CLA	A	402	15	69,73,73	1.25	7 (10%)	83,113,113	1.12	5 (6%)
17	CLA	B	608	1	69,73,73	1.24	6 (8%)	83,113,113	1.06	5 (6%)
20	LHG	B	623	-	48,48,48	0.94	2 (4%)	51,54,54	0.93	2 (3%)
17	CLA	C	606	14	69,73,73	1.25	6 (8%)	83,113,113	1.05	6 (7%)
20	LHG	B	621	-	43,43,48	0.99	2 (4%)	46,49,54	1.00	2 (4%)
19	LMG	D	408	-	46,46,55	0.99	2 (4%)	54,54,63	0.86	2 (3%)
17	CLA	C	609	14	69,73,73	1.25	6 (8%)	83,113,113	1.05	5 (6%)
20	LHG	D	409	-	48,48,48	0.94	2 (4%)	51,54,54	1.01	3 (5%)
17	CLA	C	610	14	69,73,73	1.25	6 (8%)	83,113,113	1.09	4 (4%)
17	CLA	C	612	14	69,73,73	1.26	7 (10%)	83,113,113	1.11	6 (7%)
17	CLA	C	603	14	69,73,73	1.25	7 (10%)	83,113,113	1.18	5 (6%)
17	CLA	C	602	14	69,73,73	1.25	7 (10%)	83,113,113	1.11	5 (6%)
17	CLA	B	601	-	69,73,73	1.25	8 (11%)	83,113,113	1.08	5 (6%)
20	LHG	L	101	-	48,48,48	0.93	2 (4%)	51,54,54	0.91	2 (3%)
20	LHG	B	622	-	46,46,48	0.97	2 (4%)	49,52,54	0.95	2 (4%)
17	CLA	B	610	-	69,73,73	1.24	5 (7%)	83,113,113	1.13	6 (7%)
17	CLA	C	613	14	69,73,73	1.25	5 (7%)	83,113,113	1.12	5 (6%)
17	CLA	B	607	-	69,73,73	1.26	6 (8%)	83,113,113	1.11	5 (6%)
17	CLA	C	604	14	69,73,73	1.24	5 (7%)	83,113,113	1.12	6 (7%)
17	CLA	B	602	1	69,73,73	1.26	7 (10%)	83,113,113	1.12	6 (7%)
17	CLA	C	611	14	69,73,73	1.26	7 (10%)	83,113,113	1.12	5 (6%)
17	CLA	B	616	1	69,73,73	1.25	6 (8%)	83,113,113	1.13	7 (8%)
17	CLA	B	605	1	69,73,73	1.24	6 (8%)	83,113,113	1.08	6 (7%)
18	BCR	B	618	-	41,41,41	0.75	0	56,56,56	1.92	20 (35%)
18	BCR	B	619	-	41,41,41	0.76	0	56,56,56	2.02	20 (35%)
26	DGD	C	618	-	58,58,67	0.92	2 (3%)	72,72,81	0.87	2 (2%)
17	CLA	B	611	1	69,73,73	1.24	5 (7%)	83,113,113	1.08	5 (6%)
17	CLA	D	403	2	69,73,73	1.25	5 (7%)	83,113,113	1.11	5 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	DGD	C	619	-	60,60,67	0.90	2 (3%)	74,74,81	0.80	2 (2%)
18	BCR	C	616	-	41,41,41	0.75	1 (2%)	56,56,56	1.94	16 (28%)
23	PHO	D	411	-	58,69,69	2.06	10 (17%)	56,99,99	1.54	8 (14%)
17	CLA	A	404	15	64,68,73	1.29	6 (9%)	77,107,113	1.11	5 (6%)
18	BCR	Z	101	-	41,41,41	0.82	1 (2%)	56,56,56	1.91	21 (37%)
17	CLA	B	613	1	69,73,73	1.25	7 (10%)	83,113,113	1.13	6 (7%)
17	CLA	B	604	1	69,73,73	1.25	6 (8%)	83,113,113	1.08	5 (6%)
19	LMG	H	102	-	48,48,55	0.96	2 (4%)	56,56,63	0.95	2 (3%)
17	CLA	C	614	14	69,73,73	1.25	6 (8%)	83,113,113	1.13	7 (8%)
17	CLA	B	609	1	69,73,73	1.25	6 (8%)	83,113,113	1.07	6 (7%)
18	BCR	H	101	-	41,41,41	0.68	0	56,56,56	2.11	20 (35%)
21	BCT	D	401	28	2,3,3	1.25	0	2,3,3	4.13	2 (100%)
23	PHO	D	412	-	58,69,69	2.05	10 (17%)	56,99,99	1.45	6 (10%)
17	CLA	B	615	1	69,73,73	1.25	5 (7%)	83,113,113	1.09	5 (6%)
18	BCR	C	615	-	41,41,41	0.78	1 (2%)	56,56,56	2.28	22 (39%)
17	CLA	A	403	-	53,57,73	1.41	8 (15%)	62,93,113	1.22	5 (8%)
17	CLA	C	607	14	69,73,73	1.25	6 (8%)	83,113,113	1.11	6 (7%)
18	BCR	D	404	-	41,41,41	0.75	0	56,56,56	2.08	22 (39%)
17	CLA	B	612	1	69,73,73	1.25	7 (10%)	83,113,113	1.13	5 (6%)
19	LMG	C	601	-	49,49,55	0.96	2 (4%)	57,57,63	0.90	2 (3%)
22	PL9	D	405	-	55,55,55	1.04	4 (7%)	68,69,69	1.53	13 (19%)
20	LHG	D	406	-	48,48,48	0.93	2 (4%)	51,54,54	1.01	2 (3%)
17	CLA	B	603	1	69,73,73	1.24	7 (10%)	83,113,113	1.10	6 (7%)
25	VTQ	X	201	-	30,32,32	1.48	5 (16%)	39,44,44	1.03	2 (5%)
27	SQD	C	620	-	50,51,54	1.22	4 (8%)	59,62,65	1.07	6 (10%)
17	CLA	B	606	1	69,73,73	1.24	6 (8%)	83,113,113	1.10	4 (4%)
18	BCR	B	617	-	41,41,41	0.78	1 (2%)	56,56,56	1.96	21 (37%)
17	CLA	B	614	1	49,53,73	1.47	6 (12%)	59,89,113	1.21	4 (6%)
17	CLA	D	402	2	69,73,73	1.25	7 (10%)	83,113,113	1.24	4 (4%)
18	BCR	A	405	-	41,41,41	0.76	1 (2%)	56,56,56	2.01	21 (37%)
17	CLA	C	608	-	69,73,73	1.26	7 (10%)	83,113,113	1.14	5 (6%)
19	LMG	B	620	-	46,46,55	0.98	2 (4%)	54,54,63	0.87	2 (3%)
19	LMG	C	621	-	48,48,55	0.99	3 (6%)	56,56,63	1.06	3 (5%)
19	LMG	K	102	-	51,51,55	0.95	2 (3%)	59,59,63	0.88	2 (3%)
24	HEM	E	101	3,4	50,50,50	1.42	6 (12%)	66,82,82	1.19	5 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	DGD	C	617	-	56,56,67	0.93	2 (3%)	70,70,81	0.92	3 (4%)
18	BCR	K	101	-	41,41,41	0.75	0	56,56,56	2.15	20 (35%)
17	CLA	C	605	-	69,73,73	1.26	7 (10%)	83,113,113	1.09	5 (6%)
20	LHG	K	103	-	40,40,48	1.03	2 (5%)	43,46,54	1.01	2 (4%)
20	LHG	D	407	-	42,42,48	1.01	2 (4%)	45,48,54	1.11	3 (6%)

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
17	CLA	D	410	-	-	6/39/115/115	-
17	CLA	A	402	15	-	11/39/115/115	-
17	CLA	B	608	1	-	10/39/115/115	-
20	LHG	B	623	-	-	11/53/53/53	-
17	CLA	C	606	14	-	16/39/115/115	-
20	LHG	B	621	-	-	10/48/48/53	-
19	LMG	D	408	-	-	6/41/61/70	0/1/1/1
17	CLA	C	609	14	-	16/39/115/115	-
20	LHG	D	409	-	-	11/53/53/53	-
17	CLA	C	610	14	-	16/39/115/115	-
17	CLA	C	612	14	-	15/39/115/115	-
17	CLA	C	603	14	-	15/39/115/115	-
17	CLA	C	602	14	-	18/39/115/115	-
17	CLA	B	601	-	-	15/39/115/115	-
20	LHG	L	101	-	-	14/53/53/53	-
20	LHG	B	622	-	-	8/51/51/53	-
17	CLA	B	610	-	-	13/39/115/115	-
17	CLA	C	613	14	-	16/39/115/115	-
17	CLA	B	607	-	-	19/39/115/115	-
17	CLA	C	604	14	-	17/39/115/115	-
17	CLA	B	602	1	-	10/39/115/115	-
17	CLA	C	611	14	-	10/39/115/115	-
17	CLA	B	616	1	-	13/39/115/115	-
17	CLA	B	605	1	-	16/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	BCR	B	618	-	-	4/29/63/63	0/2/2/2
18	BCR	B	619	-	-	4/29/63/63	0/2/2/2
26	DGD	C	618	-	-	7/46/86/95	0/2/2/2
17	CLA	B	611	1	-	15/39/115/115	-
17	CLA	D	403	2	-	20/39/115/115	-
26	DGD	C	619	-	-	5/48/88/95	0/2/2/2
18	BCR	C	616	-	-	4/29/63/63	0/2/2/2
23	PHO	D	411	-	-	12/37/103/103	0/5/6/6
17	CLA	A	404	15	-	6/33/109/115	-
18	BCR	Z	101	-	-	4/29/63/63	0/2/2/2
17	CLA	B	613	1	-	13/39/115/115	-
17	CLA	B	604	1	-	18/39/115/115	-
19	LMG	H	102	-	-	10/43/63/70	0/1/1/1
17	CLA	C	614	14	-	15/39/115/115	-
17	CLA	B	609	1	-	15/39/115/115	-
18	BCR	H	101	-	-	5/29/63/63	0/2/2/2
23	PHO	D	412	-	-	10/37/103/103	0/5/6/6
17	CLA	B	615	1	-	6/39/115/115	-
18	BCR	C	615	-	-	2/29/63/63	0/2/2/2
17	CLA	A	403	-	-	6/20/96/115	-
17	CLA	C	607	14	-	24/39/115/115	-
18	BCR	D	404	-	-	4/29/63/63	0/2/2/2
17	CLA	B	612	1	-	13/39/115/115	-
19	LMG	C	601	-	-	5/44/64/70	0/1/1/1
22	PL9	D	405	-	-	8/53/73/73	0/1/1/1
20	LHG	D	406	-	-	8/53/53/53	-
17	CLA	B	603	1	-	13/39/115/115	-
25	VTQ	X	201	-	-	7/25/49/49	0/1/1/1
27	SQD	C	620	-	-	12/46/66/69	0/1/1/1
17	CLA	B	606	1	-	13/39/115/115	-
18	BCR	B	617	-	-	4/29/63/63	0/2/2/2
17	CLA	B	614	1	-	5/15/91/115	-
17	CLA	D	402	2	-	19/39/115/115	-
18	BCR	A	405	-	-	4/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	CLA	C	608	-	-	7/39/115/115	-
19	LMG	B	620	-	-	3/41/61/70	0/1/1/1
19	LMG	C	621	-	-	8/43/63/70	0/1/1/1
19	LMG	K	102	-	-	7/46/66/70	0/1/1/1
24	HEM	E	101	3,4	-	3/14/54/54	-
26	DGD	C	617	-	-	5/44/84/95	0/2/2/2
18	BCR	K	101	-	-	4/29/63/63	0/2/2/2
17	CLA	C	605	-	-	8/39/115/115	-
20	LHG	K	103	-	-	8/45/45/53	-
20	LHG	D	407	-	-	16/47/47/53	-

The worst 5 of 300 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	D	412	PHO	C1B-C2B	9.58	1.50	1.39
23	D	411	PHO	C1B-C2B	9.50	1.50	1.39
23	D	412	PHO	C3B-C4B	7.51	1.50	1.41
23	D	411	PHO	C3B-C4B	7.47	1.50	1.41
27	C	620	SQD	O8-S	4.62	1.63	1.47

The worst 5 of 470 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	D	411	PHO	C4D-CHA-CBD	-6.63	105.52	108.52
23	D	412	PHO	C4D-CHA-CBD	-6.28	105.68	108.52
18	C	615	BCR	C3-C4-C5	-5.93	103.49	114.08
17	D	402	CLA	C4A-NA-C1A	5.52	109.19	106.71
18	C	615	BCR	C30-C25-C26	-5.52	114.84	122.61

There are no chirality outliers.

5 of 701 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	B	601	CLA	CHA-CBD-CGD-O1D
17	B	601	CLA	CHA-CBD-CGD-O2D
17	B	603	CLA	C1A-C2A-CAA-CBA
17	B	603	CLA	C3A-C2A-CAA-CBA
17	B	603	CLA	CHA-CBD-CGD-O1D

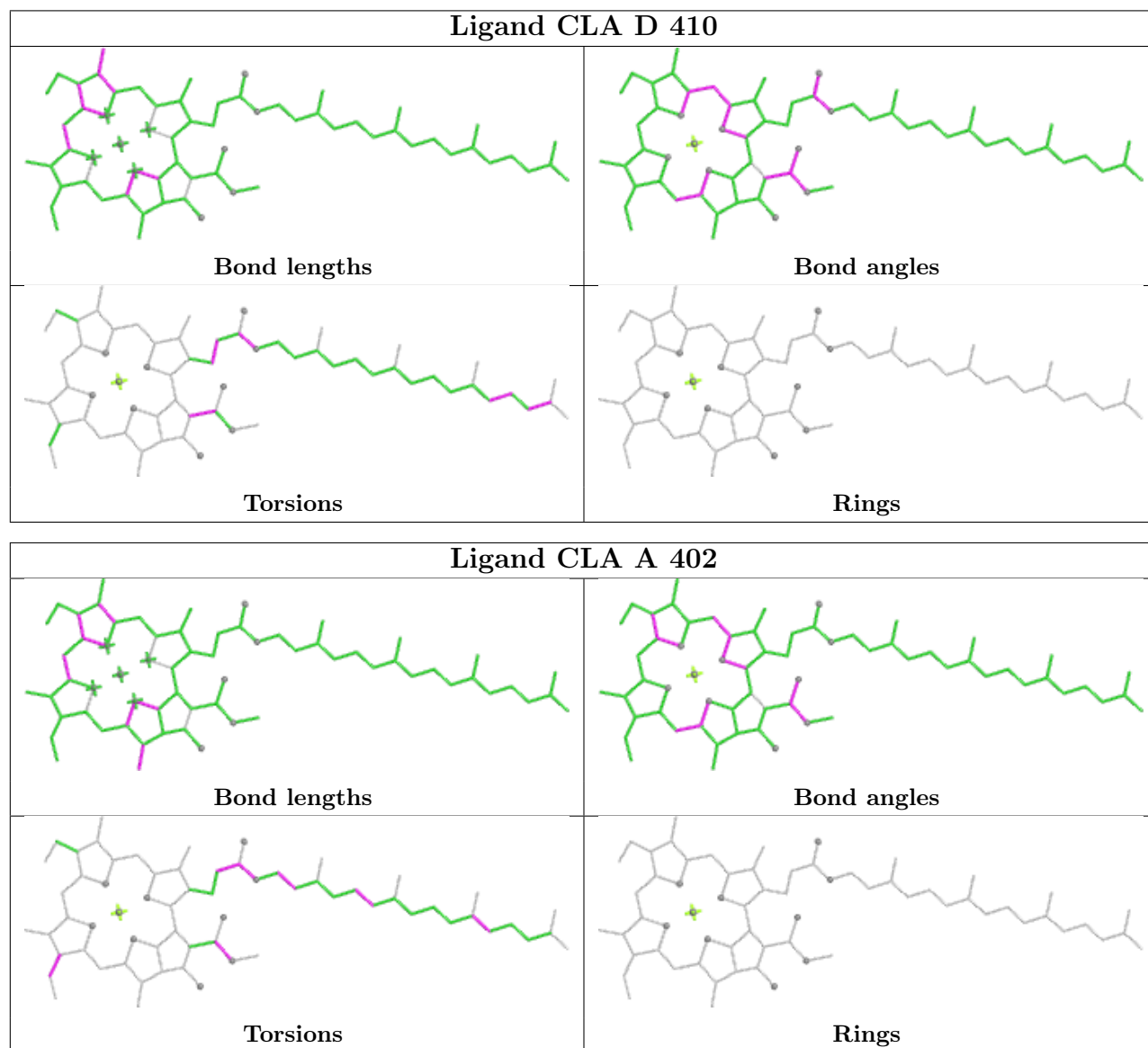
There are no ring outliers.

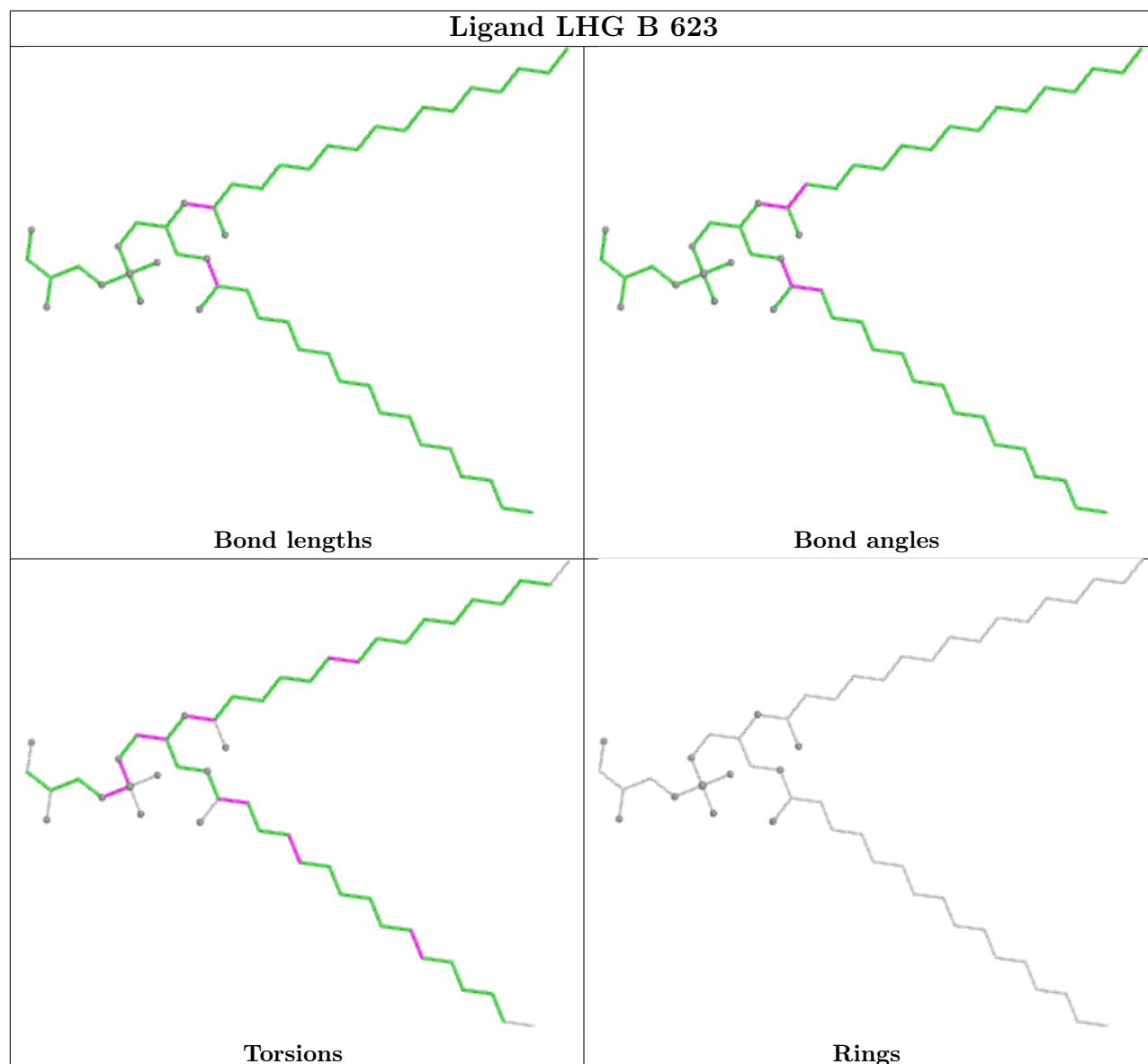
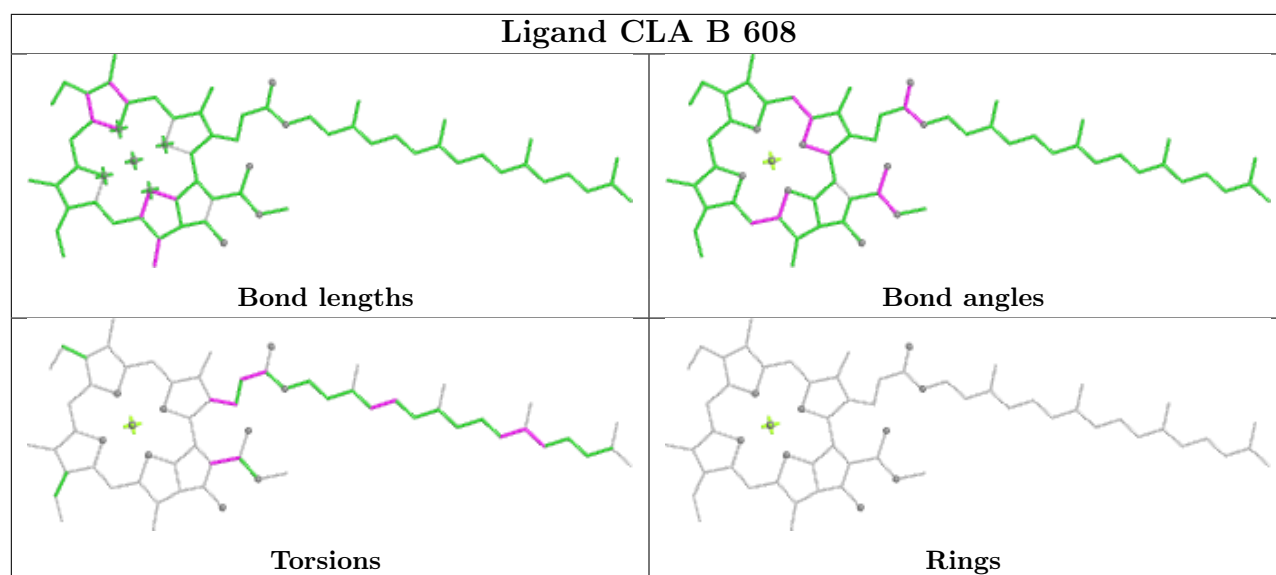
32 monomers are involved in 64 short contacts:

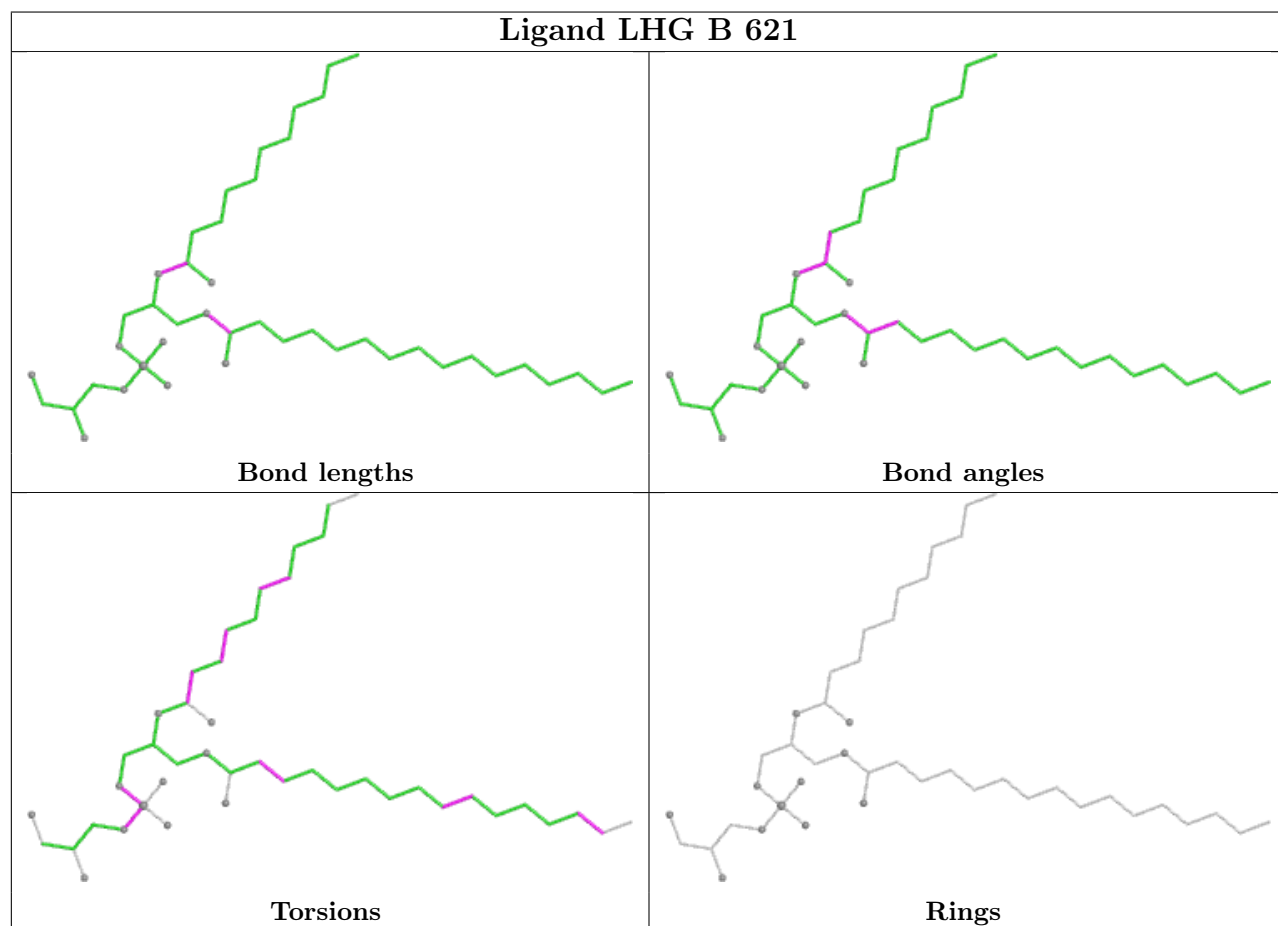
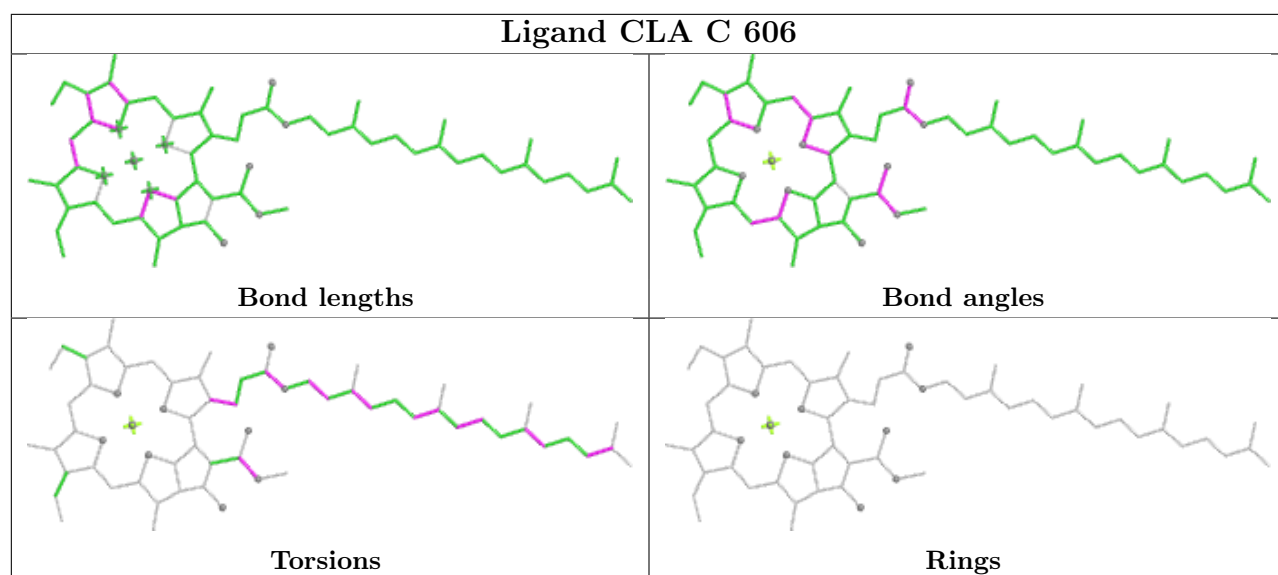
Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	D	410	CLA	2	0
17	C	606	CLA	3	0
17	C	609	CLA	1	0
17	C	612	CLA	1	0
17	C	603	CLA	3	0
17	C	602	CLA	4	0
20	L	101	LHG	1	0
17	C	604	CLA	1	0
17	B	602	CLA	4	0
17	C	611	CLA	1	0
17	B	616	CLA	1	0
18	B	618	BCR	1	0
18	B	619	BCR	1	0
17	D	403	CLA	1	0
26	C	619	DGD	2	0
18	C	616	BCR	3	0
18	Z	101	BCR	7	0
17	B	604	CLA	2	0
19	H	102	LMG	3	0
17	C	614	CLA	1	0
18	H	101	BCR	5	0
17	B	615	CLA	2	0
18	C	615	BCR	8	0
17	C	607	CLA	1	0
17	B	612	CLA	1	0
18	B	617	BCR	1	0
17	D	402	CLA	1	0
18	A	405	BCR	2	0
17	C	608	CLA	1	0
24	E	101	HEM	5	0
18	K	101	BCR	1	0
20	D	407	LHG	2	0

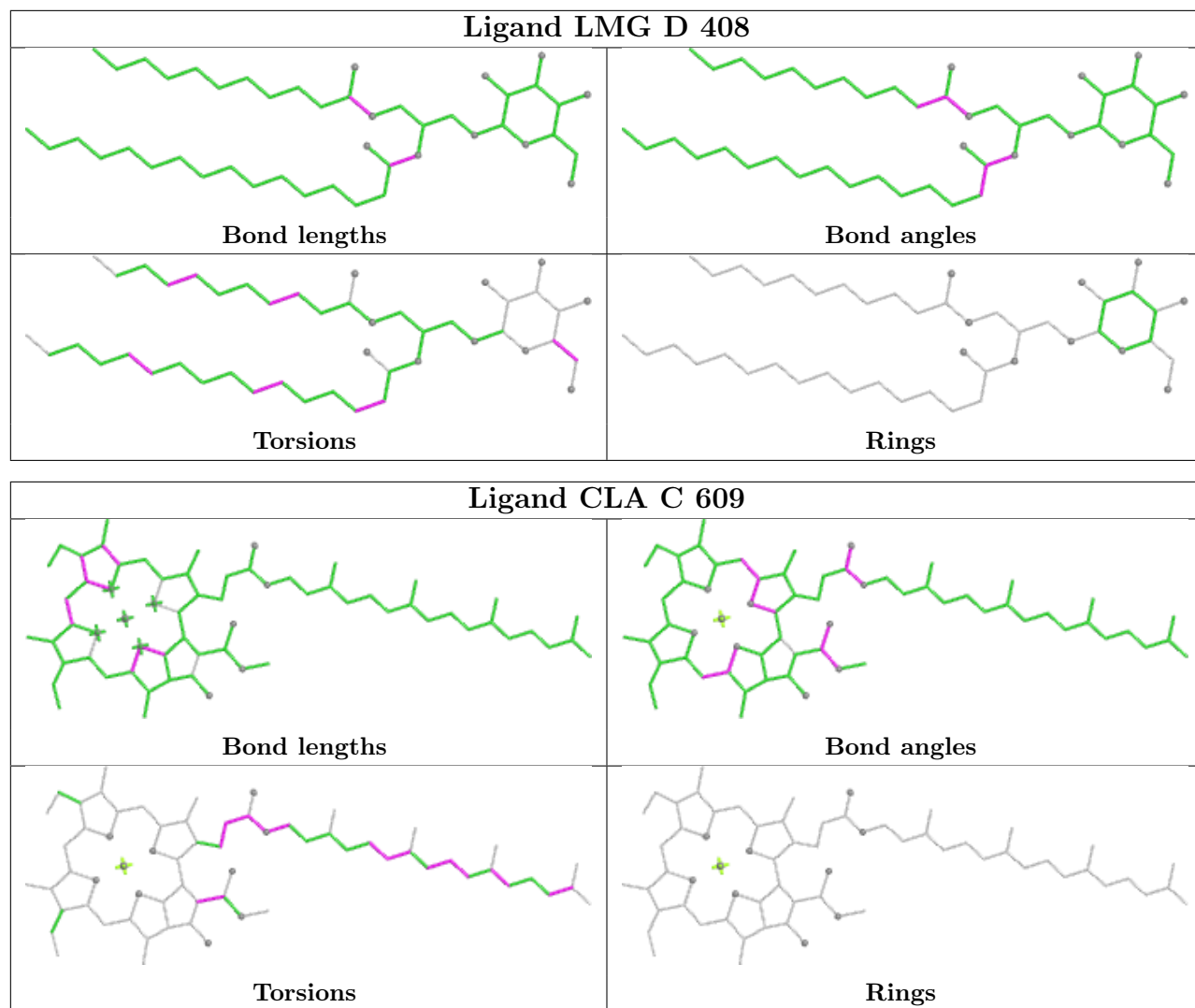
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

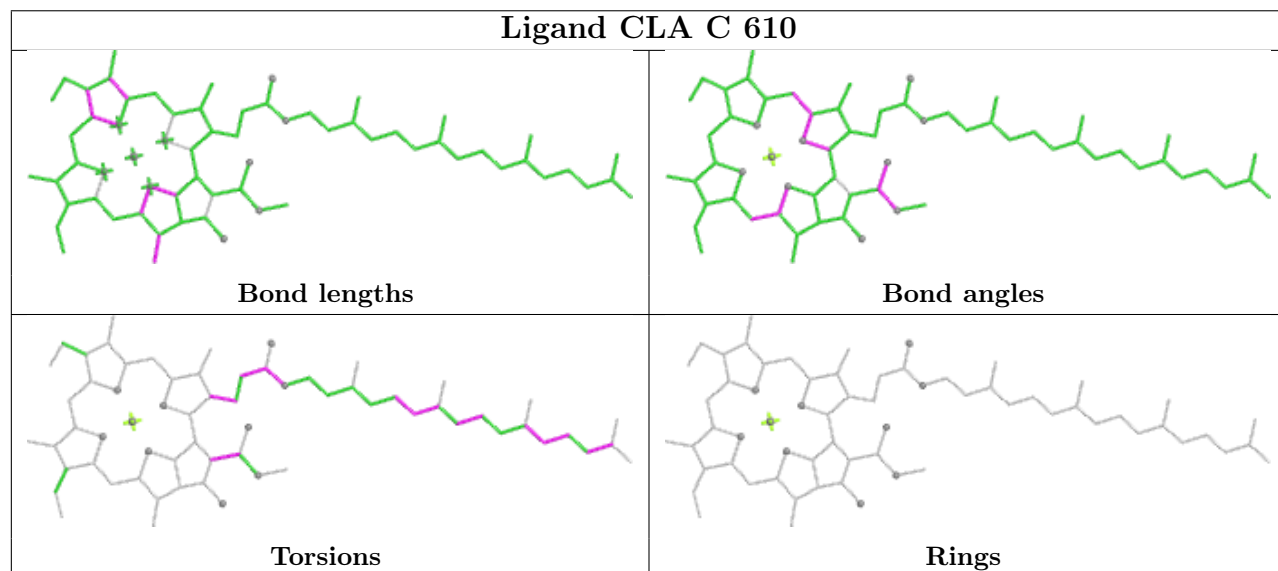
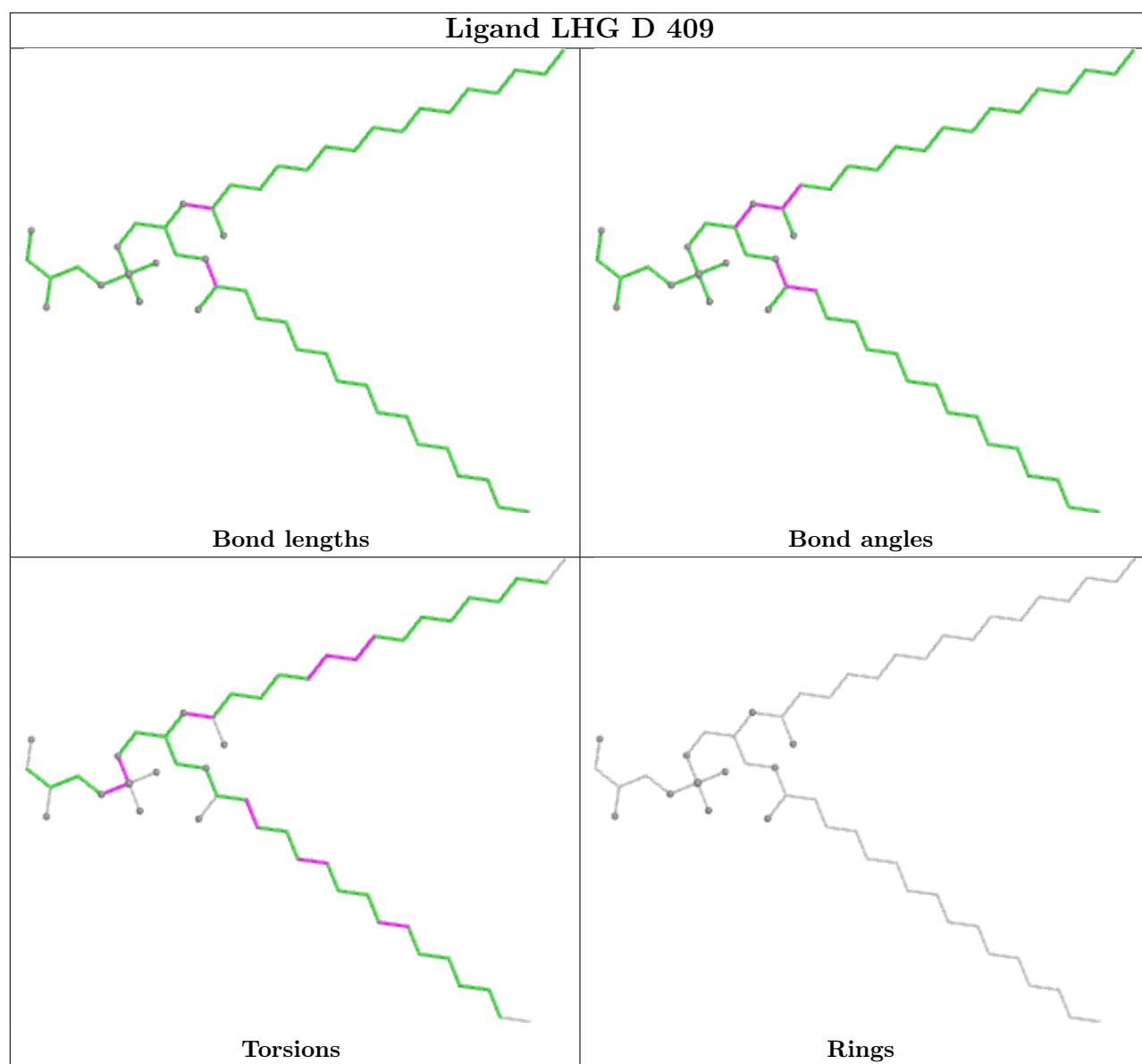
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

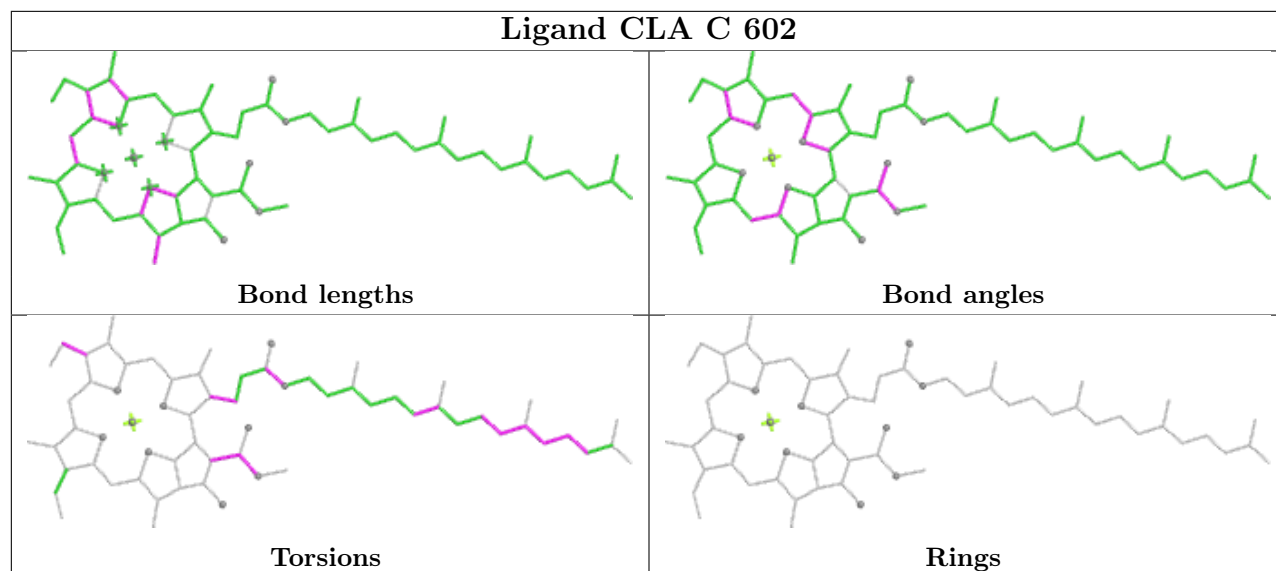
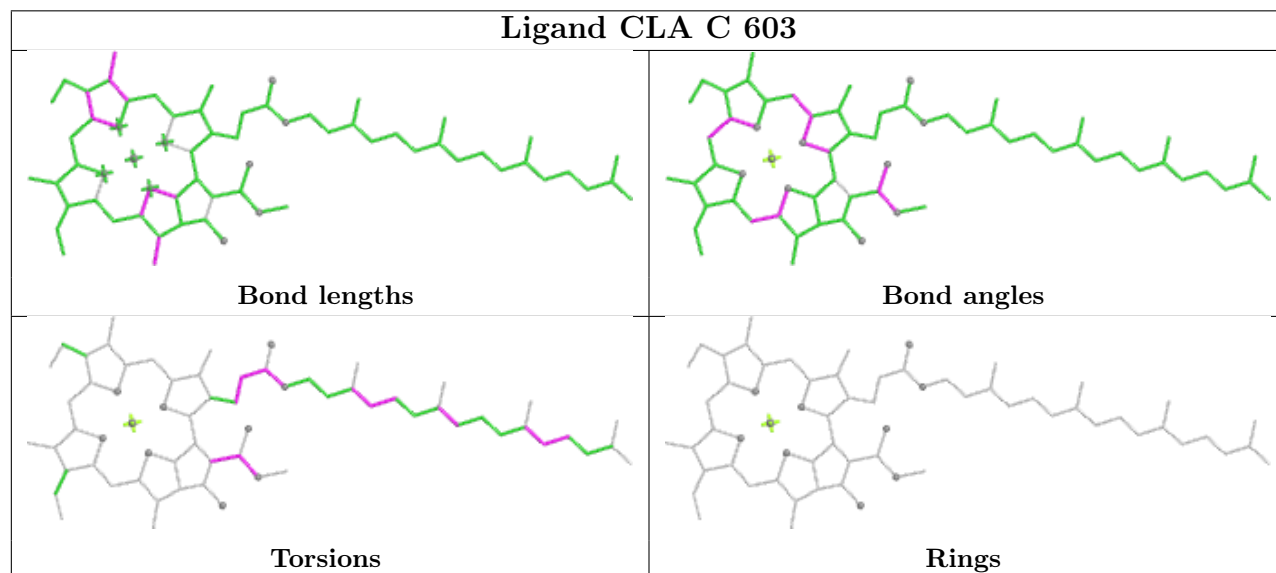
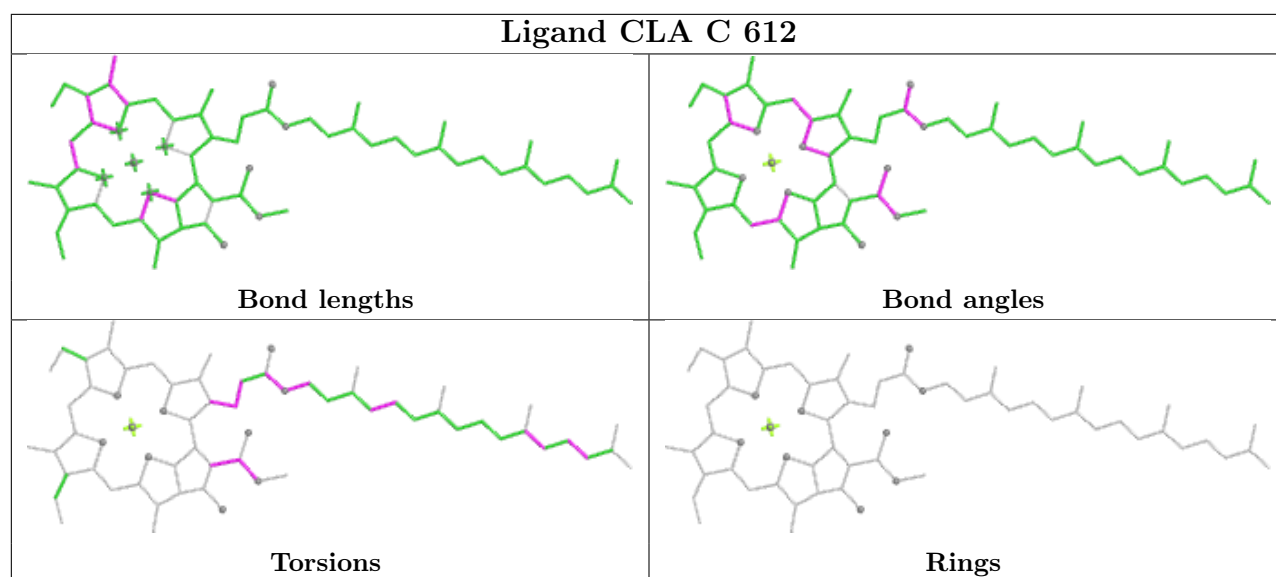


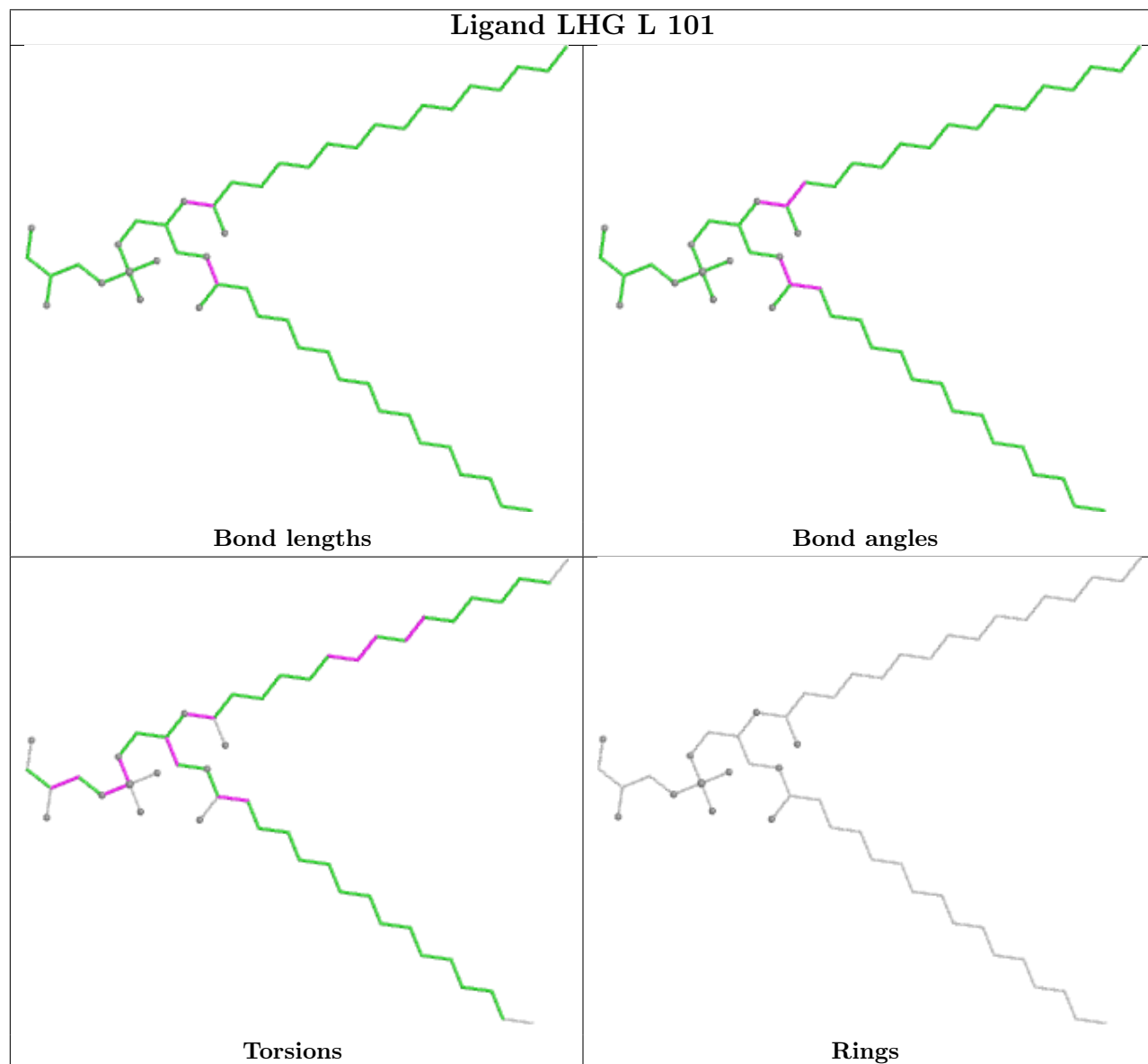
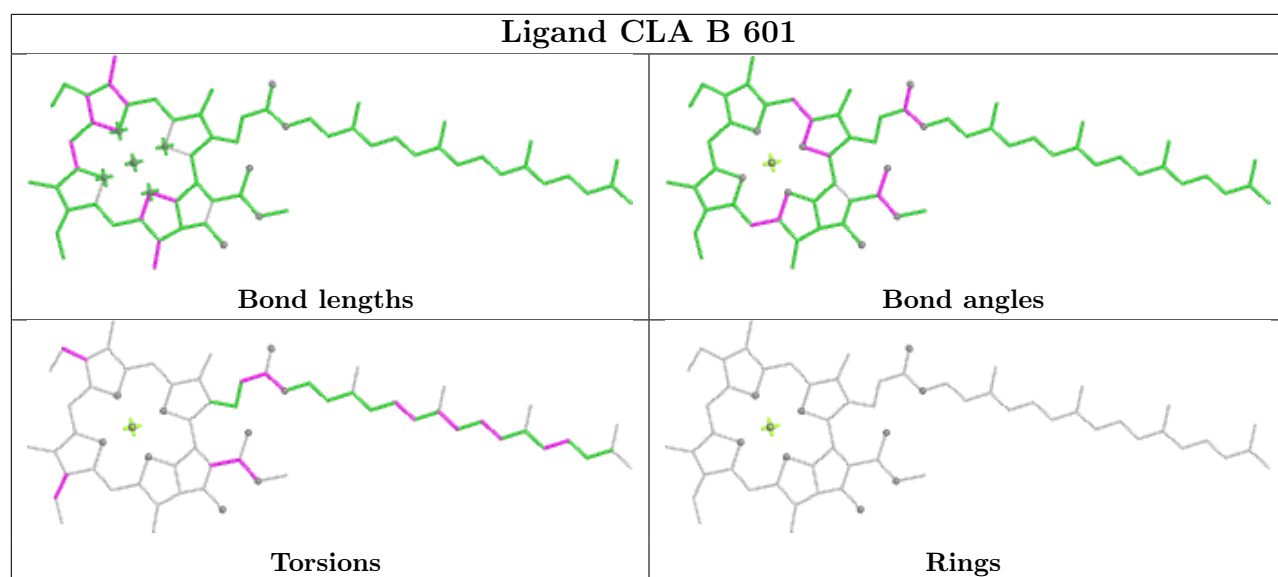


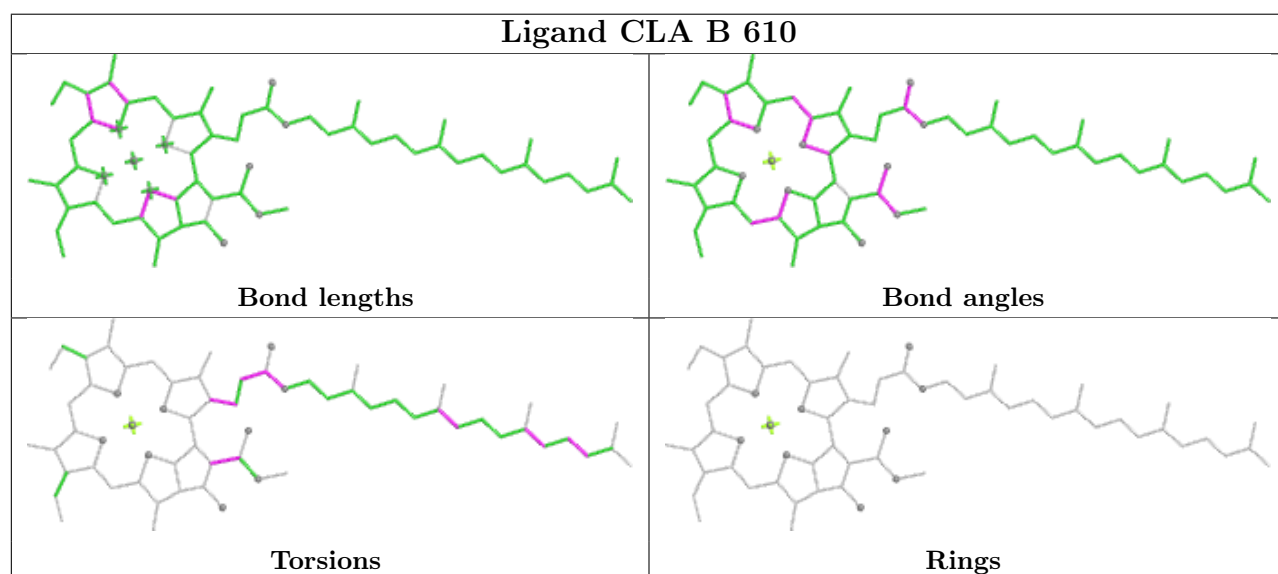
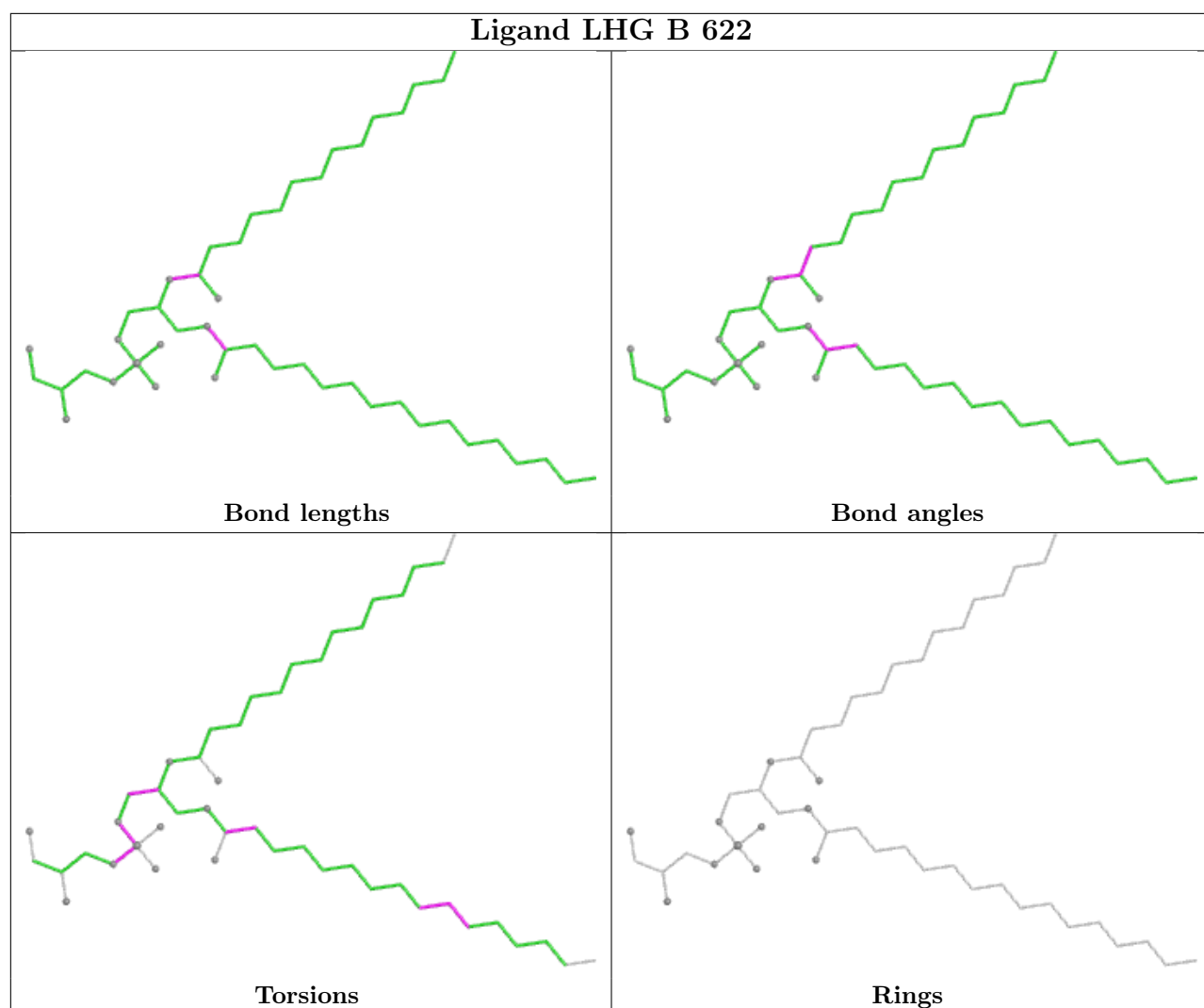


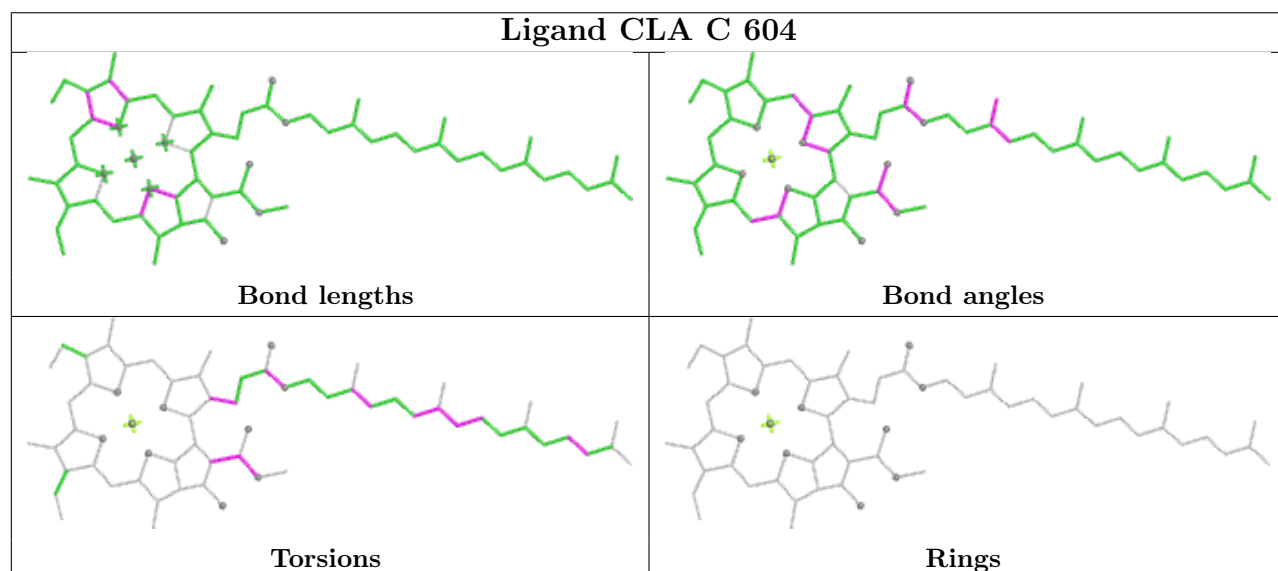
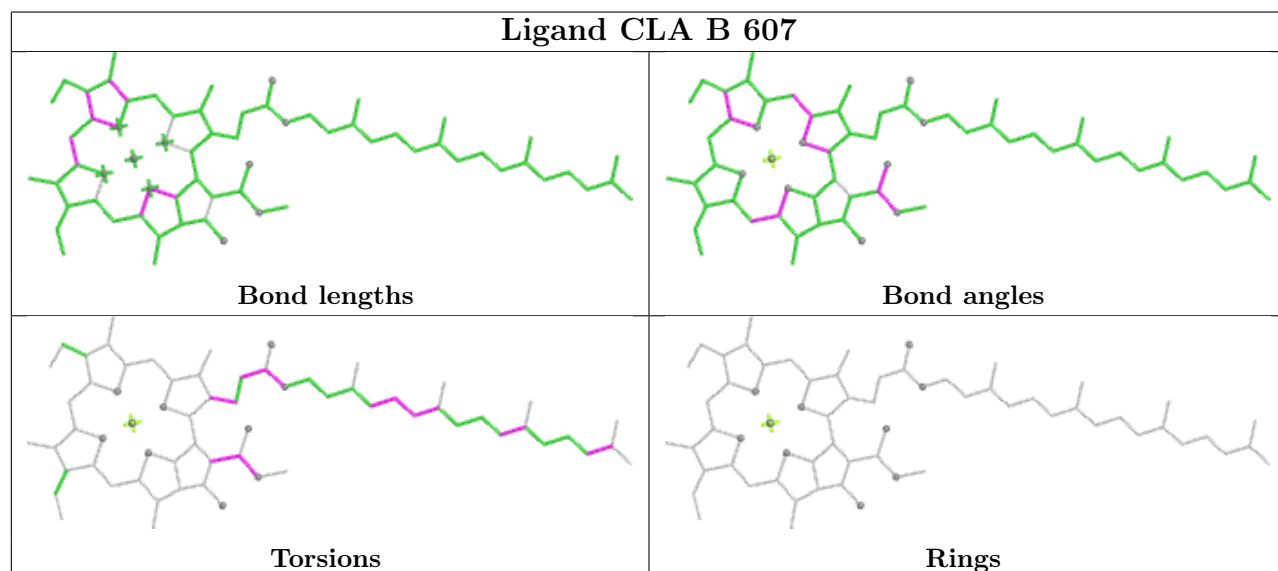
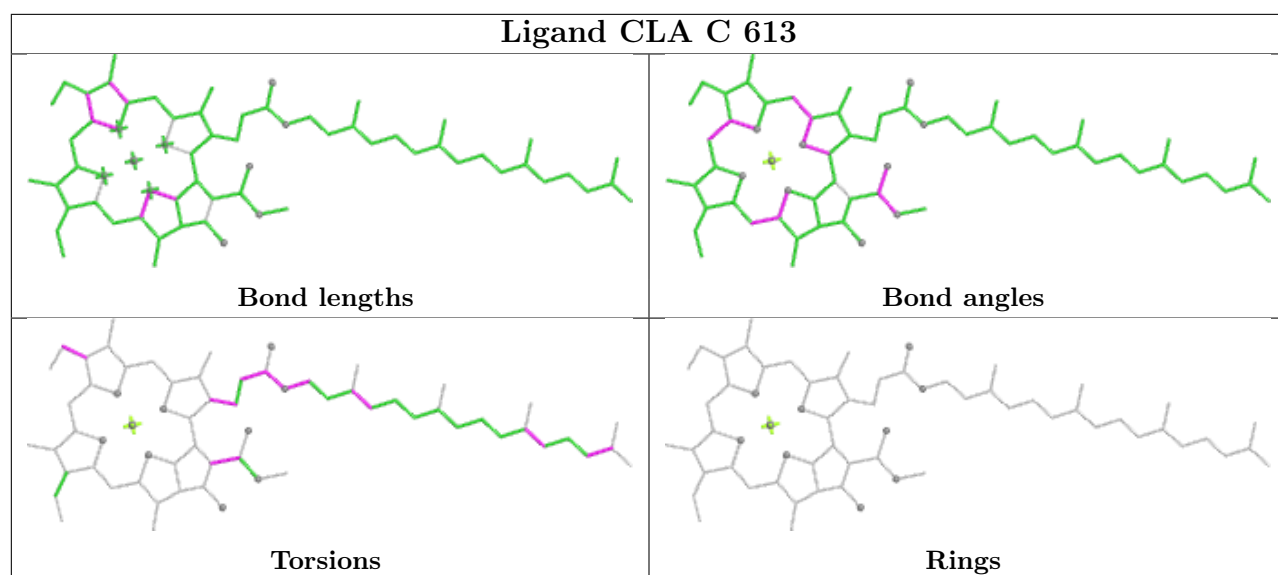


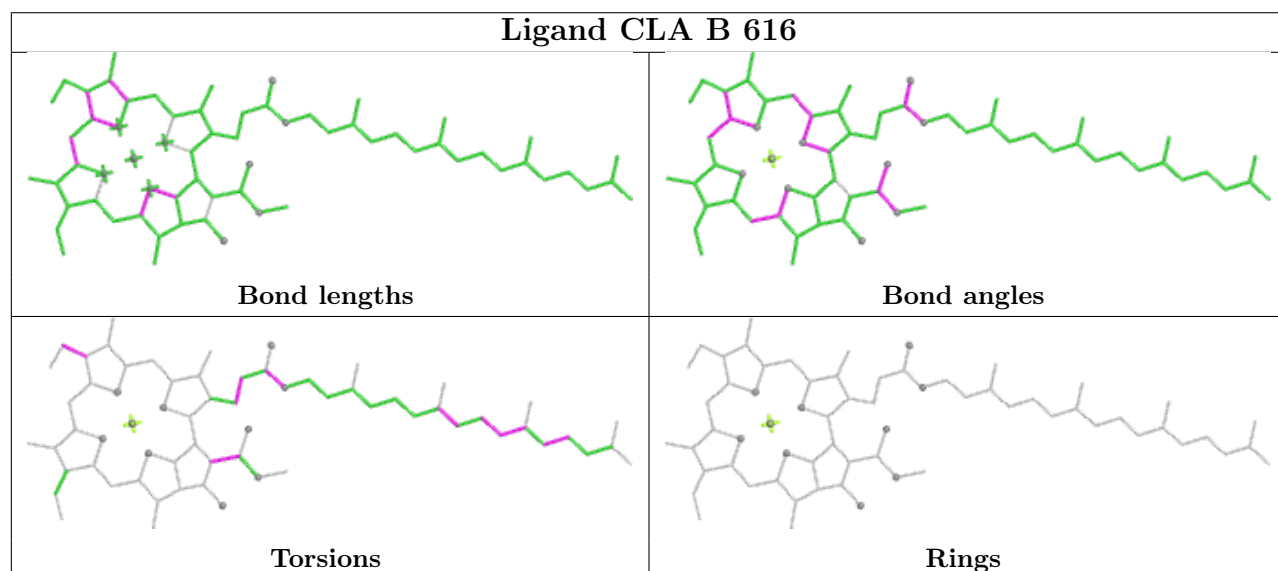
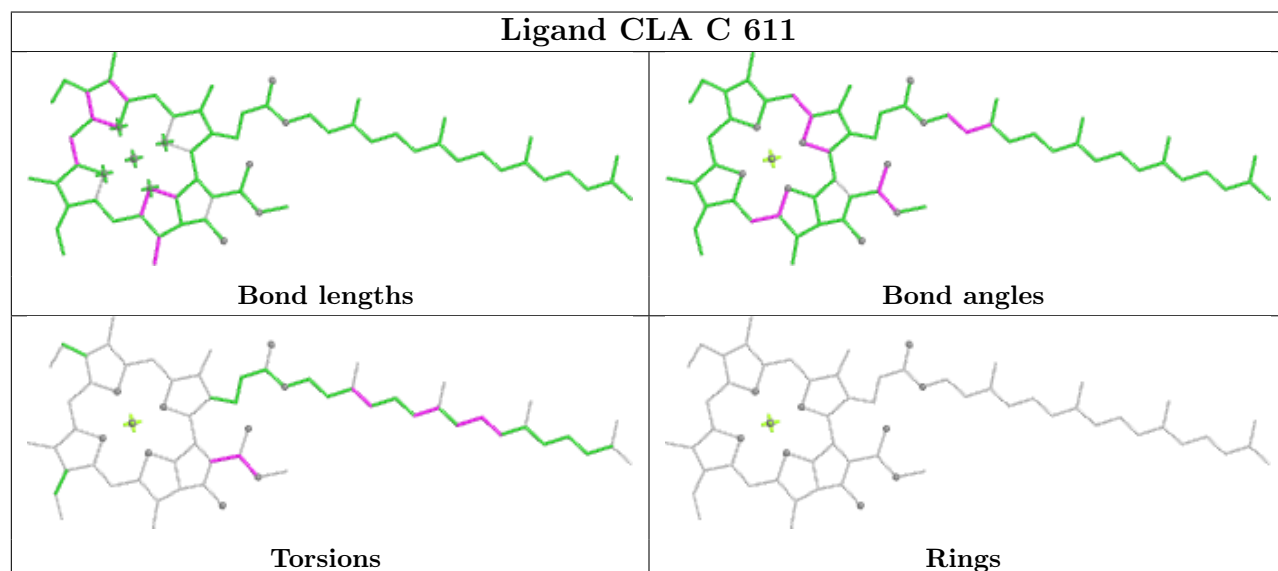
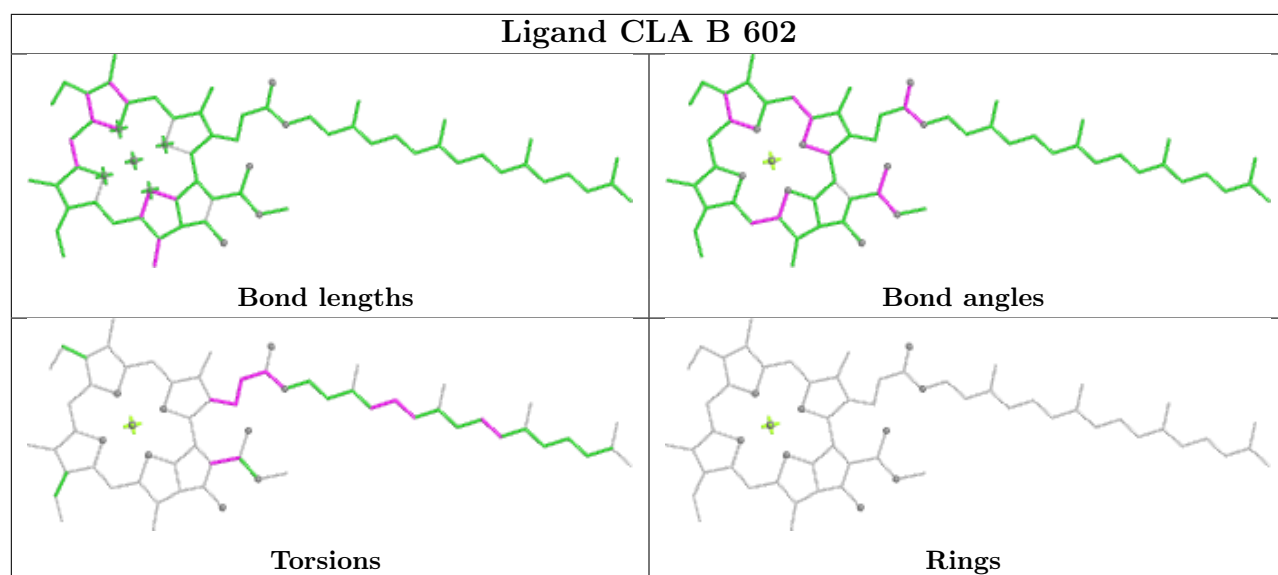


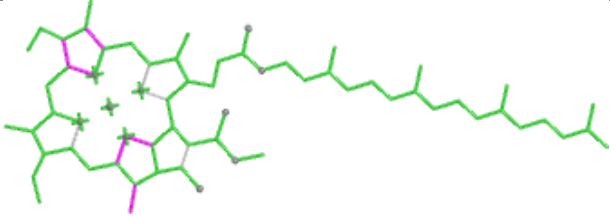
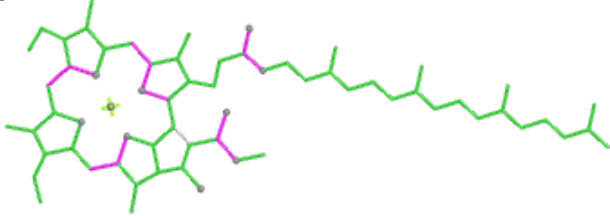
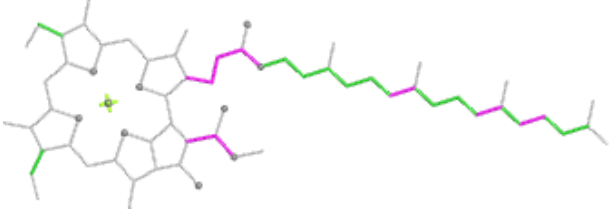
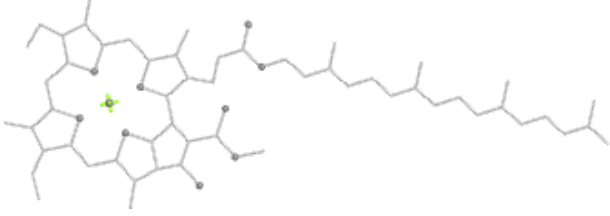
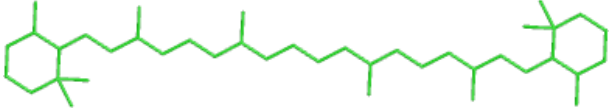
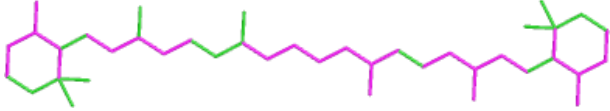
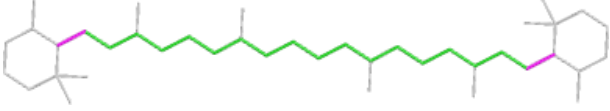
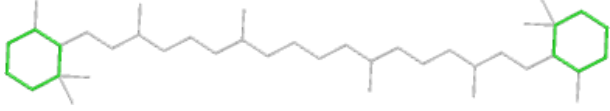
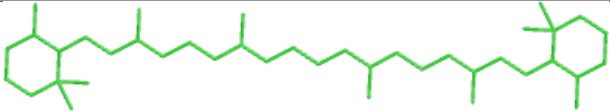
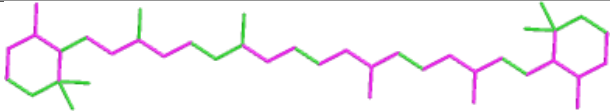
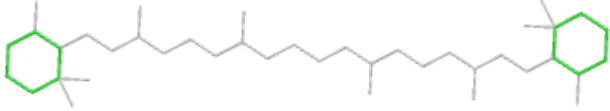


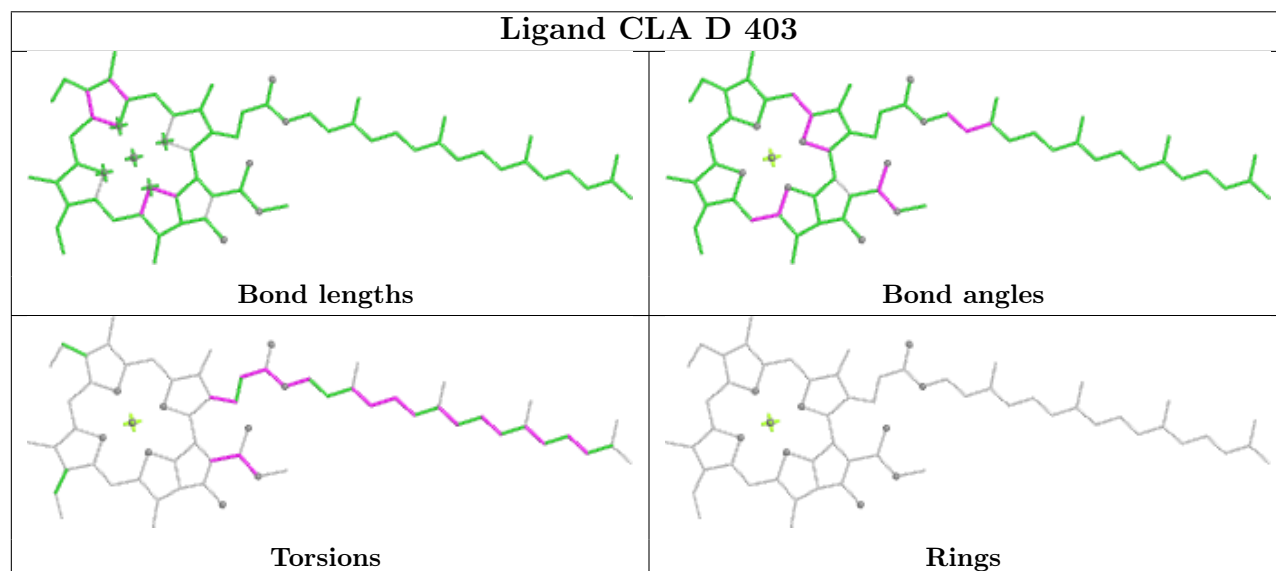
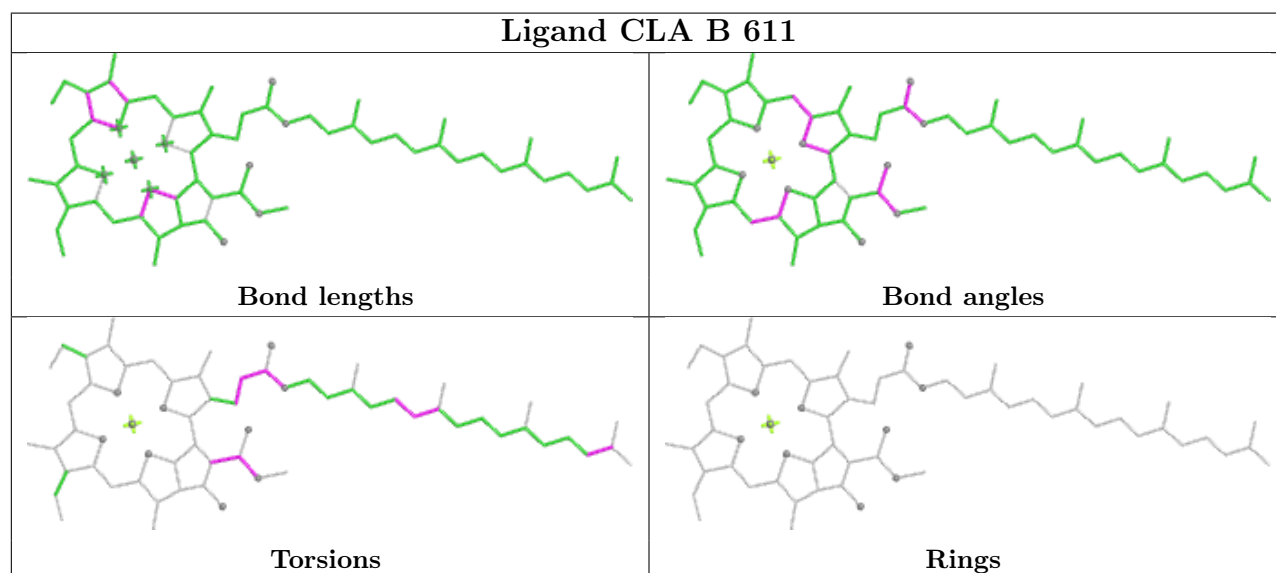
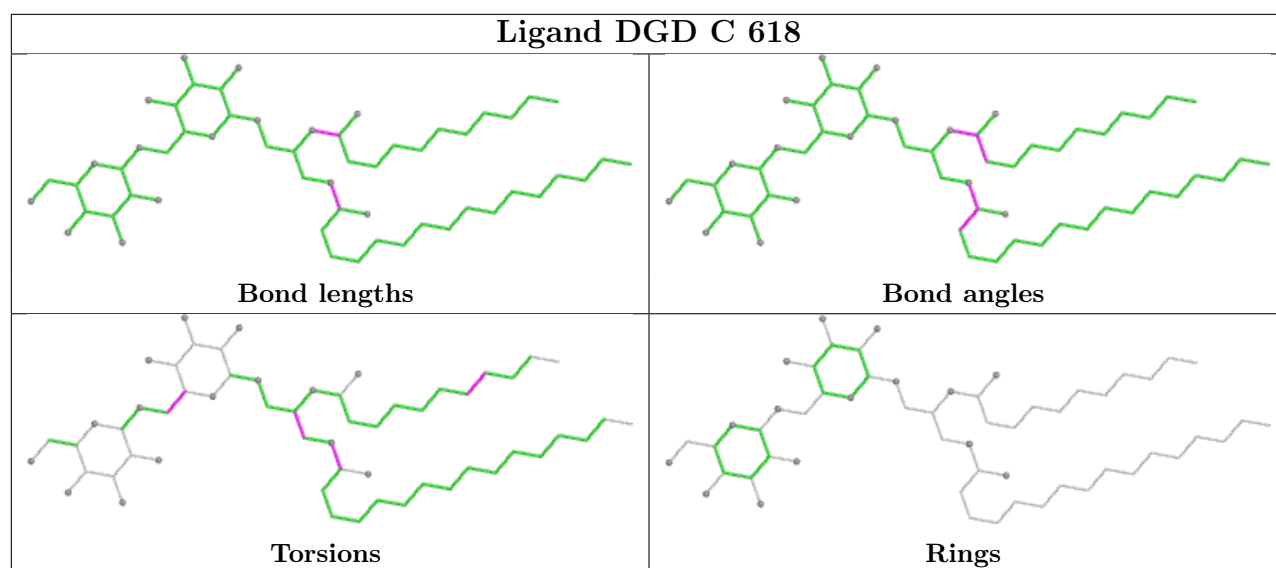


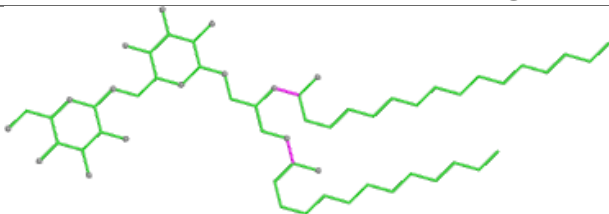
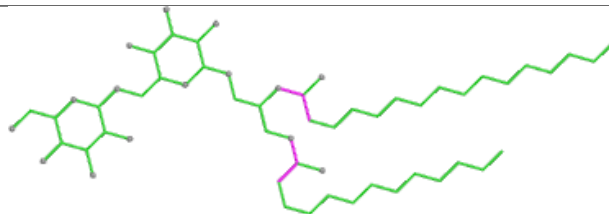
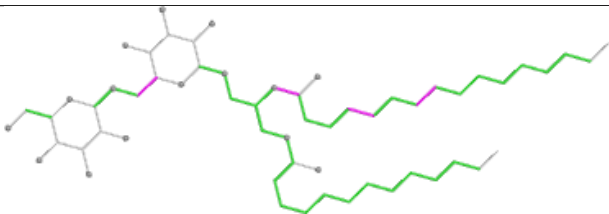
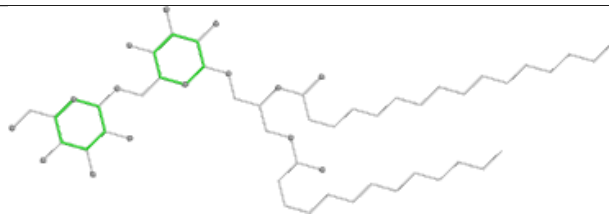


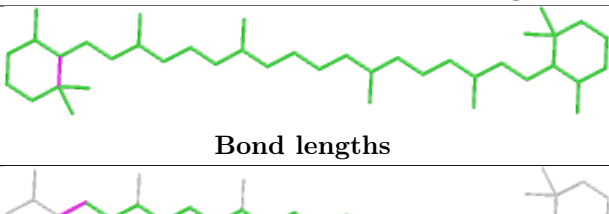
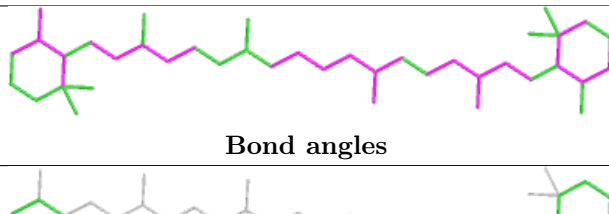
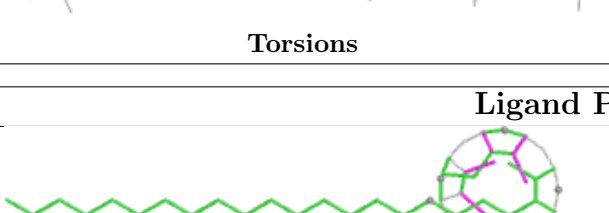


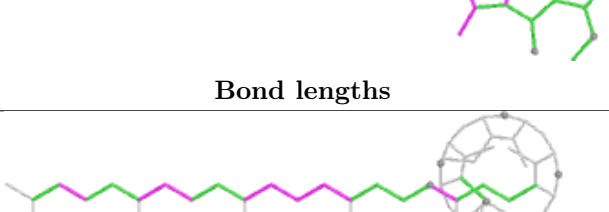
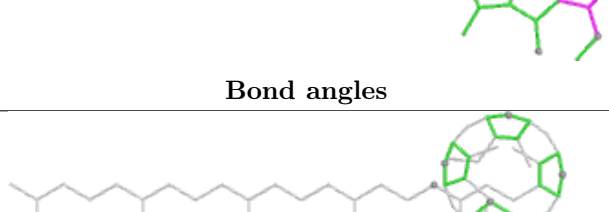


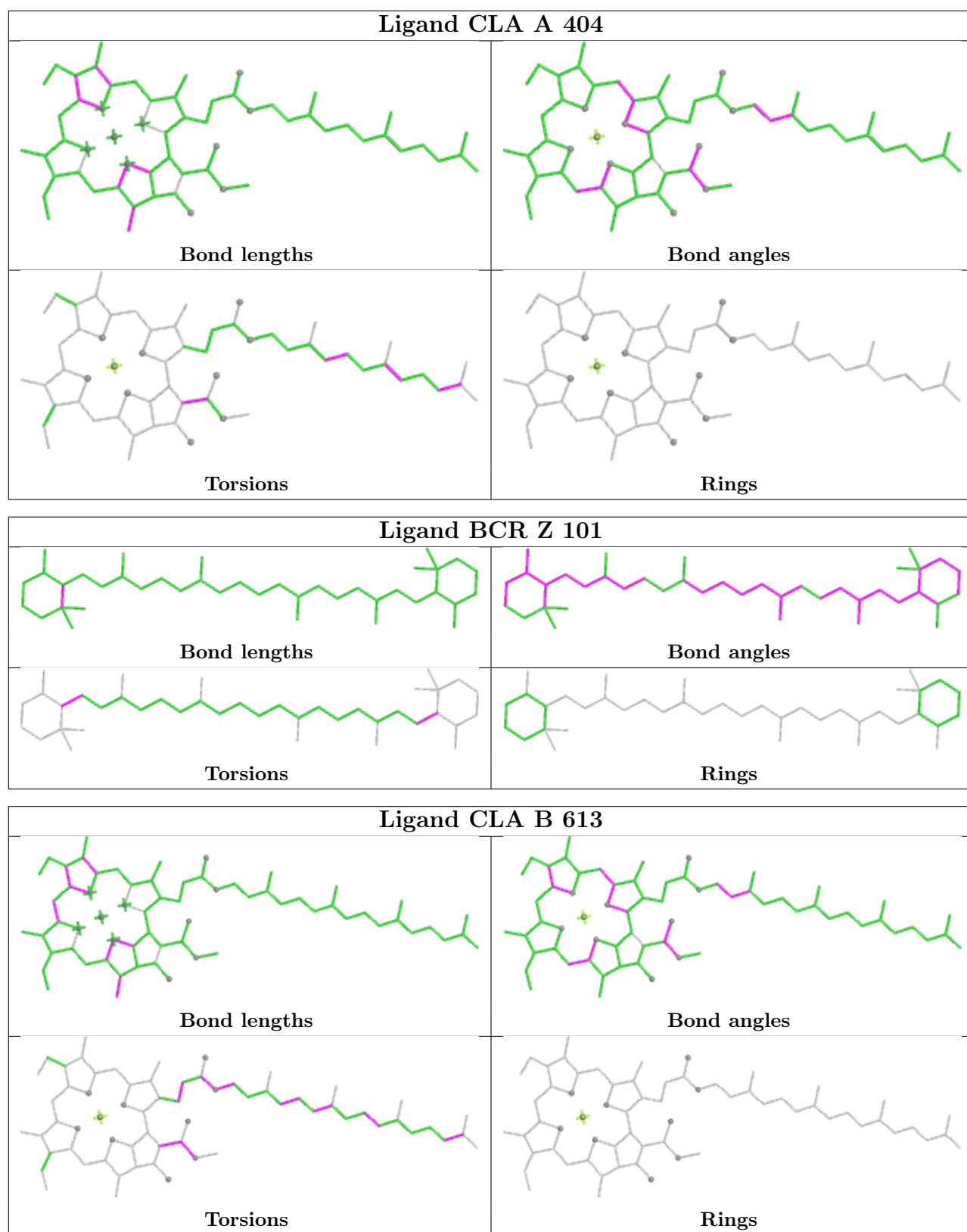
Ligand CLA B 605	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand BCR B 618	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand BCR B 619	
 Bond lengths	 Bond angles
 Torsions	 Rings

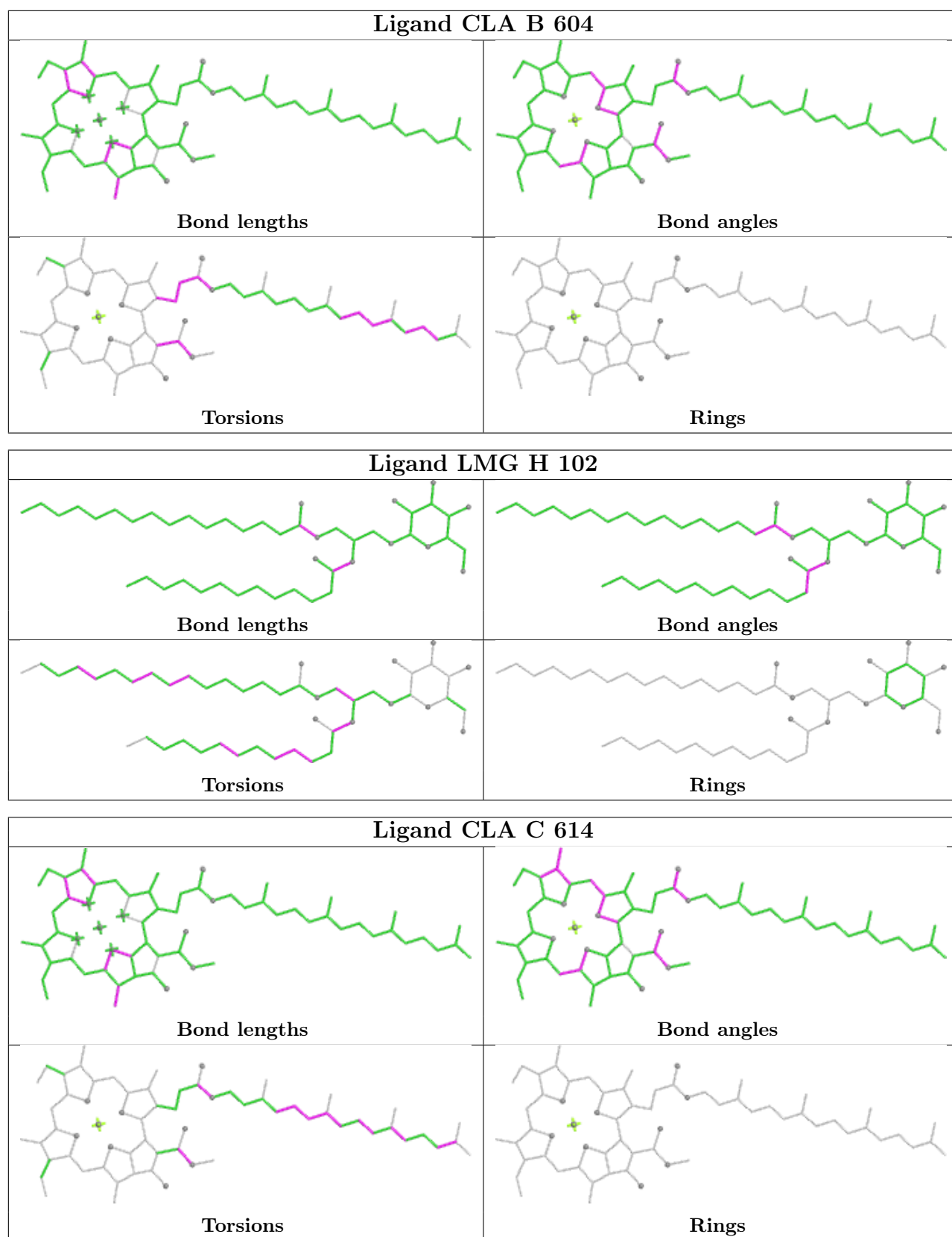


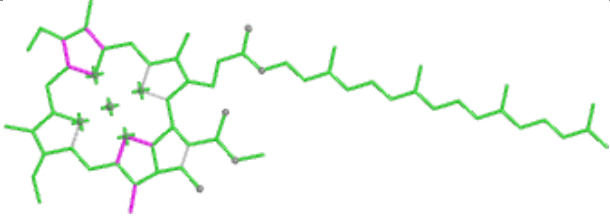
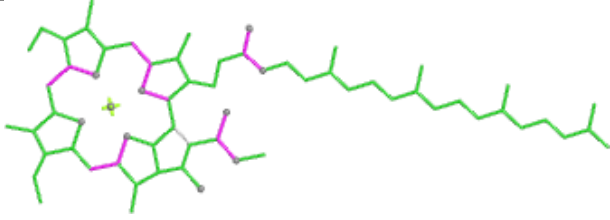
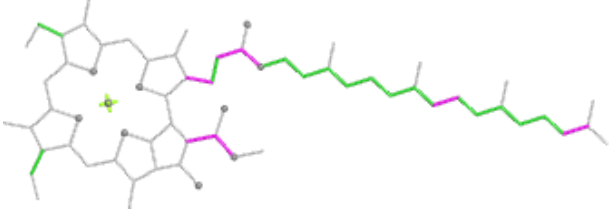
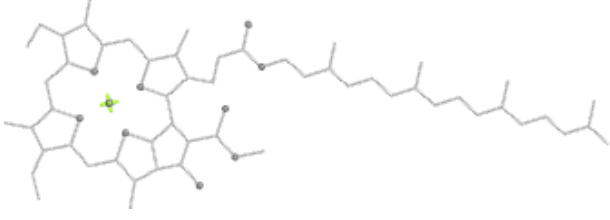
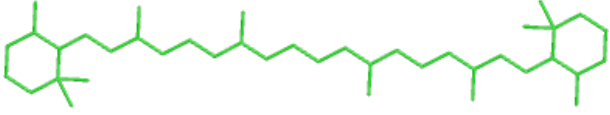
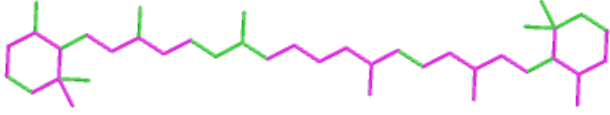
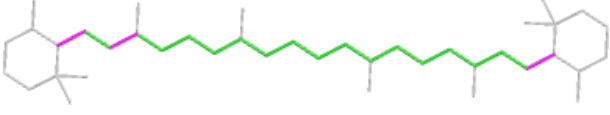
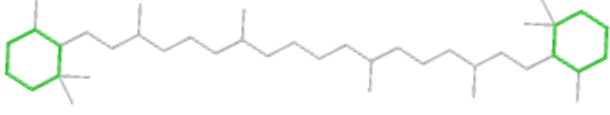
Ligand DGD C 619	
	
Bond lengths	Bond angles
	
Torsions	Rings

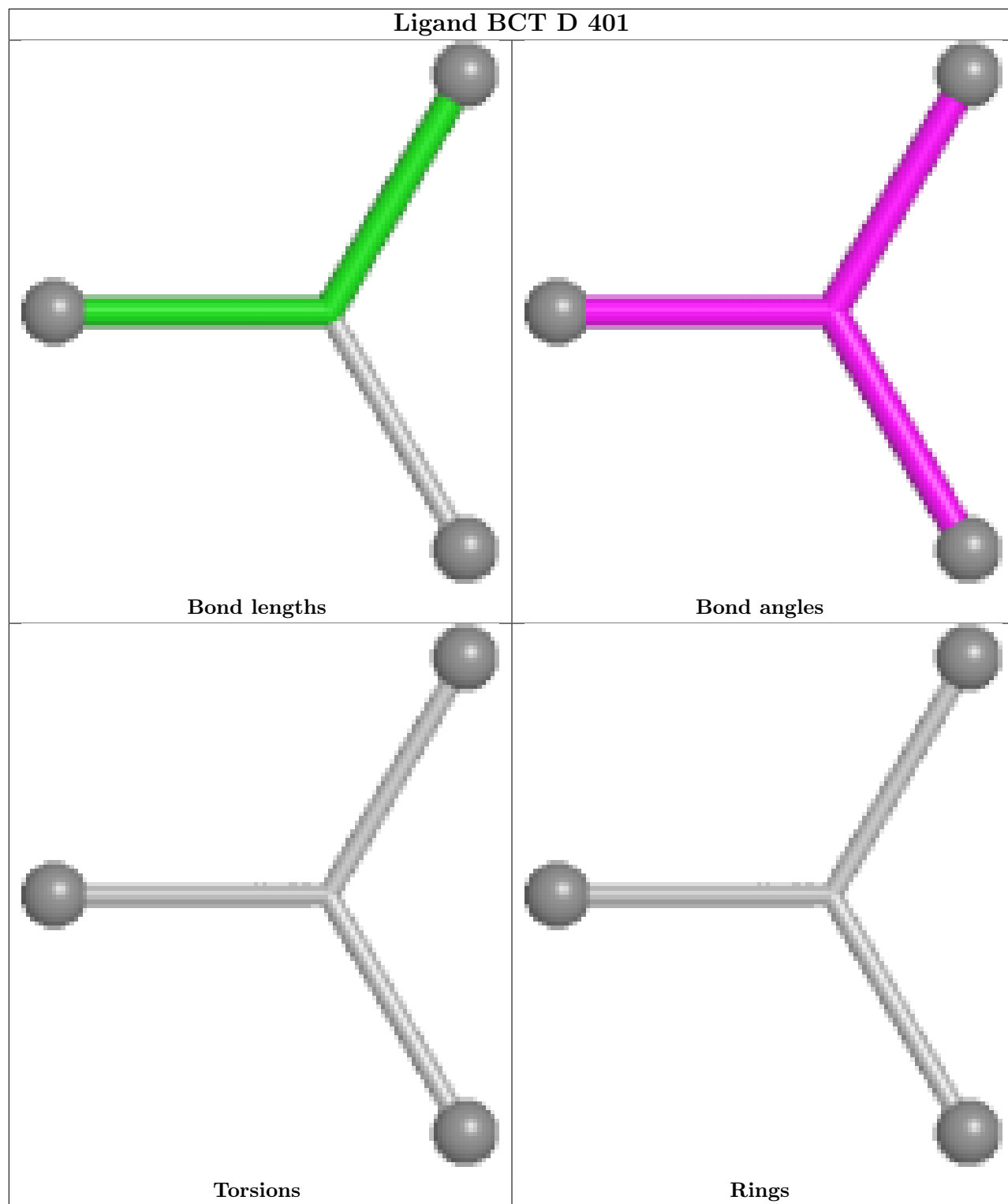
Ligand BCR C 616	
	
Bond lengths	Bond angles
	
Torsions	Rings

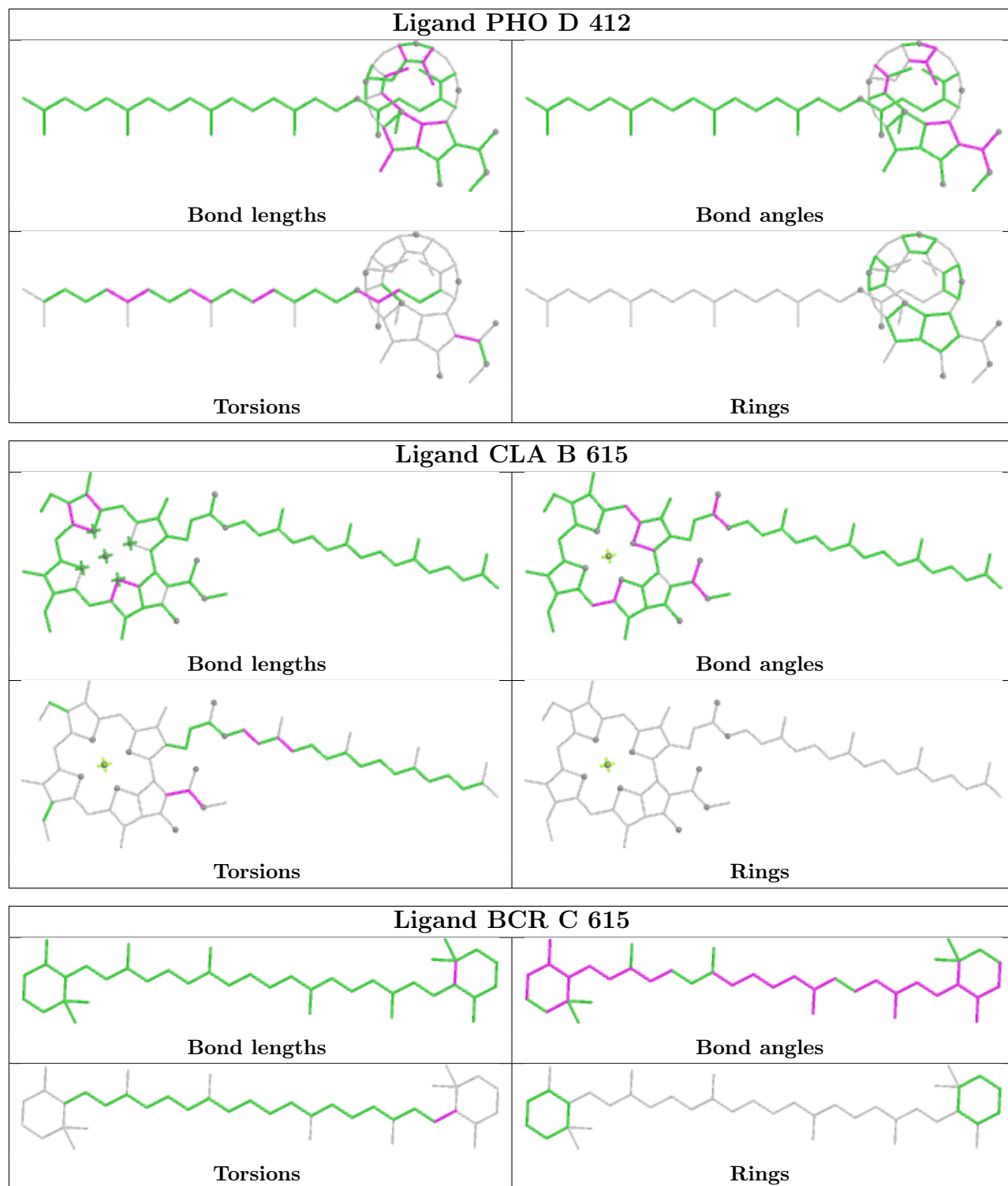
Ligand PHO D 411	
	
Bond lengths	Bond angles
	
Torsions	Rings



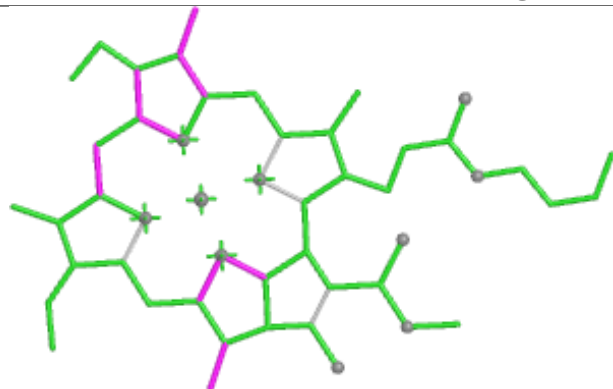


Ligand CLA B 609	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand BCR H 101	
 Bond lengths	 Bond angles
 Torsions	 Rings

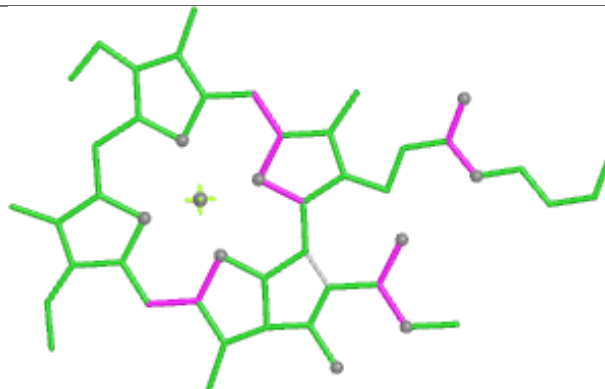




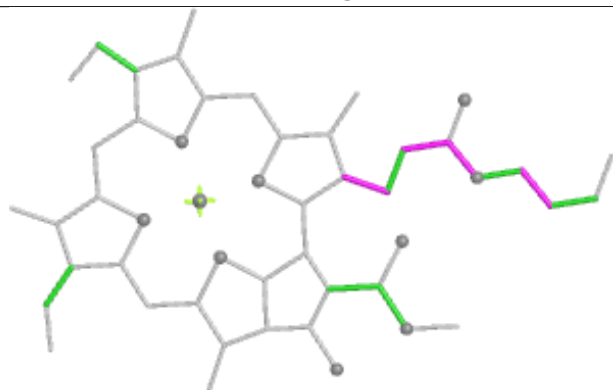
Ligand CLA A 403



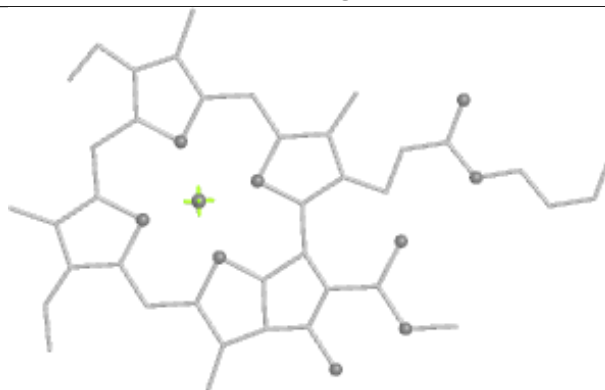
Bond lengths



Bond angles

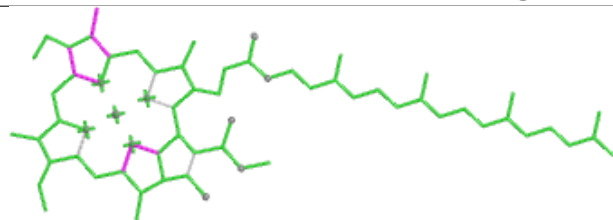


Torsions

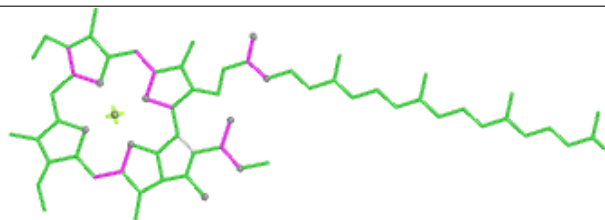


Rings

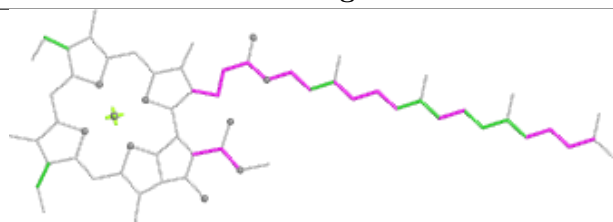
Ligand CLA C 607



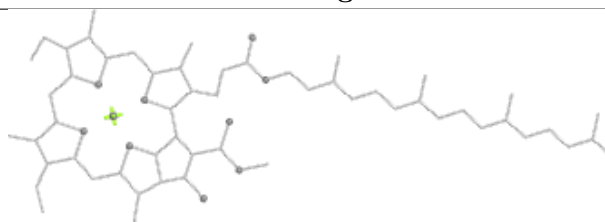
Bond lengths



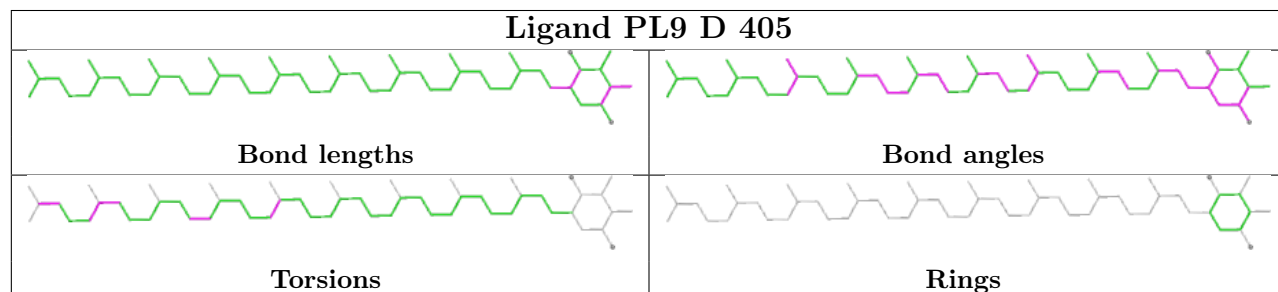
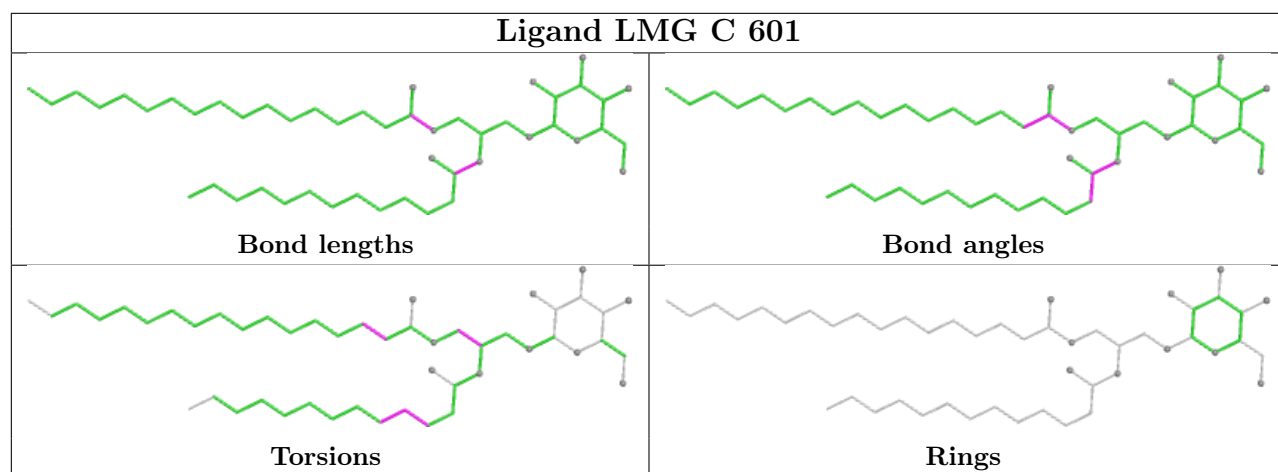
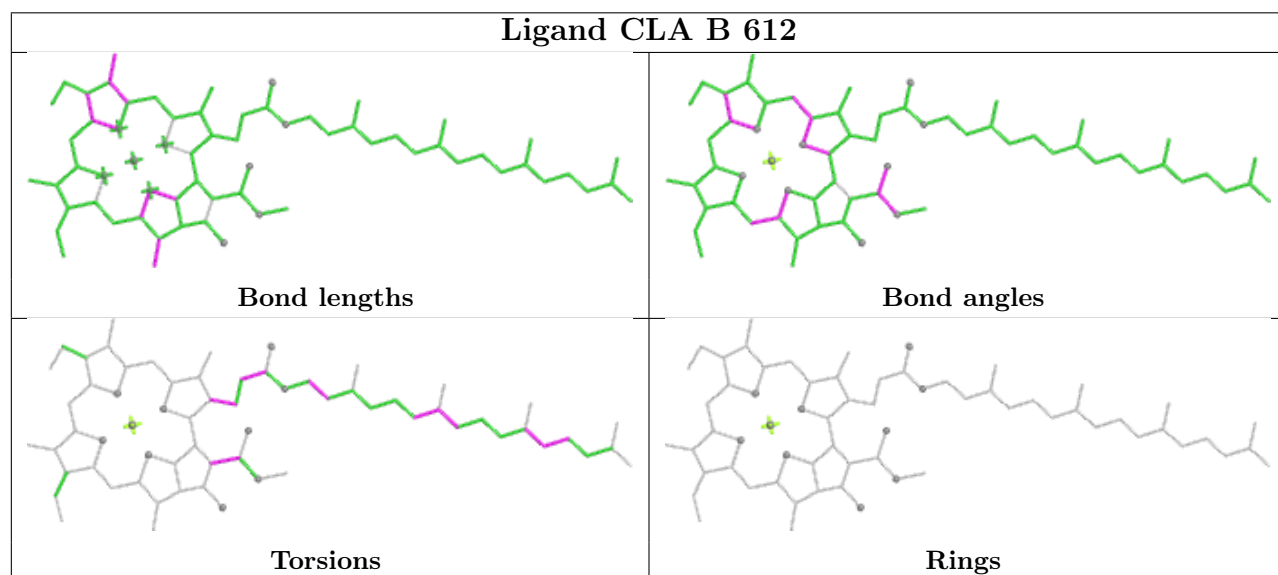
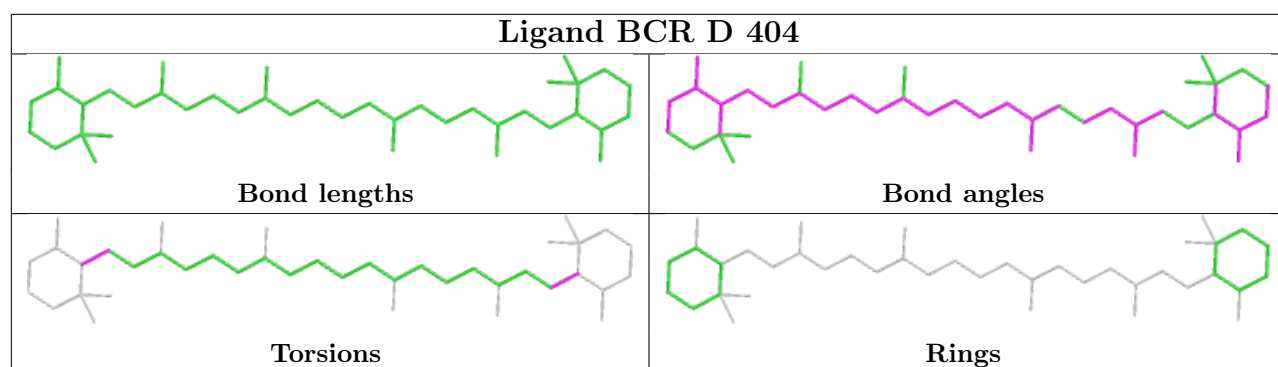
Bond angles

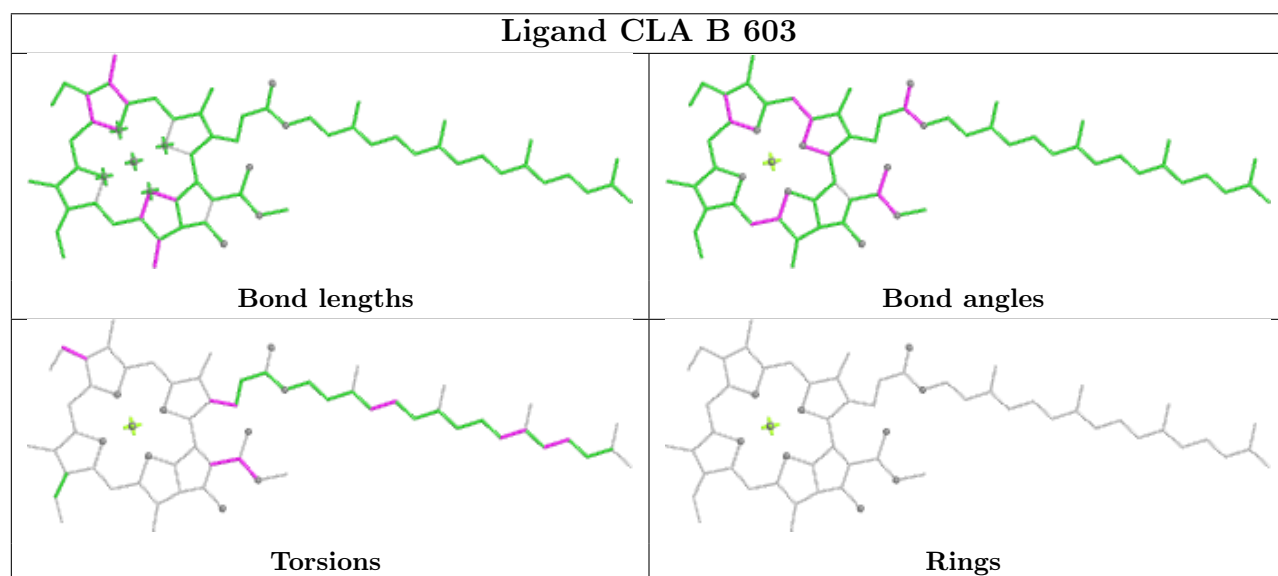
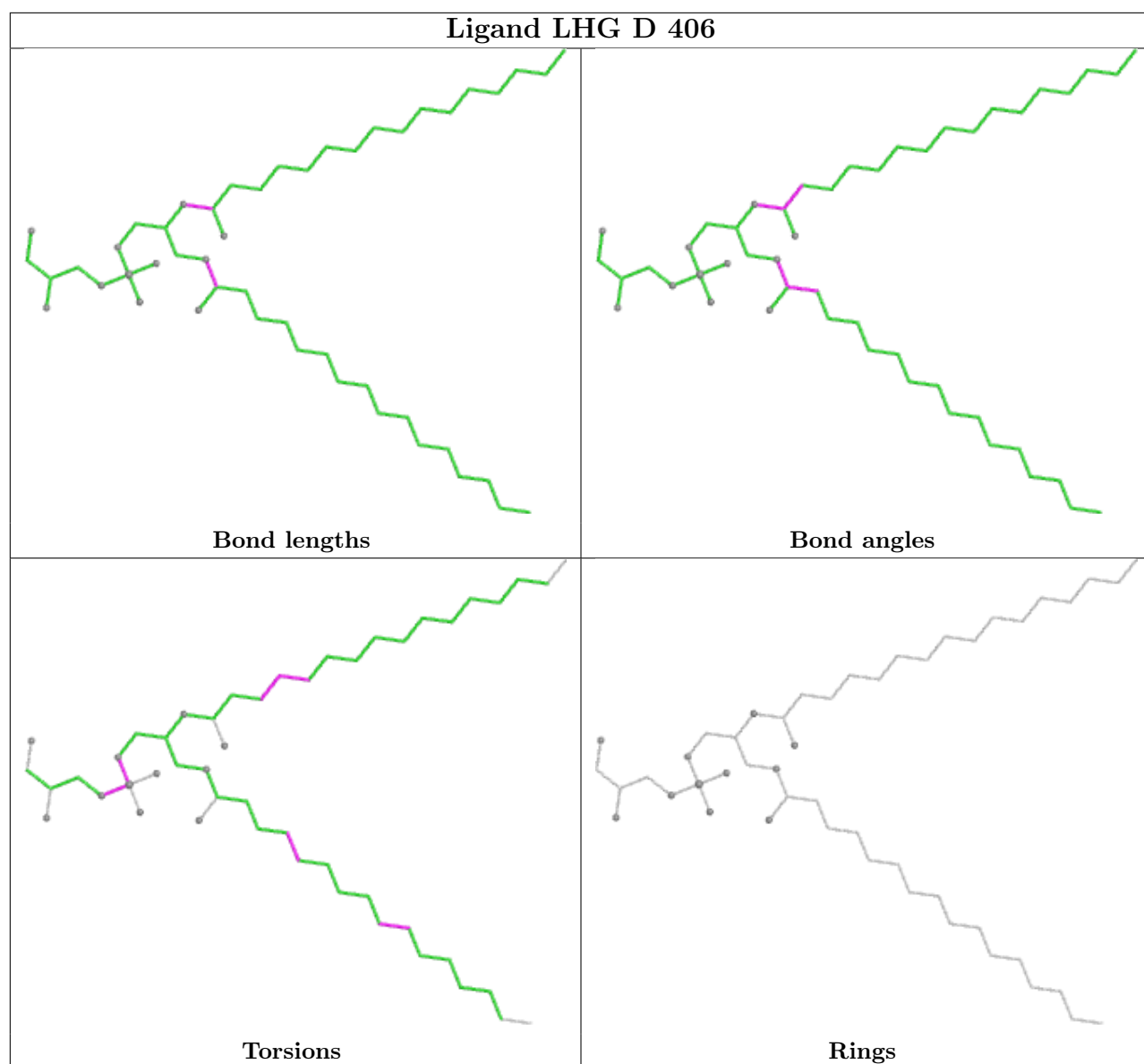


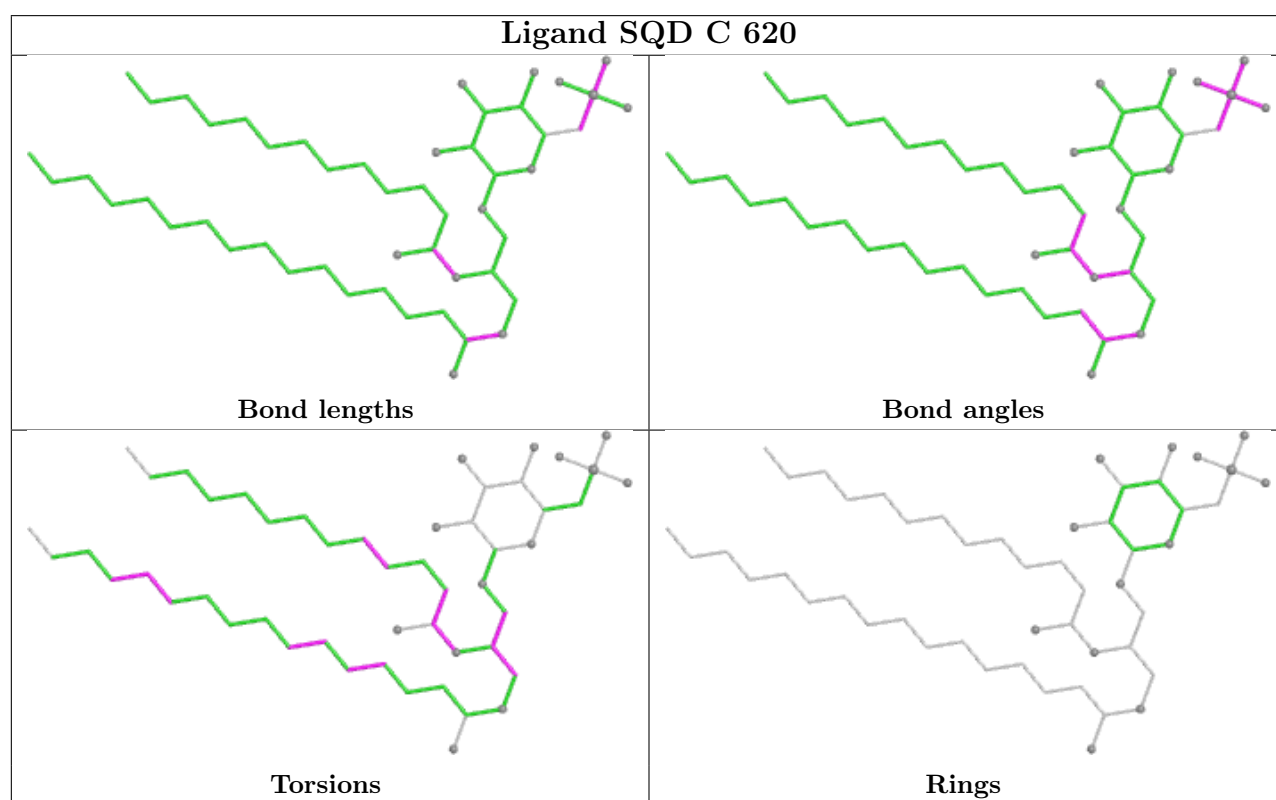
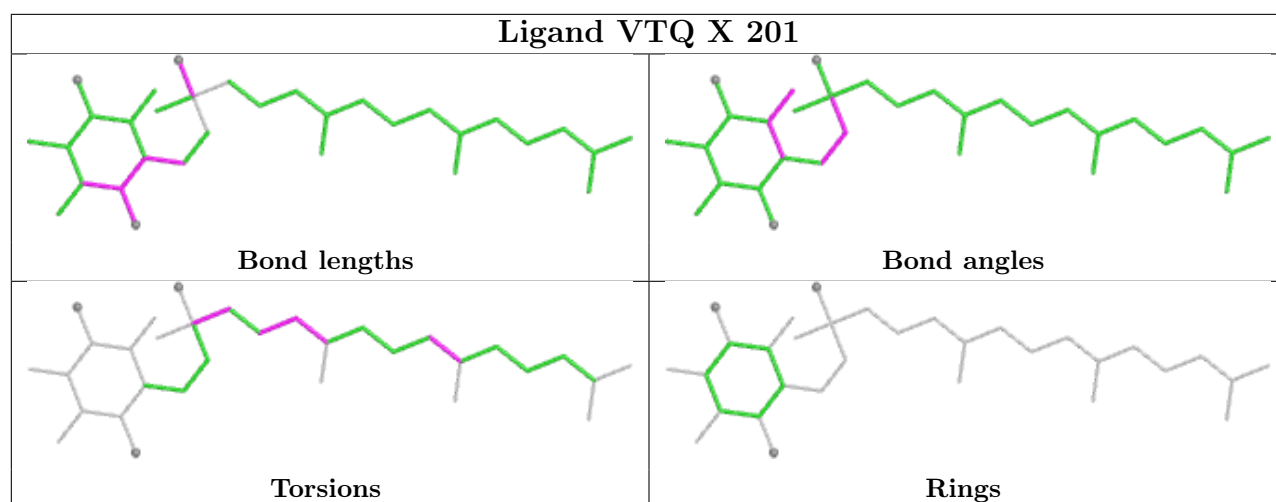
Torsions

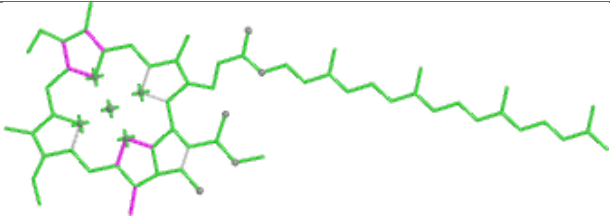
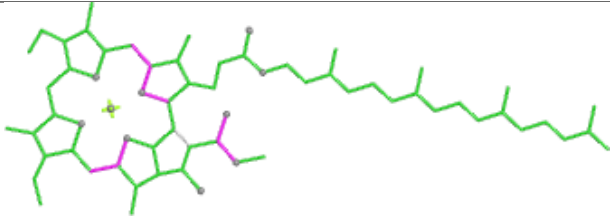
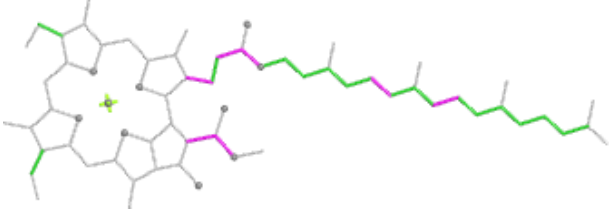
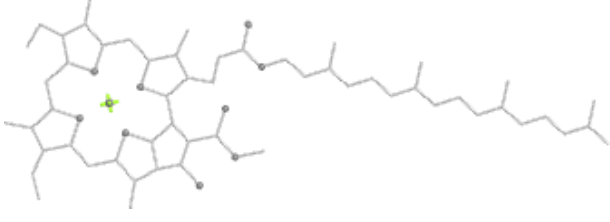
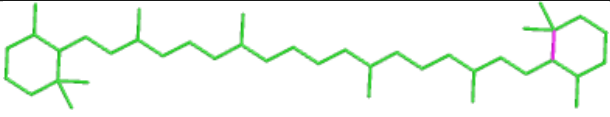
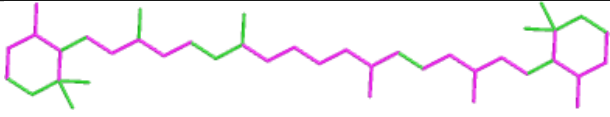
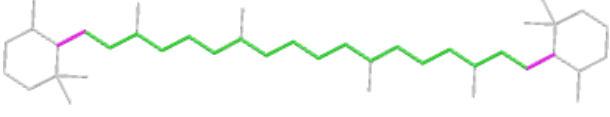
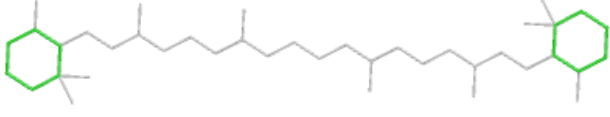


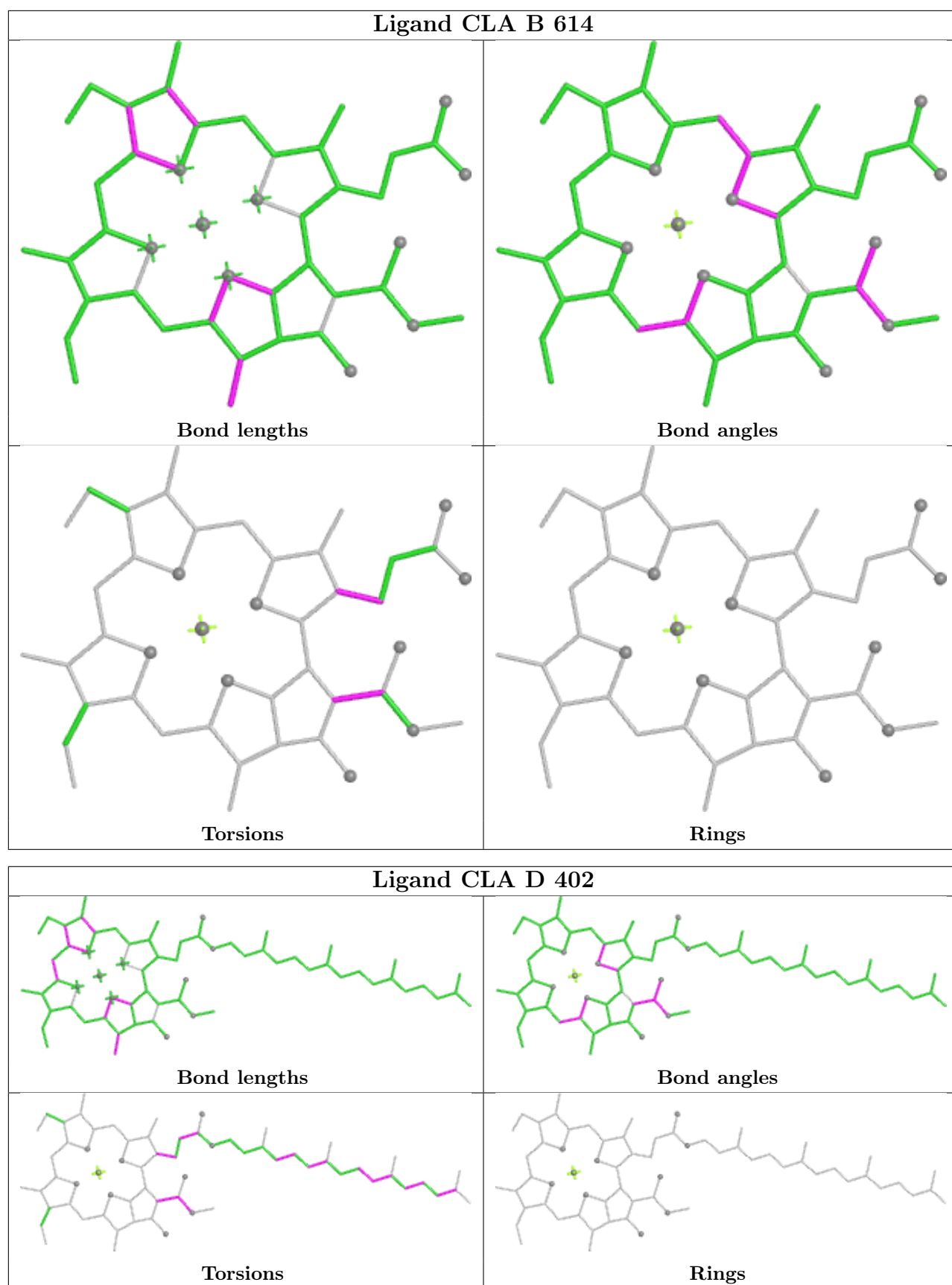
Rings

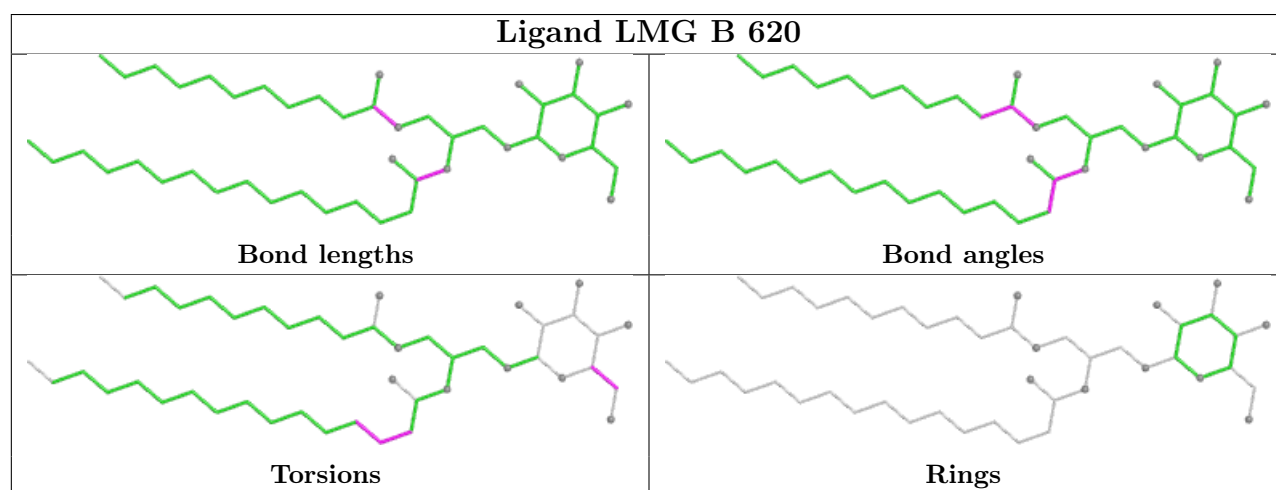
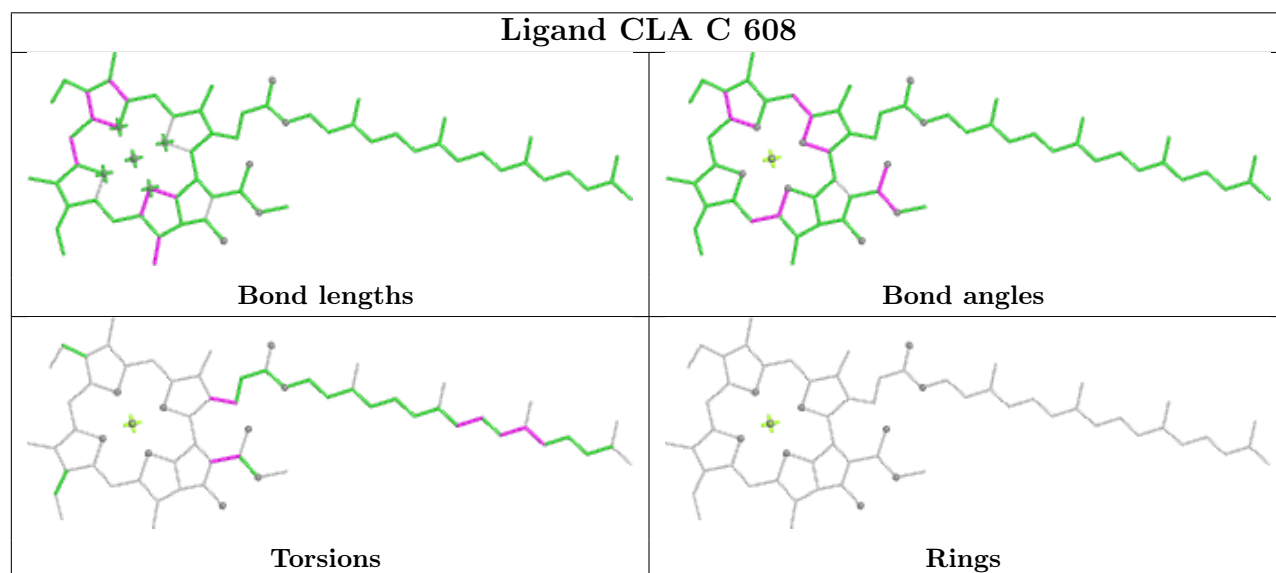
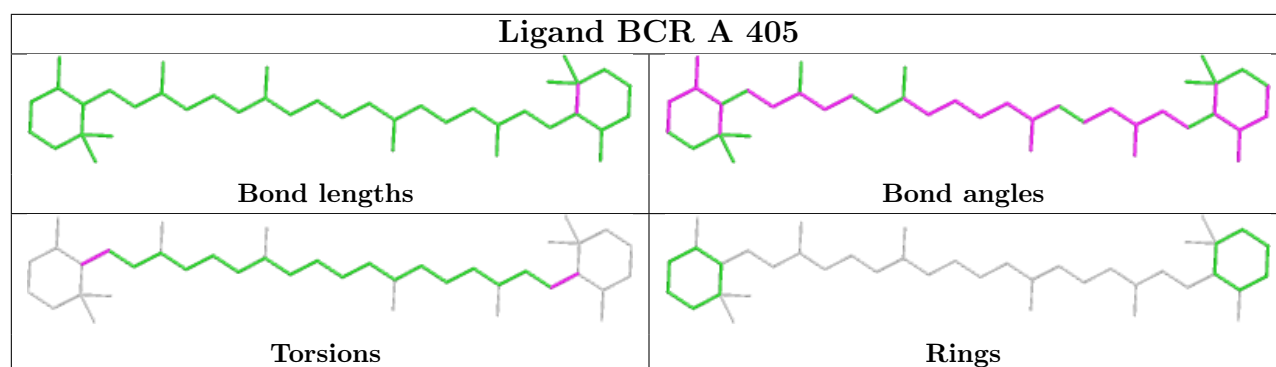


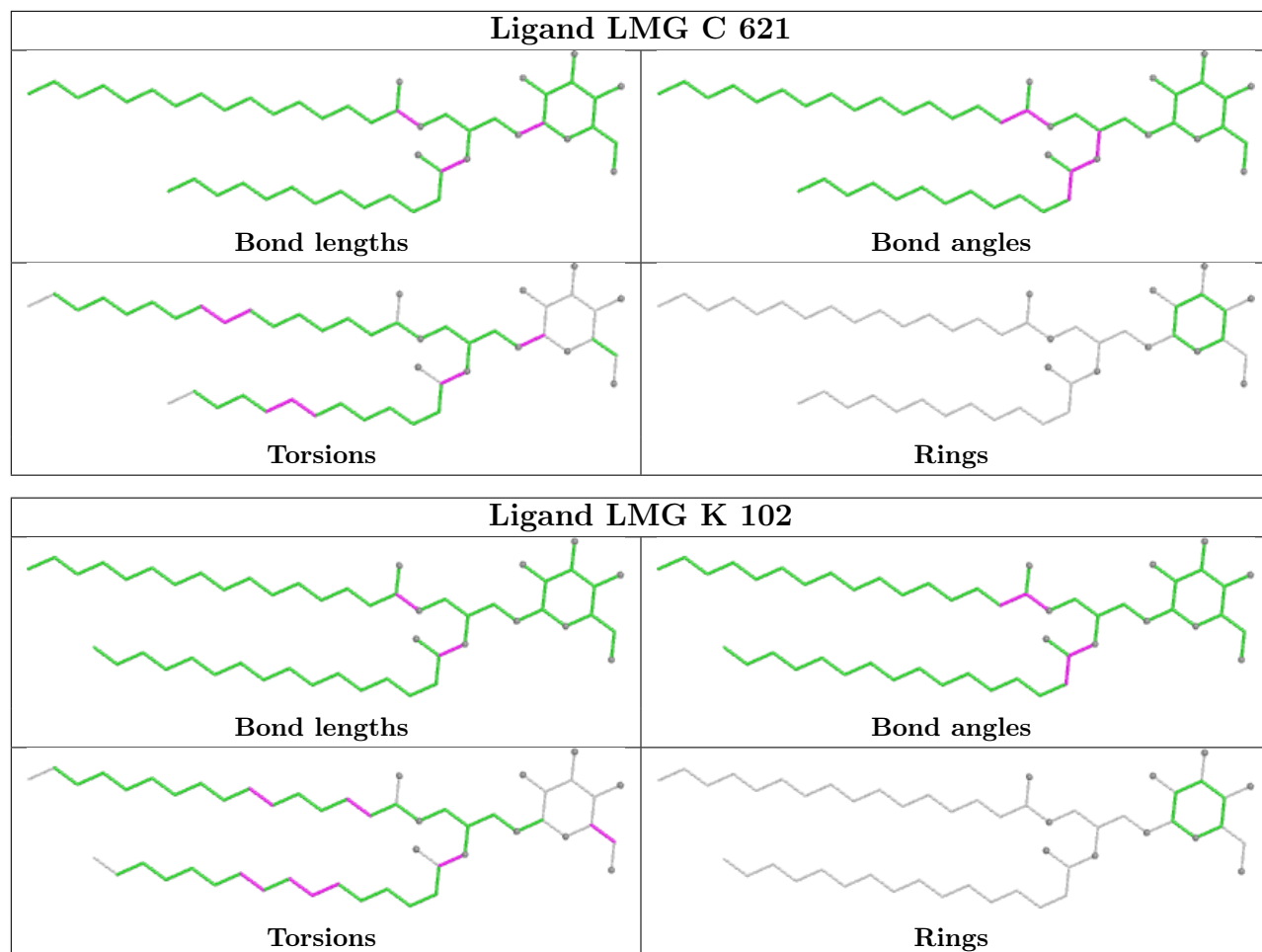


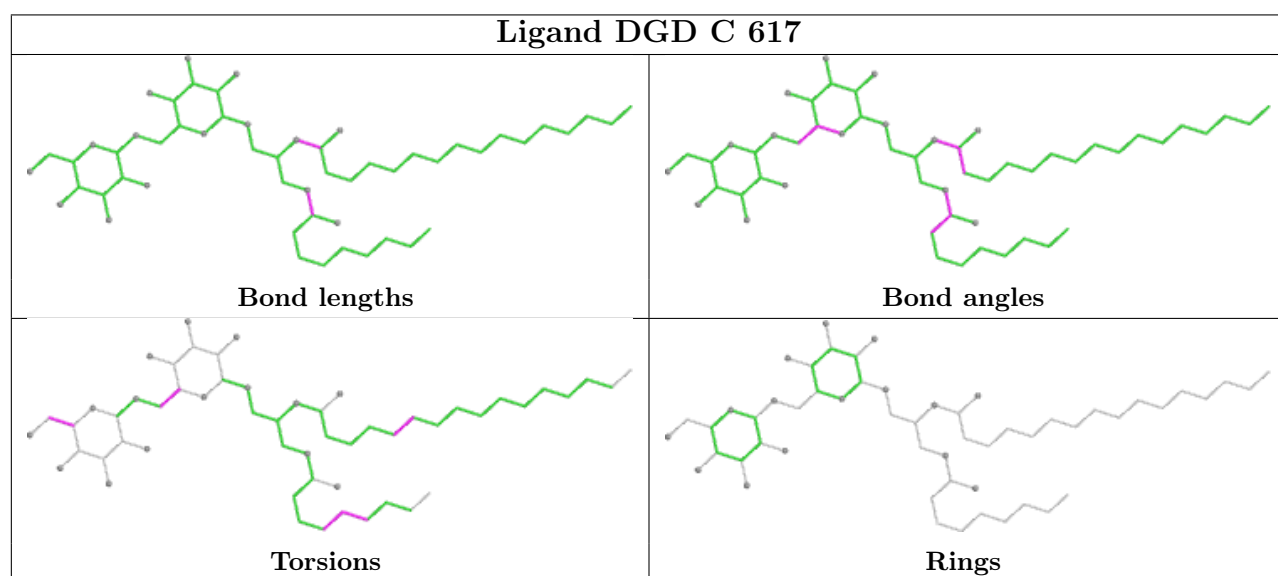
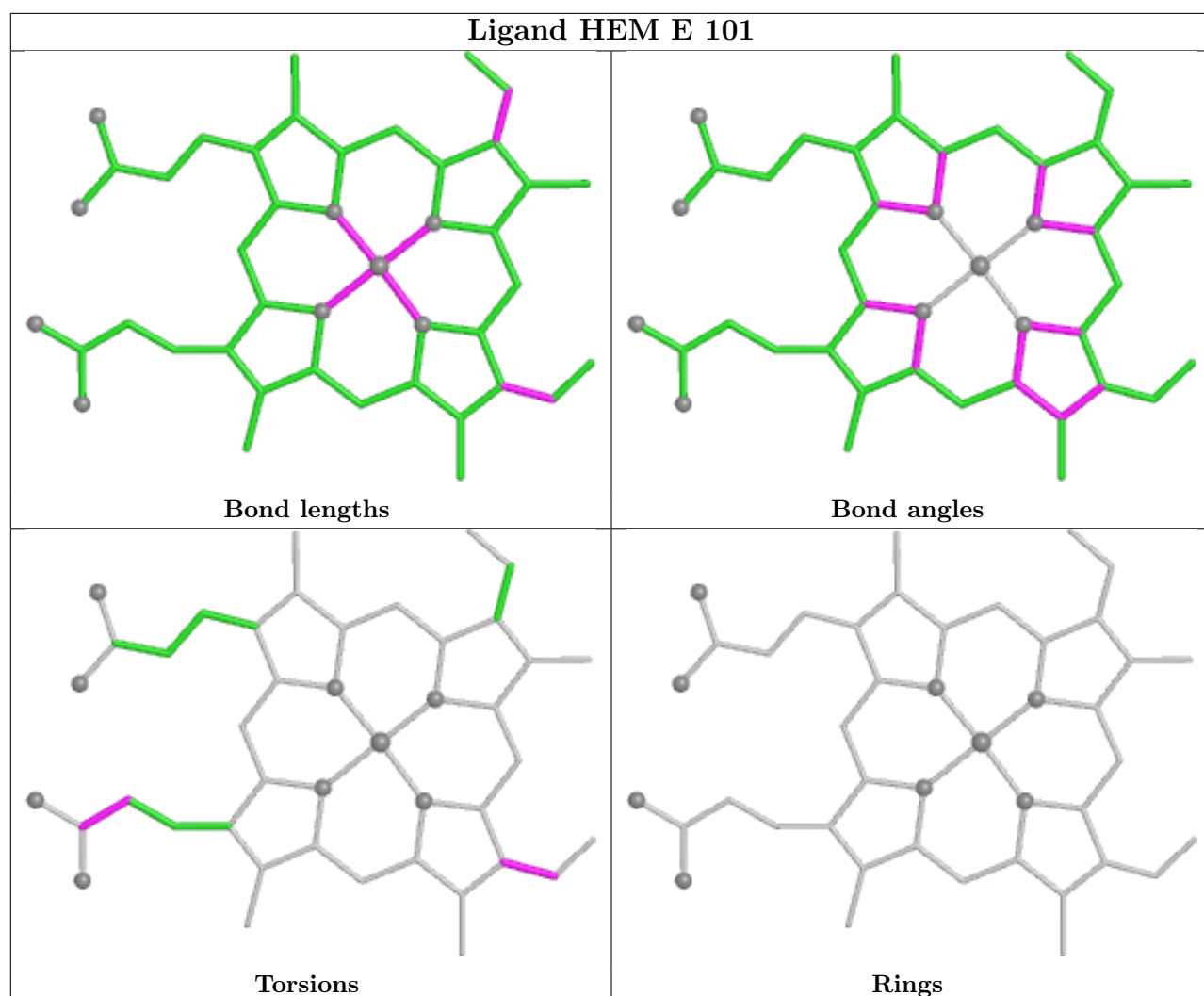


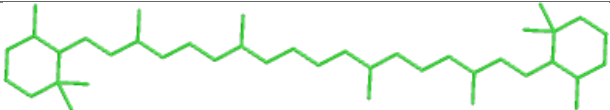
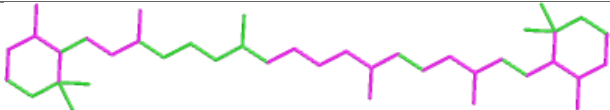
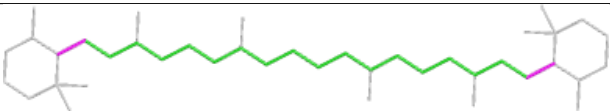
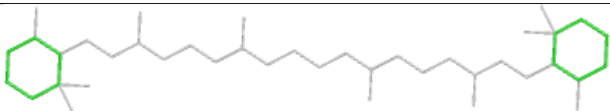
Ligand CLA B 606	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand BCR B 617	
 Bond lengths	 Bond angles
 Torsions	 Rings

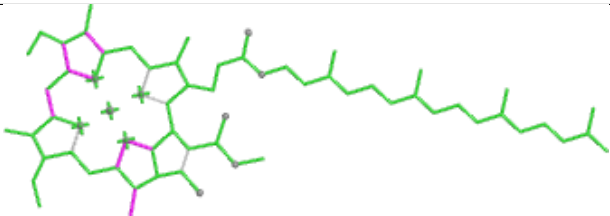
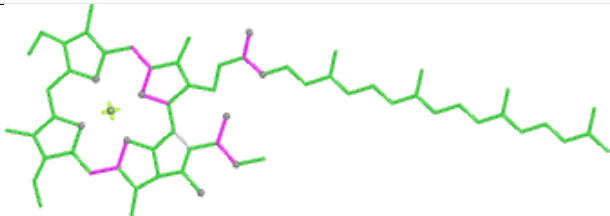
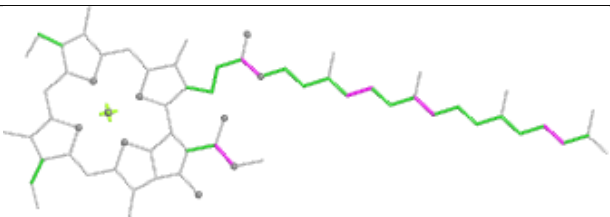
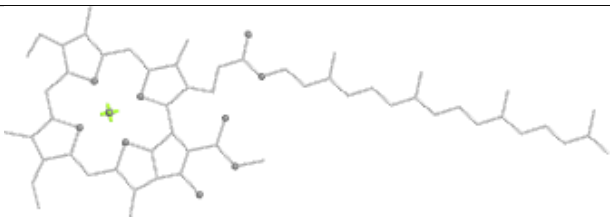


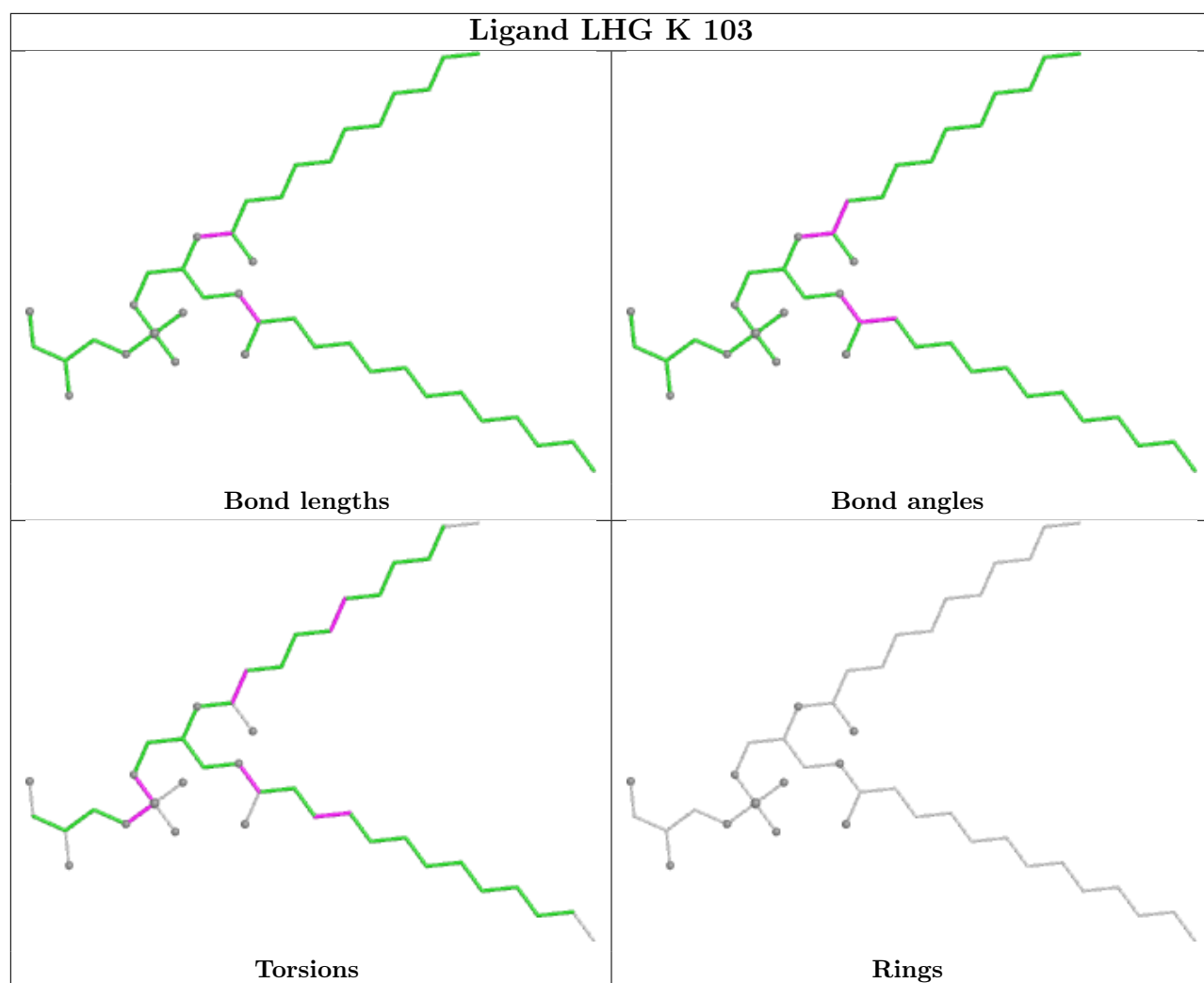


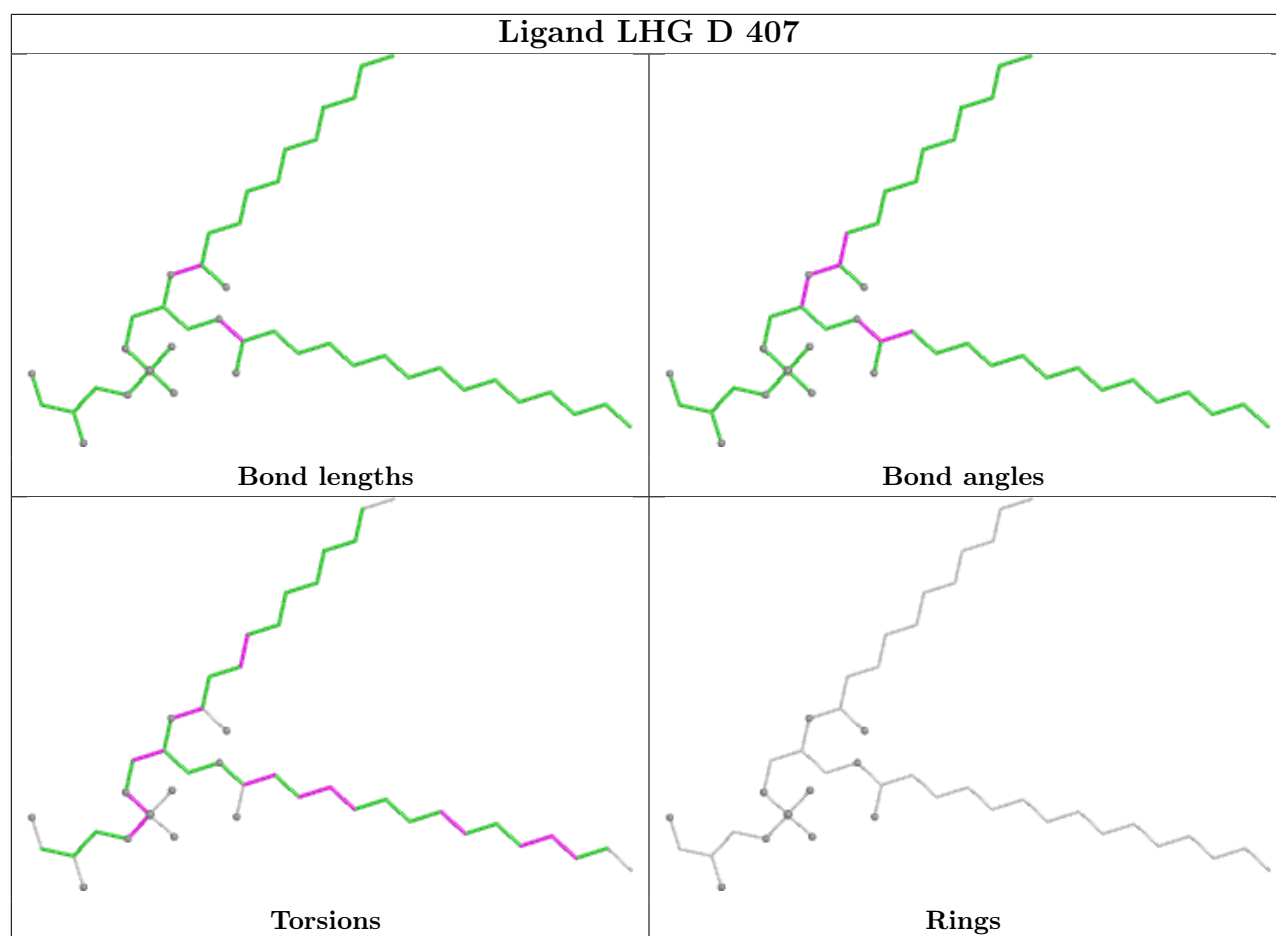




Ligand BCR K 101			
			
Bond lengths	Bond angles		
			
Torsions	Rings		

Ligand CLA C 605			
			
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.

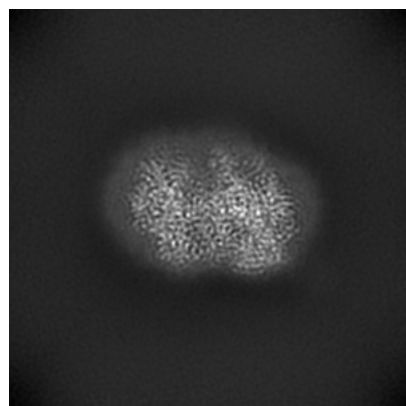
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60026. These allow visual inspection of the internal detail of the map and identification of artifacts.

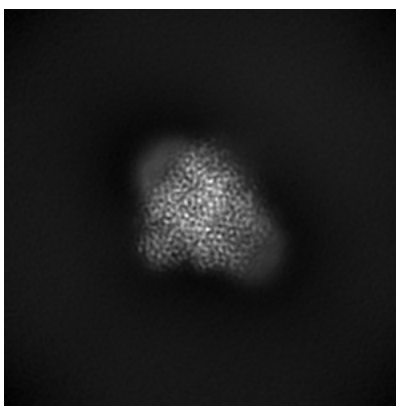
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

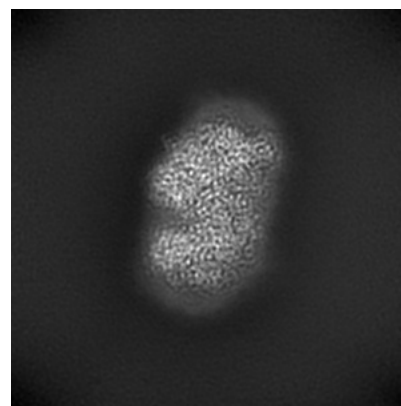
6.1.1 Primary map



X

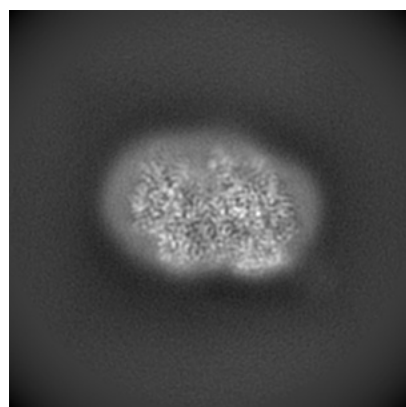


Y

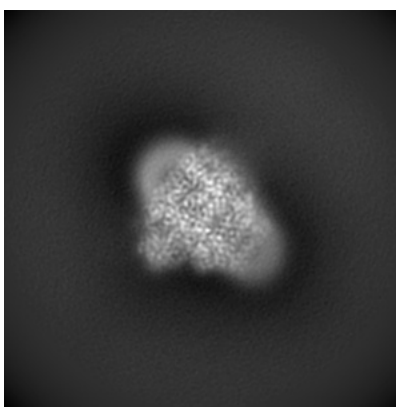


Z

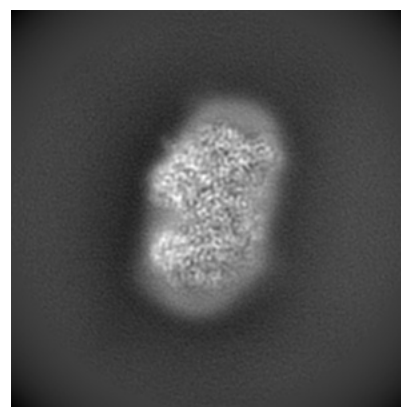
6.1.2 Raw map



X



Y

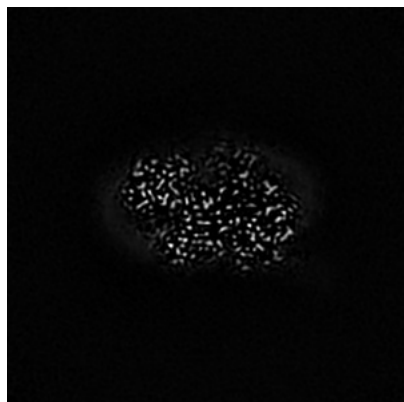


Z

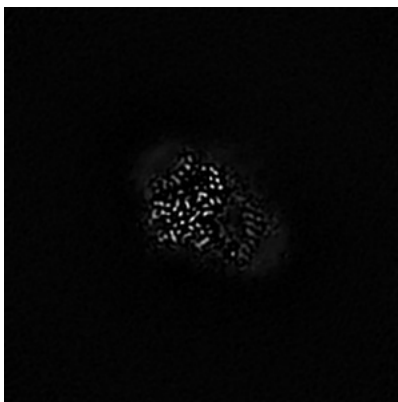
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

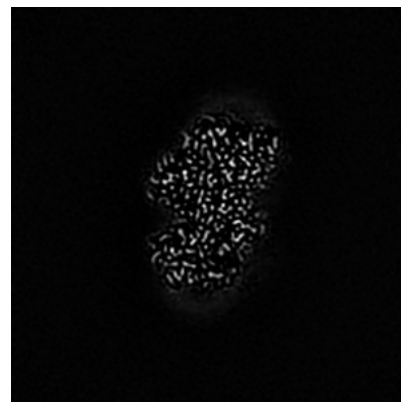
6.2.1 Primary map



X Index: 104

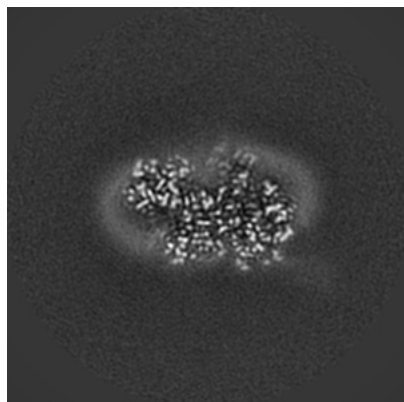


Y Index: 104

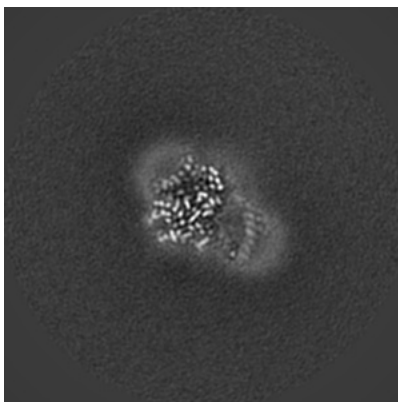


Z Index: 104

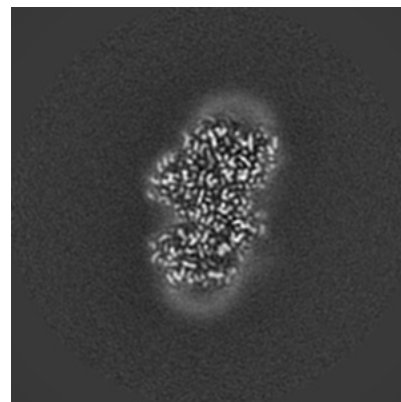
6.2.2 Raw map



X Index: 104



Y Index: 104

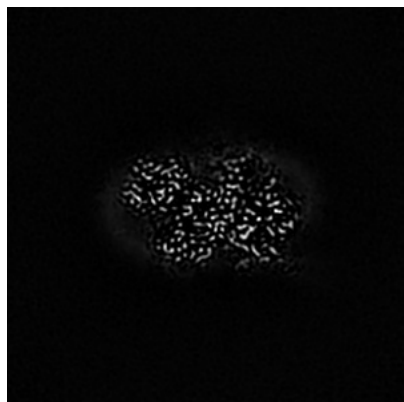


Z Index: 104

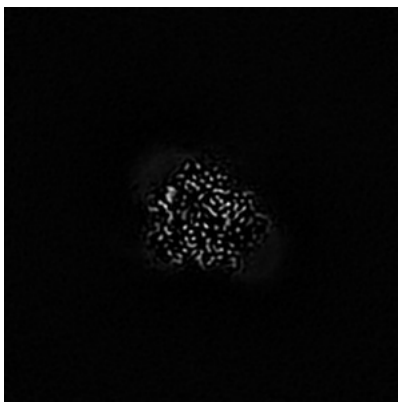
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

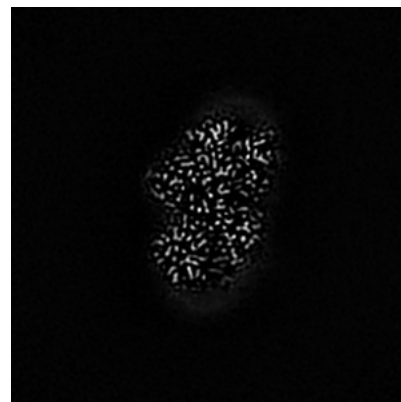
6.3.1 Primary map



X Index: 106

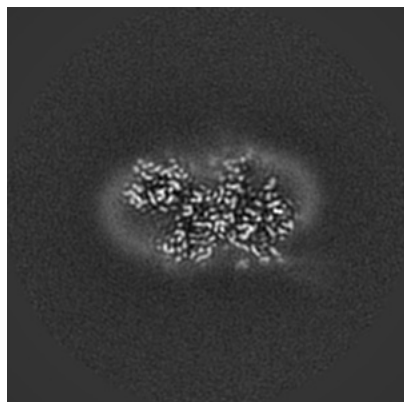


Y Index: 85

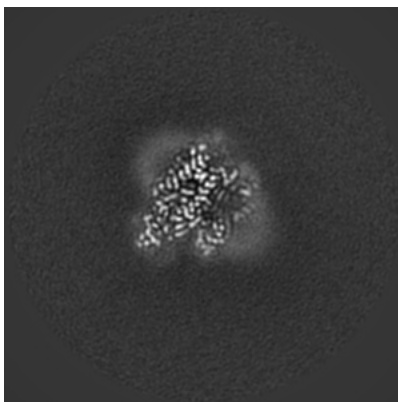


Z Index: 101

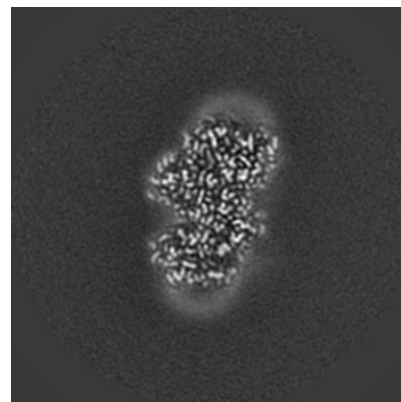
6.3.2 Raw map



X Index: 106



Y Index: 129

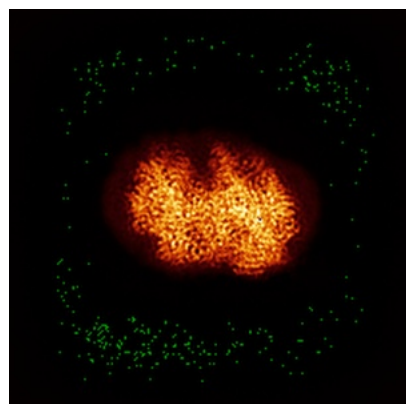


Z Index: 104

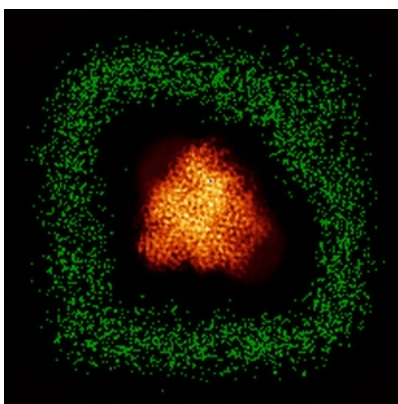
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

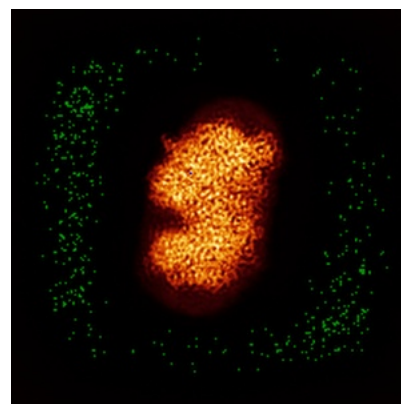
6.4.1 Primary map



X

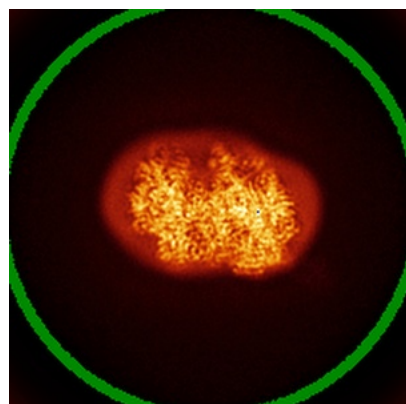


Y

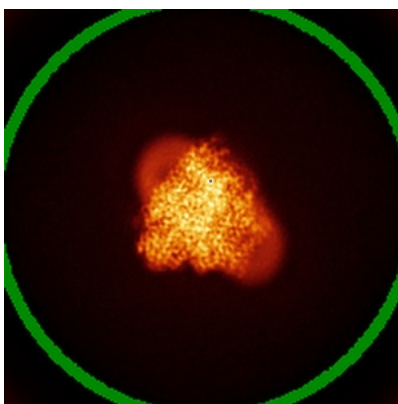


Z

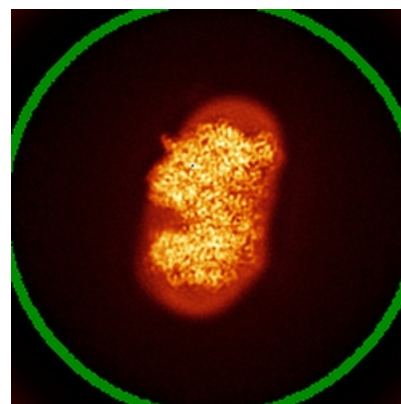
6.4.2 Raw map



X



Y

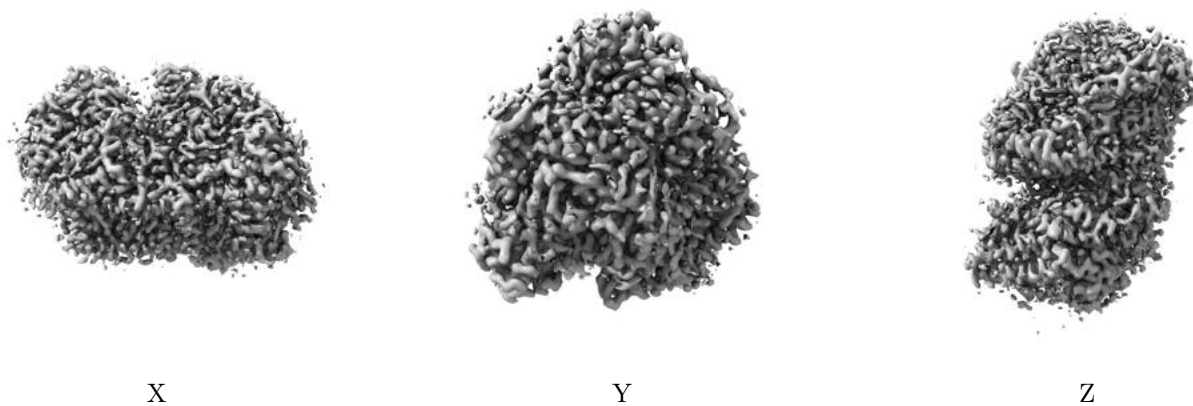


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

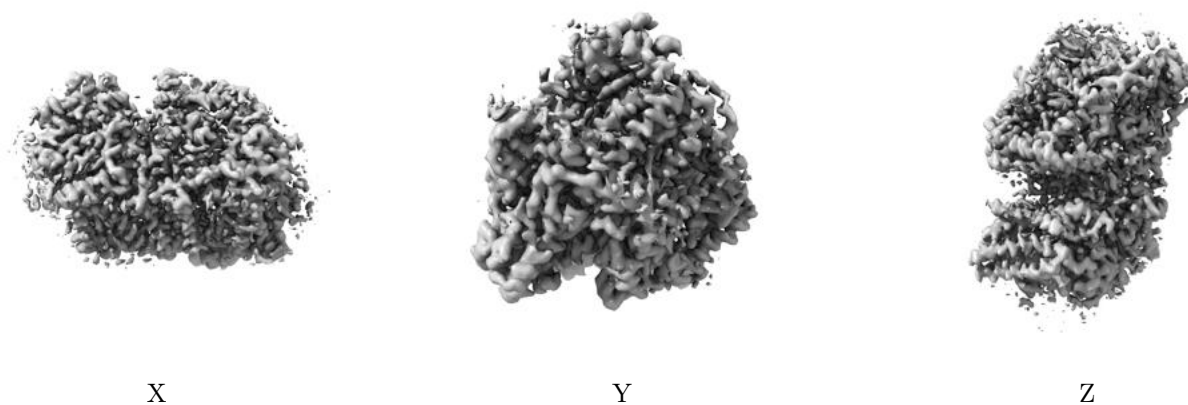
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.019. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

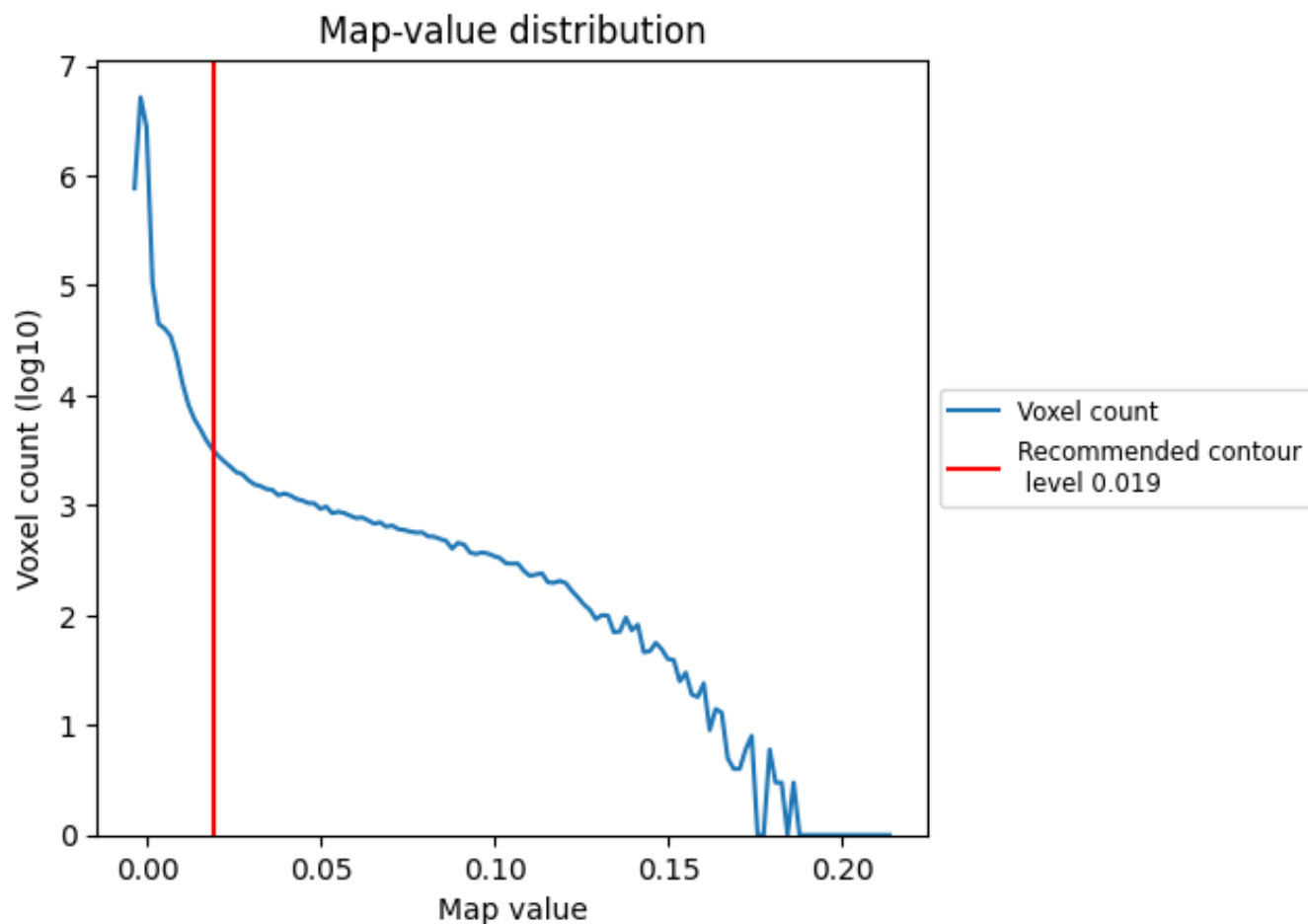
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

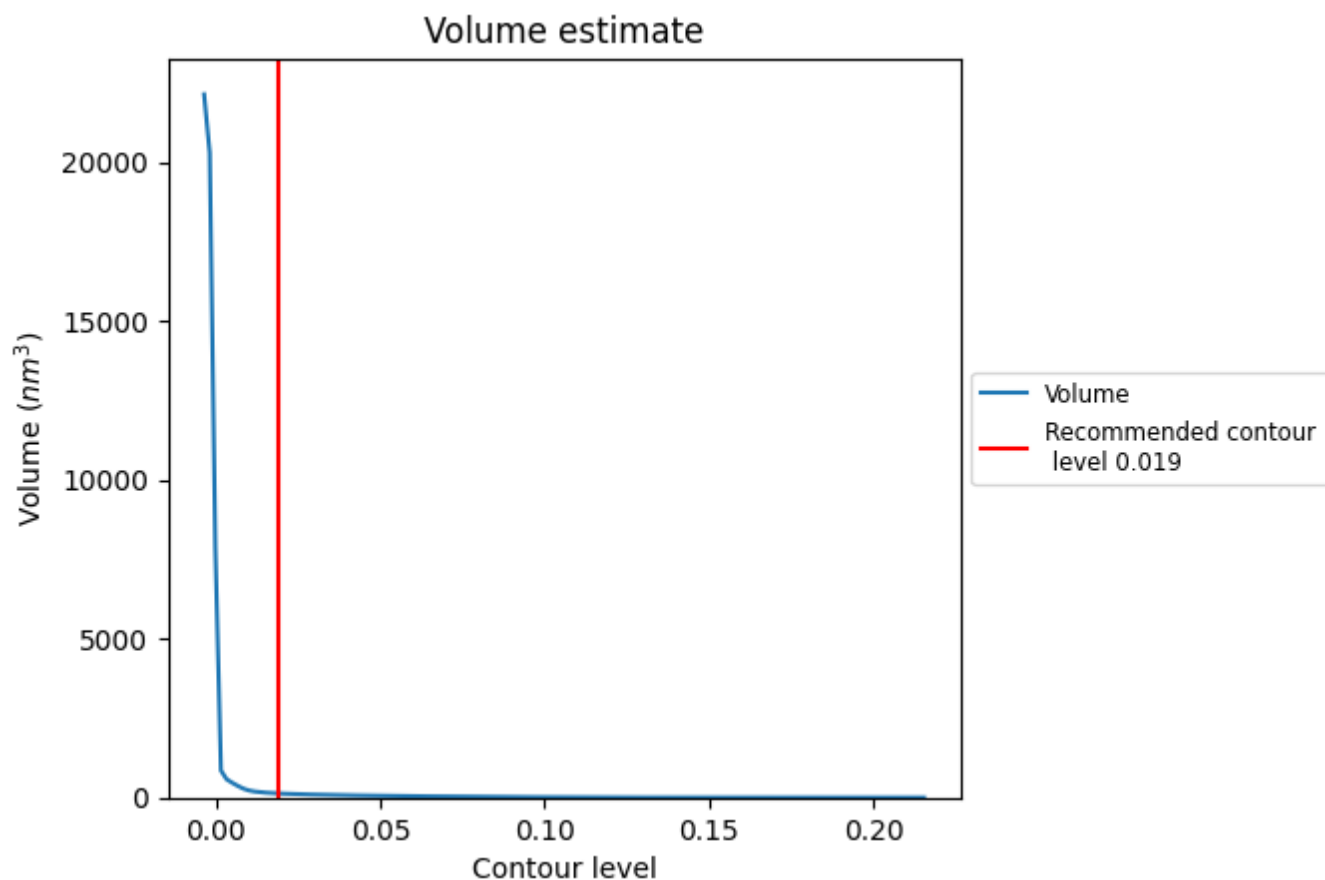
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

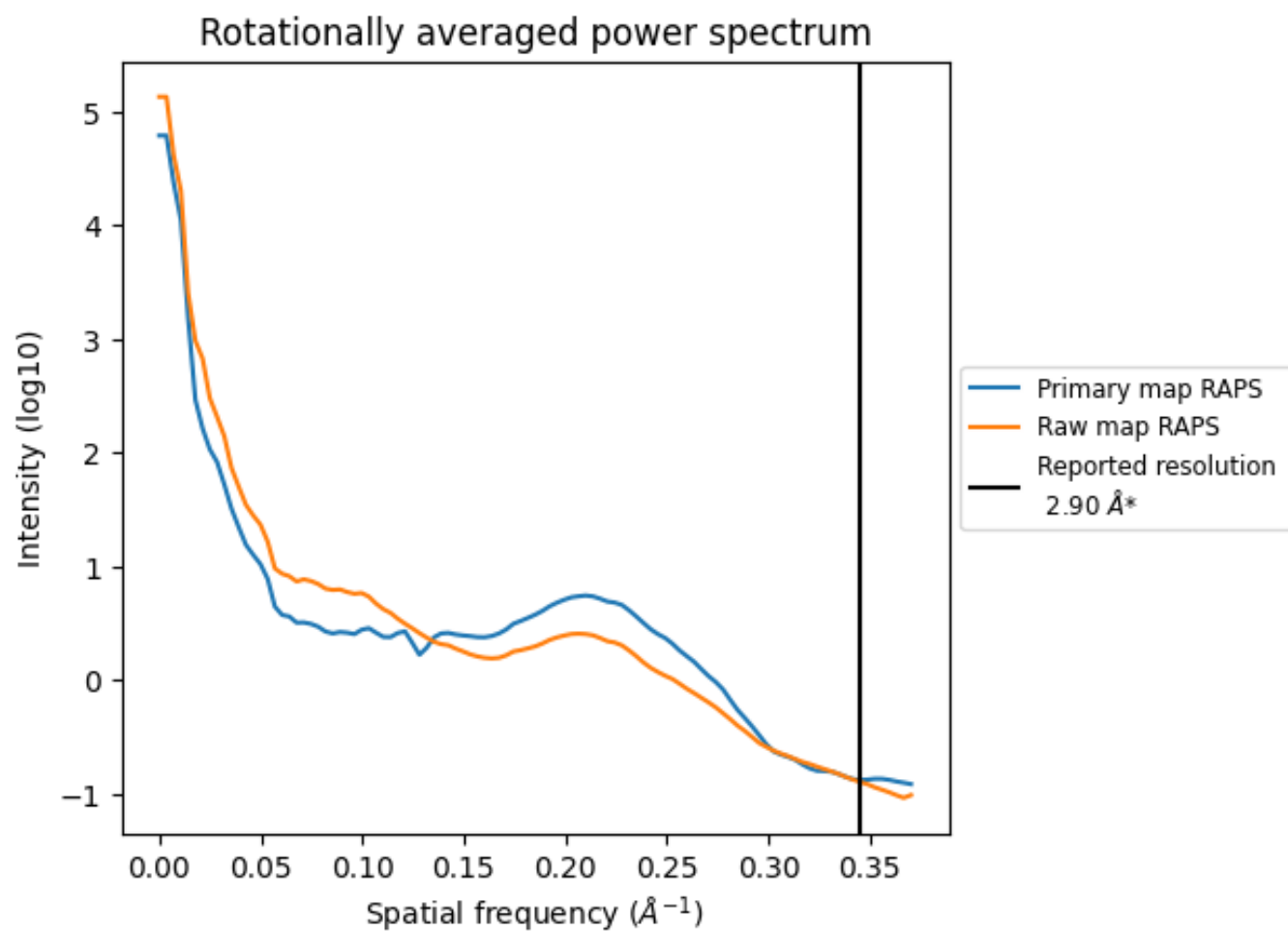
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 130 nm³; this corresponds to an approximate mass of 117 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

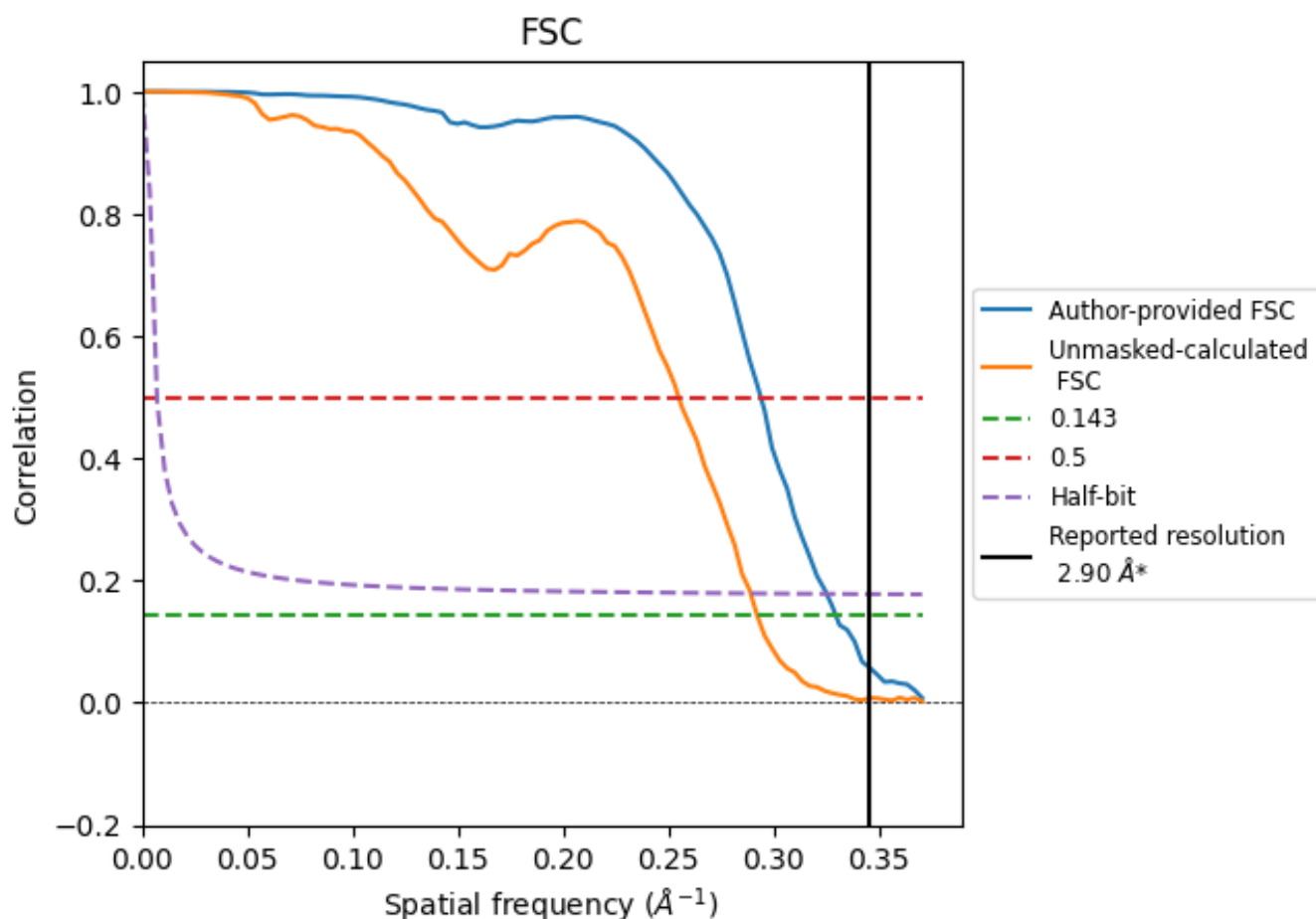


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

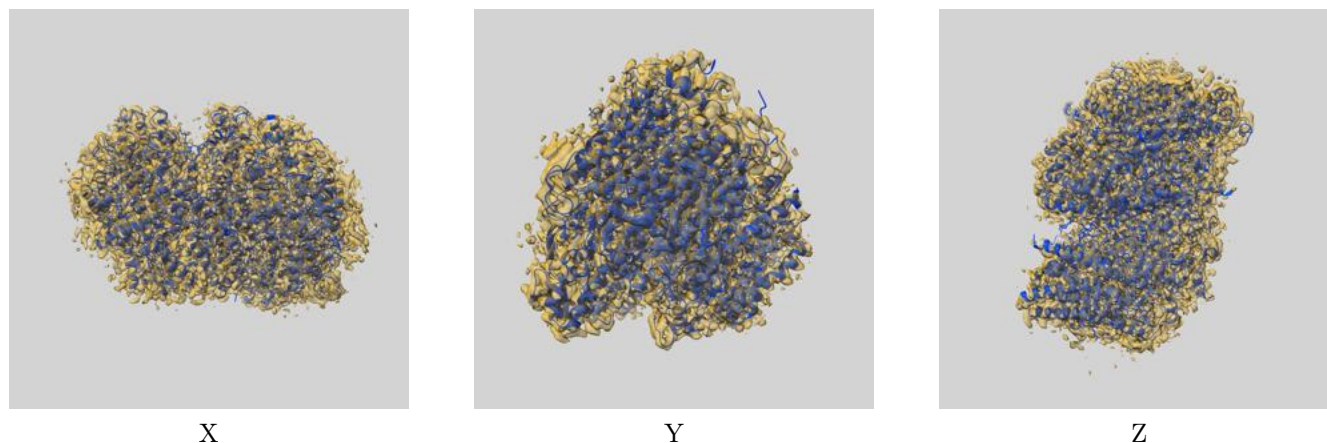
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	3.04	3.40	3.08
Unmasked-calculated*	3.42	3.92	3.46

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.42 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

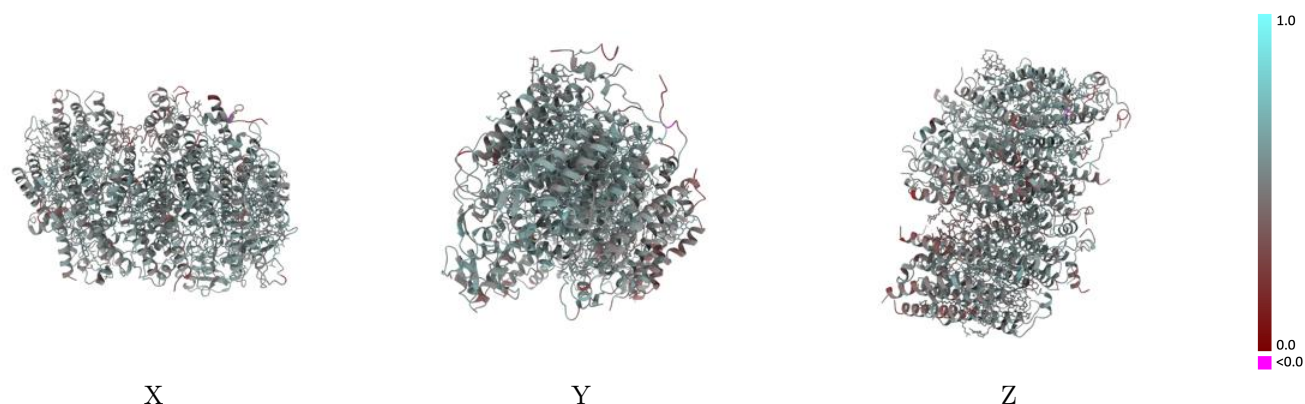
This section contains information regarding the fit between EMDB map EMD-60026 and PDB model 8ZEE. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



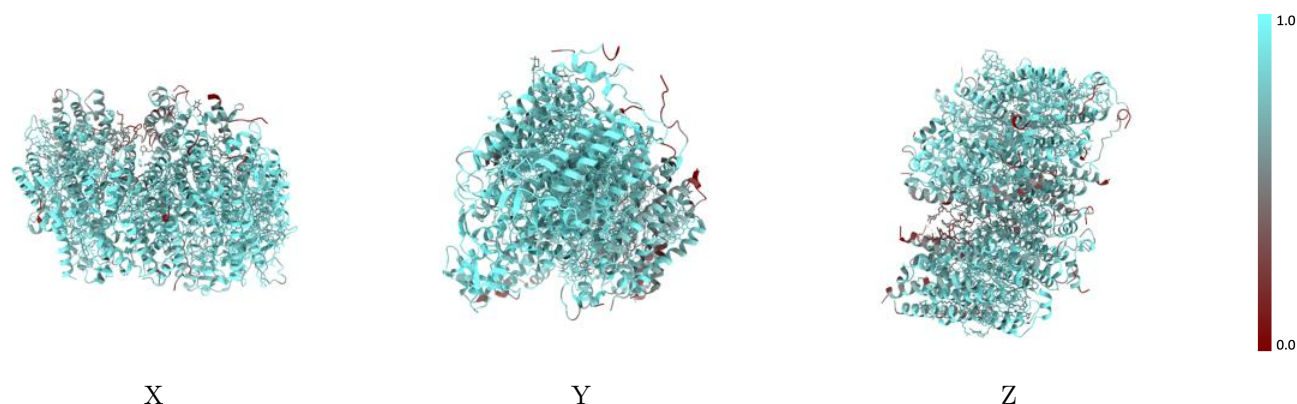
The images above show the 3D surface view of the map at the recommended contour level 0.019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



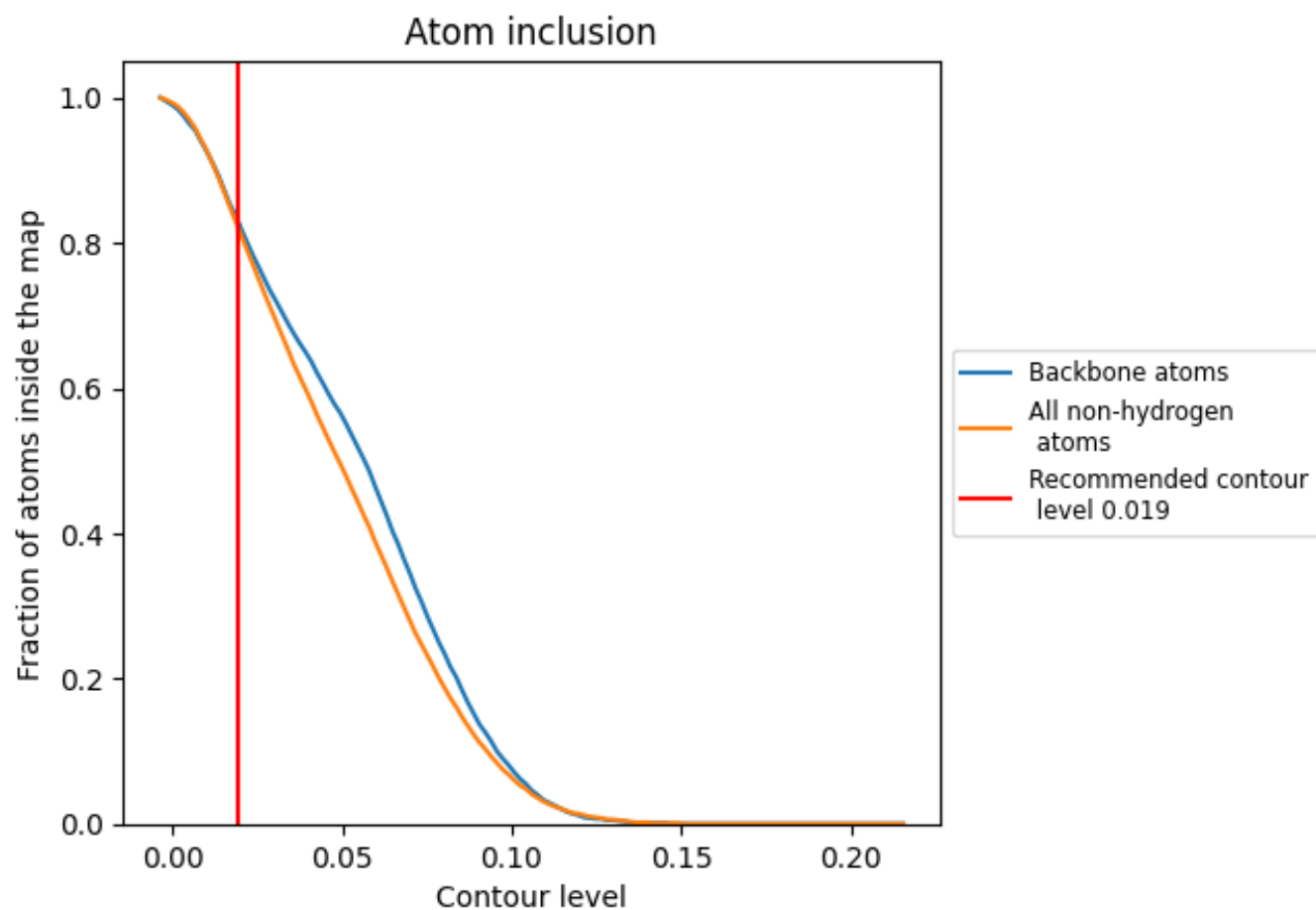
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.019).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8240	 0.5180
1	 0.5220	 0.4240
A	 0.8550	 0.5230
B	 0.8810	 0.5440
C	 0.8350	 0.5190
D	 0.8550	 0.5380
E	 0.7870	 0.4950
F	 0.7600	 0.4810
H	 0.8090	 0.5080
I	 0.7750	 0.4920
K	 0.6780	 0.4490
L	 0.7920	 0.5040
M	 0.6670	 0.4450
T	 0.7370	 0.4750
V	 0.5270	 0.4180
X	 0.6020	 0.4440
Z	 0.6390	 0.4300

