



wwPDB EM Validation Summary Report ⓘ

Aug 6, 2026 – 09:25 AM JST

PDB ID : 8YGL / pdb_00008ygl
EMDB ID : EMD-39255
Title : Rhodobacter blasticus RC-LH1 monomer
Authors : Liu, L.N.; Zhang, Y.Z.; Wang, P.; Christianson, B.M.; Ugurlar, D.
Deposited on : 2024-02-26
Resolution : 2.60 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:

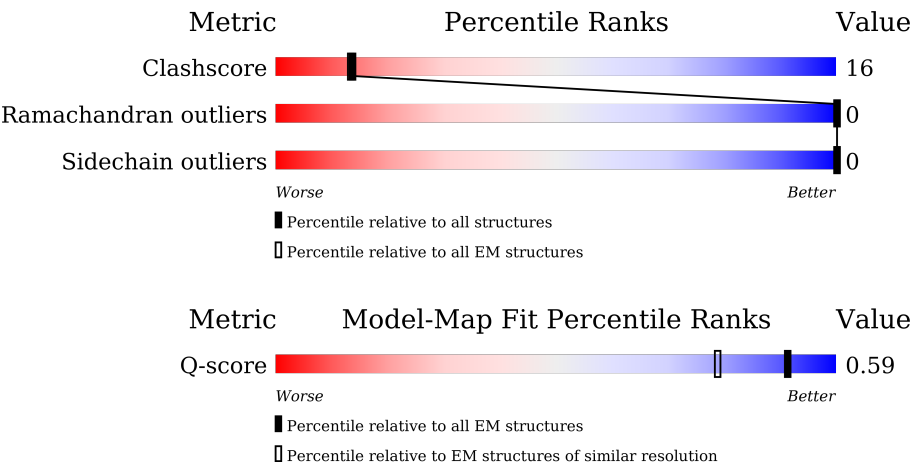
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using 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 2.60 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	8728 (2.10 - 3.10)

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	0	49	76%14%10%
1	2	49	18% 67%12%20%
1	8	49	63%24%12%
1	B	49	82%6%12%

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Mol	Chain	Length	Quality of chain
1	C	49	
1	E	49	
1	G	49	
1	J	49	
1	N	49	
1	P	49	
1	R	49	
1	T	49	
1	V	49	
1	Z	49	
1	b	49	
2	1	62	
2	3	62	
2	7	62	
2	9	62	
2	A	62	
2	D	62	
2	F	62	
2	I	62	
2	K	62	
2	O	62	
2	Q	62	
2	S	62	
2	U	62	
2	W	62	

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Mol	Chain	Length	Quality of chain
2	a	62	
3	H	256	
4	L	282	
5	M	307	
6	X	75	

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
10	CDL	H	301	-	-	X	-
7	BCL	1	101	-	-	X	-

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 23222 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 Antenna pigment protein beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	44	Total	C	N	O	S	0	0
			360	241	56	62	1		
1	2	39	Total	C	N	O	S	0	0
			319	213	51	54	1		
1	8	43	Total	C	N	O	S	0	0
			352	237	55	59	1		
1	B	43	Total	C	N	O	S	0	0
			352	237	55	59	1		
1	C	43	Total	C	N	O	S	0	0
			352	237	55	59	1		
1	E	43	Total	C	N	O	S	0	0
			352	237	55	59	1		
1	G	43	Total	C	N	O	S	0	0
			352	237	55	59	1		
1	J	43	Total	C	N	O	S	0	0
			352	237	55	59	1		
1	N	43	Total	C	N	O	S	0	0
			352	237	55	59	1		
1	P	43	Total	C	N	O	S	0	0
			352	237	55	59	1		
1	R	43	Total	C	N	O	S	0	0
			352	237	55	59	1		
1	T	43	Total	C	N	O	S	0	0
			352	237	55	59	1		
1	V	43	Total	C	N	O	S	0	0
			352	237	55	59	1		
1	Z	42	Total	C	N	O	S	0	0
			344	231	54	58	1		
1	b	37	Total	C	N	O	S	0	0
			308	207	49	51	1		

- Molecule 2 is a protein called Antenna pigment protein alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	49	Total	C	N	O	S	0	0
			412	283	65	63	1		
2	3	52	Total	C	N	O	S	0	0
			438	298	72	67	1		
2	7	45	Total	C	N	O	S	0	0
			387	266	61	58	2		
2	9	53	Total	C	N	O	S	0	0
			446	303	73	68	2		
2	A	53	Total	C	N	O	S	0	0
			446	303	73	68	2		
2	D	53	Total	C	N	O	S	0	0
			446	303	73	68	2		
2	F	53	Total	C	N	O	S	0	0
			446	303	73	68	2		
2	I	53	Total	C	N	O	S	0	0
			446	303	73	68	2		
2	K	52	Total	C	N	O	S	0	0
			438	298	72	67	1		
2	O	52	Total	C	N	O	S	0	0
			438	298	72	67	1		
2	Q	52	Total	C	N	O	S	0	0
			438	298	72	67	1		
2	S	52	Total	C	N	O	S	0	0
			438	298	72	67	1		
2	U	52	Total	C	N	O	S	0	0
			438	298	72	67	1		
2	W	52	Total	C	N	O	S	0	0
			438	298	72	67	1		
2	a	49	Total	C	N	O	S	0	0
			412	283	65	63	1		

- Molecule 3 is a protein called Photosynthetic reaction center subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	254	Total	C	N	O	S	0	0
			1980	1259	347	366	8		

- Molecule 4 is a protein called Reaction center protein L chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	281	Total	C	N	O	S	0	0
			2231	1503	349	370	9		

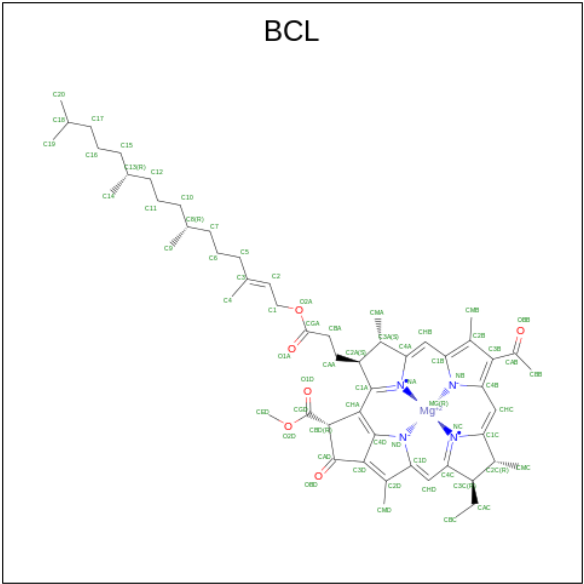
- Molecule 5 is a protein called Reaction center protein M chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	304	Total	C	N	O	S	0	0
			2432	1622	394	405	11		

- Molecule 6 is a protein called 1-deoxy-D-xylulose-5-phosphate synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	X	51	Total	C	N	O	S	0	0
			379	254	61	62	2		

- Molecule 7 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: $C_{55}H_{74}MgN_4O_6$).



Mol	Chain	Residues	Atoms					AltConf
7	0	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
7	1	1	Total	C	Mg	N	O	0
			56	45	1	4	6	
7	2	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
7	3	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
7	7	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
7	8	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
7	9	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
7	A	1	Total	C	Mg	N	O	0
			66	55	1	4	6	

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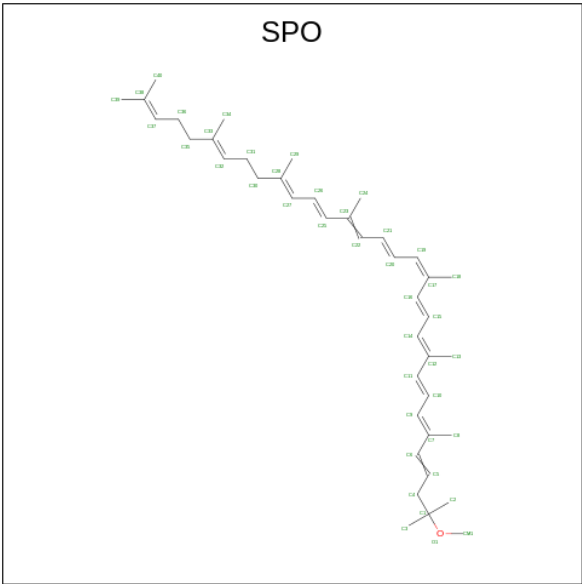
Mol	Chain	Residues	Atoms					AltConf
7	B	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	C	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	D	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	E	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	F	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	G	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	I	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	J	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	K	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	L	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	L	1	Total 63	C 52	Mg 1	N 4	O 6	0
7	M	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	M	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	N	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	O	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	P	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	Q	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	R	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	S	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	T	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	U	1	Total 66	C 55	Mg 1	N 4	O 6	0

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Mol	Chain	Residues	Atoms					AltConf
7	V	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
7	W	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
7	Z	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
7	a	1	Total	C	Mg	N	O	0
			56	45	1	4	6	
7	b	1	Total	C	Mg	N	O	0
			61	50	1	4	6	

- Molecule 8 is SPHEROIDENE (CCD ID: SPO) (formula: C₄₁H₆₀O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
8	0	1	Total	C	O	0
			42	41	1	
8	0	1	Total	C	O	0
			42	41	1	
8	1	1	Total	C	O	0
			42	41	1	
8	2	1	Total	C	O	0
			42	41	1	
8	3	1	Total	C	O	0
			42	41	1	
8	9	1	Total	C	O	0
			42	41	1	

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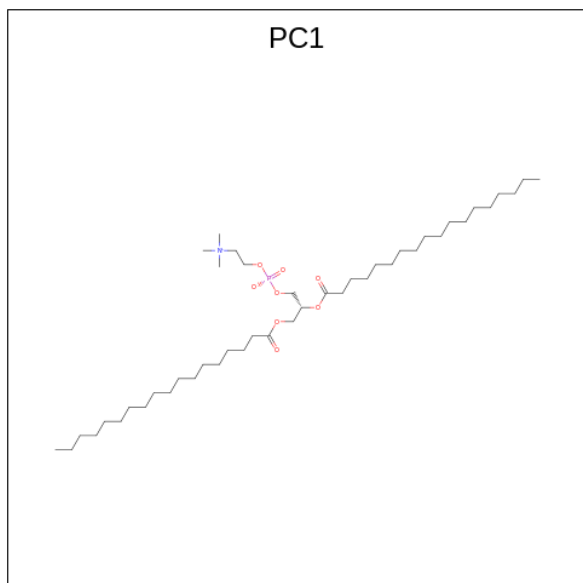
Mol	Chain	Residues	Atoms			AltConf
8	C	1	Total 42	C 41	O 1	0
8	D	1	Total 42	C 41	O 1	0
8	D	1	Total 42	C 41	O 1	0
8	F	1	Total 42	C 41	O 1	0
8	F	1	Total 42	C 41	O 1	0
8	G	1	Total 42	C 41	O 1	0
8	I	1	Total 42	C 41	O 1	0
8	J	1	Total 42	C 41	O 1	0
8	J	1	Total 42	C 41	O 1	0
8	M	1	Total 42	C 41	O 1	0
8	N	1	Total 42	C 41	O 1	0
8	O	1	Total 42	C 41	O 1	0
8	O	1	Total 42	C 41	O 1	0
8	P	1	Total 42	C 41	O 1	0
8	P	1	Total 42	C 41	O 1	0
8	S	1	Total 42	C 41	O 1	0
8	T	1	Total 42	C 41	O 1	0
8	U	1	Total 42	C 41	O 1	0
8	U	1	Total 42	C 41	O 1	0
8	V	1	Total 42	C 41	O 1	0
8	X	1	Total 39	C 38	O 1	0

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Mol	Chain	Residues	Atoms			AltConf
8	Z	1	Total	C	O	0
			42	41	1	
8	b	1	Total	C	O	0
			42	41	1	

- Molecule 9 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$) (labeled as "Ligand of Interest" by depositor).



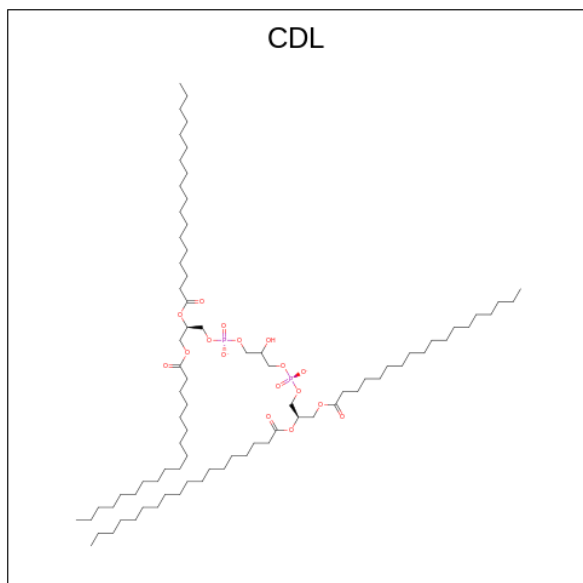
Mol	Chain	Residues	Atoms					AltConf
9	A	1	Total	C	N	O	P	0
			45	35	1	8	1	
9	A	1	Total	C	N	O	P	0
			32	22	1	8	1	
9	A	1	Total	C	N	O	P	0
			32	22	1	8	1	
9	D	1	Total	C	N	O	P	0
			37	27	1	8	1	
9	L	1	Total	C	N	O	P	0
			35	25	1	8	1	
9	L	1	Total	C	N	O	P	0
			36	26	1	8	1	
9	L	1	Total	C	N	O	P	0
			32	22	1	8	1	
9	M	1	Total	C	N	O	P	0
			40	30	1	8	1	
9	M	1	Total	C	N	O	P	0
			47	37	1	8	1	

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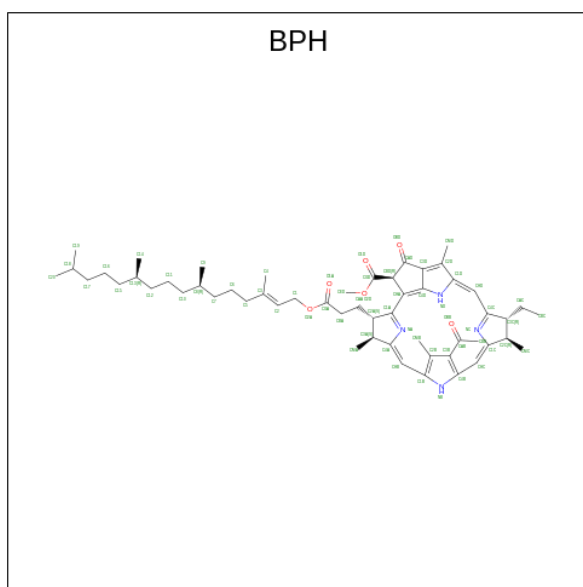
Mol	Chain	Residues	Atoms					AltConf
9	M	1	Total	C	N	O	P	0
			45	35	1	8	1	
9	O	1	Total	C	N	O	P	0
			32	22	1	8	1	

- Molecule 10 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$) (labeled as "Ligand of Interest" by depositor).



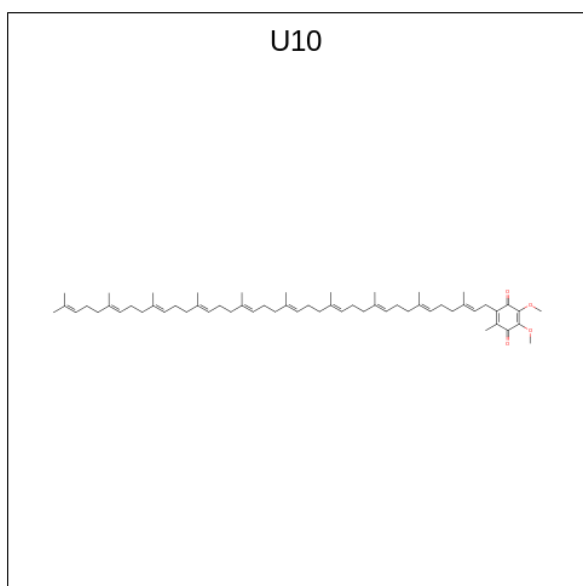
Mol	Chain	Residues	Atoms				AltConf
10	H	1	Total	C	O	P	0
			78	59	17	2	
10	M	1	Total	C	O	P	0
			100	81	17	2	
10	M	1	Total	C	O	P	0
			78	59	17	2	

- Molecule 11 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: $C_{55}H_{76}N_4O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
11	L	1	Total	C	N	O	0
			62	52	4	6	
11	L	1	Total	C	N	O	0
			55	45	4	6	

- Molecule 12 is UBIQUINONE-10 (CCD ID: U10) (formula: $C_{59}H_{90}O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
12	L	1	Total	C	O	0
			43	39	4	

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Mol	Chain	Residues	Atoms			AltConf
12	L	1	Total	C	O	0
			48	44	4	
12	L	1	Total	C	O	0
			19	15	4	
12	L	1	Total	C	O	0
			38	34	4	
12	M	1	Total	C	O	0
			43	39	4	
12	M	1	Total	C	O	0
			48	44	4	
12	X	1	Total	C	O	0
			48	44	4	

- Molecule 13 is FE (II) ION (CCD ID: FE2) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

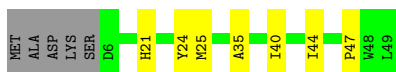
Mol	Chain	Residues	Atoms		AltConf
13	M	1	Total	Fe	0
			1	1	

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.

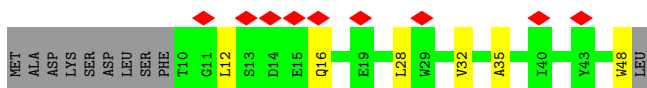
- Molecule 1: Antenna pigment protein beta chain

Chain 0: 



- Molecule 1: Antenna pigment protein beta chain

Chain 2: 



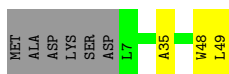
- Molecule 1: Antenna pigment protein beta chain

Chain 8: 



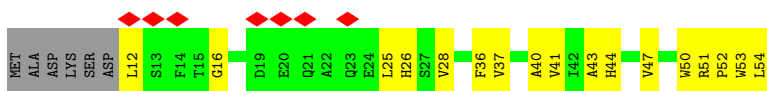
- Molecule 1: Antenna pigment protein beta chain

Chain B: 



- Molecule 1: Antenna pigment protein beta chain

Chain C: 



- Molecule 1: Antenna pigment protein beta chain

Chain E:  65% 22% 12%



- Molecule 1: Antenna pigment protein beta chain

Chain G:  71% 16% 12%



- Molecule 1: Antenna pigment protein beta chain

Chain J:  57% 31% 12%



- Molecule 1: Antenna pigment protein beta chain

Chain N:  71% 16% 12%



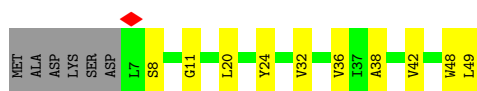
- Molecule 1: Antenna pigment protein beta chain

Chain P:  65% 22% 12%



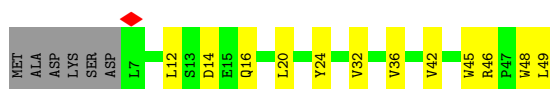
- Molecule 1: Antenna pigment protein beta chain

Chain R:  67% 20% 12%

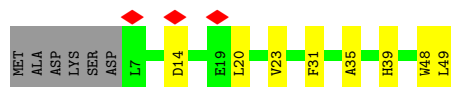
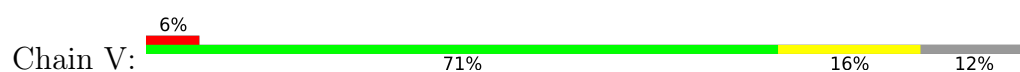


- Molecule 1: Antenna pigment protein beta chain

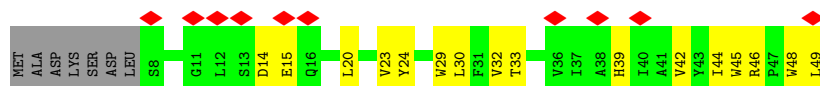
Chain T:  63% 24% 12%



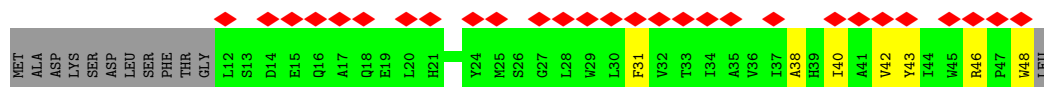
- Molecule 1: Antenna pigment protein beta chain



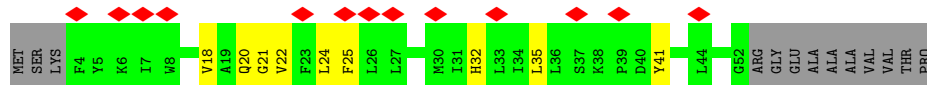
- Molecule 1: Antenna pigment protein beta chain



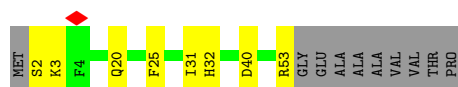
- Molecule 1: Antenna pigment protein beta chain



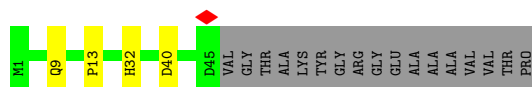
- Molecule 2: Antenna pigment protein alpha chain



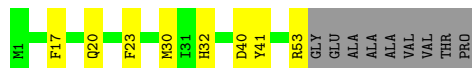
- Molecule 2: Antenna pigment protein alpha chain



- Molecule 2: Antenna pigment protein alpha chain



- Molecule 2: Antenna pigment protein alpha chain



- Molecule 2: Antenna pigment protein alpha chain

Chain A:  77% 8% 15%



- Molecule 2: Antenna pigment protein alpha chain

Chain D:  61% 24% 15%



- Molecule 2: Antenna pigment protein alpha chain

Chain F:  66% 19% 15%



- Molecule 2: Antenna pigment protein alpha chain

Chain I:  69% 16% 15%



- Molecule 2: Antenna pigment protein alpha chain

Chain K:  71% 13% 16%



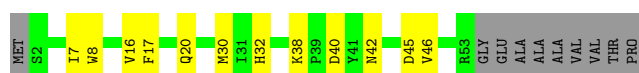
- Molecule 2: Antenna pigment protein alpha chain

Chain O:  68% 16% 16%



- Molecule 2: Antenna pigment protein alpha chain

Chain Q:  65% 19% 16%



- Molecule 2: Antenna pigment protein alpha chain

Chain S:  53% 31% 16%



- Molecule 2: Antenna pigment protein alpha chain

Chain U:  69% 15% 16%



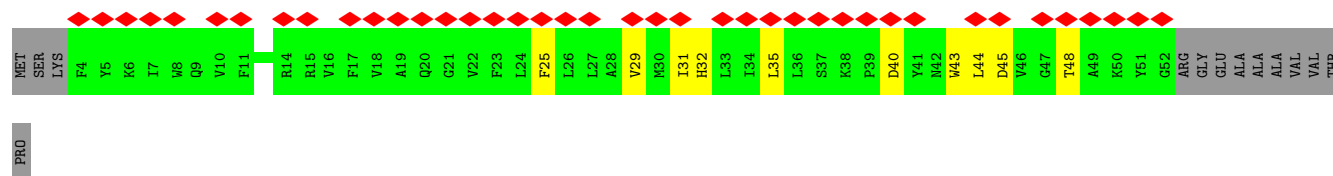
- Molecule 2: Antenna pigment protein alpha chain

Chain W:  63% 21% 16%



- Molecule 2: Antenna pigment protein alpha chain

Chain a:  65% 63% 16% 21%



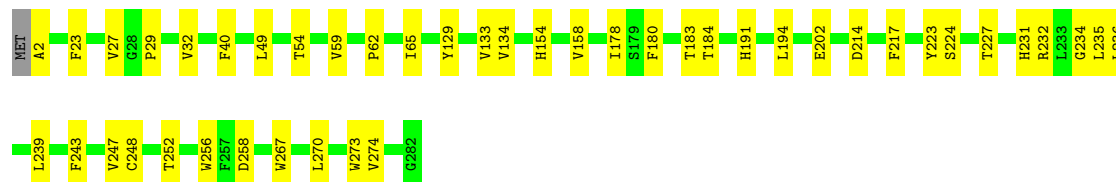
- Molecule 3: Photosynthetic reaction center subunit H

Chain H:  88% 11%



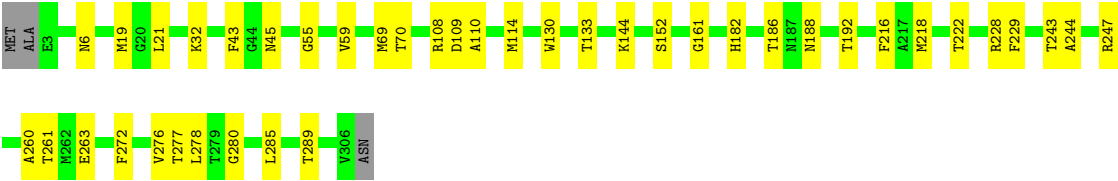
- Molecule 4: Reaction center protein L chain

Chain L:  84% 16%

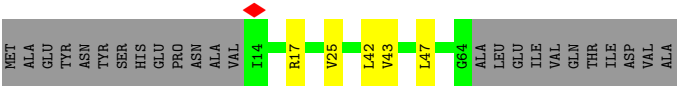


- Molecule 5: Reaction center protein M chain

Chain M:  86% 13%



• Molecule 6: 1-deoxy-D-xylulose-5-phosphate synthase



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45399	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.792	Depositor
Minimum map value	-0.912	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.17	Depositor
Map size (Å)	297.28, 297.28, 297.28	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.929, 0.929, 0.929	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BCL, PC1, BPH, CDL, FE2, SPO, U10

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	0	0.31	0/372	0.31	0/510
1	2	0.18	0/330	0.28	0/453
1	8	0.27	0/364	0.28	0/499
1	B	0.31	0/364	0.28	0/499
1	C	0.20	0/364	0.31	0/499
1	E	0.30	0/364	0.30	0/499
1	G	0.28	0/364	0.31	0/499
1	J	0.30	0/364	0.34	0/499
1	N	0.27	0/364	0.32	0/499
1	P	0.27	0/364	0.34	0/499
1	R	0.27	0/364	0.32	0/499
1	T	0.27	0/364	0.38	0/499
1	V	0.23	0/364	0.27	0/499
1	Z	0.19	0/356	0.34	0/488
1	b	0.17	0/319	0.38	0/438
2	1	0.19	0/426	0.36	0/579
2	3	0.19	0/452	0.31	0/612
2	7	0.29	0/400	0.32	0/542
2	9	0.31	0/460	0.37	0/622
2	A	0.32	0/460	0.35	0/622
2	D	0.32	0/460	0.39	0/622
2	F	0.31	0/460	0.31	0/622
2	I	0.29	0/460	0.33	0/622
2	K	0.29	0/452	0.34	0/612
2	O	0.28	0/452	0.35	0/612
2	Q	0.34	0/452	0.34	0/612
2	S	0.32	0/452	0.40	0/612
2	U	0.28	0/452	0.37	0/612
2	W	0.23	0/452	0.36	0/612
2	a	0.18	0/426	0.35	0/579
3	H	0.26	0/2030	0.37	0/2757
4	L	0.31	0/2317	0.36	0/3172

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	M	0.32	0/2525	0.38	0/3453
6	X	0.30	0/388	0.38	0/532
All	All	0.28	0/19357	0.35	0/26386

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	0	360	0	350	5	0
1	2	319	0	310	8	0
1	8	352	0	346	10	0
1	B	352	0	346	2	0
1	C	352	0	346	15	0
1	E	352	0	346	10	0
1	G	352	0	346	8	0
1	J	352	0	346	14	0
1	N	352	0	346	9	0
1	P	352	0	346	14	0
1	R	352	0	346	7	0
1	T	352	0	346	14	0
1	V	352	0	346	13	0
1	Z	344	0	335	14	0
1	b	308	0	300	9	0
2	1	412	0	420	12	0
2	3	438	0	451	8	0
2	7	387	0	401	4	0
2	9	446	0	463	9	0
2	A	446	0	463	8	0
2	D	446	0	463	16	0
2	F	446	0	463	15	0
2	I	446	0	463	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	438	0	451	8	0
2	O	438	0	451	9	0
2	Q	438	0	451	10	0
2	S	438	0	451	25	0
2	U	438	0	451	11	0
2	W	438	0	451	18	0
2	a	412	0	420	7	0
3	H	1980	0	1952	23	0
4	L	2231	0	2169	36	0
5	M	2432	0	2331	31	0
6	X	379	0	401	6	0
7	0	61	0	61	7	0
7	1	56	0	51	27	0
7	2	61	0	61	11	0
7	3	66	0	74	13	0
7	7	61	0	61	5	0
7	8	66	0	74	5	0
7	9	66	0	74	10	0
7	A	66	0	74	5	0
7	B	66	0	74	7	0
7	C	66	0	74	8	0
7	D	66	0	74	5	0
7	E	66	0	74	20	0
7	F	66	0	74	6	0
7	G	66	0	74	11	0
7	I	66	0	74	14	0
7	J	66	0	74	19	0
7	K	66	0	74	5	0
7	L	129	0	139	13	0
7	M	132	0	148	19	0
7	N	66	0	74	16	0
7	O	66	0	74	10	0
7	P	66	0	74	5	0
7	Q	66	0	74	8	0
7	R	66	0	74	8	0
7	S	66	0	74	14	0
7	T	66	0	74	7	0
7	U	66	0	74	10	0
7	V	66	0	74	6	0
7	W	66	0	74	9	0
7	Z	66	0	74	18	0
7	a	56	0	51	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	b	61	0	61	7	0
8	0	84	0	120	13	0
8	1	42	0	60	16	0
8	2	42	0	60	12	0
8	3	42	0	60	19	0
8	9	42	0	60	5	0
8	C	42	0	60	8	0
8	D	84	0	120	14	0
8	F	84	0	120	4	0
8	G	42	0	60	6	0
8	I	42	0	60	12	0
8	J	84	0	120	39	0
8	M	42	0	60	4	0
8	N	42	0	60	5	0
8	O	84	0	120	14	0
8	P	84	0	120	13	0
8	S	42	0	60	17	0
8	T	42	0	60	7	0
8	U	84	0	120	13	0
8	V	42	0	60	10	0
8	X	39	0	53	5	0
8	Z	42	0	60	8	0
8	b	42	0	60	15	0
9	A	109	0	143	22	0
9	D	37	0	48	3	0
9	L	103	0	128	4	0
9	M	132	0	192	10	0
9	O	32	0	38	0	0
10	H	78	0	106	21	0
10	M	178	0	262	3	0
11	L	117	0	120	8	0
12	L	148	0	182	18	0
12	M	91	0	118	5	0
12	X	48	0	63	10	0
13	M	1	0	0	0	0
All	All	23222	0	24209	754	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 16.

The worst 5 of 754 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)
8:O:103:SPO:H9	8:O:103:SPO:H42	1.30	1.06
5:M:152:SER:HG	5:M:277:THR:HG1	0.97	0.97
7:1:101:BCL:HMB2	8:3:102:SPO:H42	1.48	0.95
7:J:101:BCL:H62	8:J:103:SPO:H241	1.49	0.95
8:O:104:SPO:H6	7:S:201:BCL:HMB1	1.49	0.93

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	0	42/49 (86%)	42 (100%)	0	0	100	100
1	2	37/49 (76%)	37 (100%)	0	0	100	100
1	8	41/49 (84%)	39 (95%)	2 (5%)	0	100	100
1	B	41/49 (84%)	41 (100%)	0	0	100	100
1	C	41/49 (84%)	38 (93%)	3 (7%)	0	100	100
1	E	41/49 (84%)	41 (100%)	0	0	100	100
1	G	41/49 (84%)	40 (98%)	1 (2%)	0	100	100
1	J	41/49 (84%)	41 (100%)	0	0	100	100
1	N	41/49 (84%)	39 (95%)	2 (5%)	0	100	100
1	P	41/49 (84%)	40 (98%)	1 (2%)	0	100	100
1	R	41/49 (84%)	41 (100%)	0	0	100	100
1	T	41/49 (84%)	41 (100%)	0	0	100	100
1	V	41/49 (84%)	41 (100%)	0	0	100	100
1	Z	40/49 (82%)	40 (100%)	0	0	100	100
1	b	35/49 (71%)	35 (100%)	0	0	100	100
2	1	47/62 (76%)	47 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	3	50/62 (81%)	49 (98%)	1 (2%)	0	100	100
2	7	43/62 (69%)	42 (98%)	1 (2%)	0	100	100
2	9	51/62 (82%)	50 (98%)	1 (2%)	0	100	100
2	A	51/62 (82%)	51 (100%)	0	0	100	100
2	D	51/62 (82%)	51 (100%)	0	0	100	100
2	F	51/62 (82%)	50 (98%)	1 (2%)	0	100	100
2	I	51/62 (82%)	50 (98%)	1 (2%)	0	100	100
2	K	50/62 (81%)	50 (100%)	0	0	100	100
2	O	50/62 (81%)	50 (100%)	0	0	100	100
2	Q	50/62 (81%)	48 (96%)	2 (4%)	0	100	100
2	S	50/62 (81%)	47 (94%)	3 (6%)	0	100	100
2	U	50/62 (81%)	49 (98%)	1 (2%)	0	100	100
2	W	50/62 (81%)	48 (96%)	2 (4%)	0	100	100
2	a	47/62 (76%)	44 (94%)	3 (6%)	0	100	100
3	H	252/256 (98%)	252 (100%)	0	0	100	100
4	L	279/282 (99%)	274 (98%)	5 (2%)	0	100	100
5	M	302/307 (98%)	301 (100%)	1 (0%)	0	100	100
6	X	49/75 (65%)	49 (100%)	0	0	100	100
All	All	2229/2585 (86%)	2198 (99%)	31 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	0	38/42 (90%)	38 (100%)	0	100	100
1	2	33/42 (79%)	33 (100%)	0	100	100
1	8	37/42 (88%)	37 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	37/42 (88%)	37 (100%)	0	100	100
1	C	37/42 (88%)	37 (100%)	0	100	100
1	E	37/42 (88%)	37 (100%)	0	100	100
1	G	37/42 (88%)	37 (100%)	0	100	100
1	J	37/42 (88%)	37 (100%)	0	100	100
1	N	37/42 (88%)	37 (100%)	0	100	100
1	P	37/42 (88%)	37 (100%)	0	100	100
1	R	37/42 (88%)	37 (100%)	0	100	100
1	T	37/42 (88%)	37 (100%)	0	100	100
1	V	37/42 (88%)	37 (100%)	0	100	100
1	Z	36/42 (86%)	36 (100%)	0	100	100
1	b	32/42 (76%)	32 (100%)	0	100	100
2	1	43/52 (83%)	43 (100%)	0	100	100
2	3	46/52 (88%)	46 (100%)	0	100	100
2	7	42/52 (81%)	42 (100%)	0	100	100
2	9	47/52 (90%)	47 (100%)	0	100	100
2	A	47/52 (90%)	47 (100%)	0	100	100
2	D	47/52 (90%)	47 (100%)	0	100	100
2	F	47/52 (90%)	47 (100%)	0	100	100
2	I	47/52 (90%)	47 (100%)	0	100	100
2	K	46/52 (88%)	46 (100%)	0	100	100
2	O	46/52 (88%)	46 (100%)	0	100	100
2	Q	46/52 (88%)	46 (100%)	0	100	100
2	S	46/52 (88%)	46 (100%)	0	100	100
2	U	46/52 (88%)	46 (100%)	0	100	100
2	W	46/52 (88%)	46 (100%)	0	100	100
2	a	43/52 (83%)	43 (100%)	0	100	100
3	H	207/208 (100%)	207 (100%)	0	100	100
4	L	223/224 (100%)	223 (100%)	0	100	100
5	M	237/239 (99%)	237 (100%)	0	100	100
6	X	39/59 (66%)	39 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1937/2140 (90%)	1937 (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 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	21	HIS
1	Z	16	GLN
1	b	39	HIS
1	b	21	HIS
2	F	32	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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 87 ligands modelled in this entry, 1 is monoatomic - leaving 86 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	$\# Z > 2$
7	BCL	9	101	-	69,74,74	0.84	1 (1%)	83,115,115	1.23	10 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	SPO	U	103	-	40,41,41	0.15	0	47,50,50	0.45	0
8	SPO	X	101	-	37,38,41	0.17	0	43,46,50	0.56	1 (2%)
7	BCL	L	301	-	69,74,74	0.84	2 (2%)	83,115,115	1.30	15 (18%)
7	BCL	U	101	-	69,74,74	0.89	2 (2%)	83,115,115	1.25	11 (13%)
11	BPH	L	303	-	56,67,70	1.11	3 (5%)	57,97,101	1.05	5 (8%)
8	SPO	M	408	-	40,41,41	0.18	0	47,50,50	0.63	1 (2%)
12	U10	M	407	-	48,48,63	0.19	0	58,61,79	0.47	1 (1%)
8	SPO	F	103	-	40,41,41	0.17	0	47,50,50	0.59	1 (2%)
12	U10	L	309	-	38,38,63	0.20	0	46,49,79	0.52	1 (2%)
9	PC1	A	103	-	31,31,53	0.36	0	37,39,61	0.36	0
8	SPO	b	101	-	40,41,41	0.14	0	47,50,50	0.46	1 (2%)
7	BCL	P	101	1	69,74,74	0.87	1 (1%)	83,115,115	1.30	13 (15%)
7	BCL	B	101	1	69,74,74	0.89	2 (2%)	83,115,115	1.27	13 (15%)
8	SPO	V	101	-	40,41,41	0.13	0	47,50,50	0.49	0
8	SPO	0	102	-	40,41,41	0.12	0	47,50,50	0.48	1 (2%)
8	SPO	O	102	-	40,41,41	0.19	0	47,50,50	0.56	1 (2%)
8	SPO	D	103	-	40,41,41	0.15	0	47,50,50	0.71	3 (6%)
8	SPO	P	102	-	40,41,41	0.17	0	47,50,50	0.49	1 (2%)
7	BCL	0	101	1	64,69,74	0.91	2 (3%)	77,109,115	1.34	12 (15%)
7	BCL	K	101	-	69,74,74	0.87	1 (1%)	83,115,115	1.18	10 (12%)
9	PC1	M	401	-	39,39,53	0.34	0	45,47,61	0.31	0
9	PC1	O	103	-	31,31,53	0.36	0	37,39,61	0.32	0
9	PC1	A	104	-	31,31,53	0.36	0	37,39,61	0.30	0
8	SPO	Z	102	-	40,41,41	0.14	0	47,50,50	0.40	0
7	BCL	T	101	1	69,74,74	0.90	3 (4%)	83,115,115	1.27	13 (15%)
9	PC1	M	411	-	44,44,53	0.30	0	50,52,61	0.31	0
7	BCL	L	302	-	66,71,74	0.91	1 (1%)	79,111,115	1.25	13 (16%)
8	SPO	T	102	-	40,41,41	0.30	0	47,50,50	1.06	4 (8%)
9	PC1	L	306	-	35,35,53	0.34	0	41,43,61	0.31	0
7	BCL	I	101	-	69,74,74	0.91	1 (1%)	83,115,115	1.19	9 (10%)
8	SPO	9	102	-	40,41,41	0.13	0	47,50,50	0.37	0
8	SPO	U	102	-	40,41,41	0.13	0	47,50,50	0.48	1 (2%)
7	BCL	7	101	-	64,69,74	0.89	2 (3%)	77,109,115	1.32	14 (18%)
8	SPO	S	202	-	40,41,41	0.16	0	47,50,50	0.56	0
8	SPO	I	102	-	40,41,41	0.14	0	47,50,50	0.39	0
7	BCL	a	101	-	59,64,74	0.85	1 (1%)	71,103,115	1.49	12 (16%)
9	PC1	L	311	-	31,31,53	0.36	0	37,39,61	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	U10	L	307	-	48,48,63	0.20	0	58,61,79	0.57	1 (1%)
7	BCL	M	404	-	69,74,74	0.88	1 (1%)	83,115,115	1.22	11 (13%)
7	BCL	8	101	-	69,74,74	0.88	3 (4%)	83,115,115	1.28	13 (15%)
7	BCL	1	101	-	59,64,74	0.89	2 (3%)	71,103,115	1.29	11 (15%)
7	BCL	N	102	1	69,74,74	0.90	2 (2%)	83,115,115	1.26	13 (15%)
8	SPO	0	103	-	40,41,41	0.18	0	47,50,50	0.65	1 (2%)
9	PC1	A	102	-	44,44,53	0.31	0	50,52,61	0.26	0
7	BCL	3	101	-	69,74,74	0.81	1 (1%)	83,115,115	1.25	12 (14%)
7	BCL	S	201	-	69,74,74	0.86	1 (1%)	83,115,115	1.28	9 (10%)
9	PC1	D	104	-	36,36,53	0.34	0	42,44,61	0.30	0
7	BCL	J	101	1	69,74,74	0.88	2 (2%)	83,115,115	1.30	13 (15%)
9	PC1	L	304	-	34,34,53	0.35	0	40,42,61	0.31	0
7	BCL	Z	101	1	69,74,74	0.84	1 (1%)	83,115,115	1.28	13 (15%)
12	U10	L	308	-	19,19,63	0.29	0	23,26,79	0.66	1 (4%)
8	SPO	O	104	-	40,41,41	0.15	0	47,50,50	0.39	1 (2%)
8	SPO	C	102	-	40,41,41	0.12	0	47,50,50	0.51	1 (2%)
8	SPO	2	102	-	40,41,41	0.14	0	47,50,50	0.65	1 (2%)
7	BCL	G	101	1	69,74,74	0.89	2 (2%)	83,115,115	1.26	13 (15%)
7	BCL	V	102	1	69,74,74	0.87	1 (1%)	83,115,115	1.23	11 (13%)
10	CDL	M	410	-	77,77,99	0.34	0	83,89,111	0.36	0
8	SPO	P	103	-	40,41,41	0.12	0	47,50,50	0.53	1 (2%)
7	BCL	C	101	1	69,74,74	0.85	2 (2%)	83,115,115	1.27	13 (15%)
8	SPO	1	102	-	40,41,41	0.19	0	47,50,50	0.98	4 (8%)
12	U10	M	403	-	43,43,63	0.21	0	52,55,79	0.51	1 (1%)
10	CDL	M	409	-	99,99,99	0.31	0	105,111,111	0.39	0
8	SPO	G	102	-	40,41,41	0.16	0	47,50,50	0.56	0
7	BCL	W	101	-	69,74,74	0.85	2 (2%)	83,115,115	1.24	12 (14%)
12	U10	X	102	-	48,48,63	0.21	0	58,61,79	0.50	1 (1%)
8	SPO	F	101	-	40,41,41	0.20	0	47,50,50	0.56	1 (2%)
9	PC1	M	402	-	46,46,53	0.31	0	52,54,61	0.30	0
8	SPO	N	101	-	40,41,41	0.15	0	47,50,50	0.40	0
7	BCL	D	102	-	69,74,74	0.88	1 (1%)	83,115,115	1.24	13 (15%)
8	SPO	3	102	-	40,41,41	0.15	0	47,50,50	0.58	1 (2%)
7	BCL	O	101	-	69,74,74	0.87	2 (2%)	83,115,115	1.19	9 (10%)
7	BCL	R	101	1	69,74,74	0.90	1 (1%)	83,115,115	1.27	13 (15%)
11	BPH	L	310	-	49,60,70	1.18	3 (6%)	49,89,101	1.04	4 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	BCL	Q	101	2	69,74,74	0.85	2 (2%)	83,115,115	1.21	9 (10%)
7	BCL	2	101	-	64,69,74	0.89	2 (3%)	77,109,115	1.31	12 (15%)
8	SPO	J	102	-	40,41,41	0.14	0	47,50,50	1.00	4 (8%)
7	BCL	M	405	-	69,74,74	0.86	1 (1%)	83,115,115	1.22	12 (14%)
12	U10	L	305	-	43,43,63	0.20	0	52,55,79	0.54	1 (1%)
7	BCL	F	102	-	69,74,74	0.89	1 (1%)	83,115,115	1.23	11 (13%)
7	BCL	E	101	1	69,74,74	0.89	3 (4%)	83,115,115	1.26	13 (15%)
10	CDL	H	301	-	77,77,99	0.32	0	83,89,111	0.31	0
7	BCL	A	101	-	69,74,74	0.87	1 (1%)	83,115,115	1.19	11 (13%)
8	SPO	D	101	-	40,41,41	0.18	0	47,50,50	0.53	1 (2%)
7	BCL	b	102	-	64,69,74	0.85	1 (1%)	77,109,115	1.42	15 (19%)
8	SPO	J	103	-	40,41,41	0.15	0	47,50,50	0.50	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
7	BCL	9	101	-	-	16/41/137/137	-
8	SPO	U	103	-	-	8/47/47/47	-
8	SPO	X	101	-	-	5/44/44/47	-
7	BCL	L	301	-	-	14/41/137/137	-
7	BCL	U	101	-	-	13/41/137/137	-
11	BPH	L	303	-	-	5/34/102/105	0/5/6/6
8	SPO	M	408	-	-	11/47/47/47	-
12	U10	M	407	-	-	6/45/69/87	0/1/1/1
8	SPO	F	103	-	-	11/47/47/47	-
12	U10	L	309	-	-	9/33/57/87	0/1/1/1
9	PC1	A	103	-	-	13/35/35/57	-
8	SPO	b	101	-	-	10/47/47/47	-
7	BCL	P	101	1	-	26/41/137/137	-
7	BCL	B	101	1	-	14/41/137/137	-
8	SPO	V	101	-	-	9/47/47/47	-
8	SPO	0	102	-	-	10/47/47/47	-
8	SPO	O	102	-	-	5/47/47/47	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	SPO	D	103	-	-	16/47/47/47	-
8	SPO	P	102	-	-	10/47/47/47	-
7	BCL	0	101	1	-	10/35/131/137	-
7	BCL	K	101	-	-	18/41/137/137	-
9	PC1	M	401	-	-	16/43/43/57	-
9	PC1	O	103	-	-	8/35/35/57	-
9	PC1	A	104	-	-	9/35/35/57	-
8	SPO	Z	102	-	-	15/47/47/47	-
7	BCL	T	101	1	-	19/41/137/137	-
9	PC1	M	411	-	-	12/48/48/57	-
7	BCL	L	302	-	-	5/38/134/137	-
8	SPO	T	102	-	-	9/47/47/47	-
9	PC1	L	306	-	-	7/39/39/57	-
7	BCL	I	101	-	-	16/41/137/137	-
8	SPO	9	102	-	-	6/47/47/47	-
8	SPO	U	102	-	-	7/47/47/47	-
7	BCL	7	101	-	-	22/35/131/137	-
8	SPO	S	202	-	-	17/47/47/47	-
8	SPO	I	102	-	-	7/47/47/47	-
7	BCL	a	101	-	-	12/29/125/137	-
9	PC1	L	311	-	-	16/35/35/57	-
12	U10	L	307	-	-	11/45/69/87	0/1/1/1
7	BCL	M	404	-	-	13/41/137/137	-
7	BCL	8	101	-	-	14/41/137/137	-
7	BCL	1	101	-	-	10/29/125/137	-
7	BCL	N	102	1	-	17/41/137/137	-
8	SPO	0	103	-	-	11/47/47/47	-
9	PC1	A	102	-	-	20/48/48/57	-
7	BCL	3	101	-	-	10/41/137/137	-
7	BCL	S	201	-	-	14/41/137/137	-
9	PC1	D	104	-	-	14/40/40/57	-
7	BCL	J	101	1	-	18/41/137/137	-
9	PC1	L	304	-	-	10/38/38/57	-
7	BCL	Z	101	1	-	21/41/137/137	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	U10	L	308	-	-	4/11/35/87	0/1/1/1
8	SPO	O	104	-	-	9/47/47/47	-
8	SPO	C	102	-	-	7/47/47/47	-
8	SPO	2	102	-	-	10/47/47/47	-
7	BCL	G	101	1	-	27/41/137/137	-
7	BCL	V	102	1	-	17/41/137/137	-
10	CDL	M	410	-	-	28/88/88/110	-
8	SPO	P	103	-	-	14/47/47/47	-
7	BCL	C	101	1	-	19/41/137/137	-
8	SPO	1	102	-	-	11/47/47/47	-
12	U10	M	403	-	-	11/39/63/87	0/1/1/1
10	CDL	M	409	-	-	51/110/110/110	-
8	SPO	G	102	-	-	10/47/47/47	-
7	BCL	W	101	-	-	13/41/137/137	-
12	U10	X	102	-	-	16/45/69/87	0/1/1/1
8	SPO	F	101	-	-	6/47/47/47	-
9	PC1	M	402	-	-	17/50/50/57	-
8	SPO	N	101	-	-	8/47/47/47	-
7	BCL	D	102	-	-	21/41/137/137	-
8	SPO	3	102	-	-	11/47/47/47	-
7	BCL	O	101	-	-	17/41/137/137	-
7	BCL	R	101	1	-	24/41/137/137	-
11	BPH	L	310	-	-	6/25/93/105	0/5/6/6
7	BCL	Q	101	2	-	15/41/137/137	-
7	BCL	2	101	-	-	21/35/131/137	-
8	SPO	J	102	-	-	8/47/47/47	-
7	BCL	M	405	-	-	11/41/137/137	-
12	U10	L	305	-	-	9/39/63/87	0/1/1/1
7	BCL	F	102	-	-	19/41/137/137	-
7	BCL	E	101	1	-	23/41/137/137	-
10	CDL	H	301	-	-	29/88/88/110	-
7	BCL	A	101	-	-	16/41/137/137	-
8	SPO	D	101	-	-	3/47/47/47	-
7	BCL	b	102	-	-	20/35/131/137	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	SPO	J	103	-	-	8/47/47/47	-

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	L	303	BPH	C1D-C2D	6.31	1.46	1.39
11	L	310	BPH	C1D-C2D	6.17	1.46	1.39
7	L	302	BCL	C4D-ND	-6.05	1.29	1.37
7	I	101	BCL	C4D-ND	-5.96	1.29	1.37
7	F	102	BCL	C4D-ND	-5.89	1.29	1.37

The worst 5 of 454 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	U	101	BCL	CAC-C3C-C2C	-4.91	101.99	114.26
7	1	101	BCL	CAC-C3C-C2C	-4.87	102.10	114.26
7	a	101	BCL	CAC-C3C-C2C	-4.77	102.34	114.26
7	N	102	BCL	CAC-C3C-C2C	-4.77	102.35	114.26
7	T	101	BCL	CAC-C3C-C2C	-4.75	102.39	114.26

There are no chirality outliers.

5 of 1164 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	0	101	BCL	C2C-C3C-CAC-CBC
7	1	101	BCL	CBD-CGD-O2D-CED
7	1	101	BCL	O1D-CGD-O2D-CED
7	1	101	BCL	C1-C2-C3-C4
7	1	101	BCL	C1-C2-C3-C5

There are no ring outliers.

84 monomers are involved in 592 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	9	101	BCL	10	0
8	U	103	SPO	8	0
8	X	101	SPO	5	0
7	L	301	BCL	7	0
7	U	101	BCL	10	0
11	L	303	BPH	4	0
8	M	408	SPO	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	M	407	U10	4	0
8	F	103	SPO	2	0
12	L	309	U10	5	0
9	A	103	PC1	1	0
8	b	101	SPO	15	0
7	P	101	BCL	5	0
7	B	101	BCL	7	0
8	V	101	SPO	10	0
8	0	102	SPO	4	0
8	O	102	SPO	5	0
8	D	103	SPO	12	0
8	P	102	SPO	7	0
7	0	101	BCL	7	0
7	K	101	BCL	5	0
9	M	401	PC1	4	0
9	A	104	PC1	7	0
8	Z	102	SPO	8	0
7	T	101	BCL	7	0
9	M	411	PC1	5	0
7	L	302	BCL	6	0
8	T	102	SPO	7	0
7	I	101	BCL	14	0
8	9	102	SPO	5	0
8	U	102	SPO	5	0
7	7	101	BCL	5	0
8	S	202	SPO	17	0
8	I	102	SPO	12	0
7	a	101	BCL	19	0
9	L	311	PC1	2	0
12	L	307	U10	4	0
7	M	404	BCL	13	0
7	8	101	BCL	5	0
7	1	101	BCL	27	0
7	N	102	BCL	16	0
8	0	103	SPO	9	0
9	A	102	PC1	14	0
7	3	101	BCL	13	0
7	S	201	BCL	14	0
9	D	104	PC1	3	0
7	J	101	BCL	19	0
9	L	304	PC1	2	0
7	Z	101	BCL	18	0

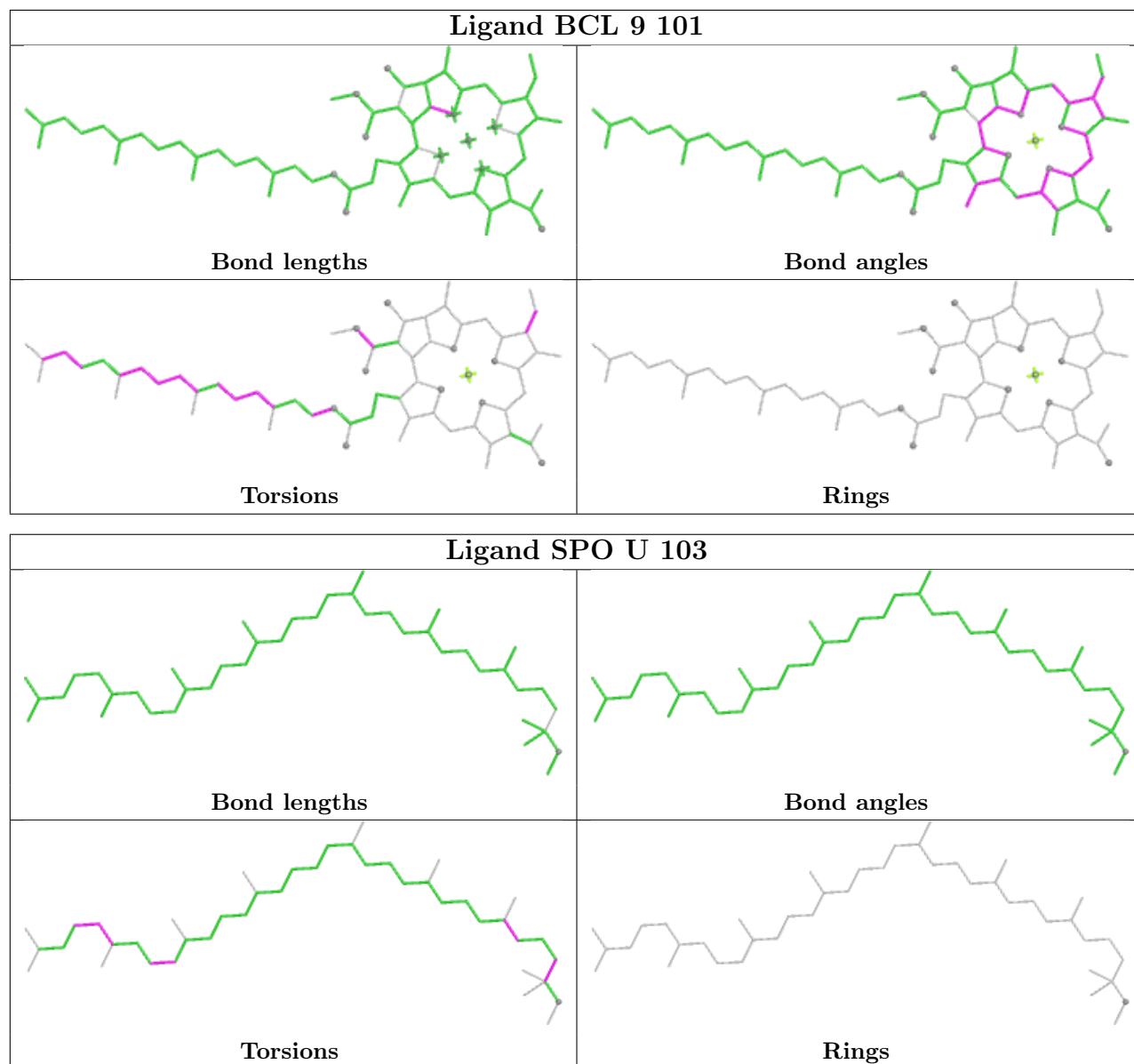
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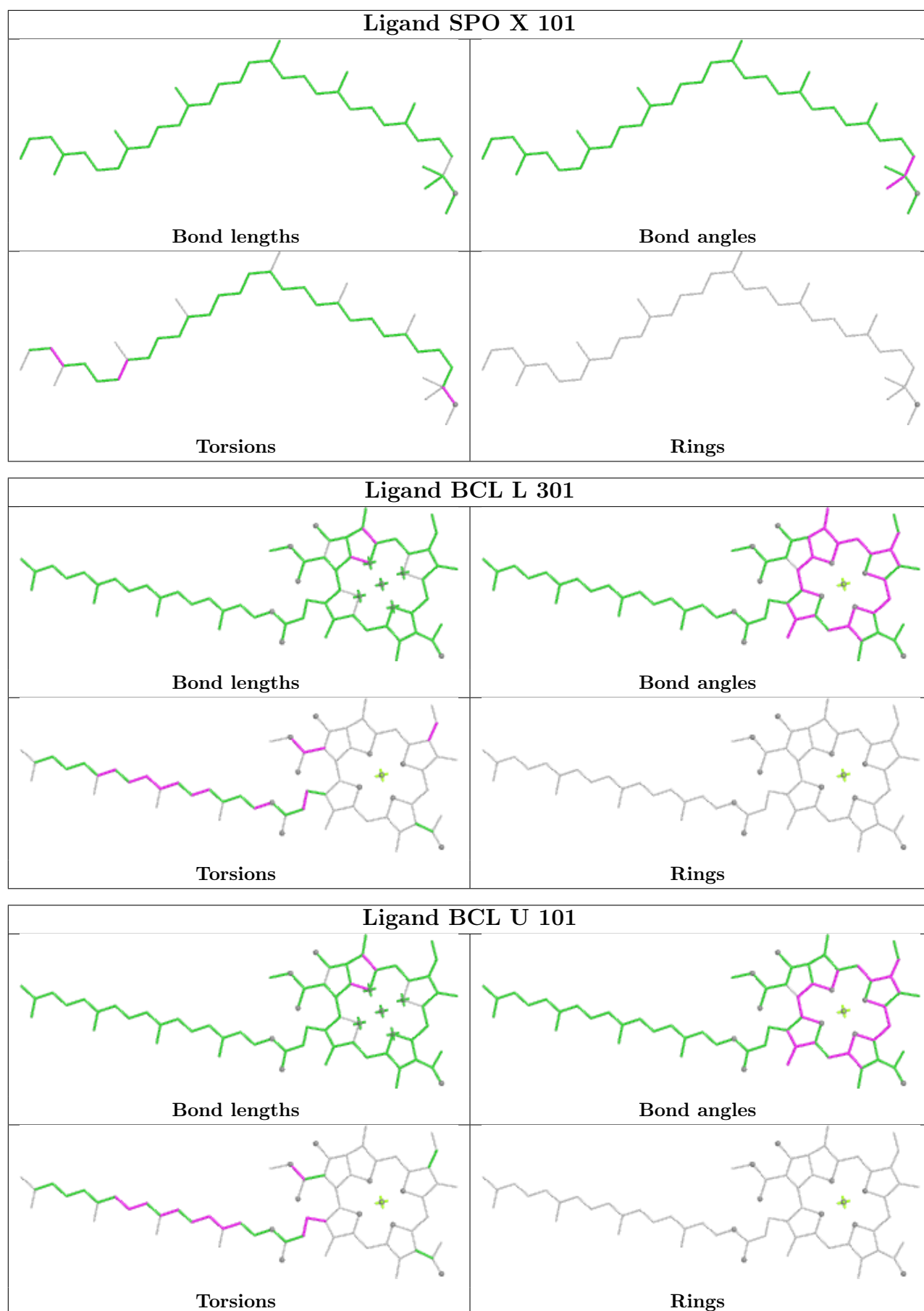
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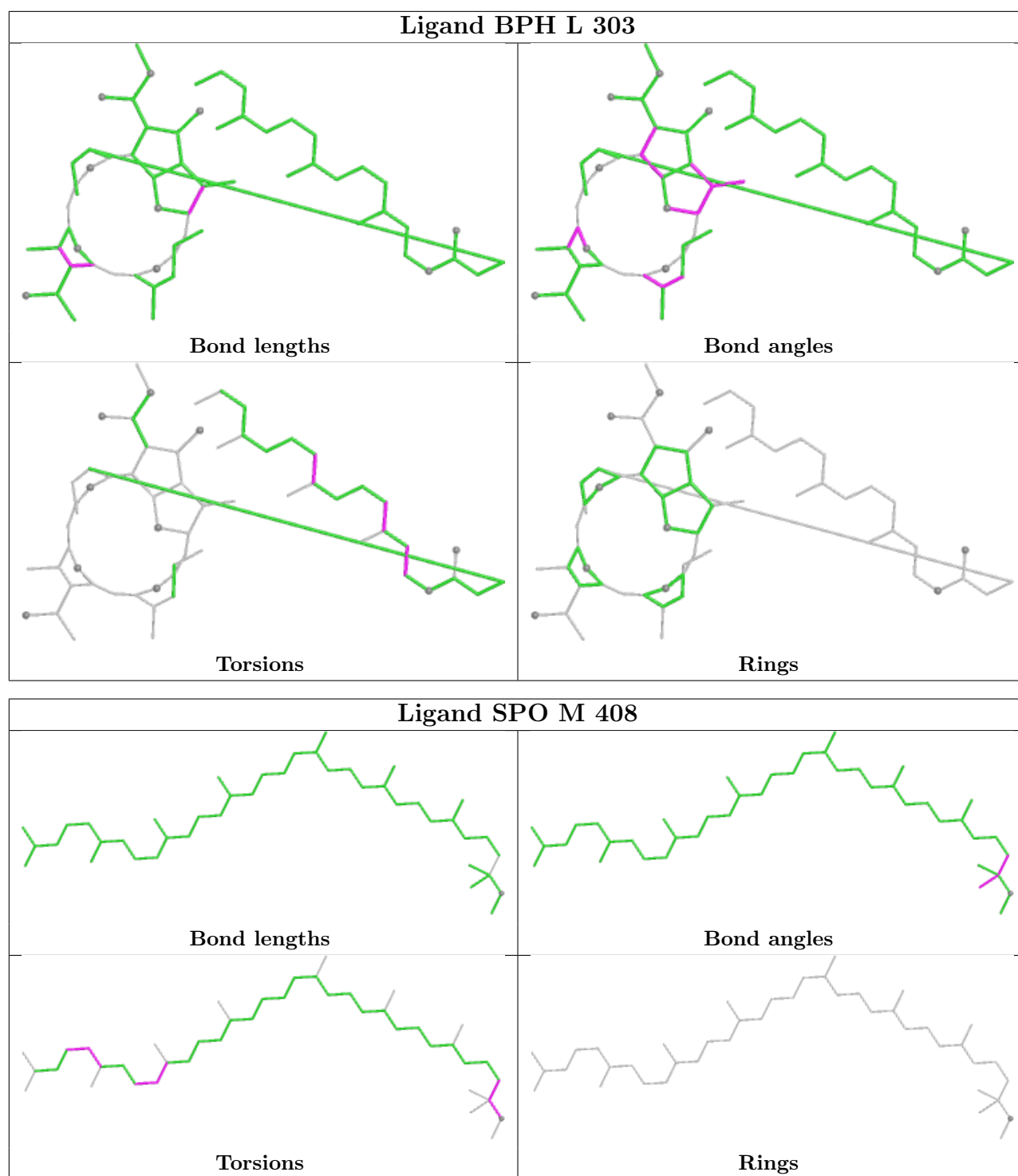
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	L	308	U10	4	0
8	O	104	SPO	9	0
8	C	102	SPO	8	0
8	2	102	SPO	12	0
7	G	101	BCL	11	0
7	V	102	BCL	6	0
10	M	410	CDL	1	0
8	P	103	SPO	6	0
7	C	101	BCL	8	0
8	1	102	SPO	16	0
12	M	403	U10	1	0
10	M	409	CDL	2	0
8	G	102	SPO	6	0
7	W	101	BCL	9	0
12	X	102	U10	10	0
8	F	101	SPO	2	0
9	M	402	PC1	1	0
8	N	101	SPO	5	0
7	D	102	BCL	5	0
8	3	102	SPO	19	0
7	O	101	BCL	10	0
7	R	101	BCL	8	0
11	L	310	BPH	4	0
7	Q	101	BCL	8	0
7	2	101	BCL	11	0
8	J	102	SPO	19	0
7	M	405	BCL	6	0
12	L	305	U10	6	0
7	F	102	BCL	6	0
7	E	101	BCL	20	0
10	H	301	CDL	21	0
7	A	101	BCL	5	0
8	D	101	SPO	2	0
7	b	102	BCL	7	0
8	J	103	SPO	20	0

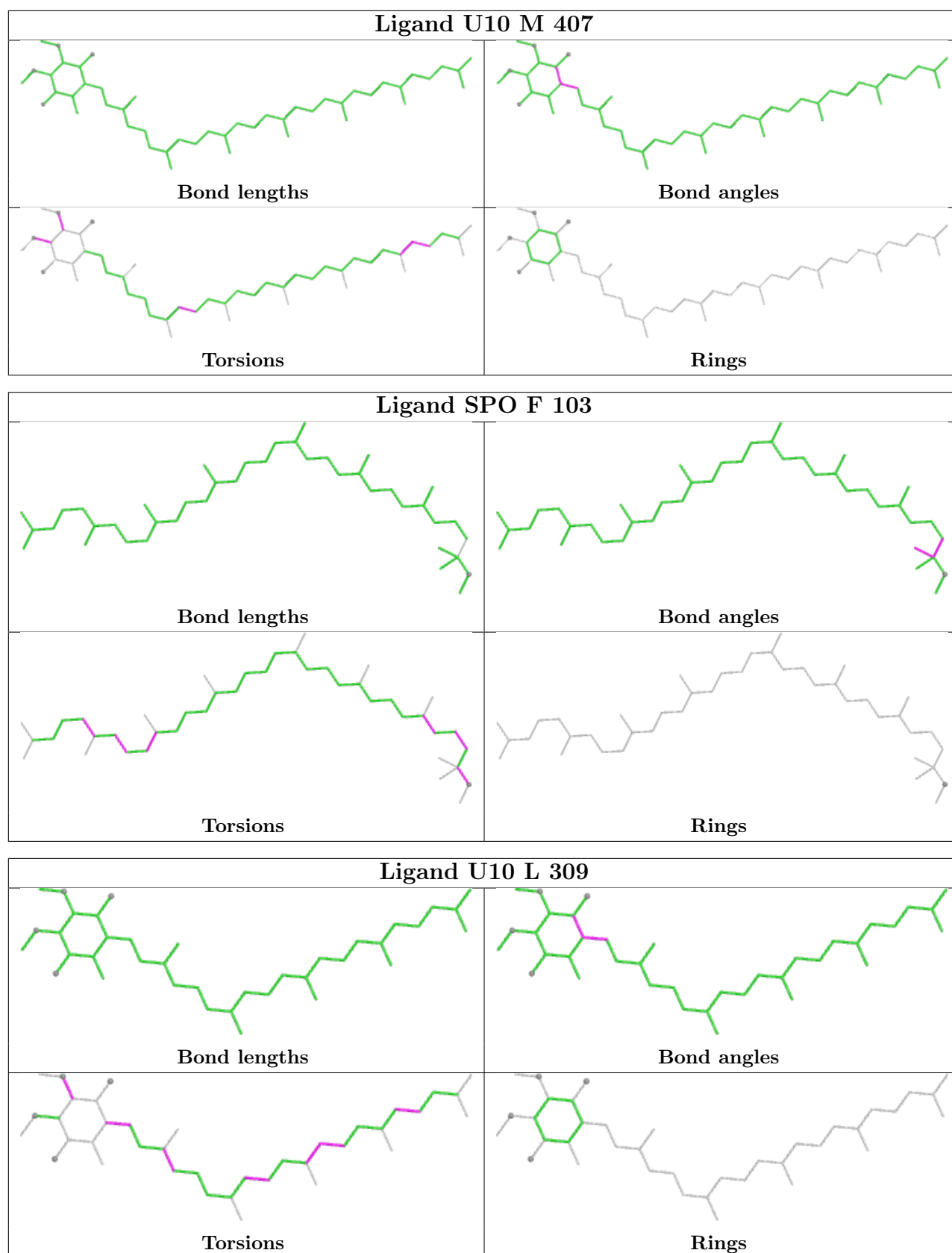
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

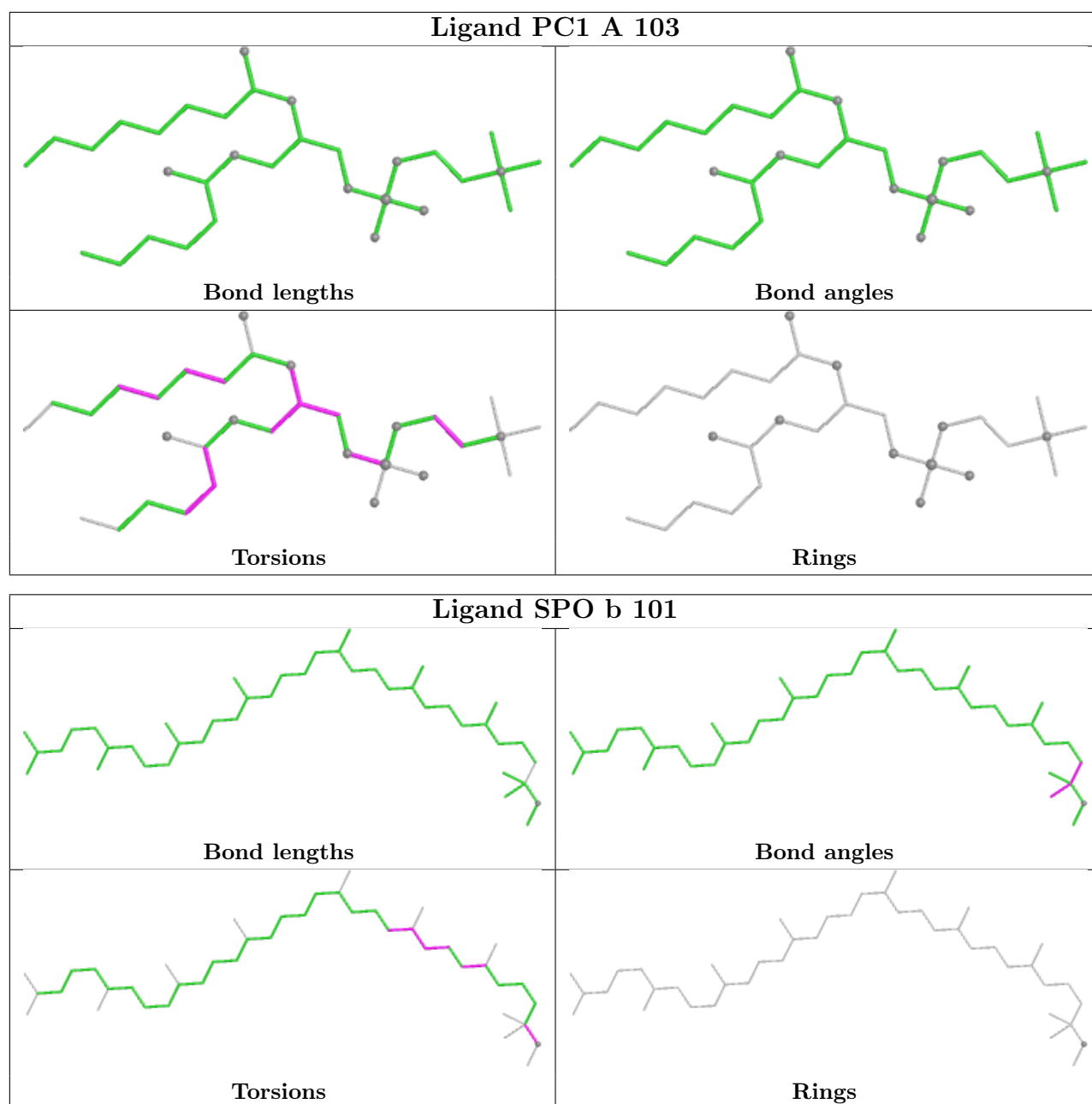
in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers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

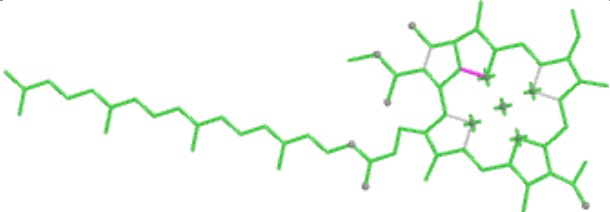
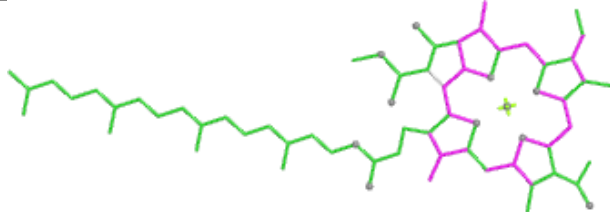
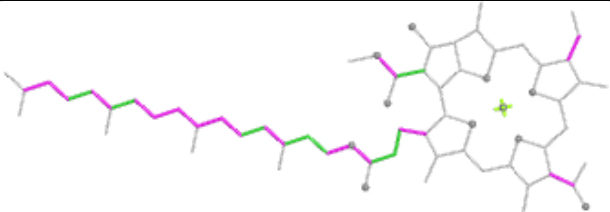
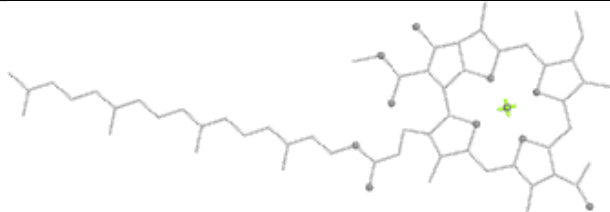
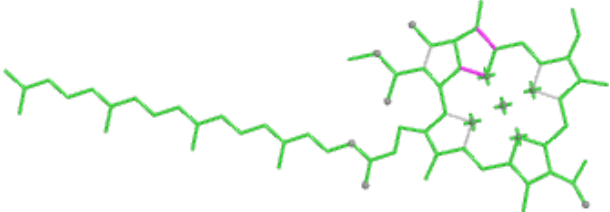
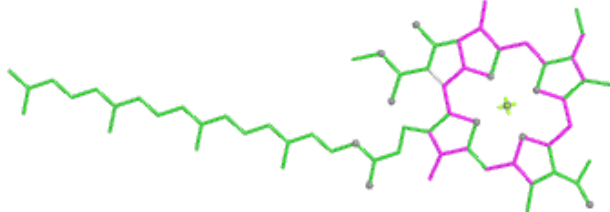
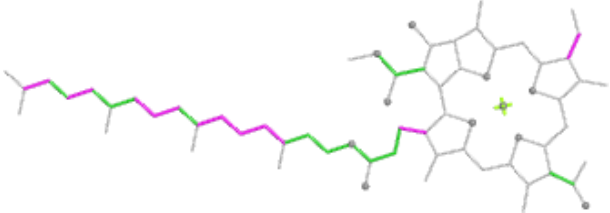
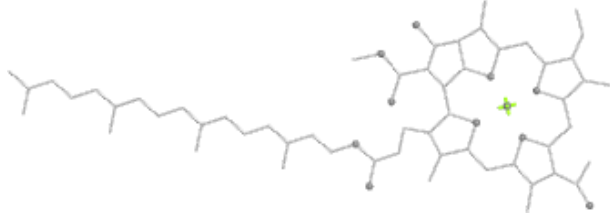
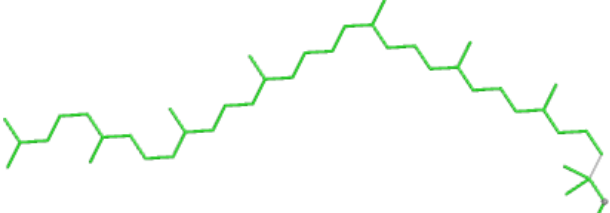
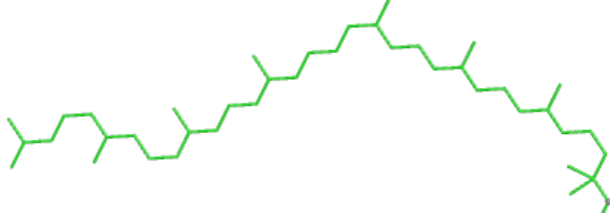
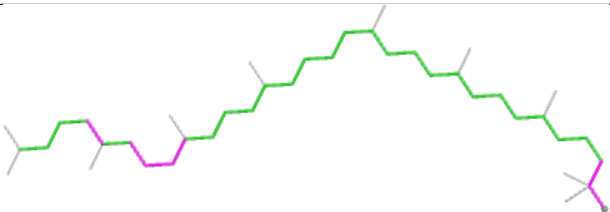
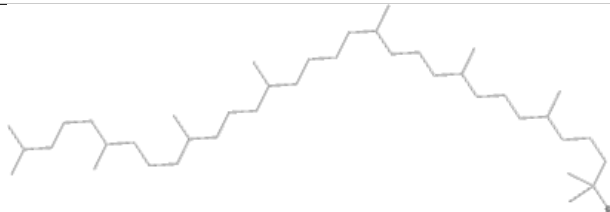


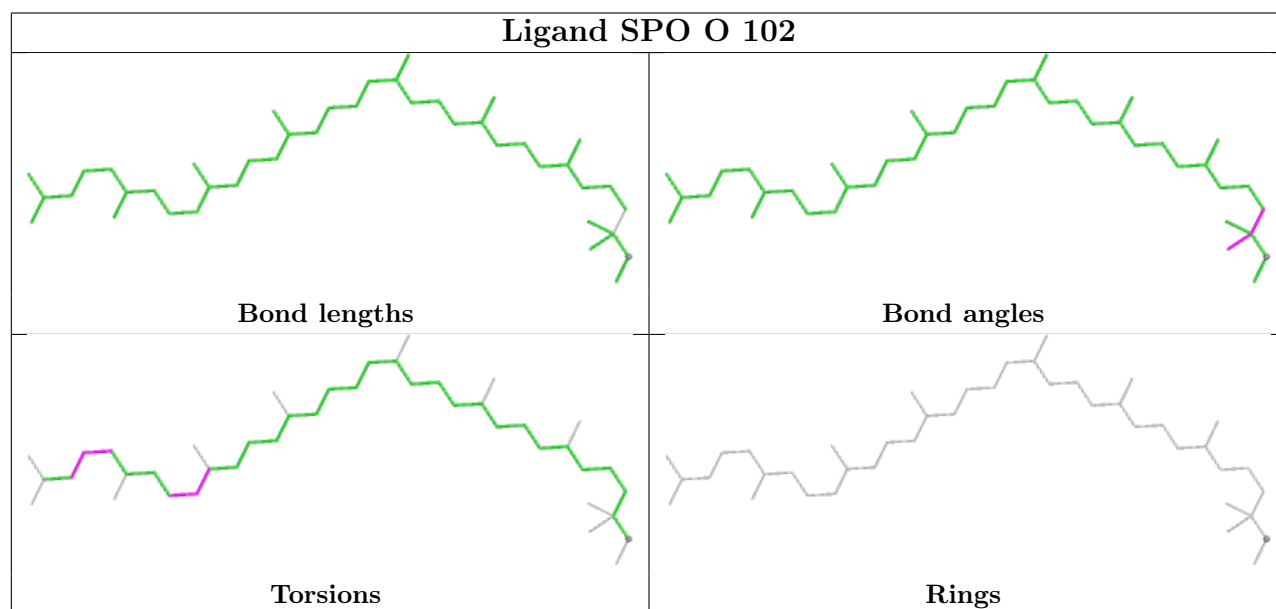
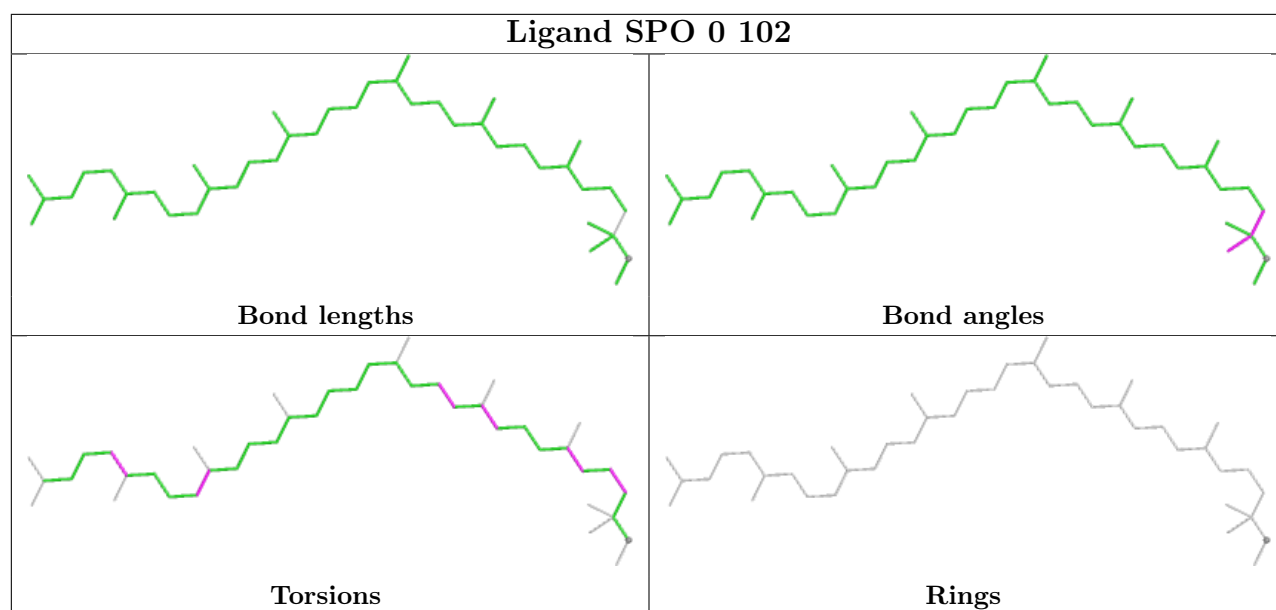


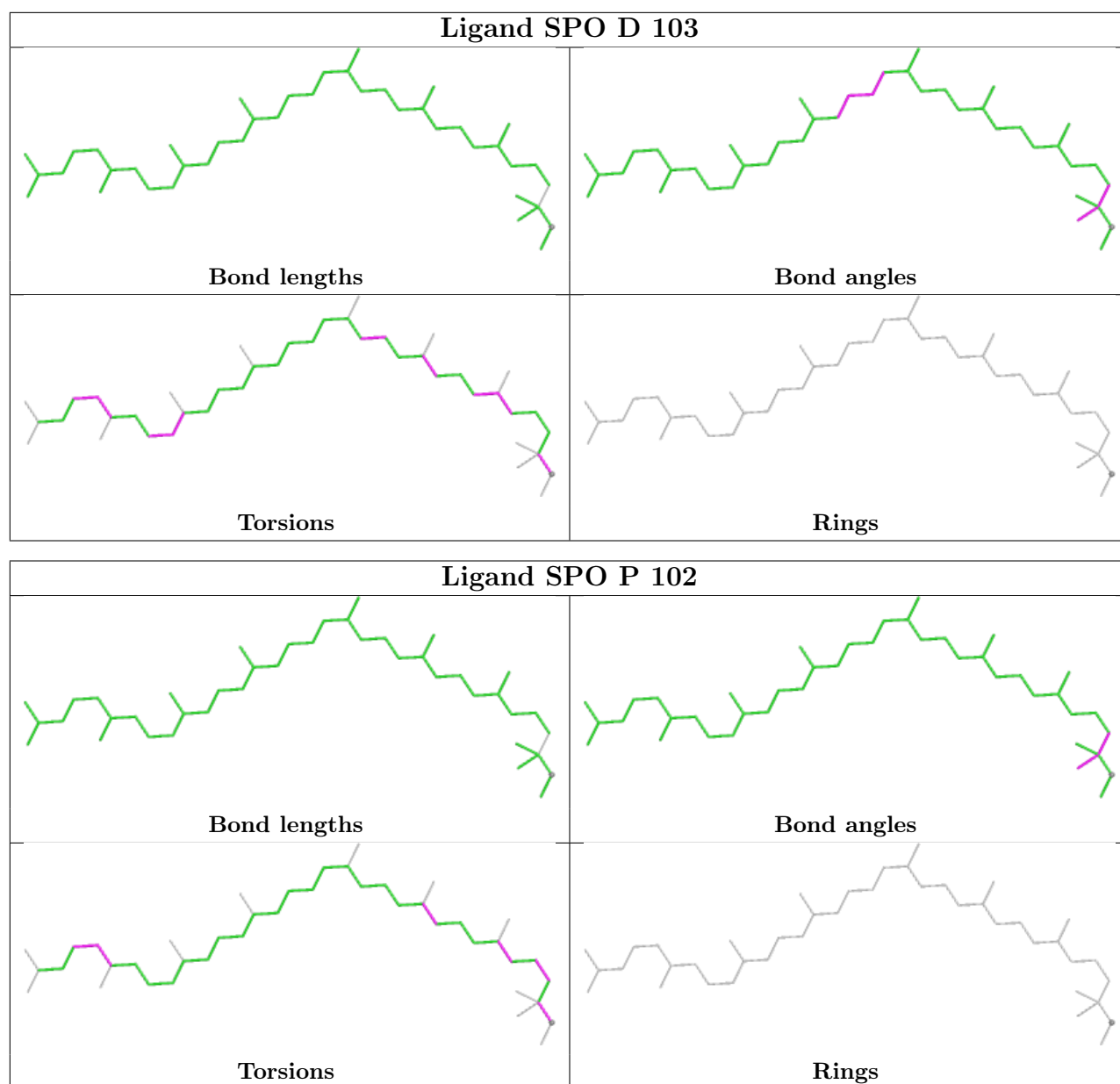


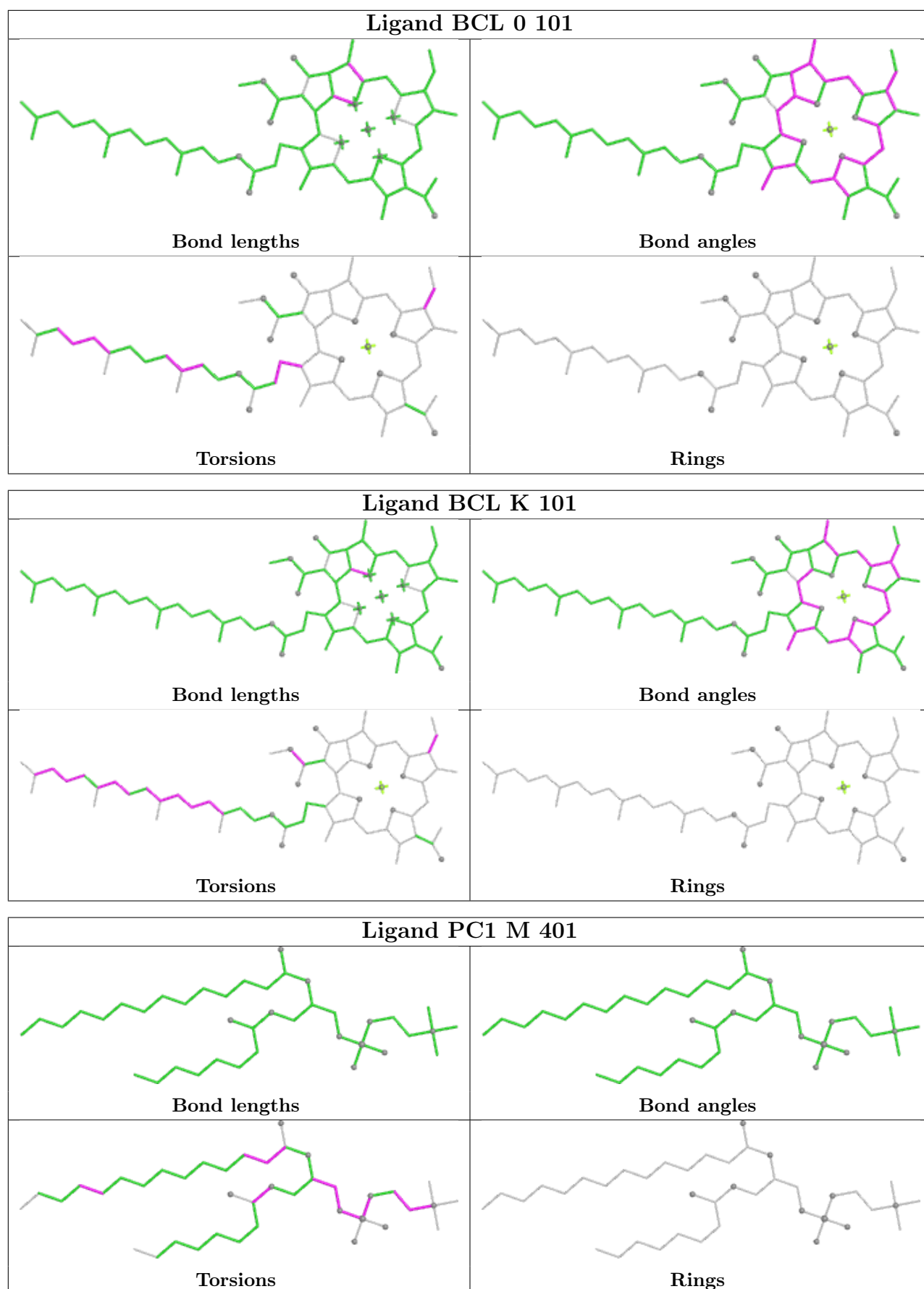


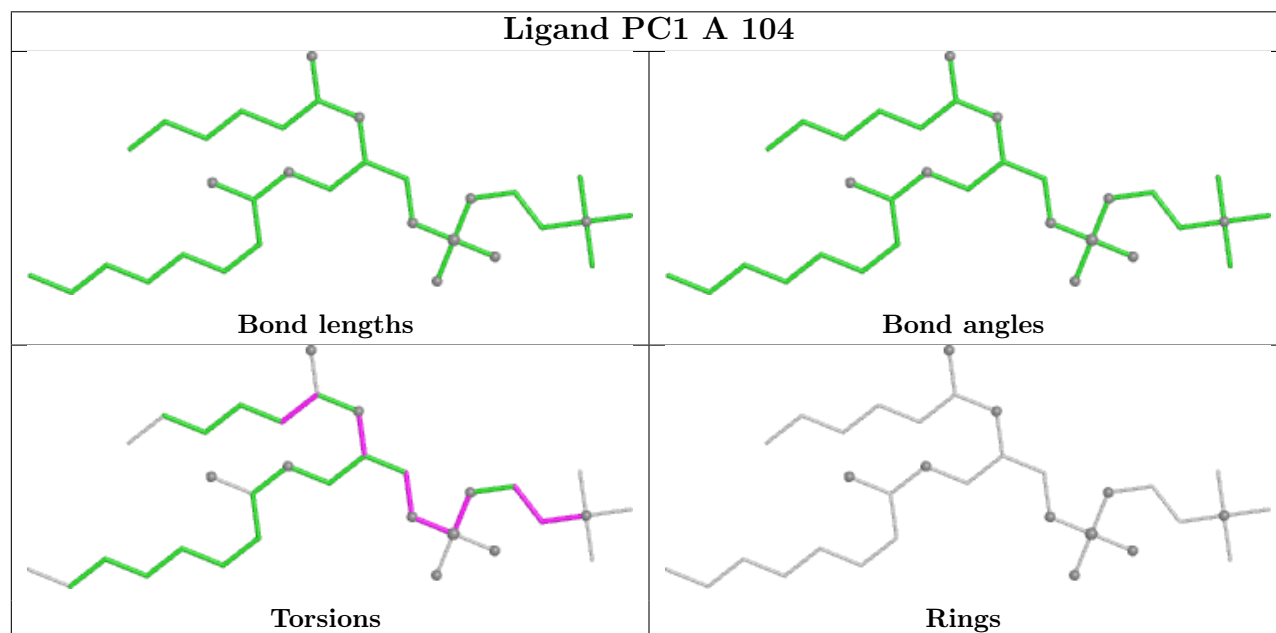
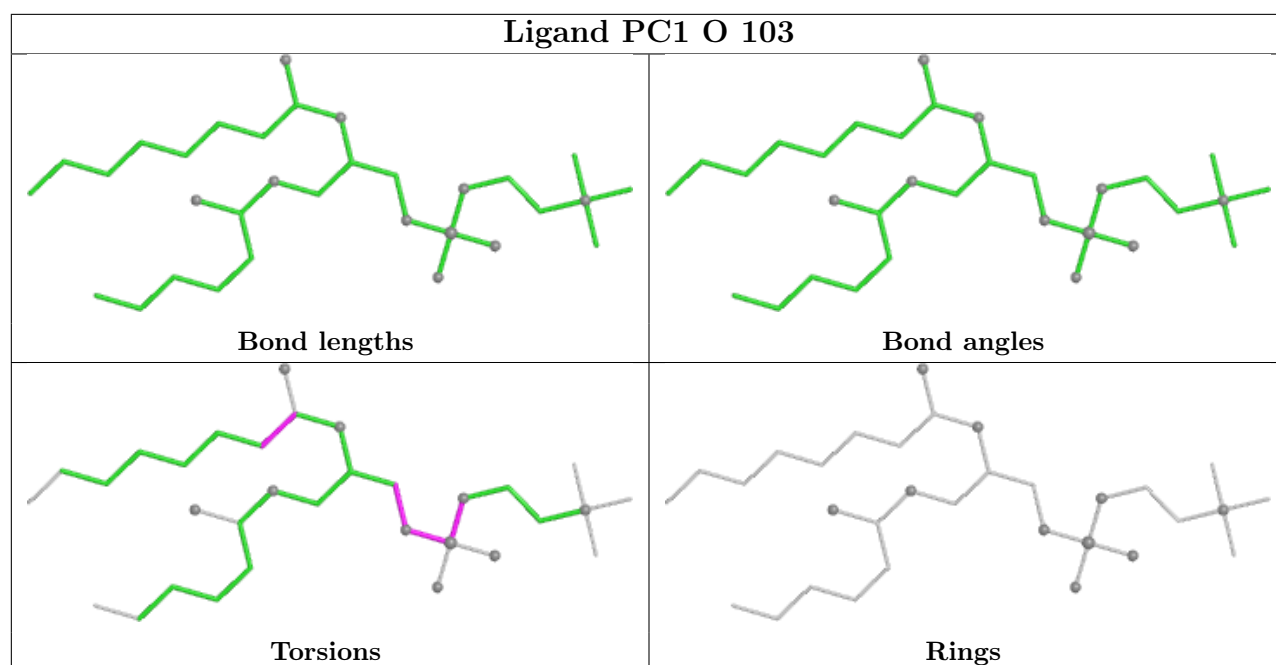


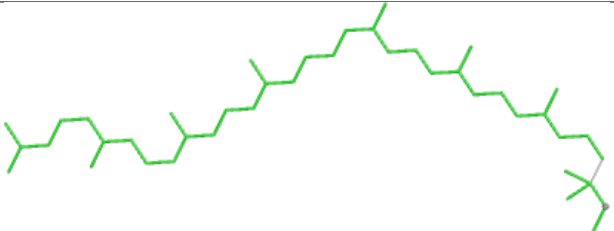
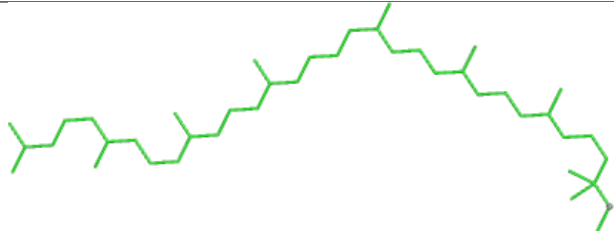
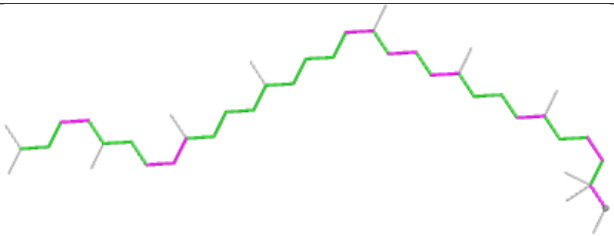
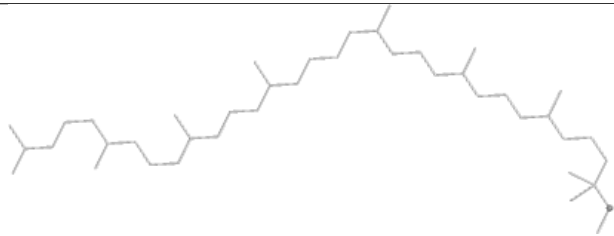
Ligand BCL P 101	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand BCL B 101	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand SPO V 101	
 Bond lengths	 Bond angles
 Torsions	 Rings

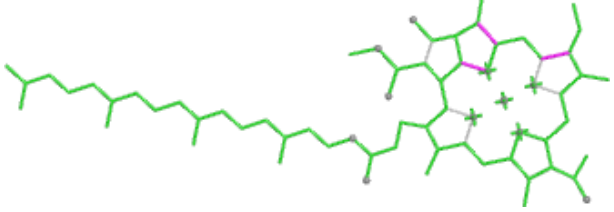
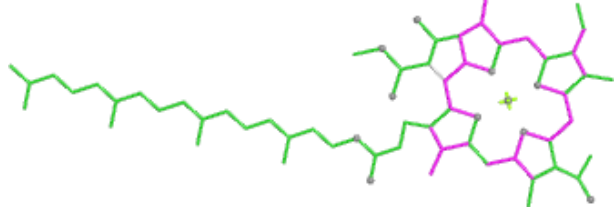
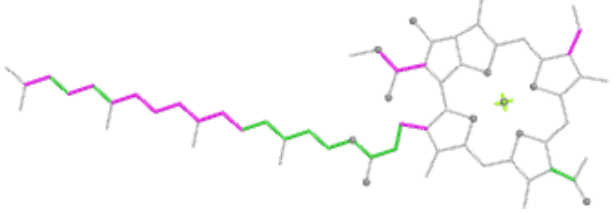
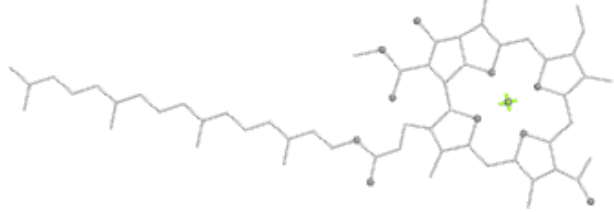


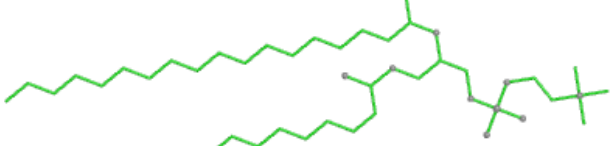
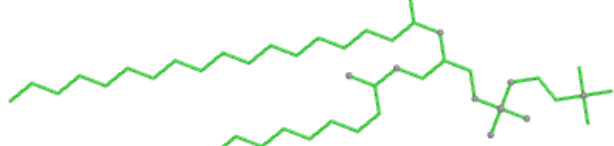
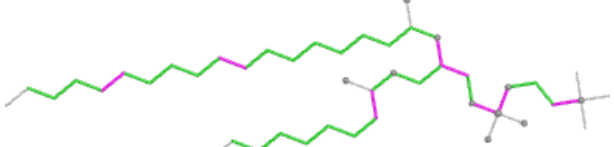


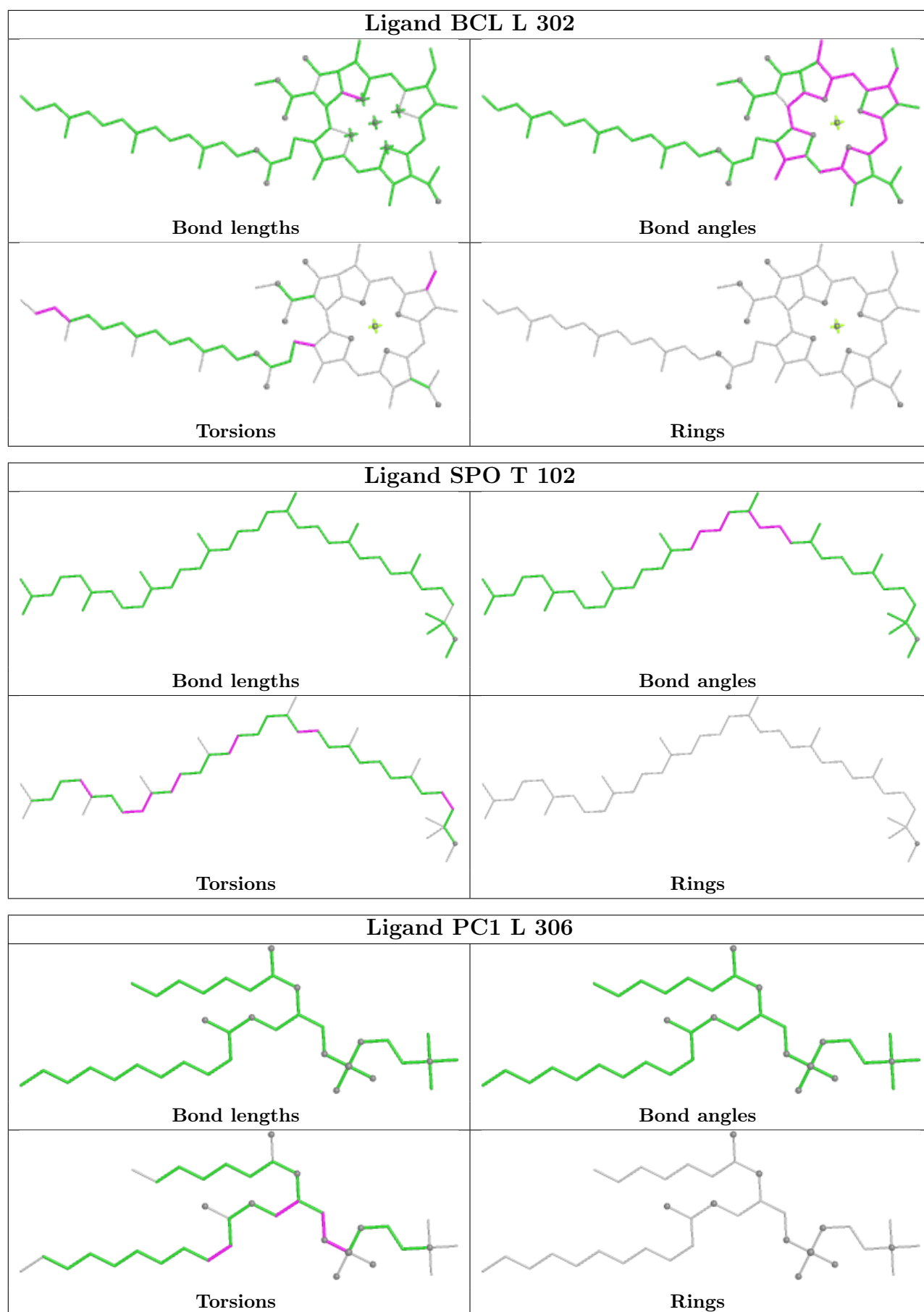


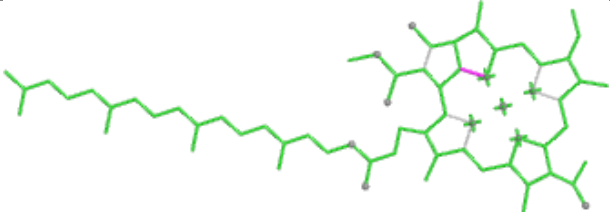
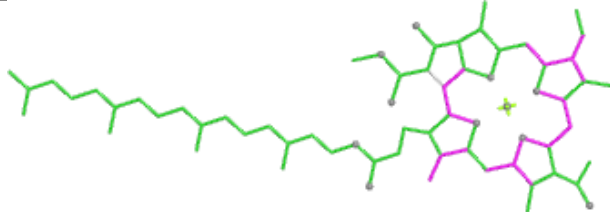
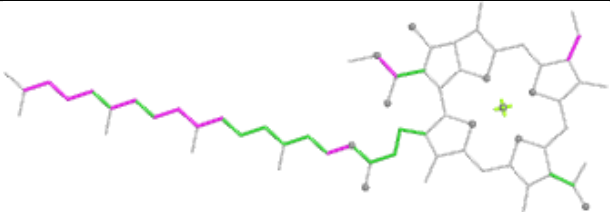
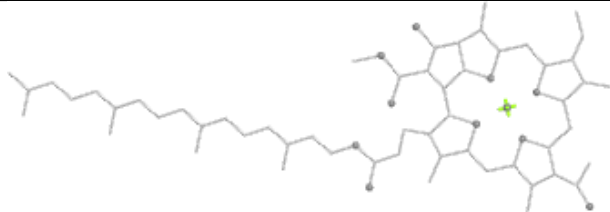
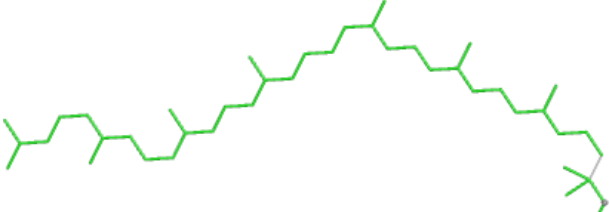
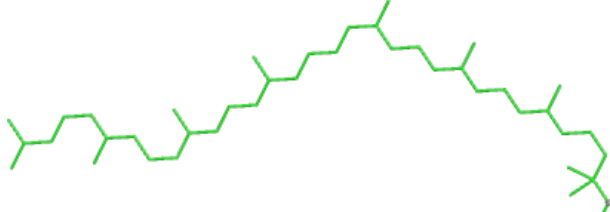
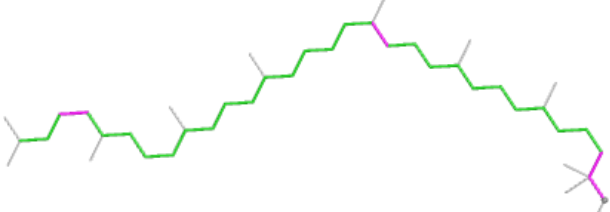
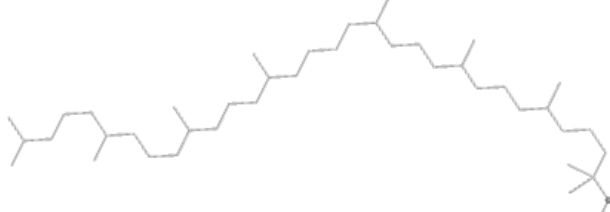


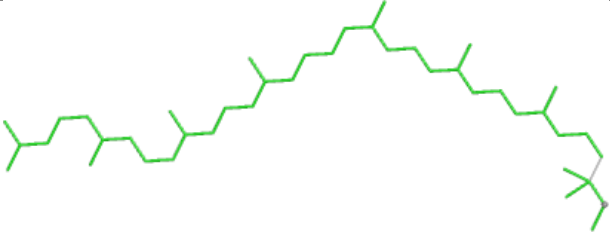
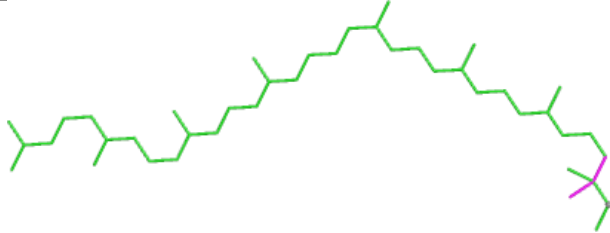
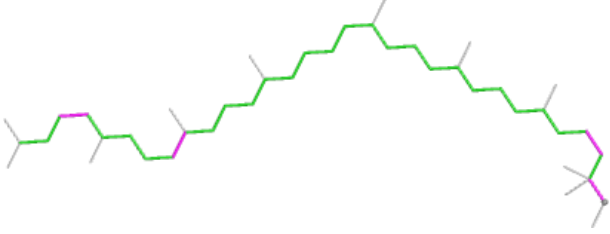
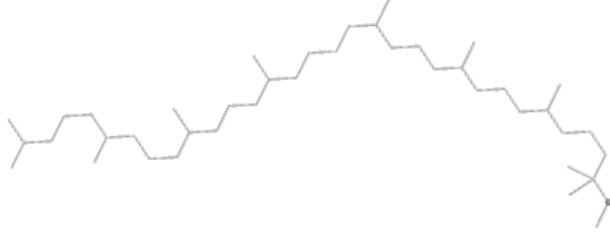
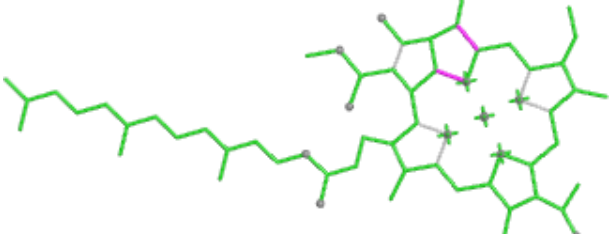
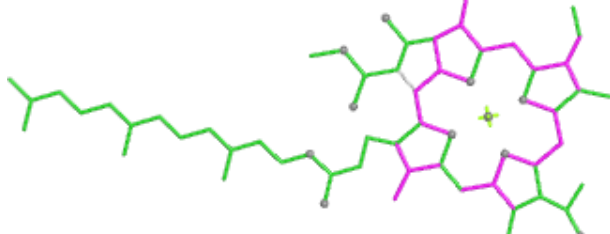
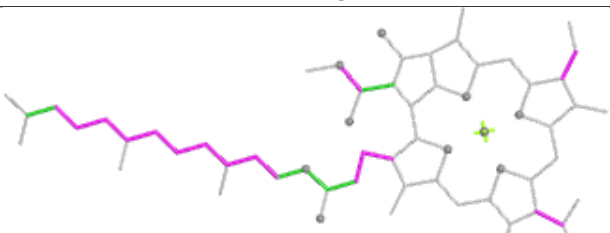
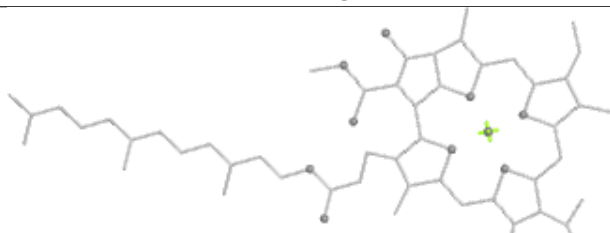
Ligand SPO Z 102	
	
Bond lengths	Bond angles
	
Torsions	Rings

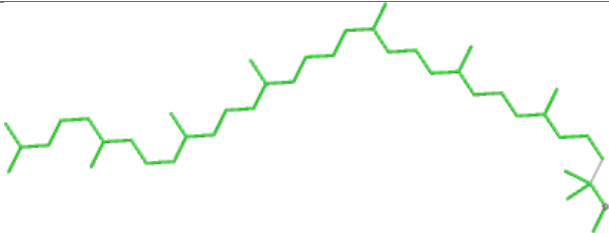
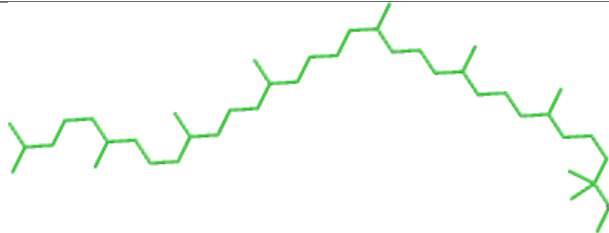
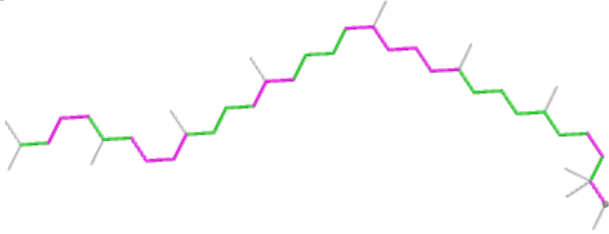
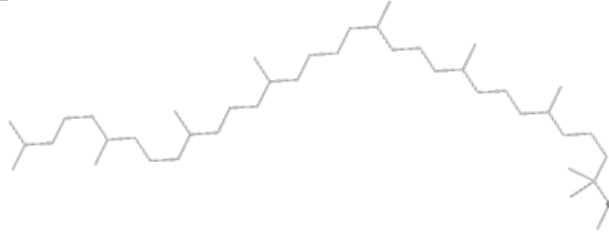
Ligand BCL T 101	
	
Bond lengths	Bond angles
	
Torsions	Rings

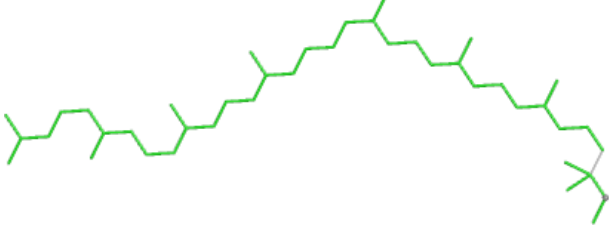
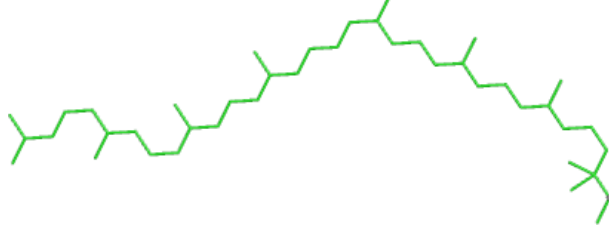
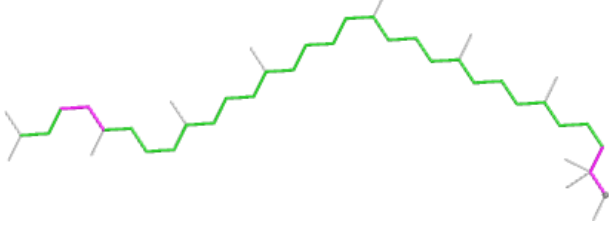
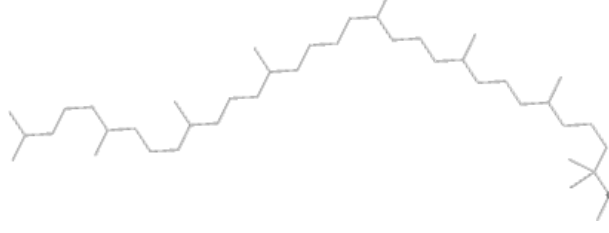
Ligand PC1 M 411	
	
Bond lengths	Bond angles
	
Torsions	Rings

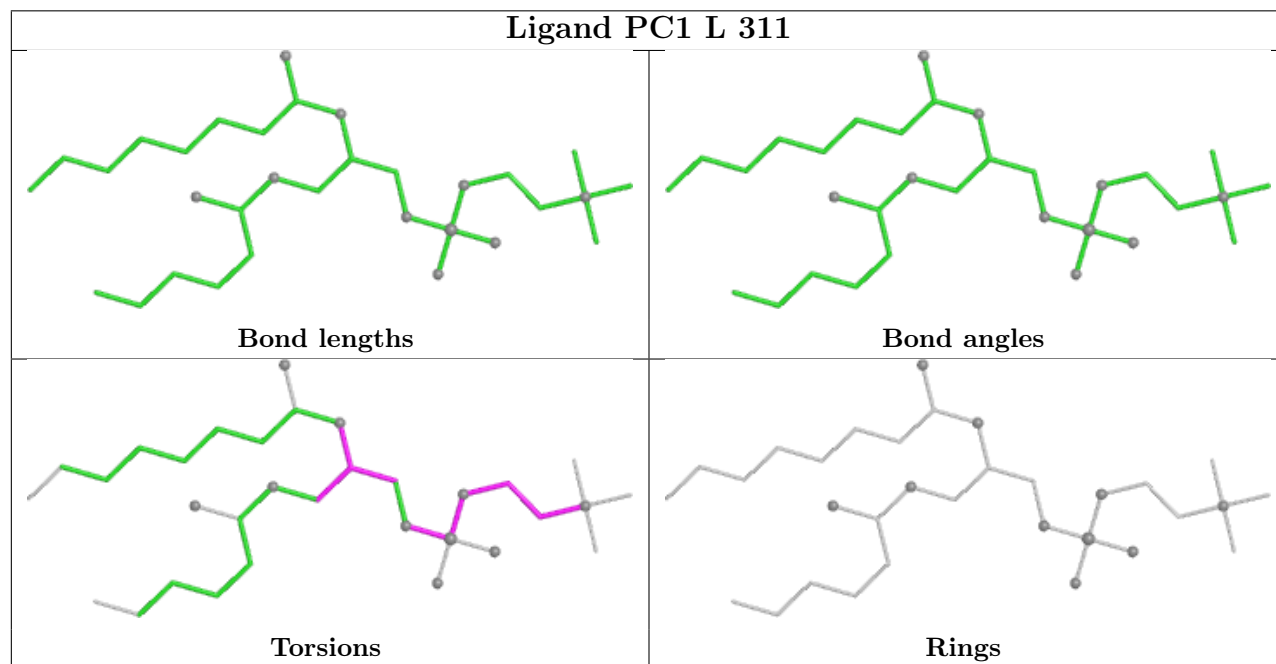
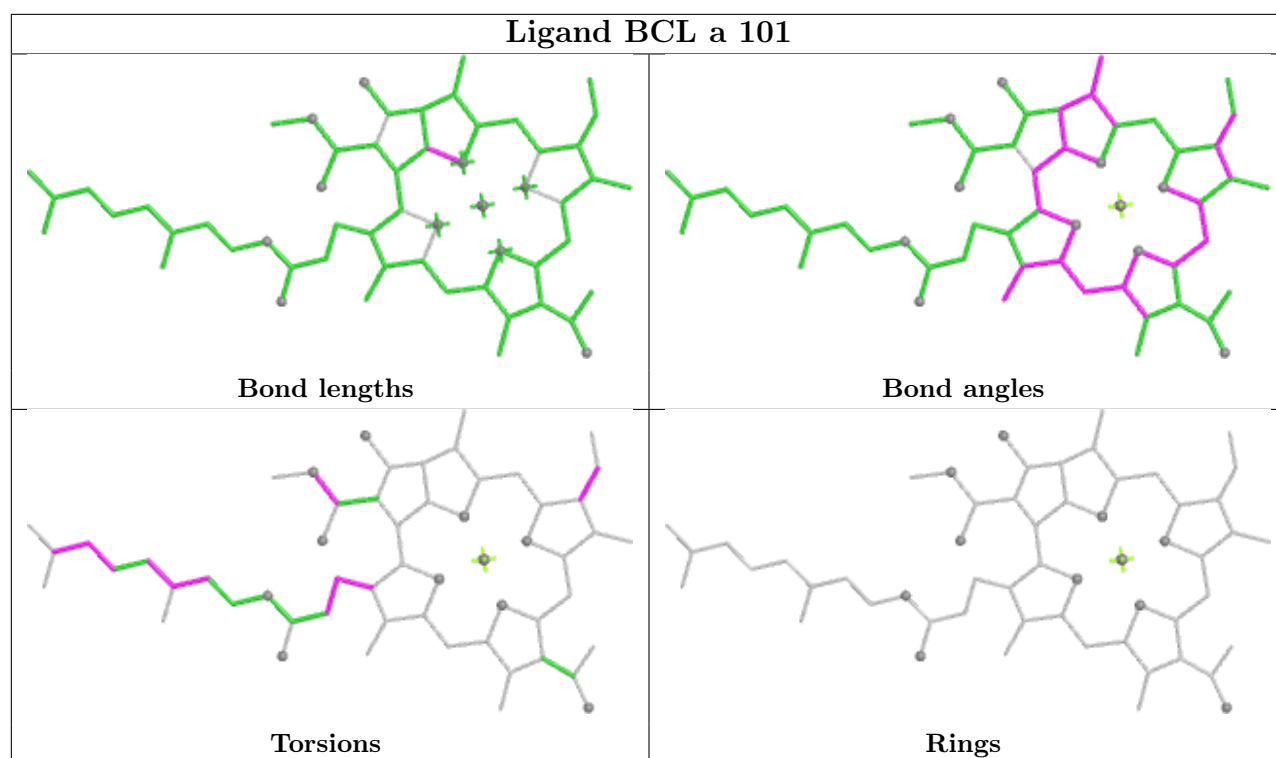


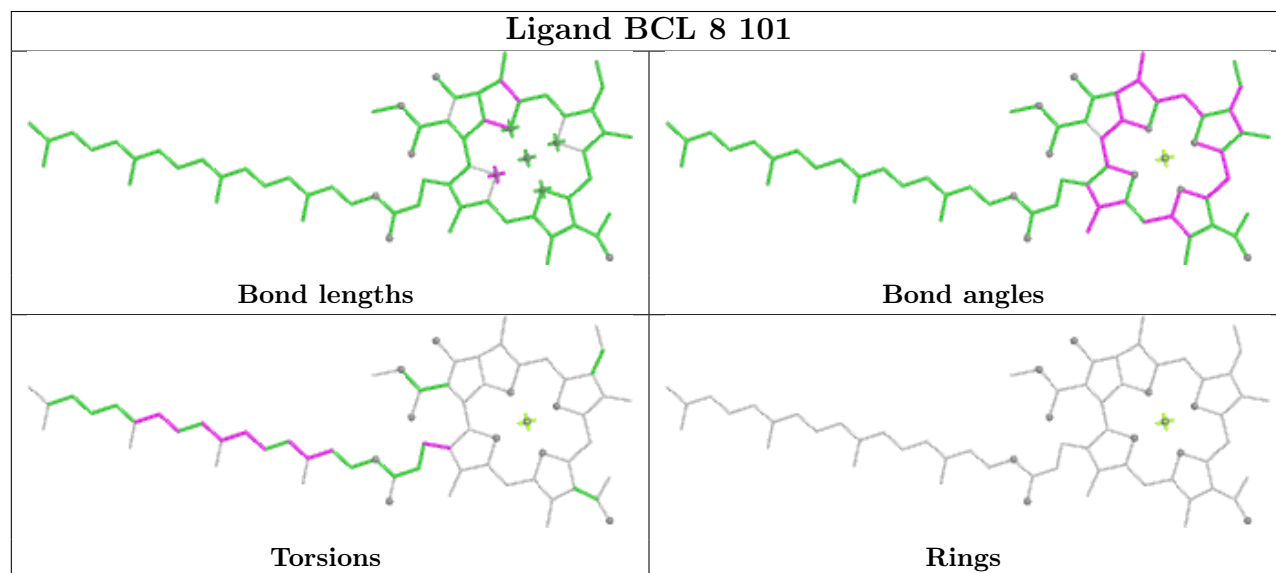
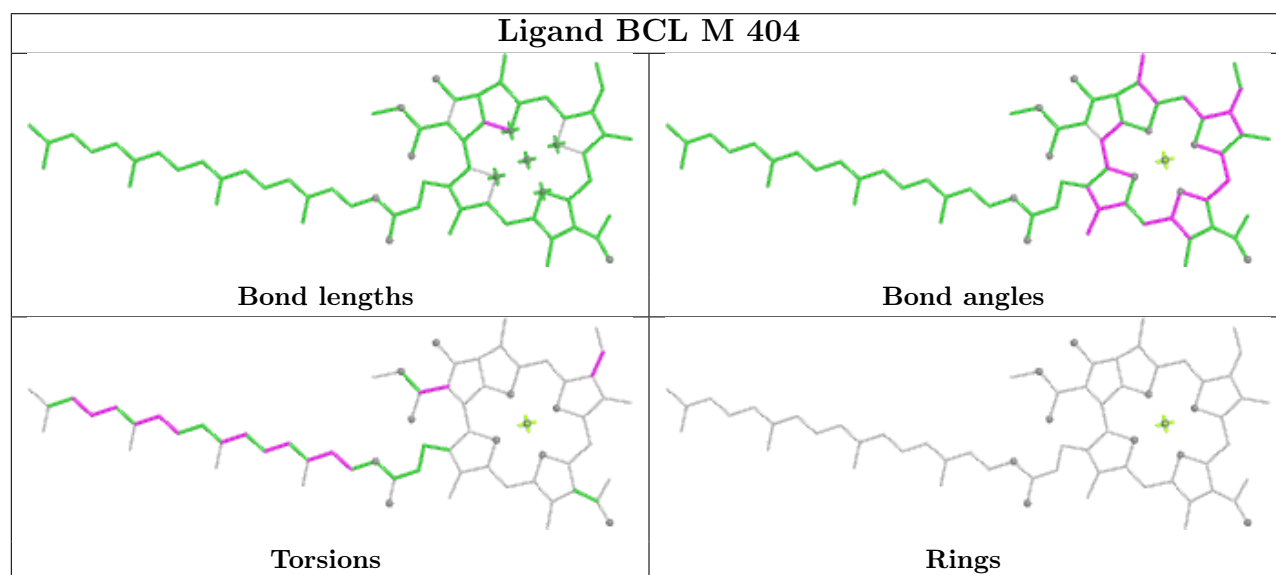
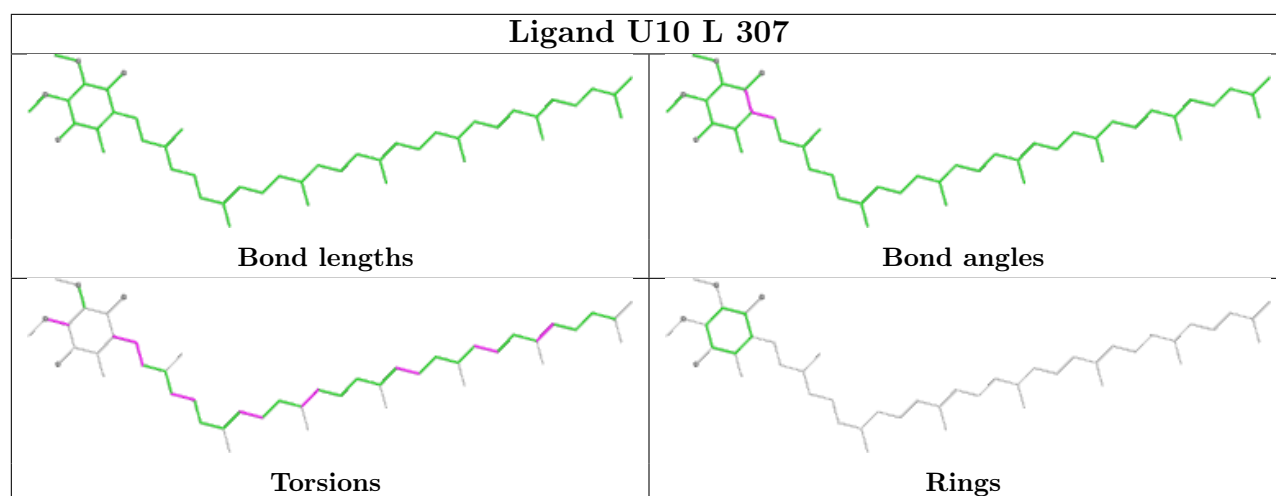
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 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand SPO 9 102	
 Bond lengths	 Bond angles
 Torsions	 Rings

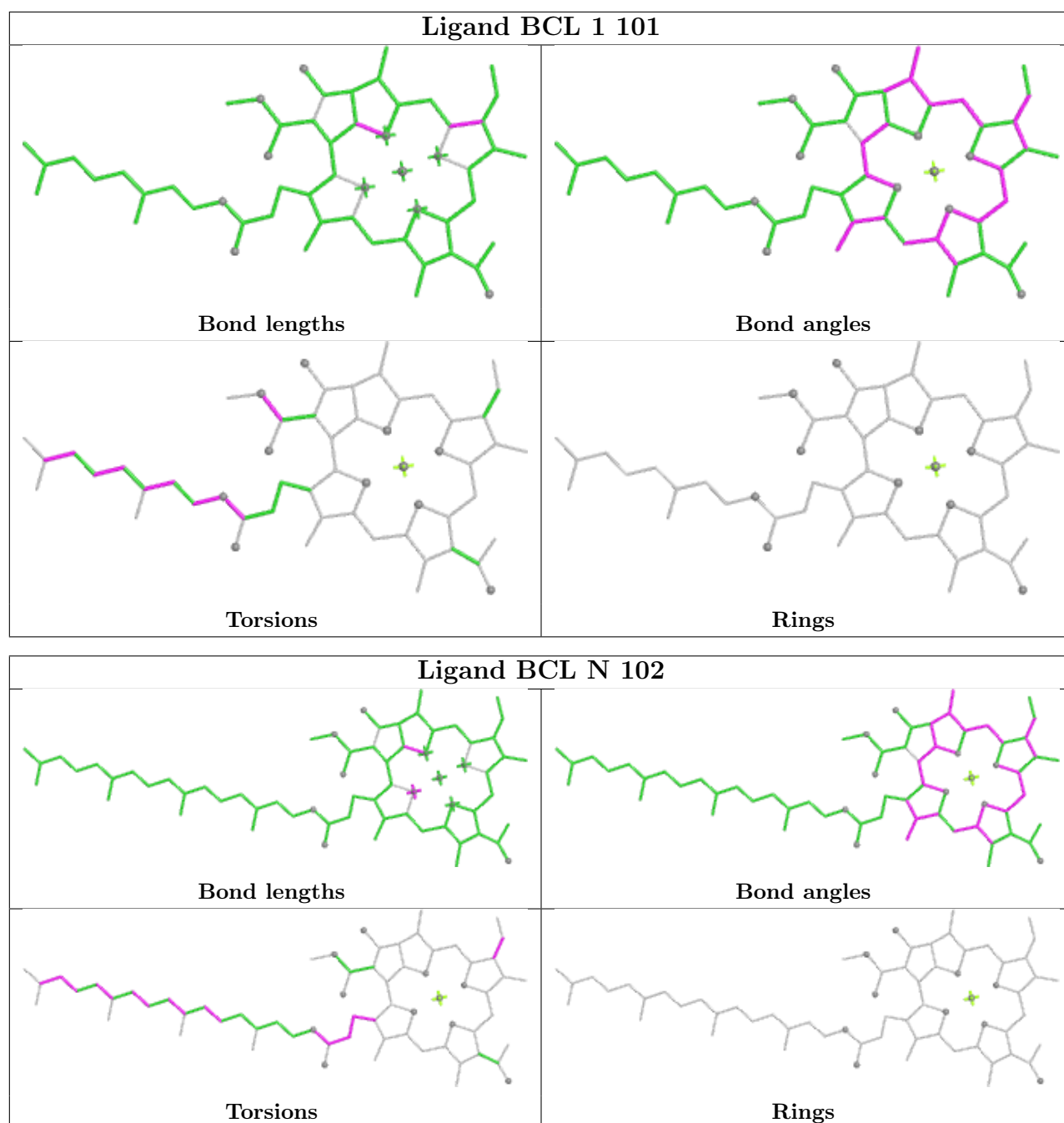
Ligand SPO U 102	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand BCL 7 101	
 Bond lengths	 Bond angles
 Torsions	 Rings

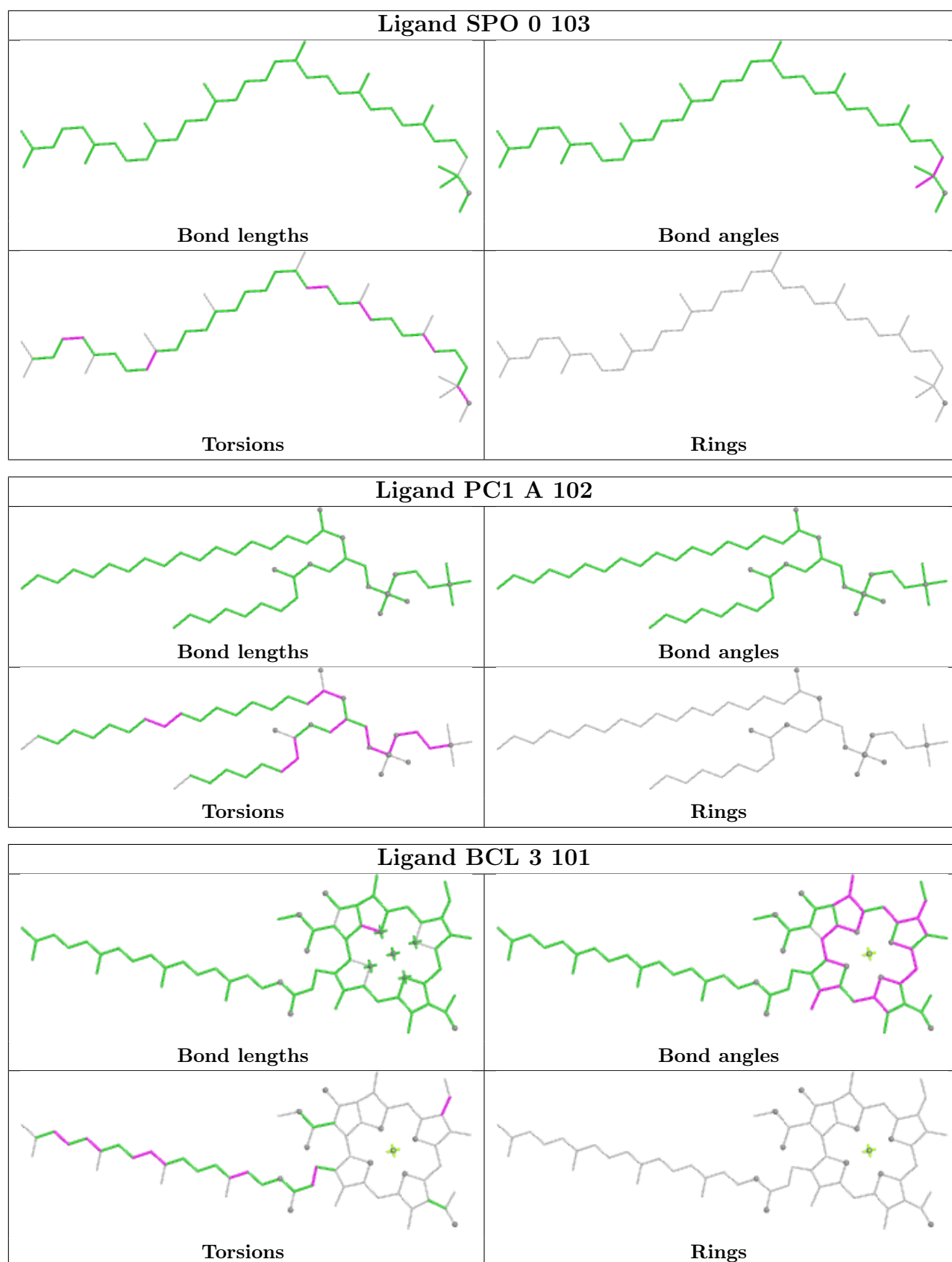
Ligand SPO S 202	
 Bond lengths	 Bond angles
 Torsions	 Rings

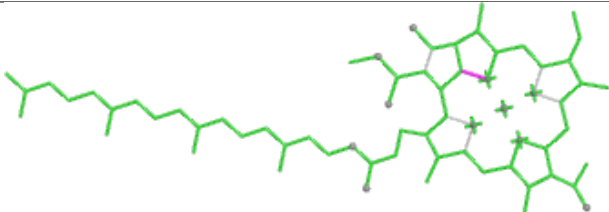
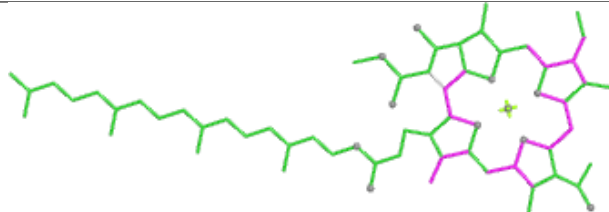
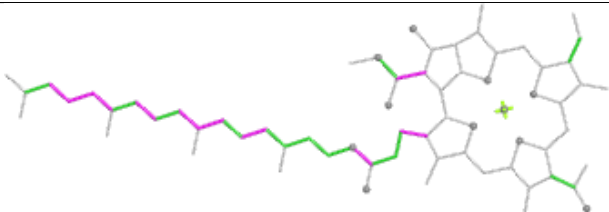
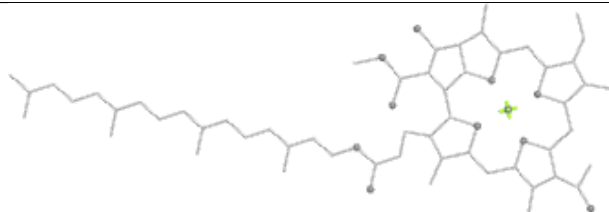
Ligand SPO I 102	
 Bond lengths	 Bond angles
 Torsions	 Rings

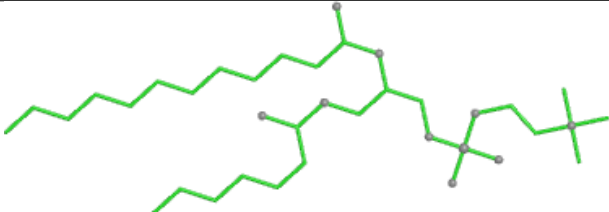
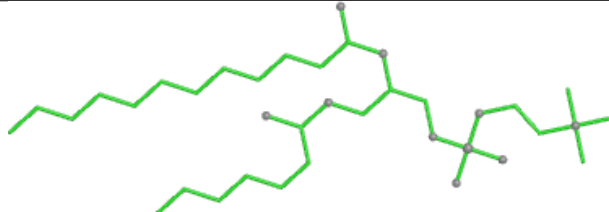
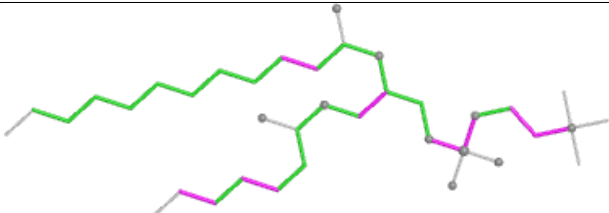
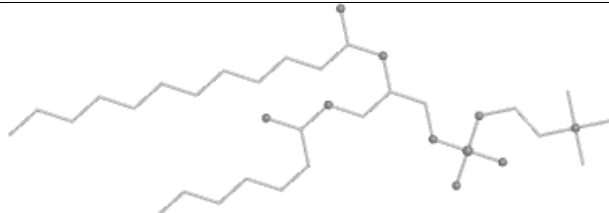


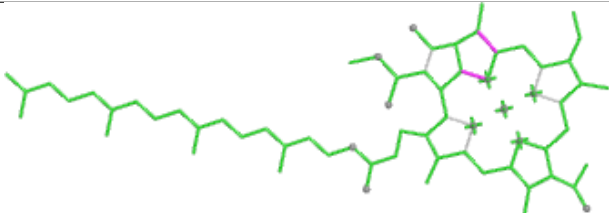
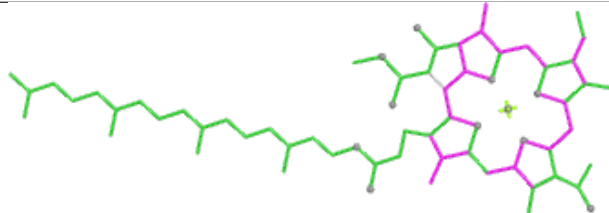
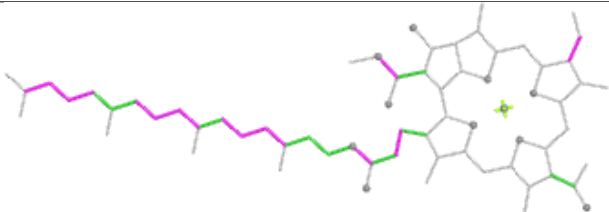
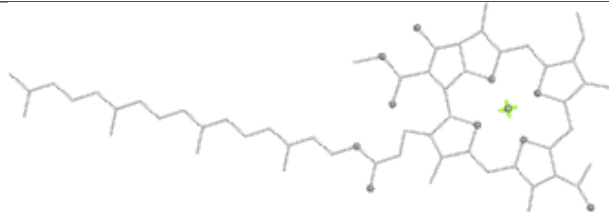


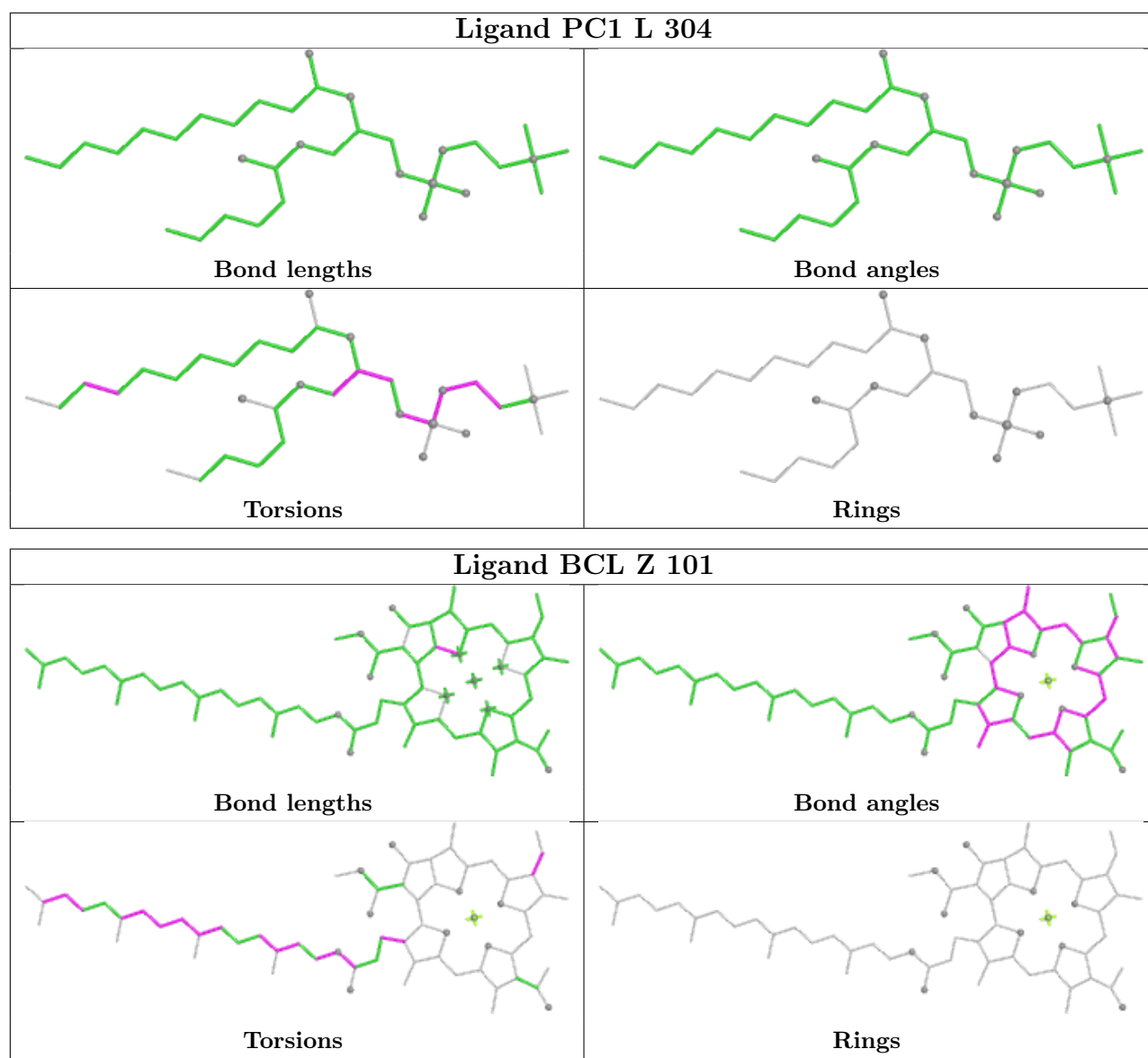


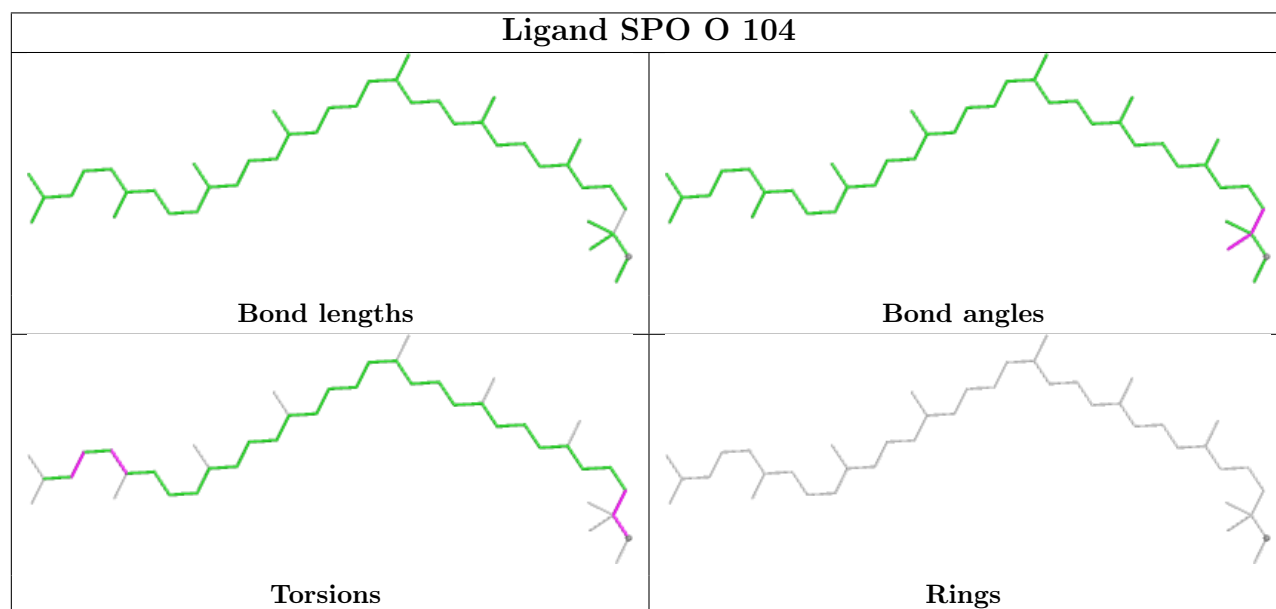
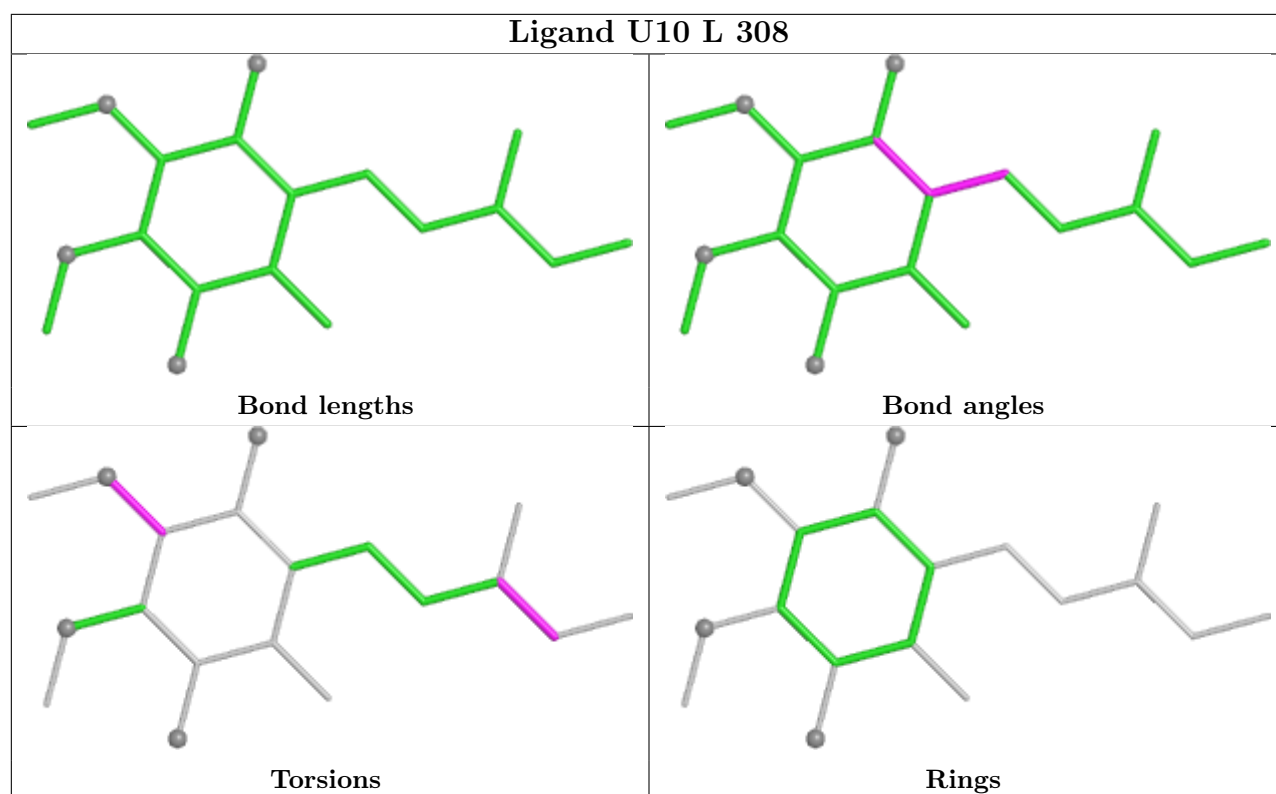


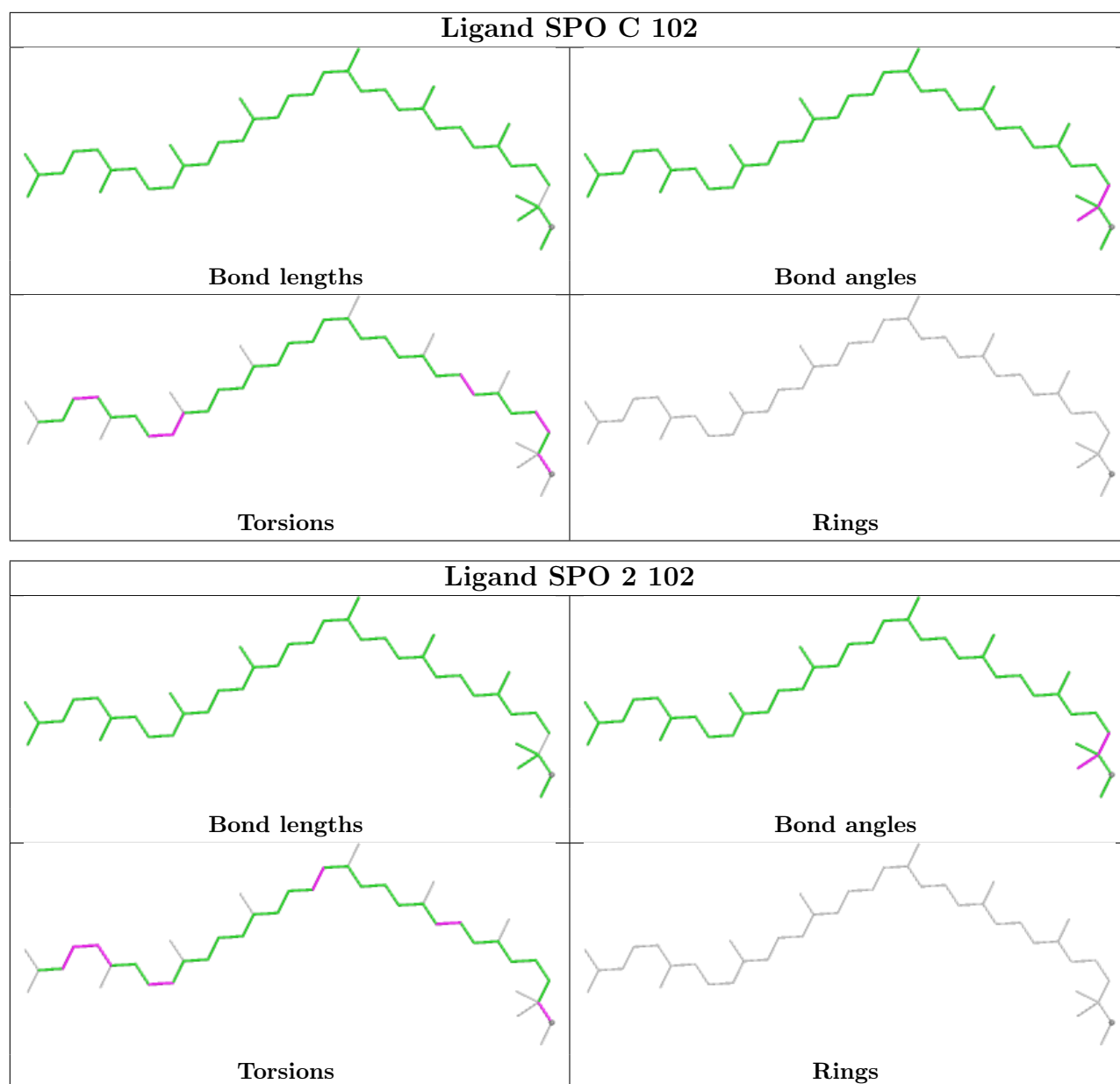
Ligand BCL S 201	
	
Bond lengths	Bond angles
	
Torsions	Rings

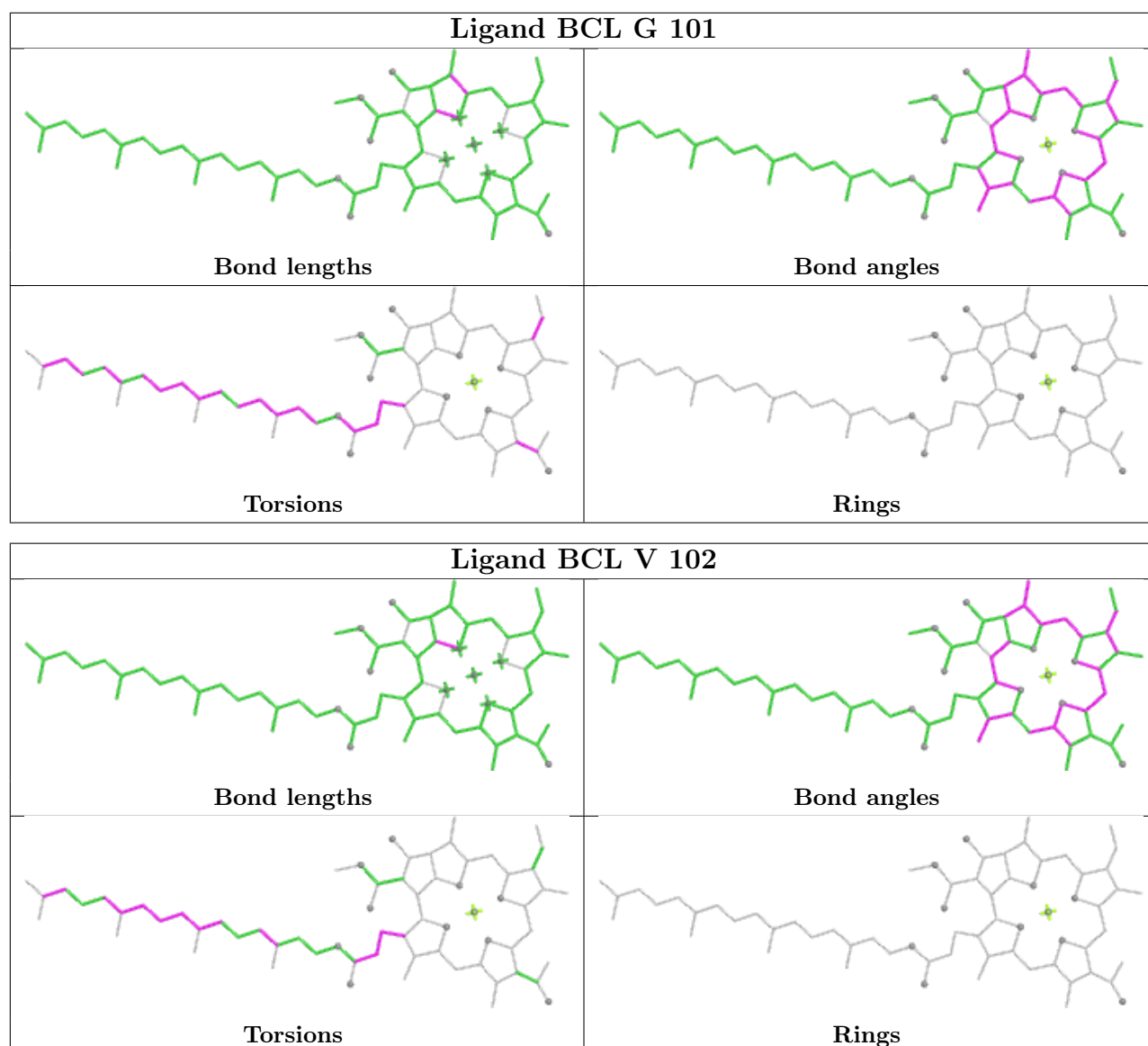
Ligand PC1 D 104	
	
Bond lengths	Bond angles
	
Torsions	Rings

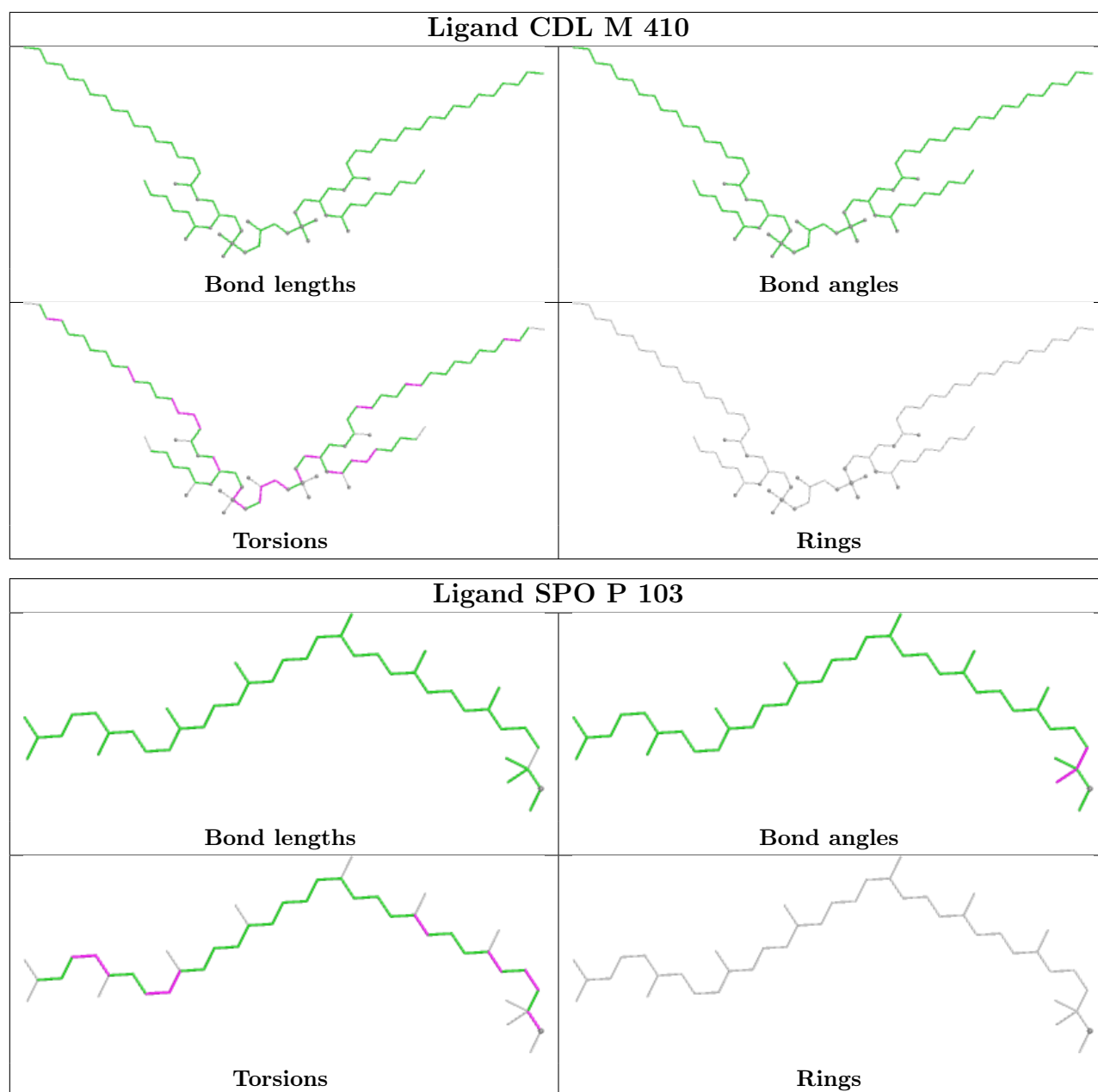
Ligand BCL J 101	
	
Bond lengths	Bond angles
	
Torsions	Rings

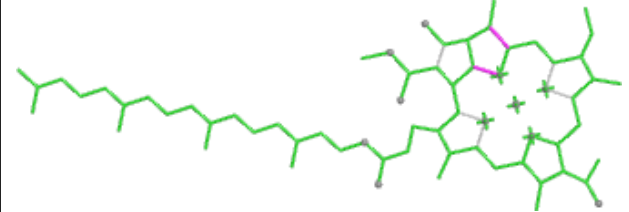
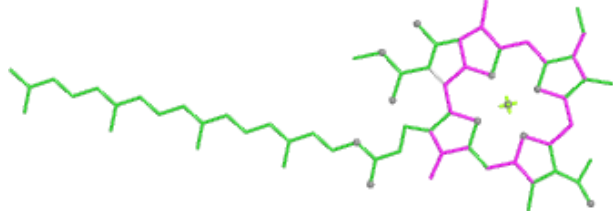
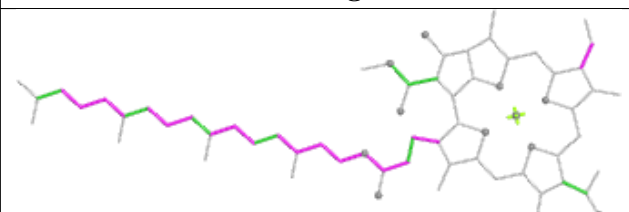
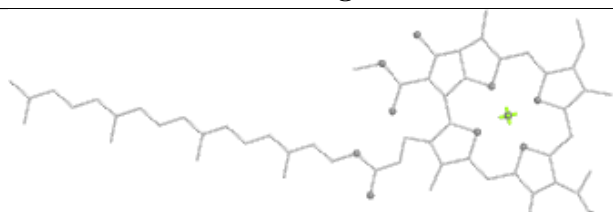
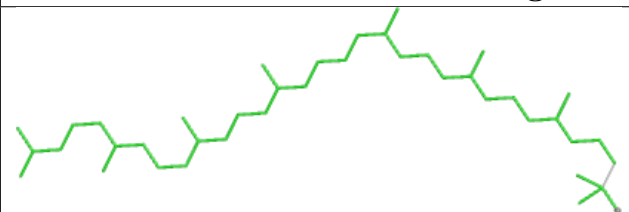
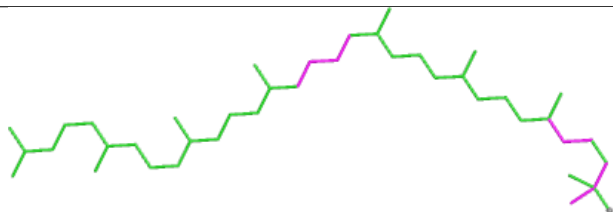
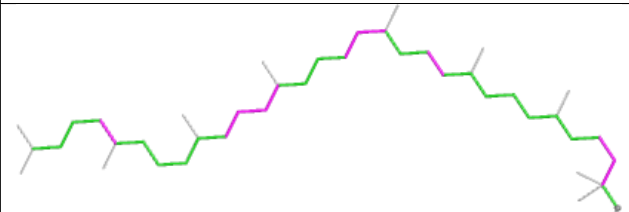
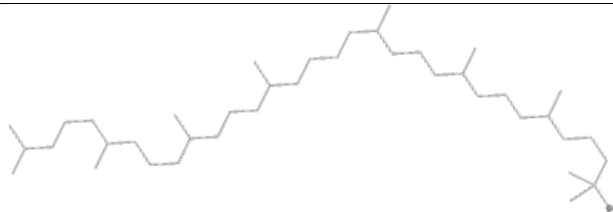
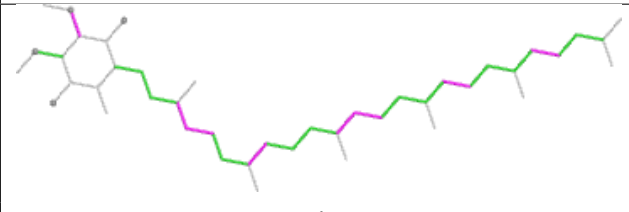
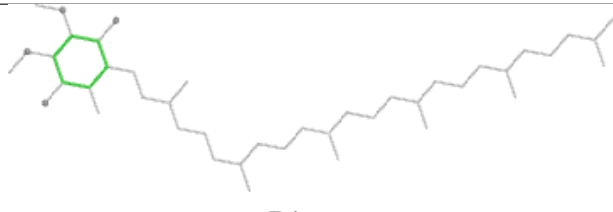


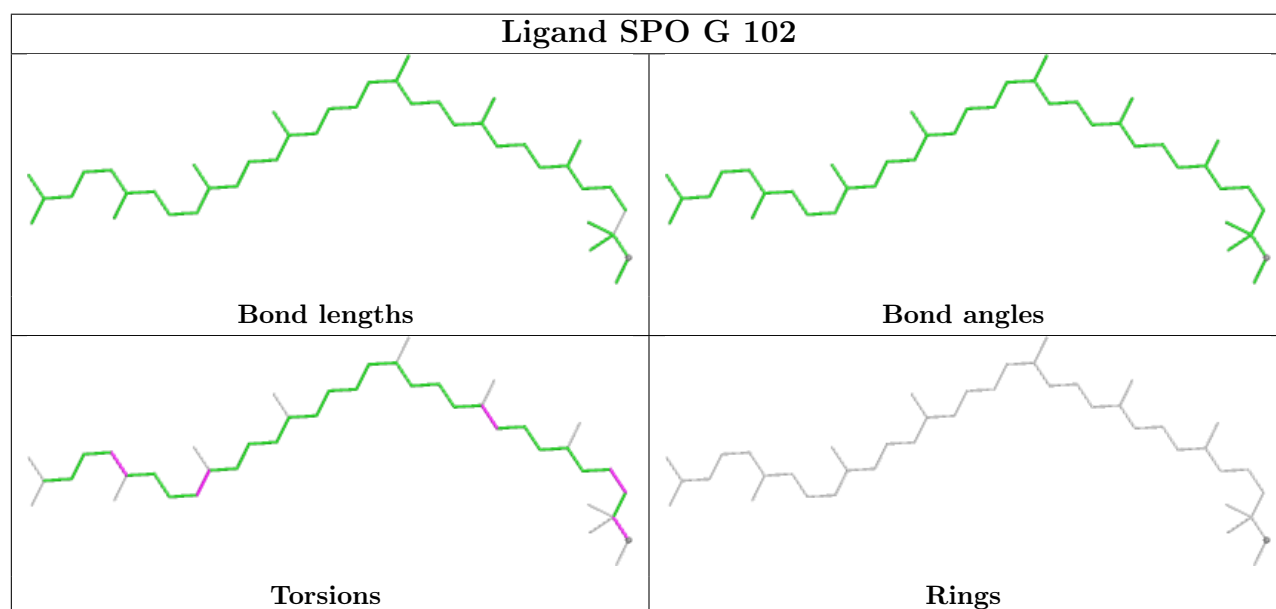
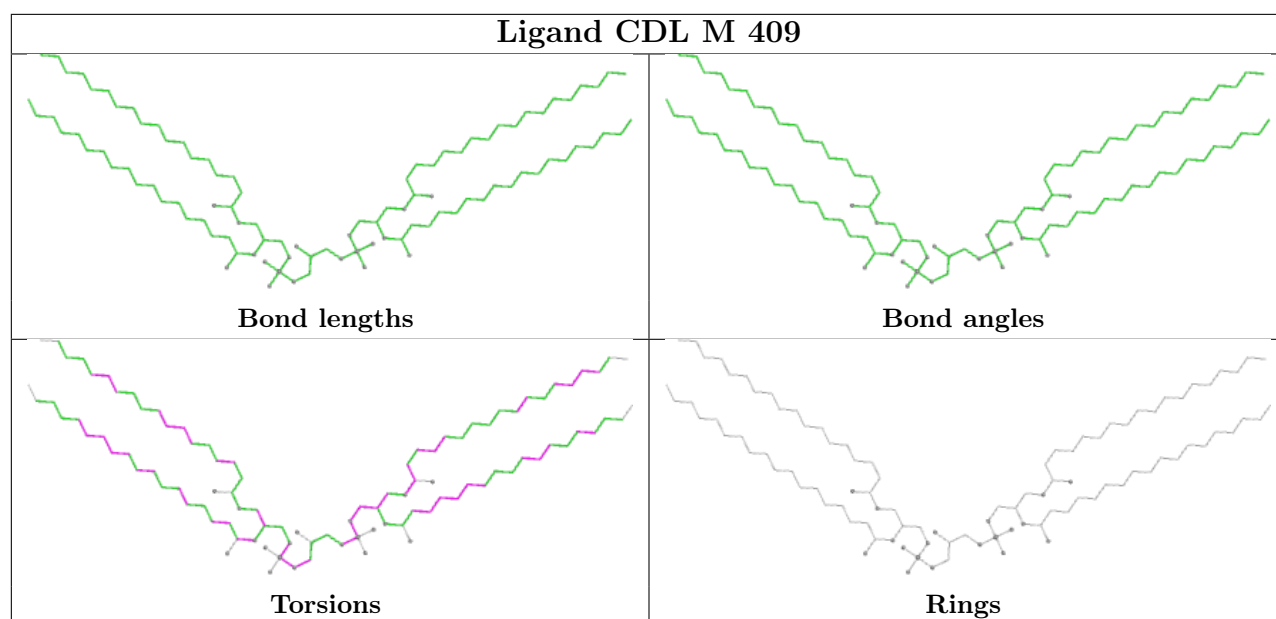


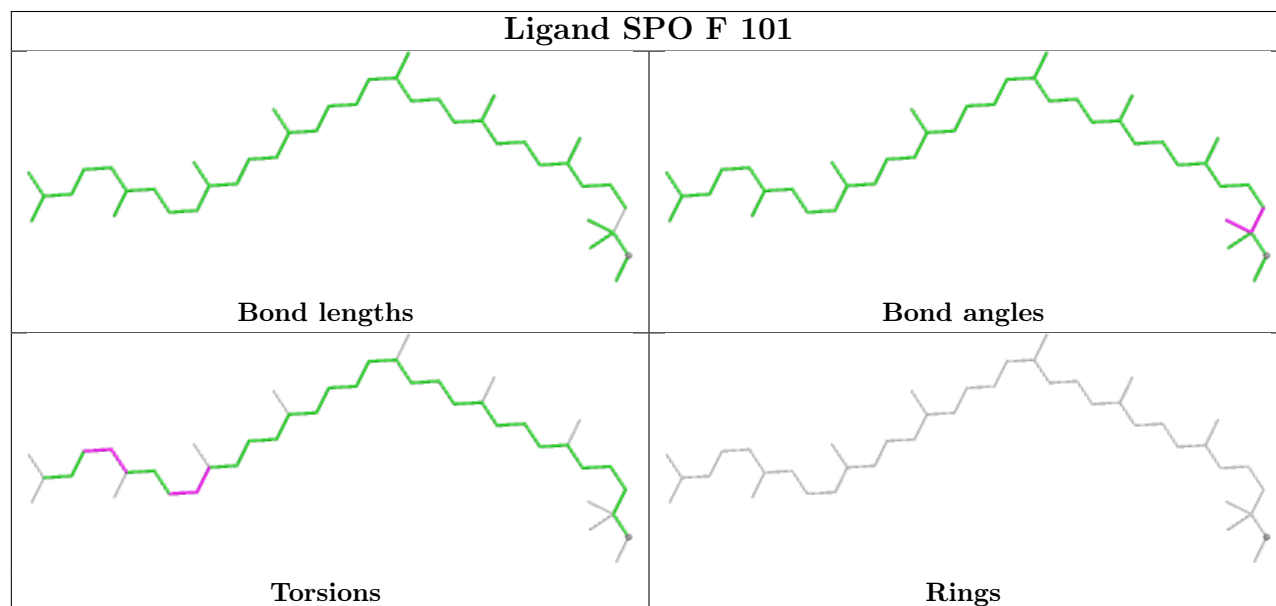
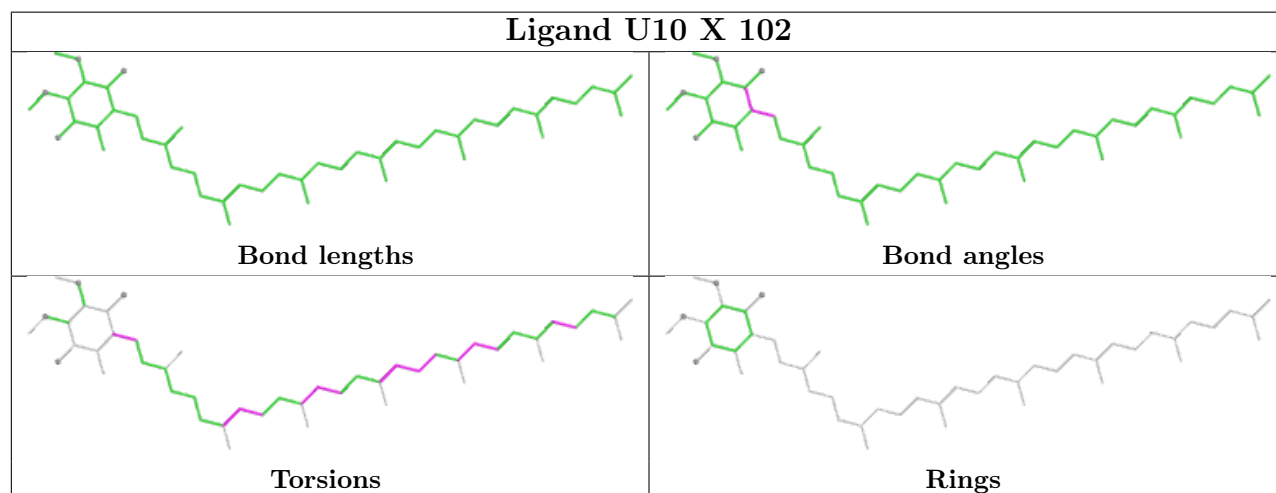
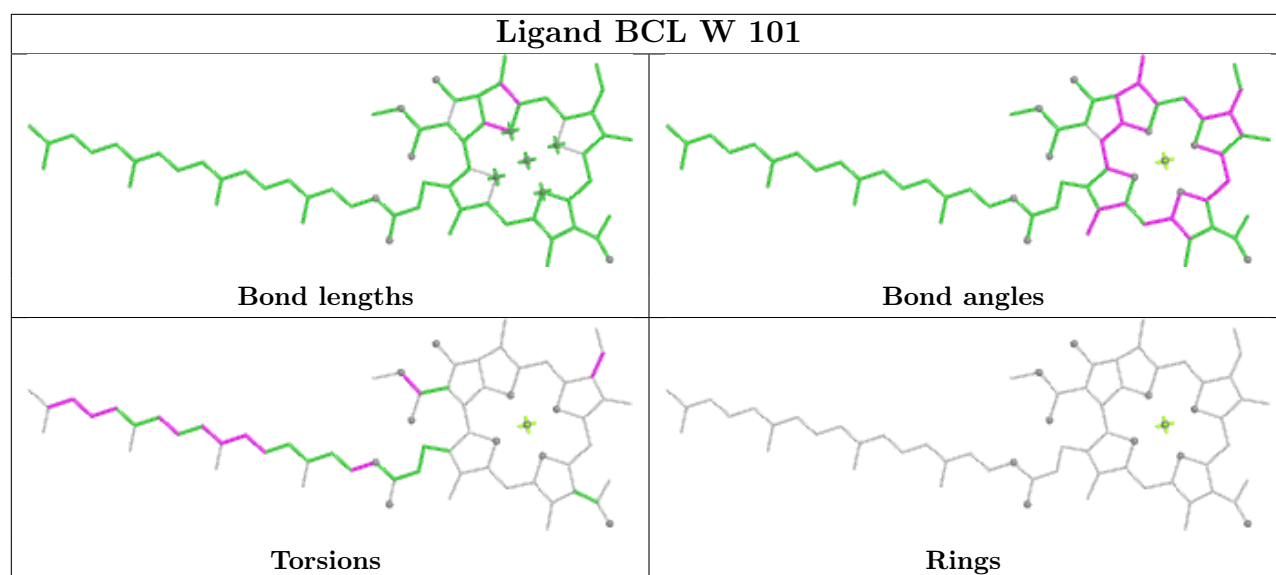


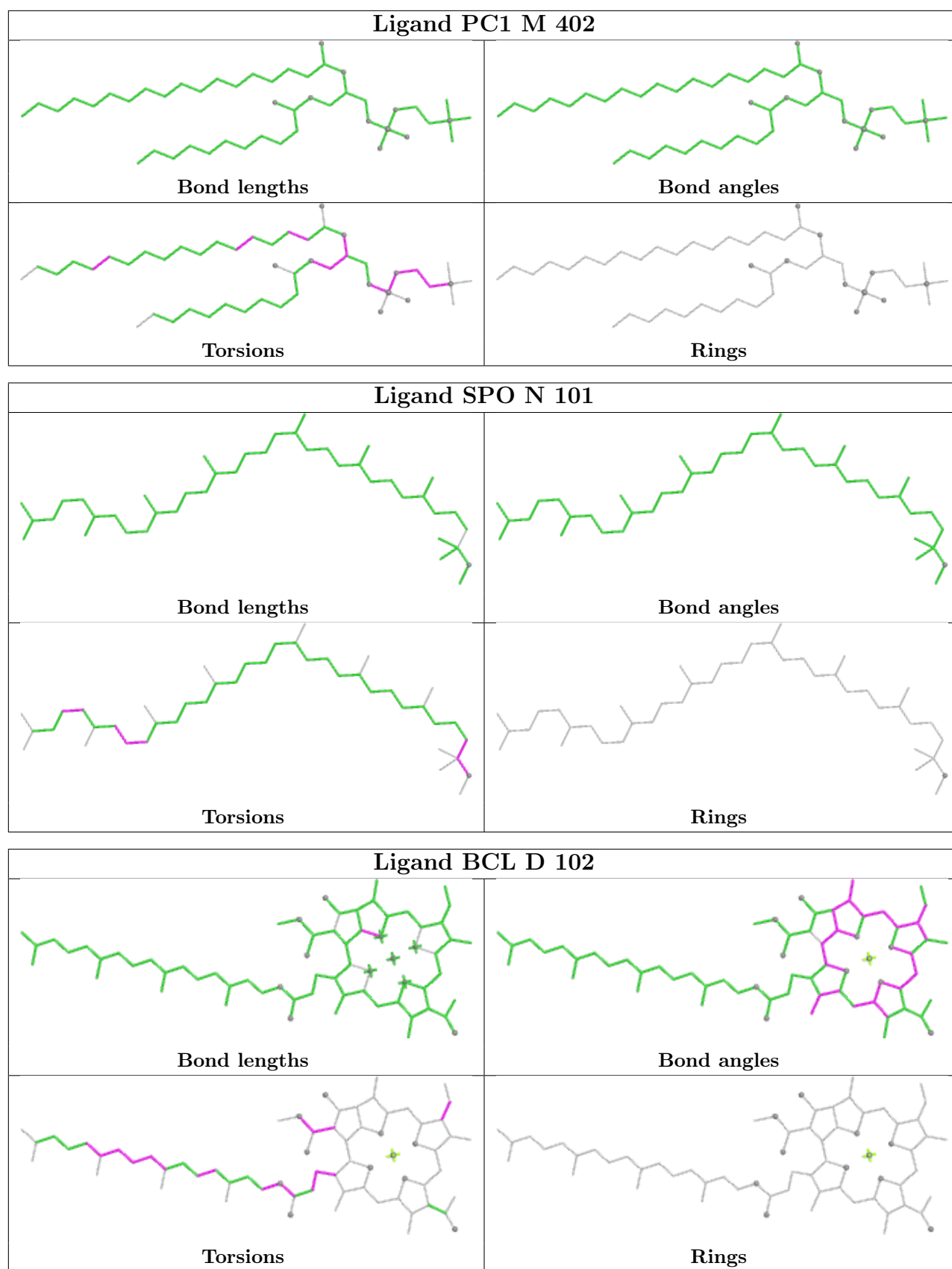


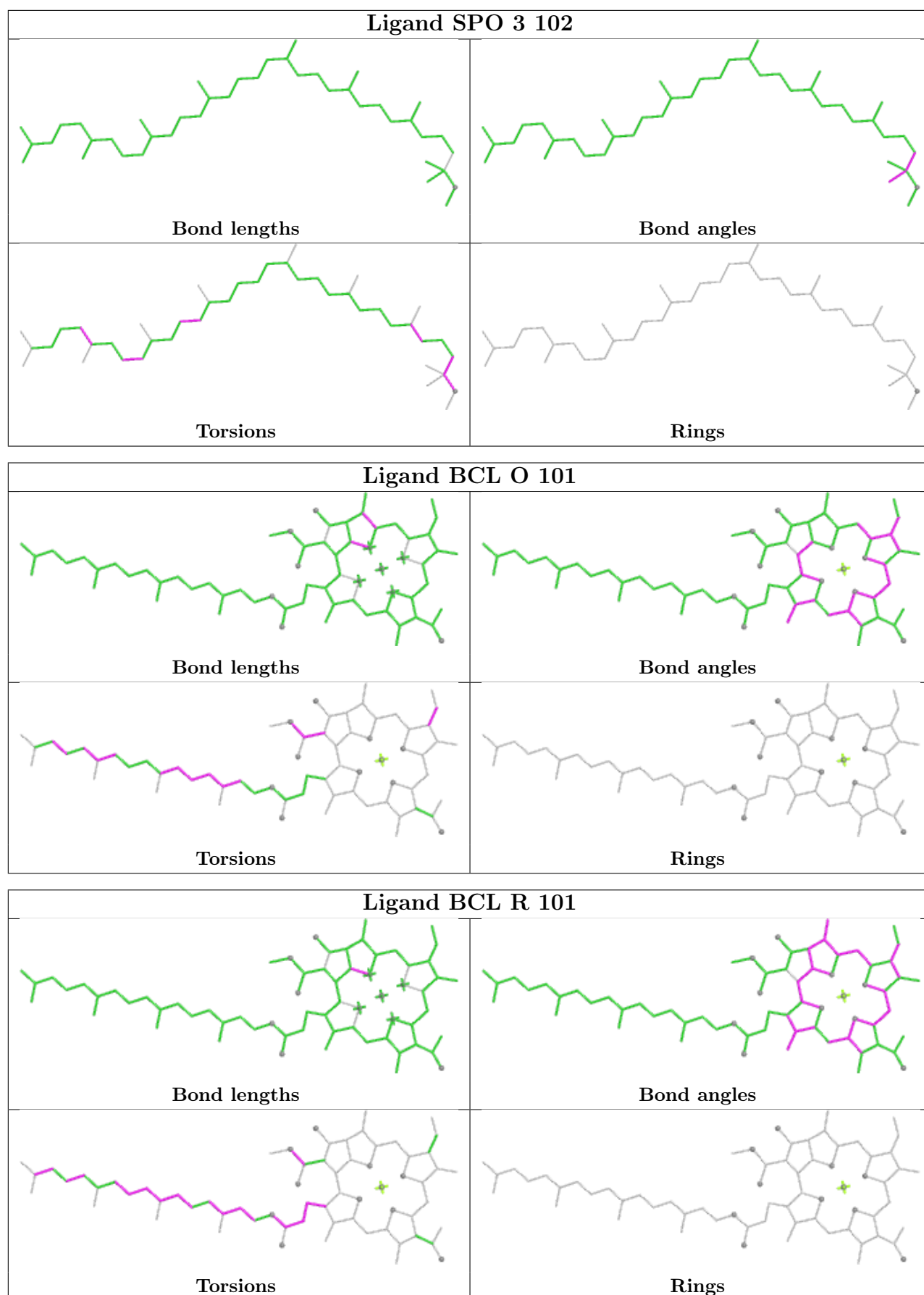


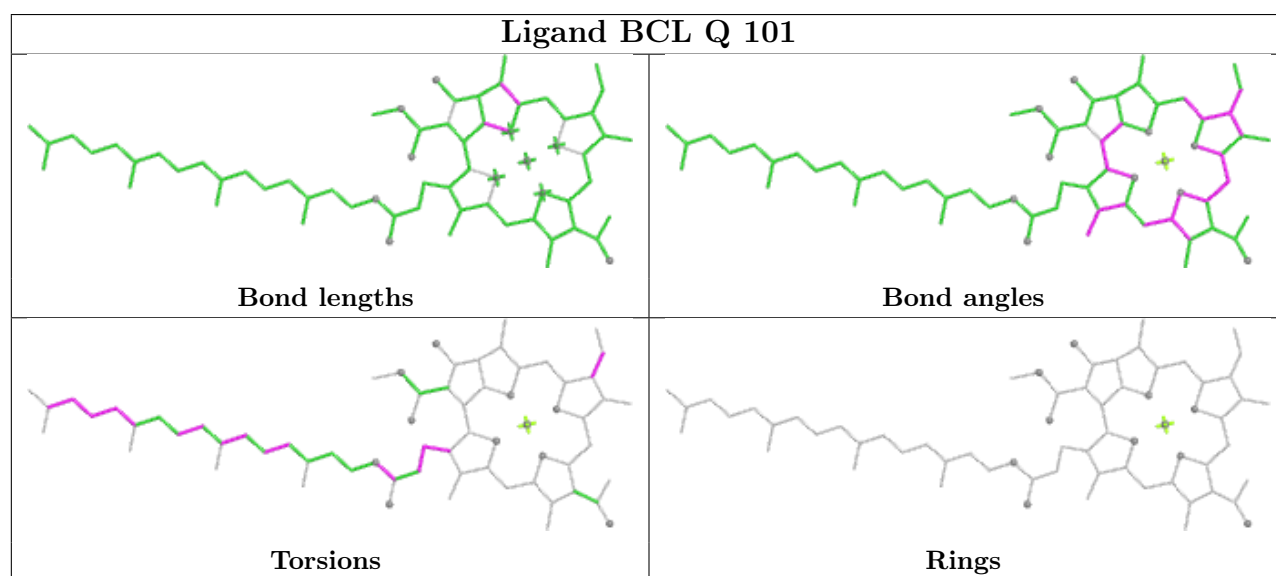
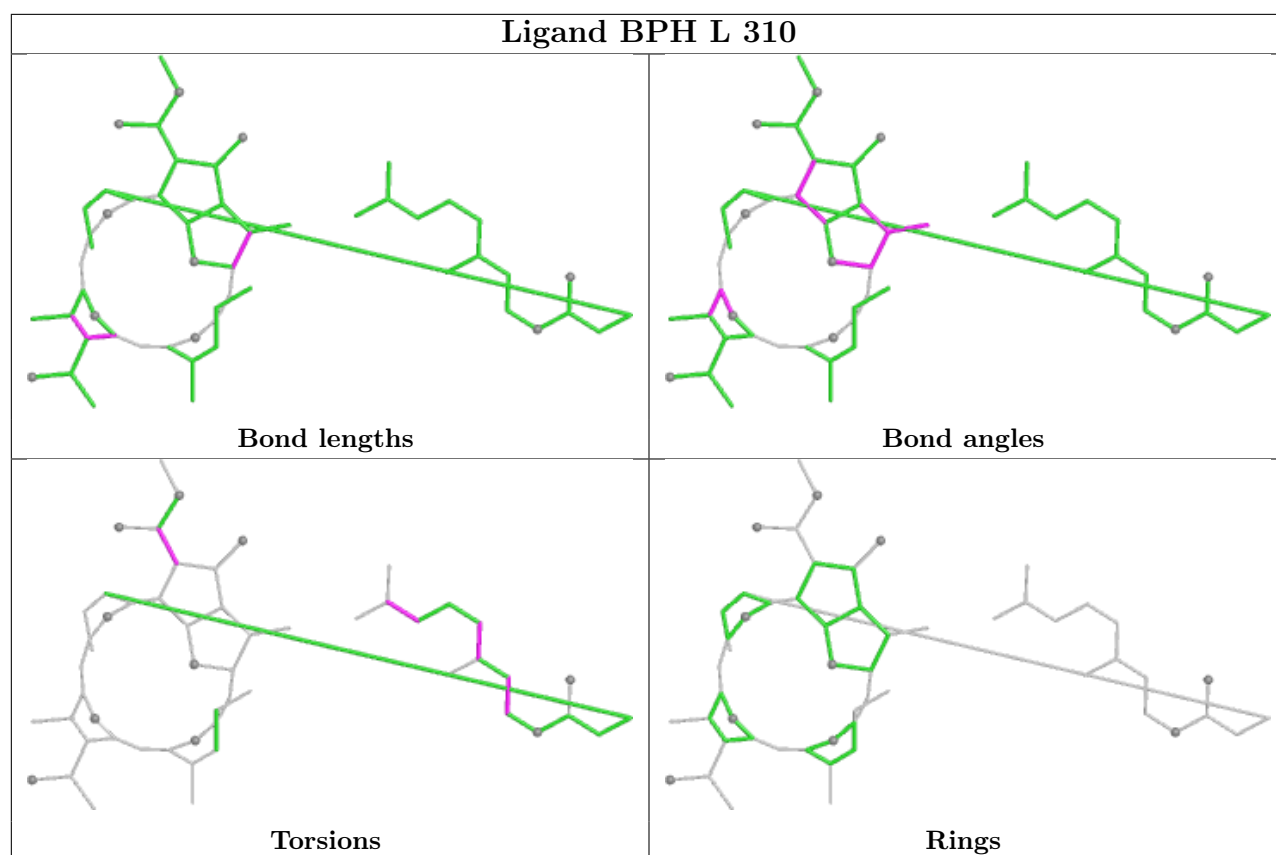
Ligand BCL C 101	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand SPO 1 102	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand U10 M 403	
 Bond lengths	 Bond angles
 Torsions	 Rings

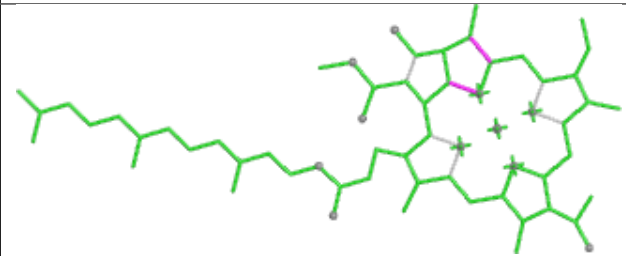
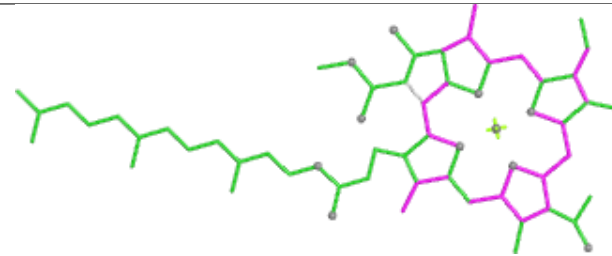
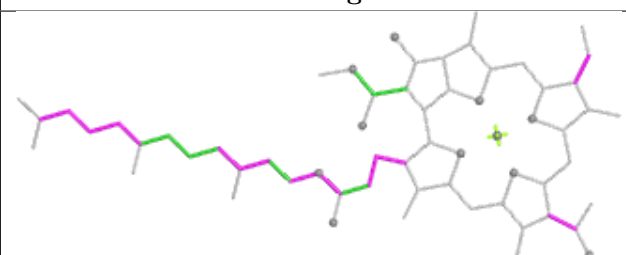
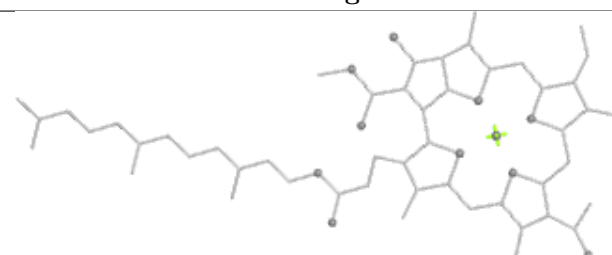


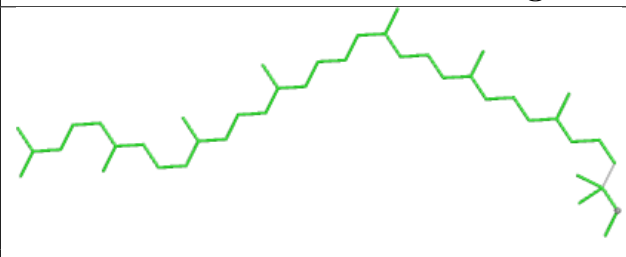
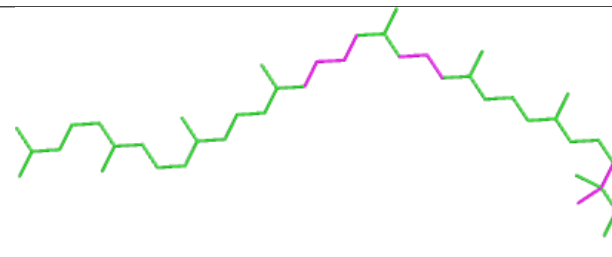
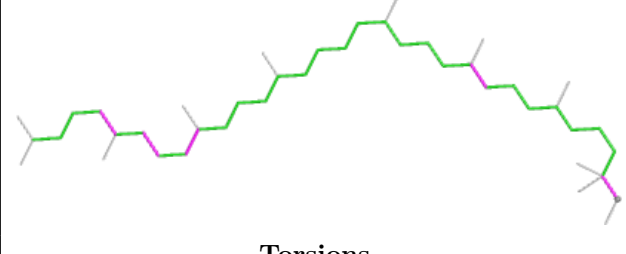


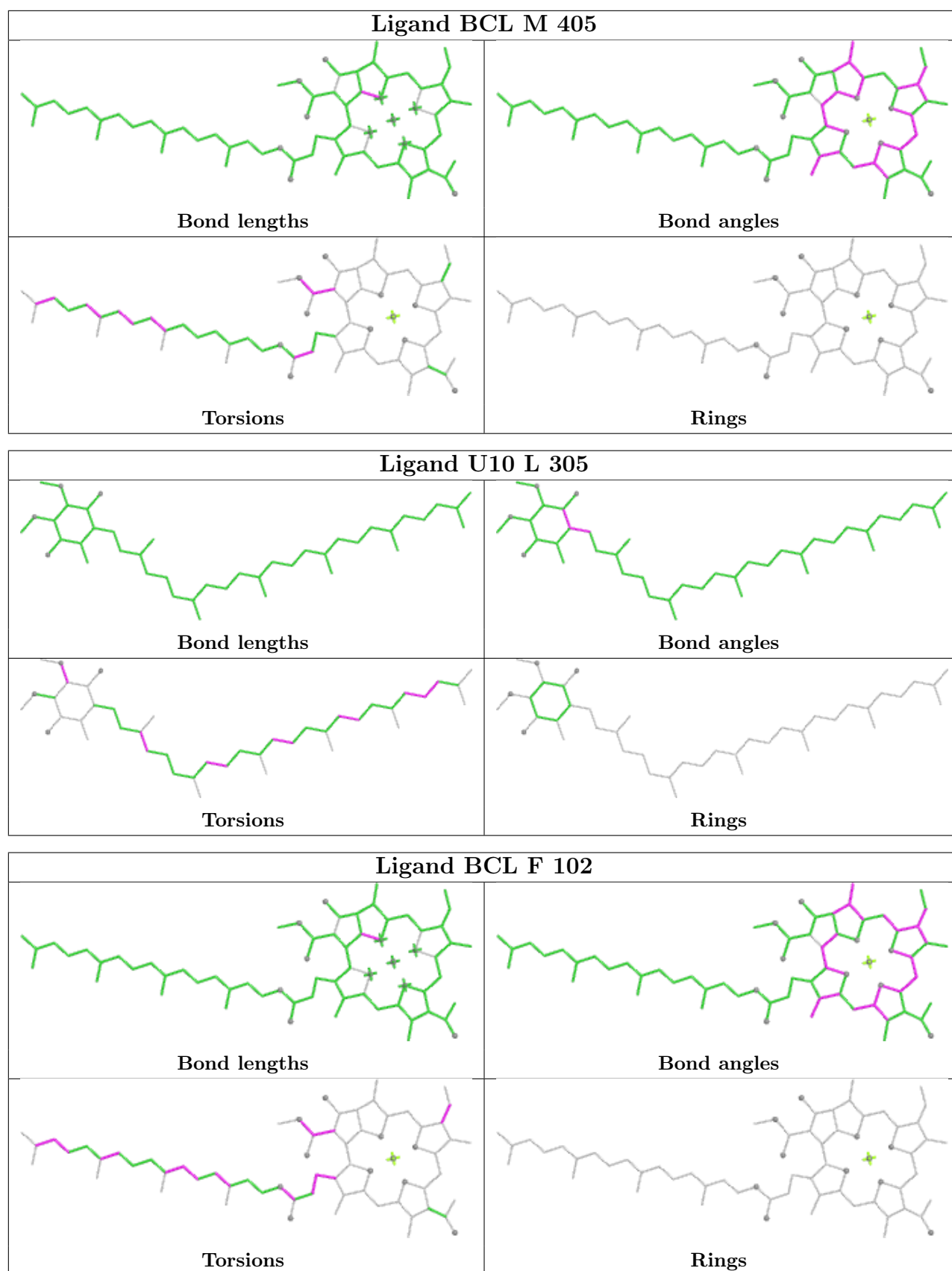


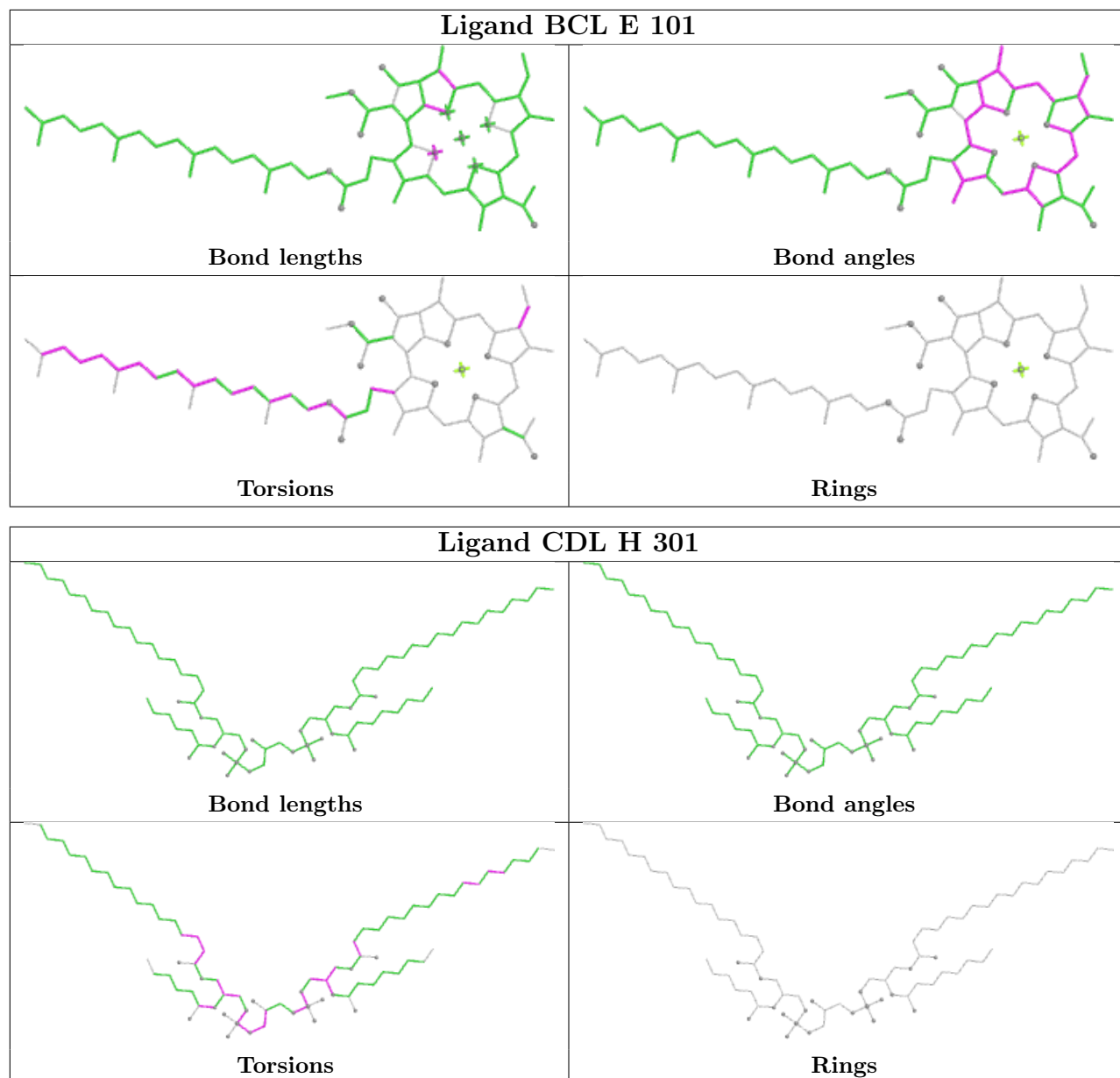


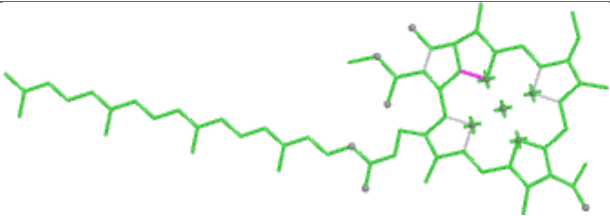
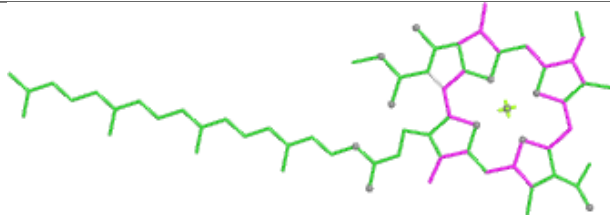
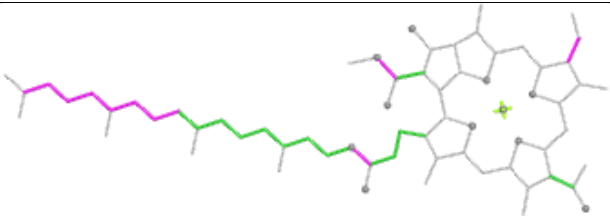
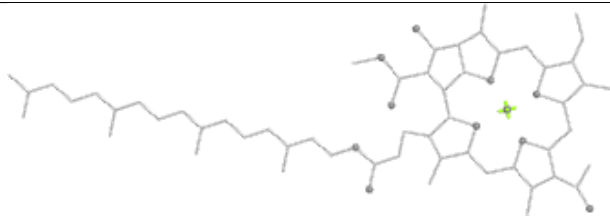
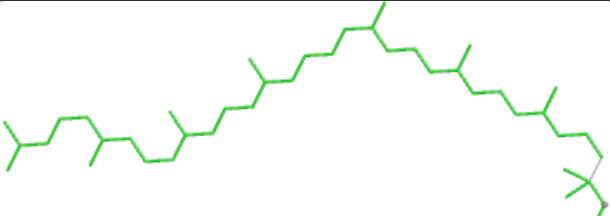
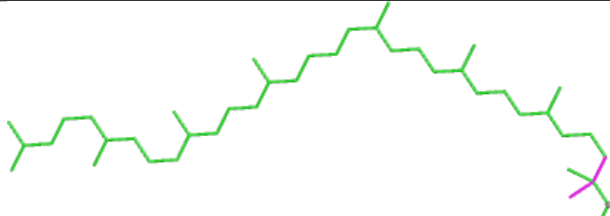
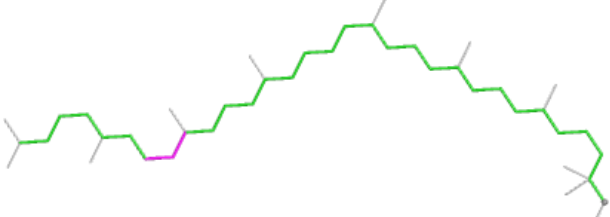
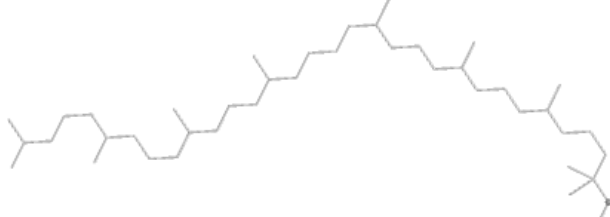


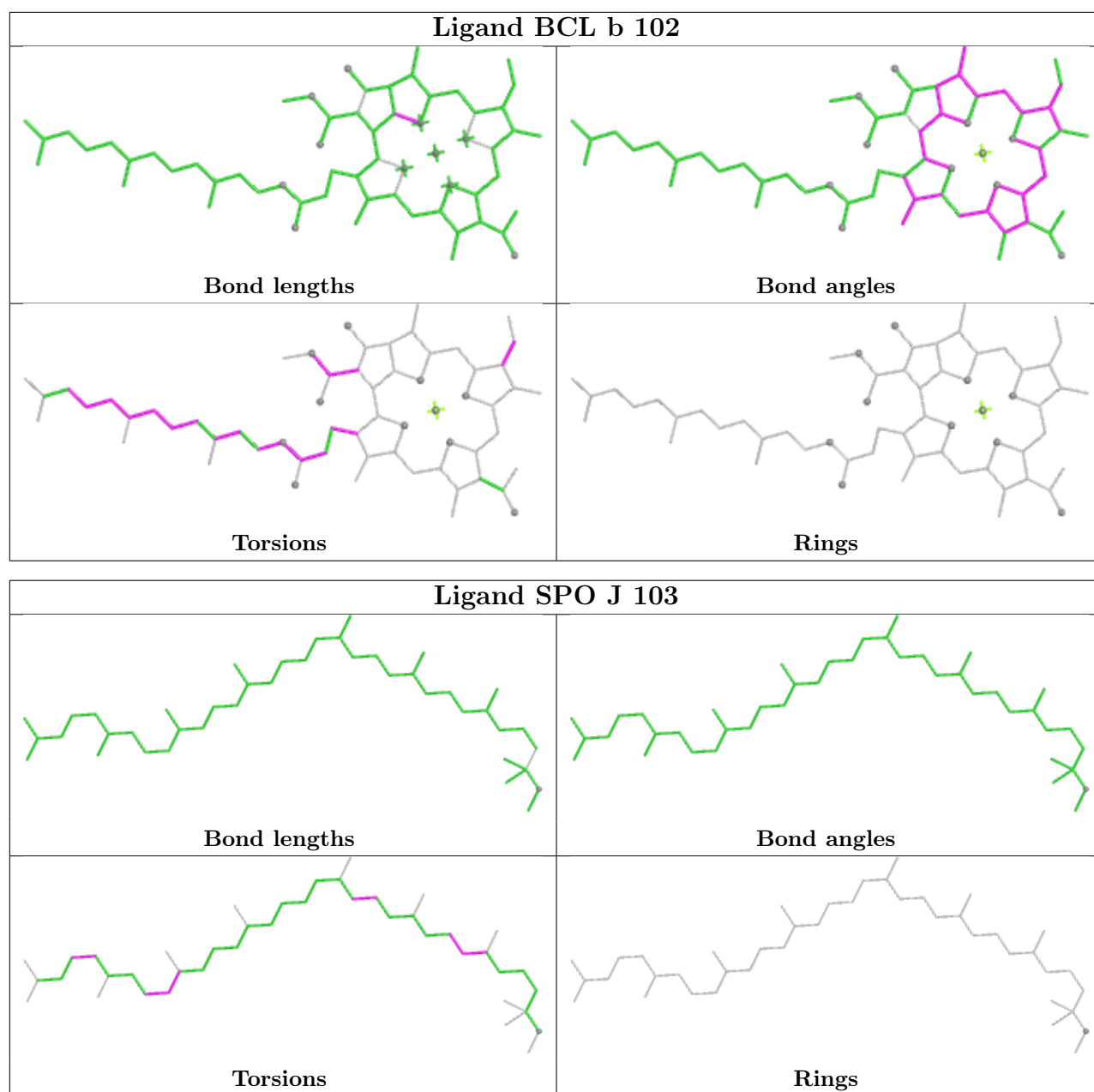
Ligand BCL 2 101	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand SPO J 102	
	
Bond lengths	Bond angles
	
Torsions	Rings





Ligand BCL A 101	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand SPO D 101	
 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.

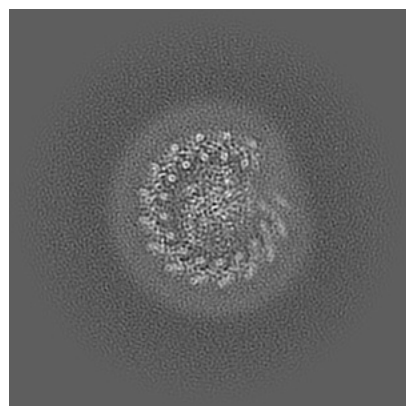
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39255. These allow visual inspection of the internal detail of the map and identification of artifacts.

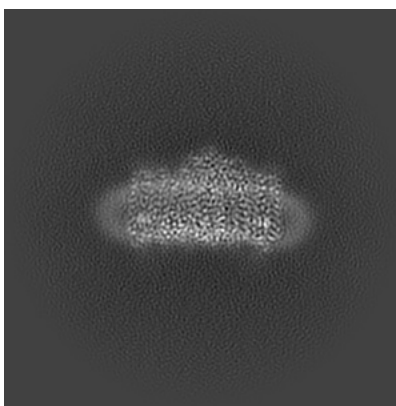
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

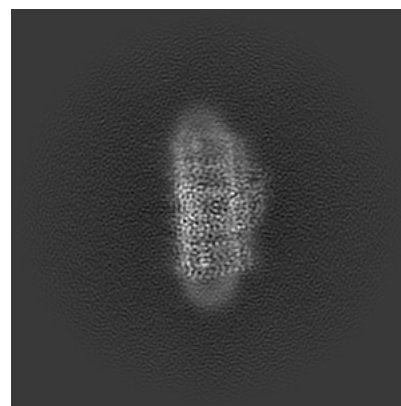
6.1.1 Primary map



X

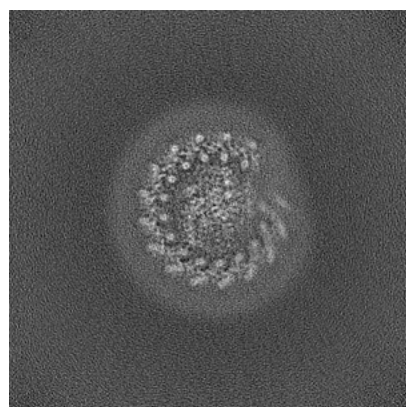


Y

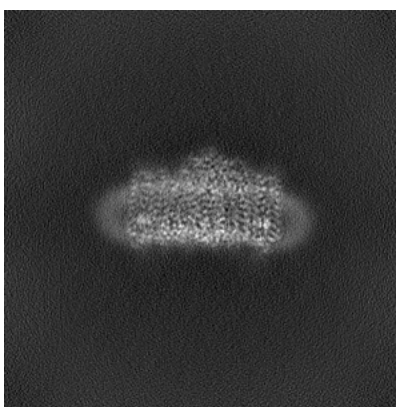


Z

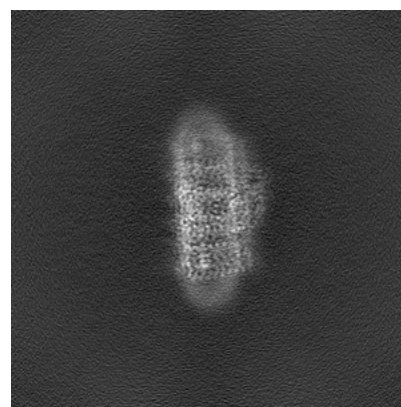
6.1.2 Raw map



X



Y

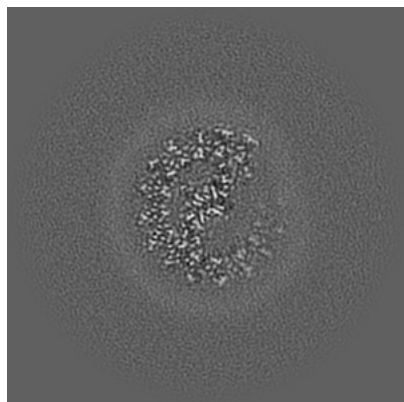


Z

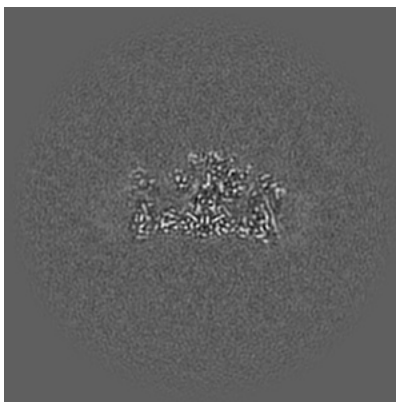
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

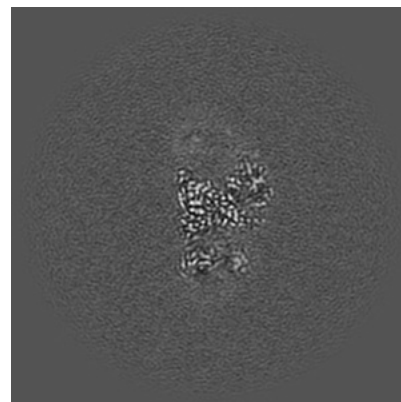
6.2.1 Primary map



X Index: 160

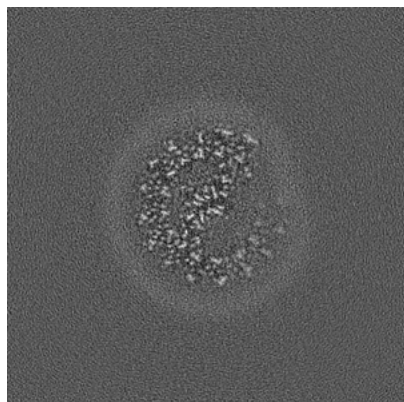


Y Index: 160

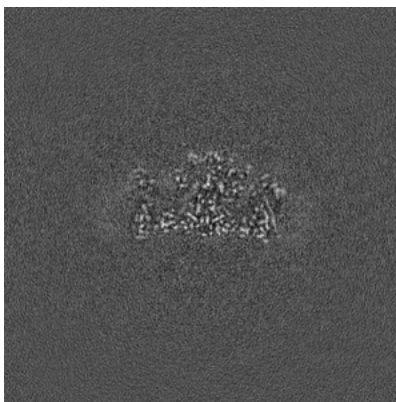


Z Index: 160

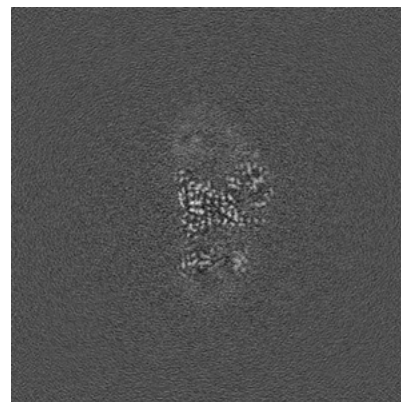
6.2.2 Raw map



X Index: 160



Y Index: 160

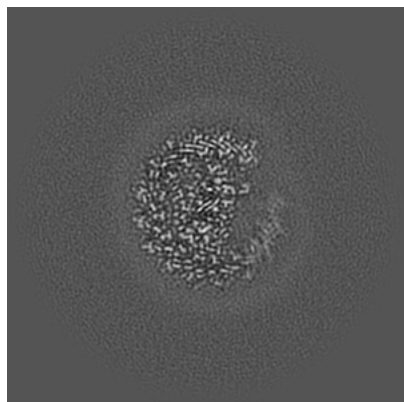


Z Index: 160

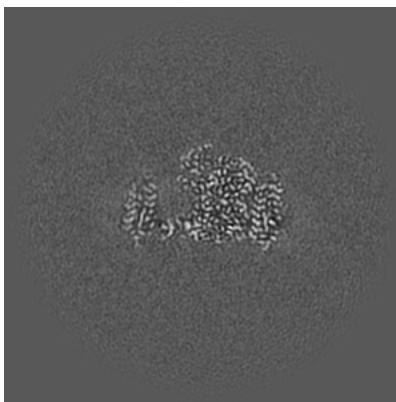
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

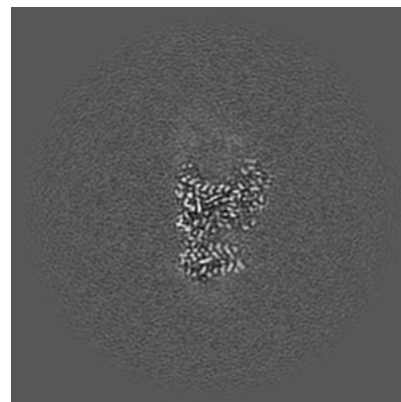
6.3.1 Primary map



X Index: 147

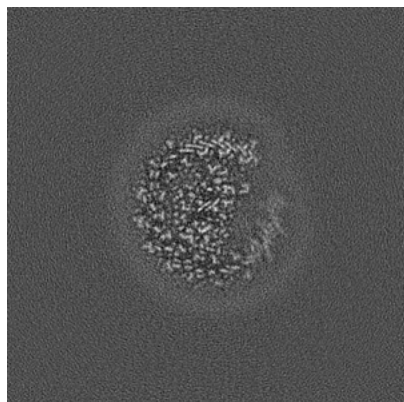


Y Index: 171

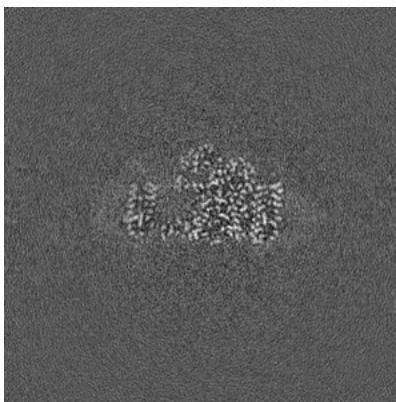


Z Index: 170

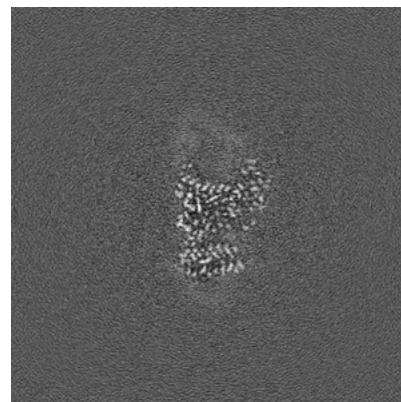
6.3.2 Raw map



X Index: 147



Y Index: 172

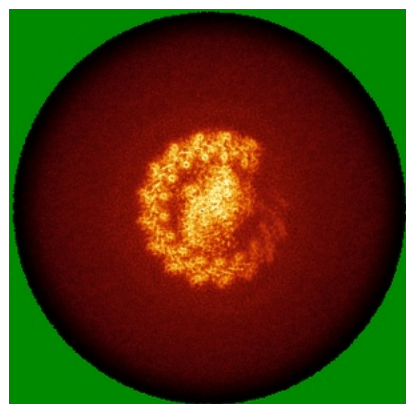


Z Index: 170

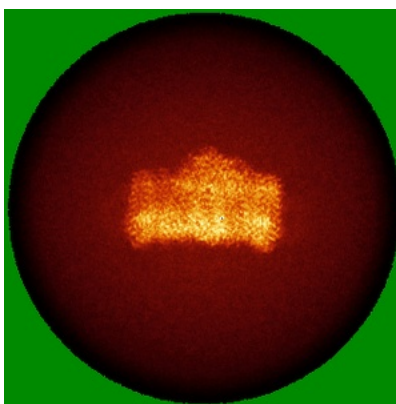
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

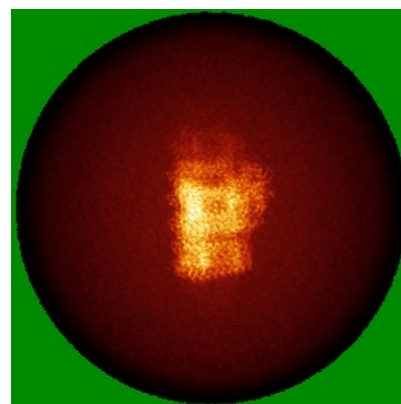
6.4.1 Primary map



X

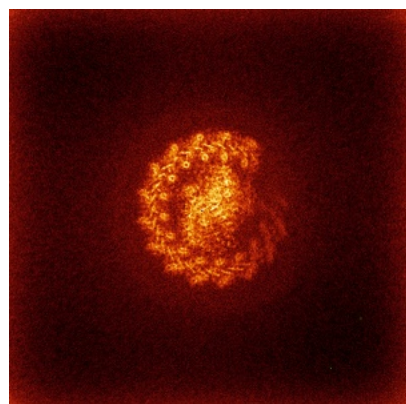


Y

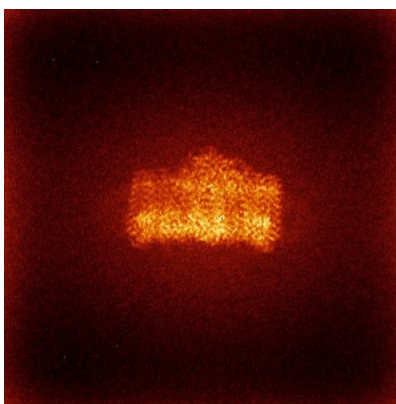


Z

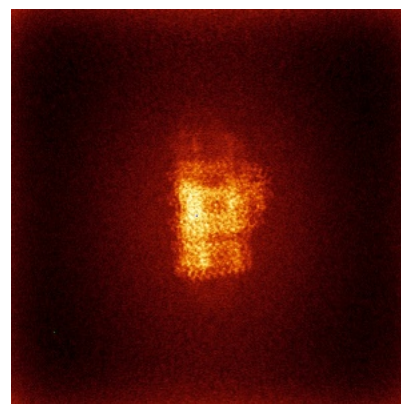
6.4.2 Raw map



X



Y

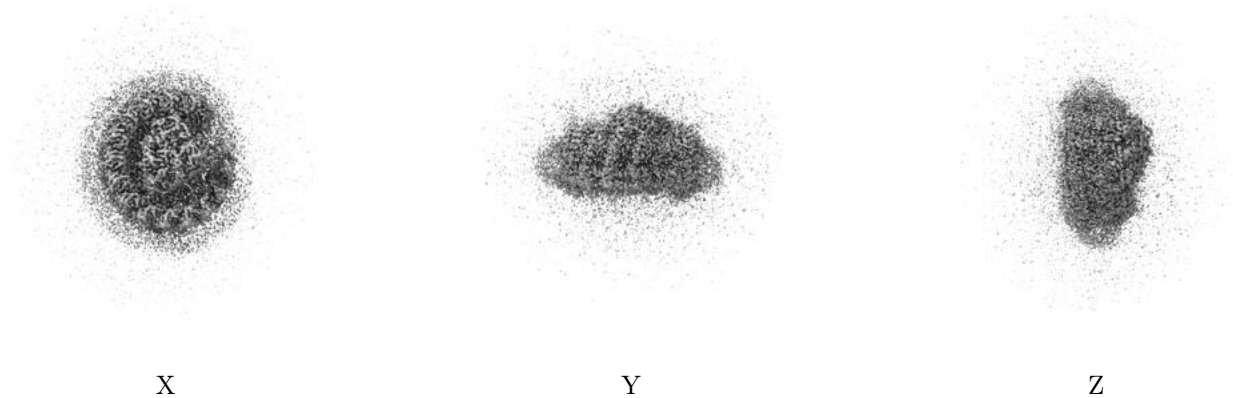


Z

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.

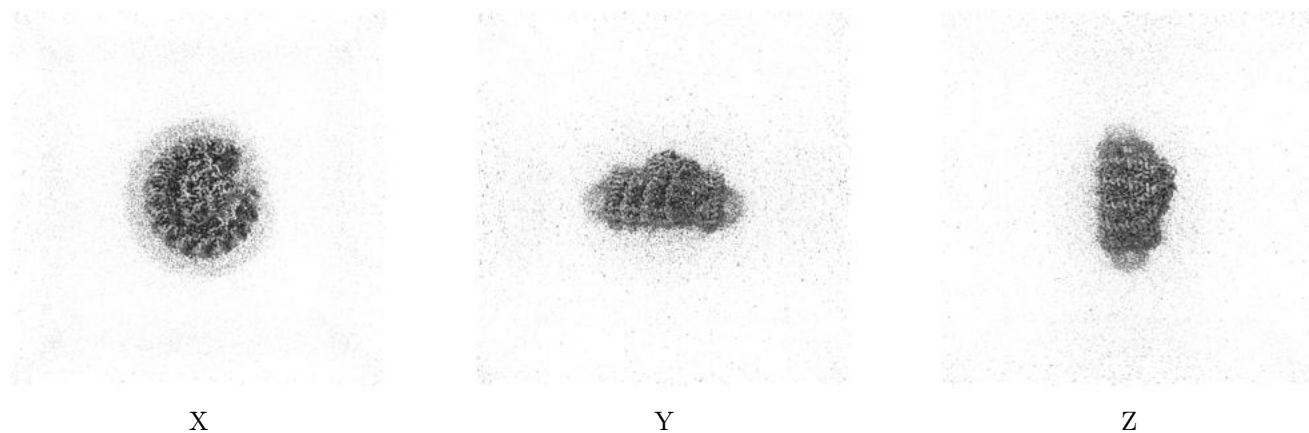
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.17. 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.

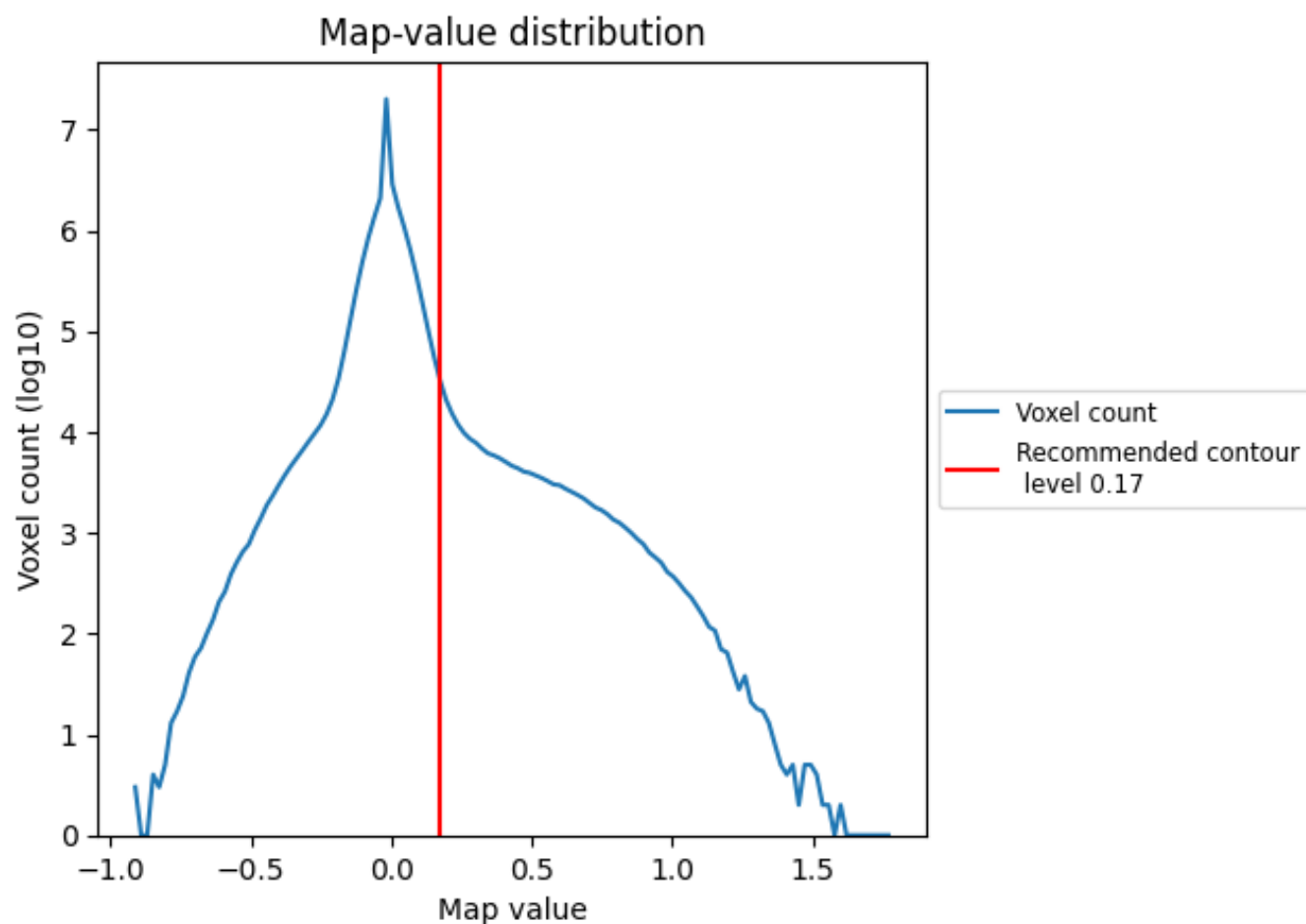
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

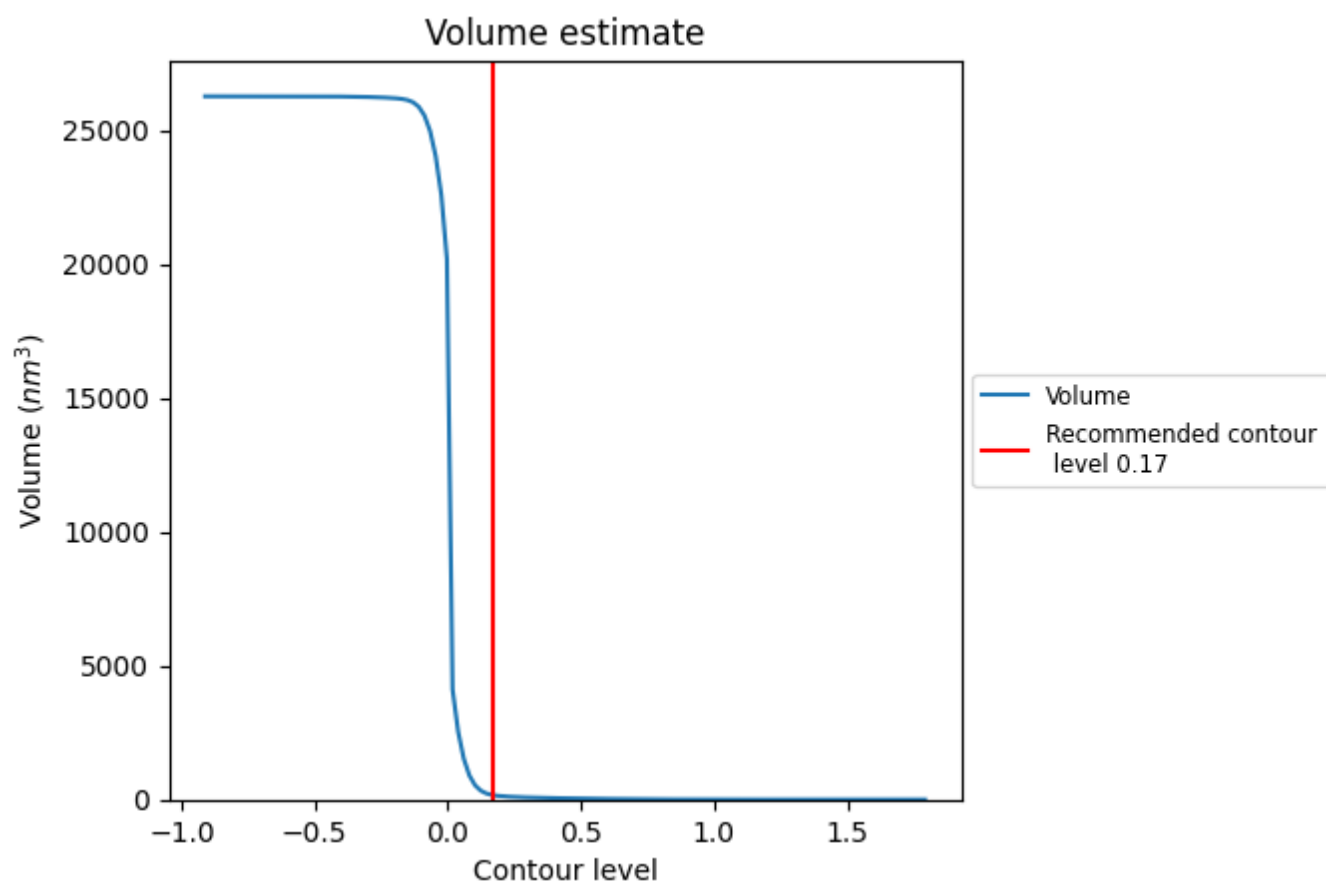
This section contains the results of statistical analysis of the map.

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.

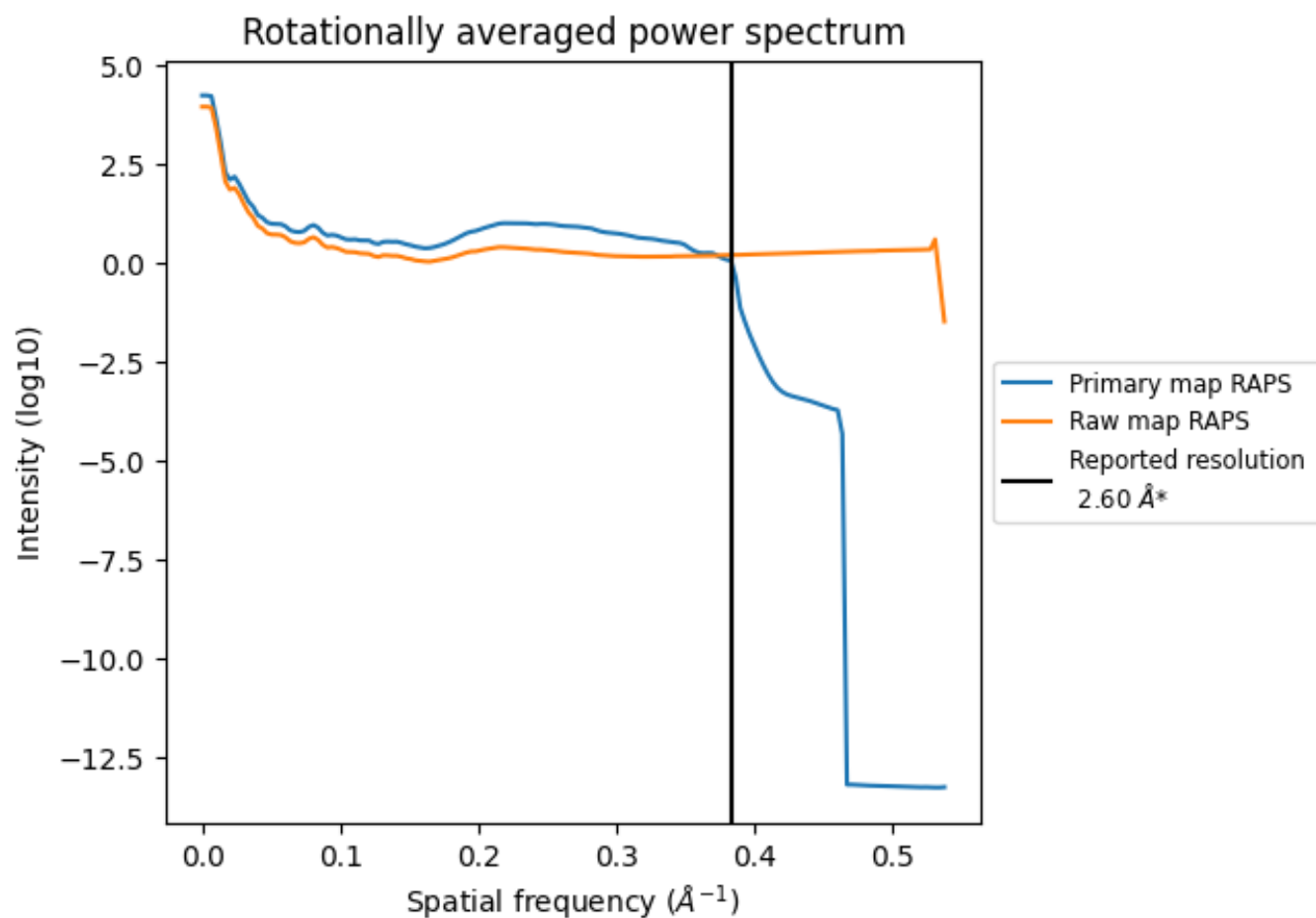
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 166 nm^3 ; this corresponds to an approximate mass of 150 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 ⓘ

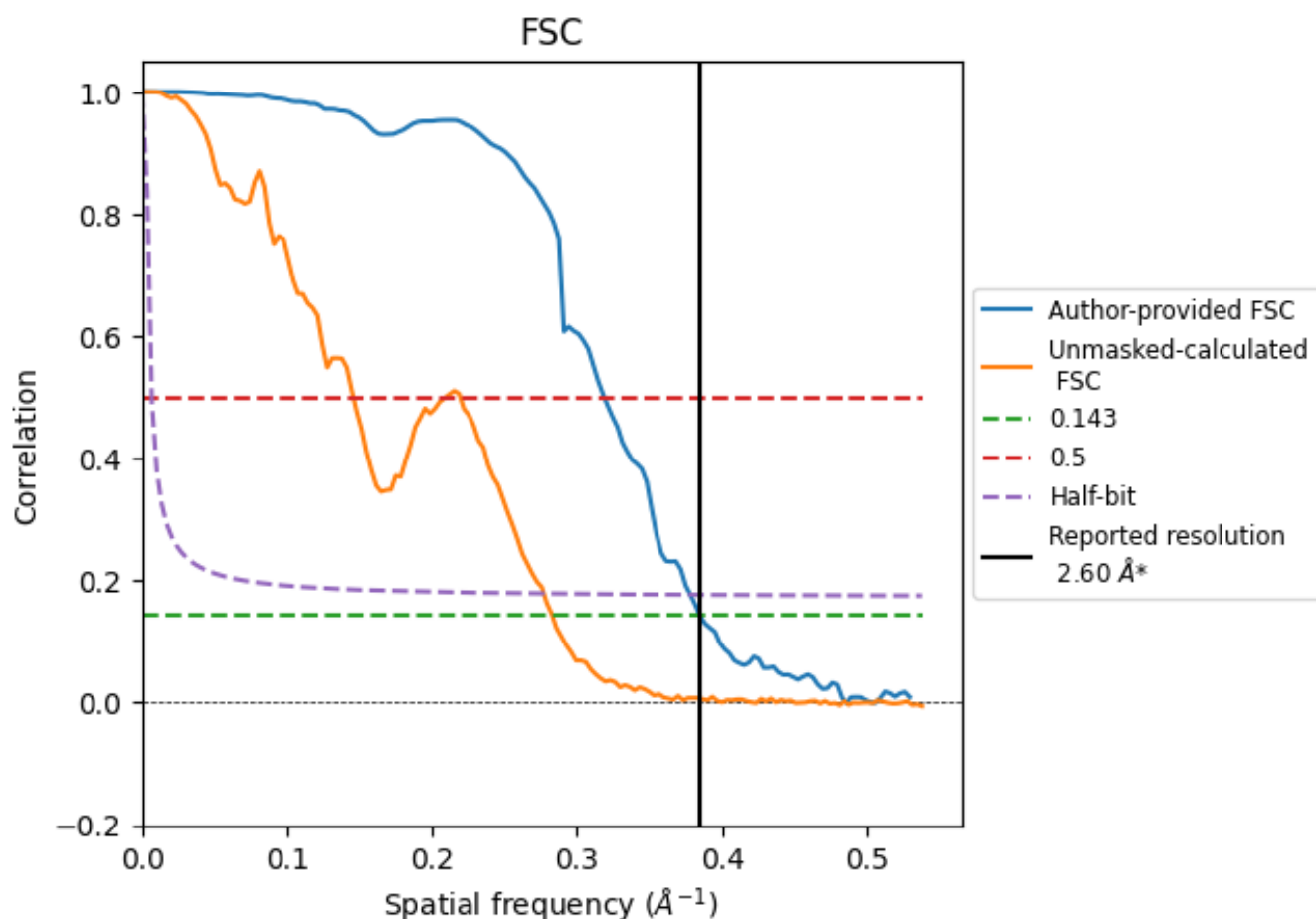


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 $0.385 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

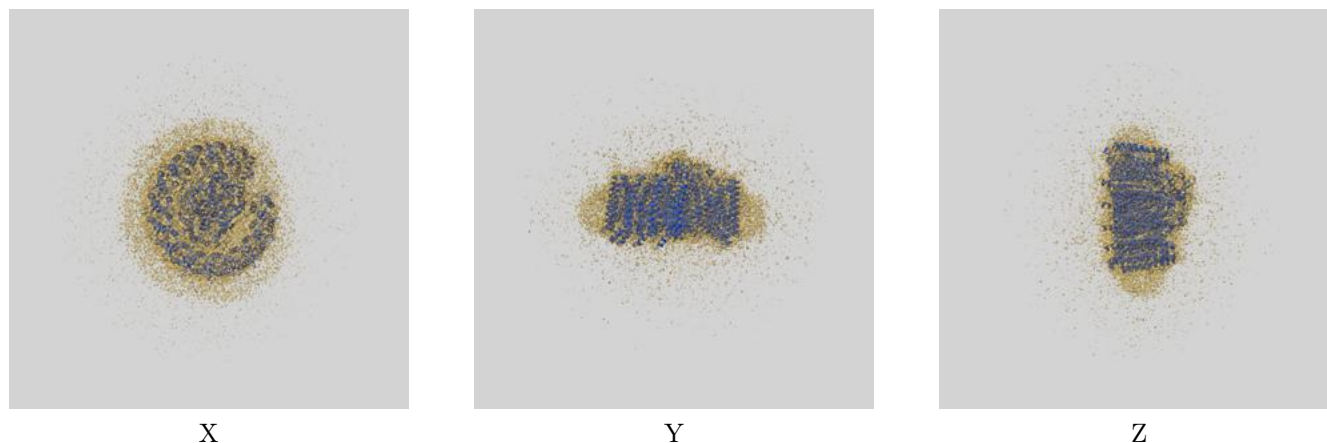
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.60	3.14	2.64
Unmasked-calculated*	3.53	6.86	3.61

*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 3.53 differs from the reported value 2.6 by more than 10 %

9 Map-model fit [i](#)

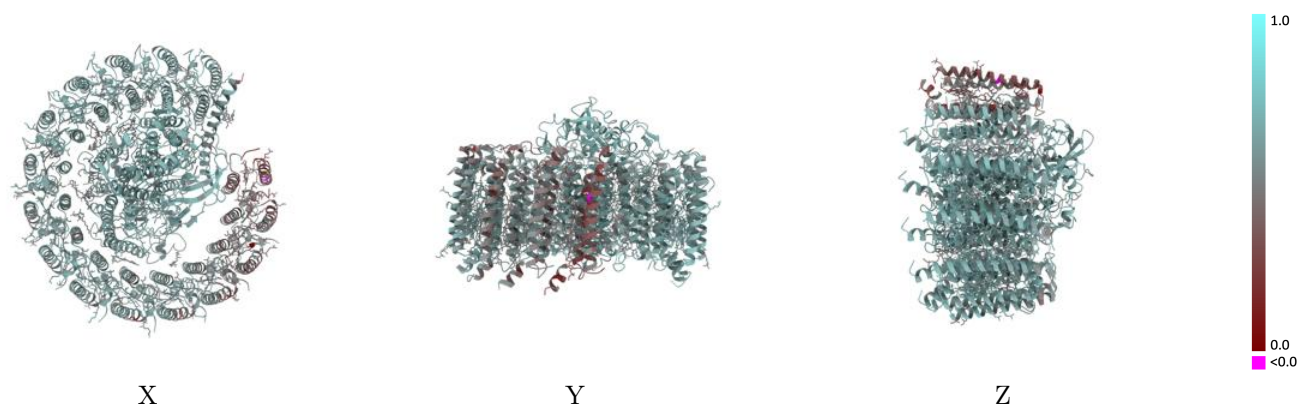
This section contains information regarding the fit between EMDB map EMD-39255 and PDB model 8YGL. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



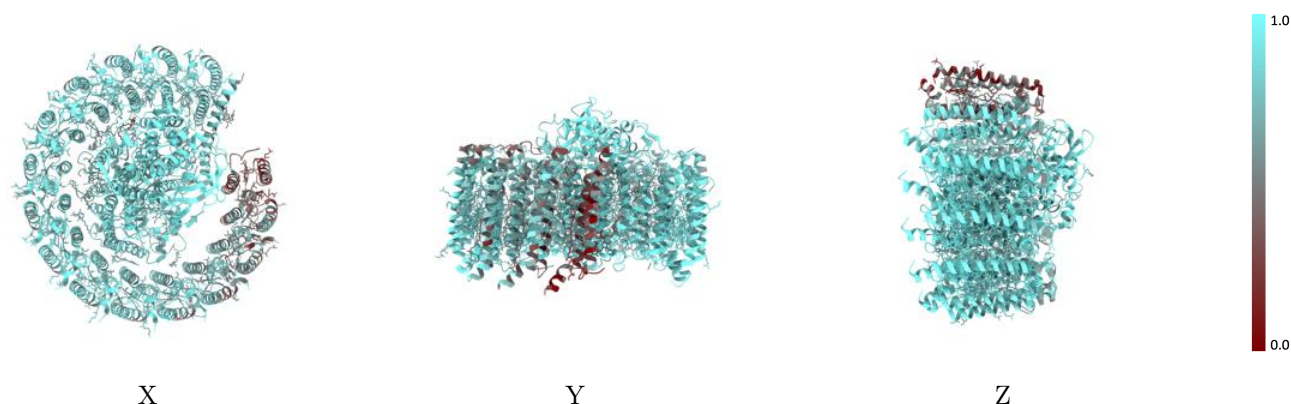
The images above show the 3D surface view of the map at the recommended contour level 0.17 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



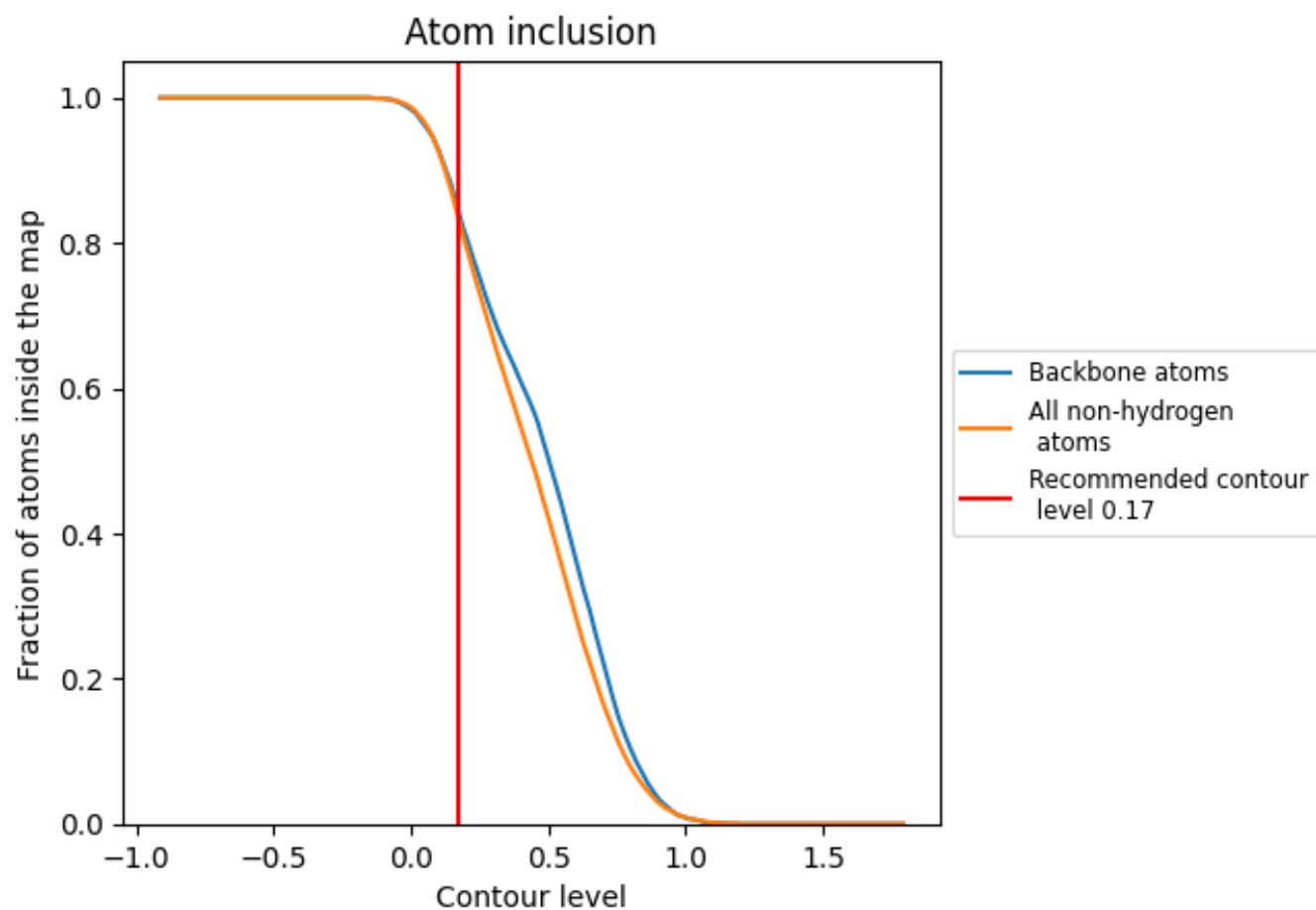
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.17).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 84% 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 (0.17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8380	 0.5900
0	 0.8640	 0.6040
1	 0.5490	 0.4500
2	 0.5300	 0.4490
3	 0.7230	 0.5090
7	 0.8760	 0.6170
8	 0.8720	 0.6090
9	 0.9310	 0.6320
A	 0.8760	 0.6090
B	 0.8820	 0.6280
C	 0.6790	 0.5110
D	 0.8980	 0.6180
E	 0.8920	 0.6180
F	 0.9330	 0.6410
G	 0.8600	 0.6060
H	 0.8980	 0.6200
I	 0.9070	 0.6260
J	 0.7980	 0.5650
K	 0.9200	 0.6200
L	 0.9210	 0.6370
M	 0.9220	 0.6380
N	 0.8350	 0.5880
O	 0.8940	 0.6120
P	 0.8390	 0.5850
Q	 0.9300	 0.6320
R	 0.8400	 0.5990
S	 0.8790	 0.5890
T	 0.8040	 0.5660
U	 0.8730	 0.6010
V	 0.8060	 0.5740
W	 0.8340	 0.5620
X	 0.8220	 0.5830
Z	 0.5810	 0.4510
a	 0.3170	 0.3490
b	 0.2530	 0.3280

