



wwPDB EM Validation Summary Report ⓘ

Aug 7, 2026 – 02:26 AM JST

PDB ID : 9LTU / pdb_00009ltu
EMDB ID : EMD-63381
Title : Cryo-EM structure of the Dinoroseobacter shibae RC-LH1 supercomplex with incomplete LH1 ring(State 1)
Authors : Liu, Z.K.; Wang, P.; Liu, L.N.
Deposited on : 2025-02-06
Resolution : 2.44 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:

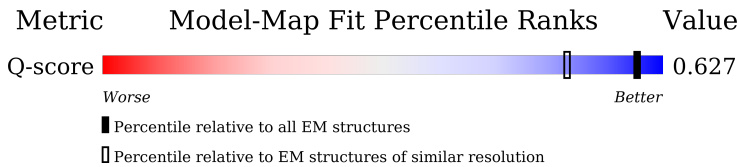
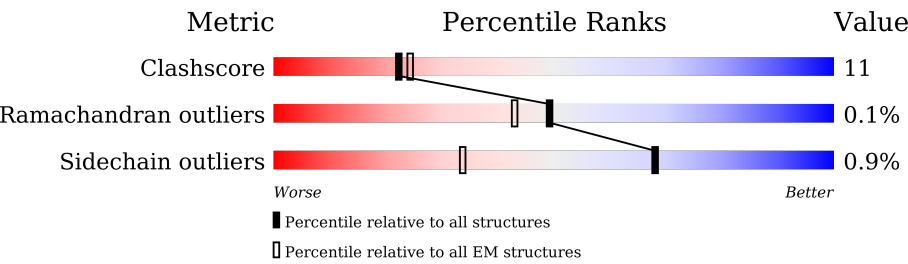
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD 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 2.44 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.



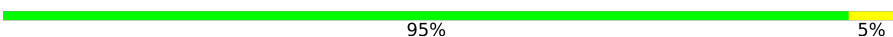
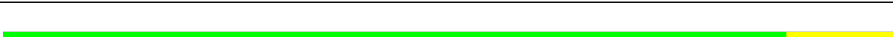
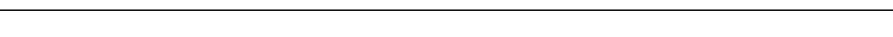
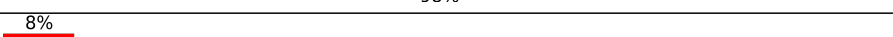
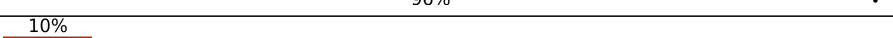
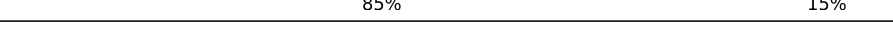
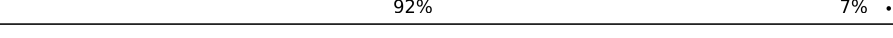
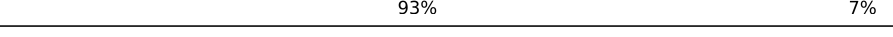
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5856 (1.94 - 2.94)

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	44	7% 82% 18%
1	8	44	41% 61% 34% 5%
1	b	44	5% 89% 11%
1	d	44	93% 7%

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Mol	Chain	Length	Quality of chain
1	f	44	
1	h	44	
1	j	44	
1	l	44	
1	n	44	
1	p	44	
2	7	51	
2	9	51	
2	a	51	
2	c	51	
2	e	51	
2	g	51	
2	i	51	
2	k	51	
2	m	51	
2	o	51	
3	C	357	
4	H	255	
5	L	273	
6	M	325	

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
11	BPH	L	305	-	-	X	-
8	SPN	0	102	-	X	-	-
8	SPN	8	102	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	SPN	9	101	-	X	-	-
8	SPN	a	102	-	X	-	-
8	SPN	a	103	-	X	-	-
8	SPN	a	104	-	X	-	-
8	SPN	e	102	-	X	-	-
8	SPN	f	101	-	X	-	-
8	SPN	g	102	-	X	-	-
8	SPN	i	102	-	X	-	-
8	SPN	i	103	-	X	-	-
8	SPN	l	102	-	X	-	-
8	SPN	m	102	-	X	-	-
8	SPN	n	102	-	X	-	-
8	SPN	p	102	-	X	-	-
8	SPN	p	103	-	X	-	-

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 20306 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
			358	239	56	62	1		
1	8	44	Total	C	N	O	S	0	0
			358	239	56	62	1		
1	b	44	Total	C	N	O	S	0	0
			358	239	56	62	1		
1	d	44	Total	C	N	O	S	0	0
			358	239	56	62	1		
1	f	44	Total	C	N	O	S	0	0
			358	239	56	62	1		
1	h	44	Total	C	N	O	S	0	0
			358	239	56	62	1		
1	j	44	Total	C	N	O	S	0	0
			358	239	56	62	1		
1	l	44	Total	C	N	O	S	0	0
			358	239	56	62	1		
1	n	44	Total	C	N	O	S	0	0
			358	239	56	62	1		
1	p	44	Total	C	N	O	S	0	0
			358	239	56	62	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	51	Total	C	N	O	S	0	0
			425	291	68	64	2		
2	9	51	Total	C	N	O	S	0	0
			425	291	68	64	2		
2	a	51	Total	C	N	O	S	0	0
			425	291	68	64	2		
2	c	51	Total	C	N	O	S	0	0
			425	291	68	64	2		
2	e	51	Total	C	N	O	S	0	0
			425	291	68	64	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	g	51	Total	C	N	O	S	0	0
			425	291	68	64	2		
2	i	51	Total	C	N	O	S	0	0
			425	291	68	64	2		
2	k	51	Total	C	N	O	S	0	0
			425	291	68	64	2		
2	m	51	Total	C	N	O	S	0	0
			425	291	68	64	2		
2	o	51	Total	C	N	O	S	0	0
			425	291	68	64	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	357	Total	C	N	O	S	0	0
			2785	1761	461	548	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	40	MET	TRP	conflict	UNP A8LQ18

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	255	Total	C	N	O	S	0	0
			2015	1279	345	383	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	44	GLU	ASP	conflict	UNP A8LQ33
H	181	LEU	ILE	conflict	UNP A8LQ33
H	197	GLN	GLU	conflict	UNP A8LQ33

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	273	Total	C	N	O	S	0	0
			2172	1466	345	352	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	176	LEU	ILE	conflict	UNP A8LQ16

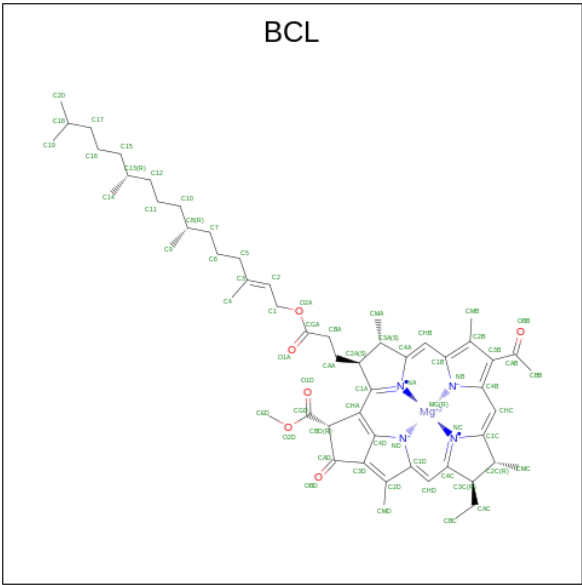
- Molecule 6 is a protein called Reaction center protein M chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	325	Total	C	N	O	S	0	0
			2634	1753	421	452	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	134	THR	SER	conflict	UNP A8LQ17

- Molecule 7 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: $C_{55}H_{74}MgN_4O_6$) (labeled as "Ligand of Interest" by depositor).



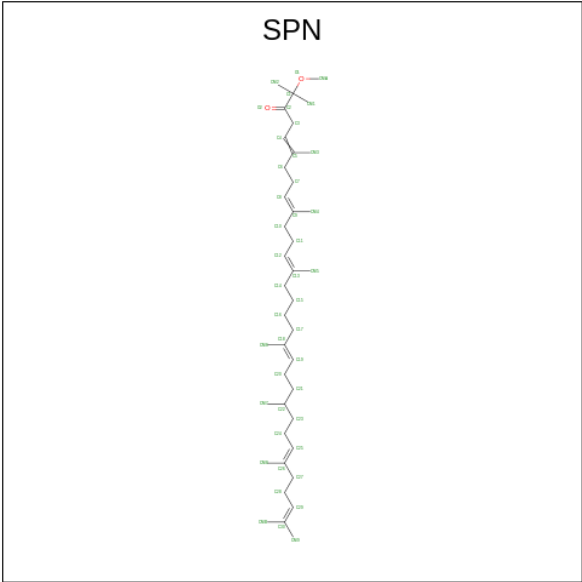
Mol	Chain	Residues	Atoms					AltConf
7	0	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
7	7	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
7	8	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
7	9	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
7	L	1	Total	C	Mg	N	O	0
			66	55	1	4	6	

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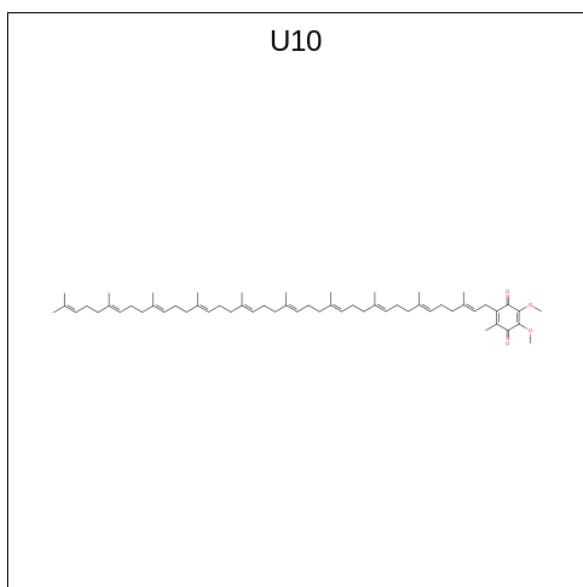
Mol	Chain	Residues	Atoms					AltConf
7	L	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	M	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	M	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	a	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	b	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	c	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	d	1	Total 66	C 55	Mg 1	N 4	O 6	0
7	e	1	Total 66	C 55	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	h	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	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

- Molecule 8 is SPEROIDENONE (CCD ID: SPN) (formula: $C_{41}H_{70}O_2$) (labeled as "Ligand of Interest" by depositor).



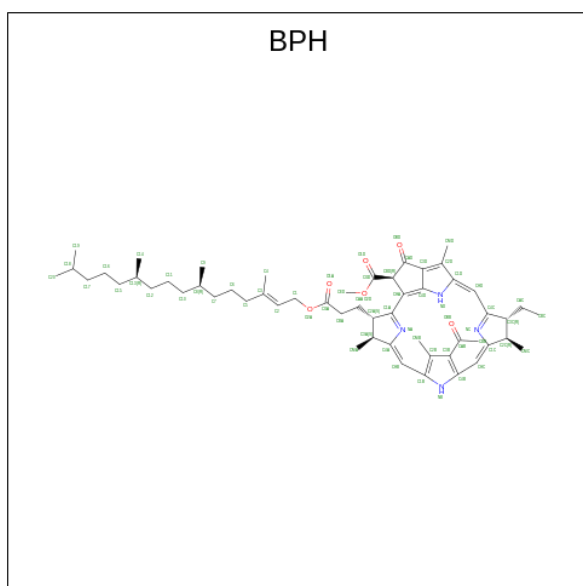
Mol	Chain	Residues	Atoms			AltConf
8	0	1	Total	C	O	0
			43	41	2	
8	8	1	Total	C	O	0
			43	41	2	
8	9	1	Total	C	O	0
			43	41	2	
8	M	1	Total	C	O	0
			43	41	2	
8	a	1	Total	C	O	0
			43	41	2	
8	a	1	Total	C	O	0
			43	41	2	
8	a	1	Total	C	O	0
			43	41	2	
8	e	1	Total	C	O	0
			43	41	2	
8	f	1	Total	C	O	0
			43	41	2	
8	f	1	Total	C	O	0
			43	41	2	
8	g	1	Total	C	O	0
			43	41	2	
8	g	1	Total	C	O	0
			43	41	2	
8	h	1	Total	C	O	0
			43	41	2	
8	i	1	Total	C	O	0
			43	41	2	

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Mol	Chain	Residues	Atoms			AltConf
10	L	1	Total	C	O	0
			38	34	4	
10	M	1	Total	C	O	0
			63	59	4	

- 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
			65	55	4	6	

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Mol	Chain	Residues	Atoms				AltConf
11	L	1	Total	C	N	O	0
			65	55	4	6	
11	M	1	Total	C	N	O	0
			65	55	4	6	

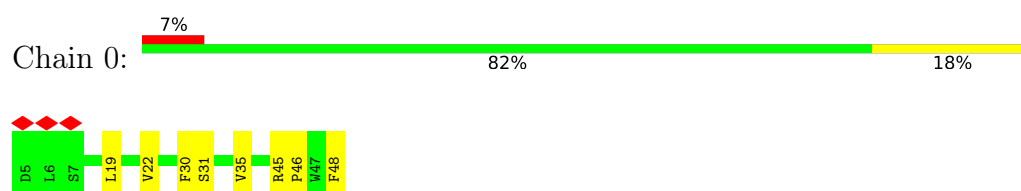
- Molecule 12 is FE (III) ION (CCD ID: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

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

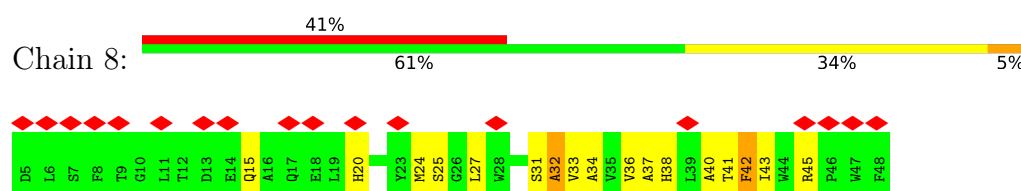
3 Residue-property plots [i](#)

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.

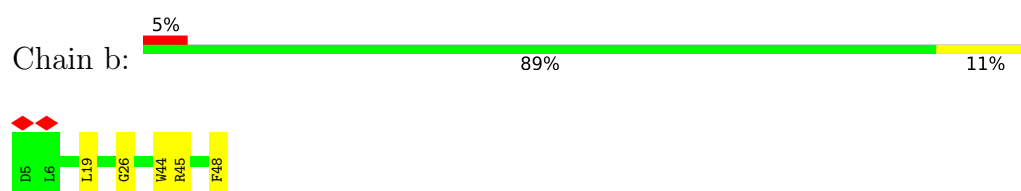
- Molecule 1: Antenna pigment protein beta chain



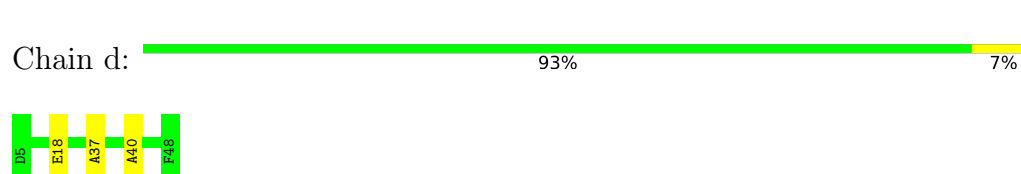
- Molecule 1: Antenna pigment protein beta chain



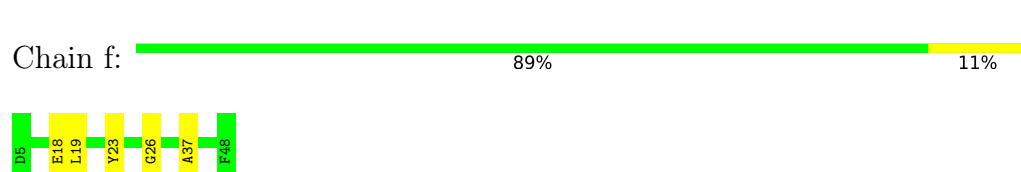
- Molecule 1: Antenna pigment protein beta chain



- Molecule 1: Antenna pigment protein beta chain



- Molecule 1: Antenna pigment protein beta chain

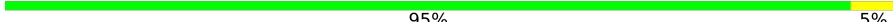


- Molecule 1: Antenna pigment protein beta chain

Chain h:  86% 14%



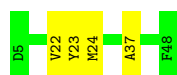
- Molecule 1: Antenna pigment protein beta chain

Chain j:  95% 5%



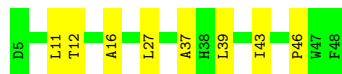
- Molecule 1: Antenna pigment protein beta chain

Chain l:  91% 9%



- Molecule 1: Antenna pigment protein beta chain

Chain n:  82% 18%



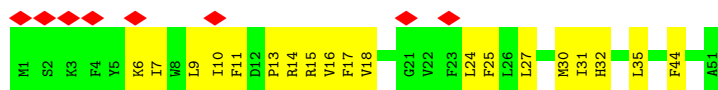
- Molecule 1: Antenna pigment protein beta chain

Chain p:  82% 18%



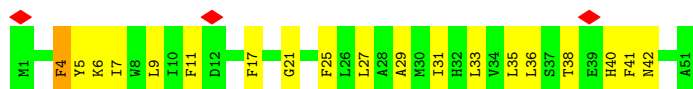
- Molecule 2: Antenna pigment protein alpha chain

Chain 7:  16% 63% 37%



- Molecule 2: Antenna pigment protein alpha chain

Chain 9:  6% 63% 35%



- Molecule 2: Antenna pigment protein alpha chain

Chain a:  73% 27%



- Molecule 2: Antenna pigment protein alpha chain

Chain c:  90% 10%



- Molecule 2: Antenna pigment protein alpha chain

Chain e:  88% 12%



- Molecule 2: Antenna pigment protein alpha chain

Chain g:  90% 10%



- Molecule 2: Antenna pigment protein alpha chain

Chain i:  92% 8%



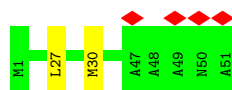
- Molecule 2: Antenna pigment protein alpha chain

Chain k:  98% .



- Molecule 2: Antenna pigment protein alpha chain

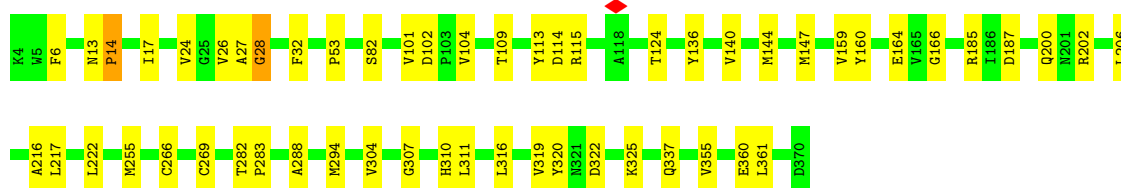
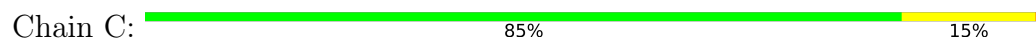
Chain m:  8% 96% .



- Molecule 2: Antenna pigment protein alpha chain



- Molecule 3: Photosynthetic reaction center cytochrome c subunit



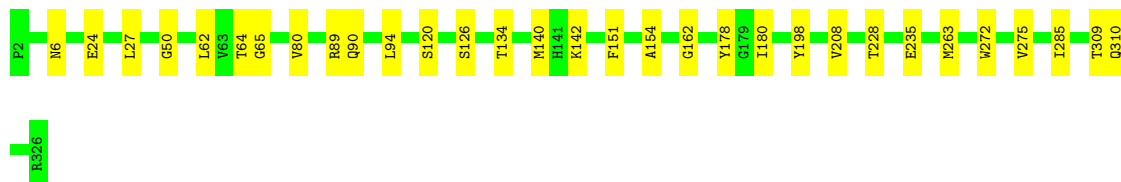
- Molecule 4: Reaction center protein H chain



- Molecule 5: Reaction center protein L chain



- Molecule 6: Reaction center protein M chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT	Depositor
Number of particles used	82830, 82830, 82830, 82830, 82830, 82830, 82830, 82830, 82830	Depositor
Resolution determination method	FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION, PHASE FLIPPING AND AMPLITUDE CORRECTION, PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.00	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.207	Depositor
Minimum map value	-1.249	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.066	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	291.0, 291.0, 291.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.97, 0.97, 0.97	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, U10, BPH, SPN, FE, 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	0	0.32	0/371	0.51	0/508
1	8	0.61	0/371	1.01	3/508 (0.6%)
1	b	0.31	0/371	0.47	0/508
1	d	0.17	0/371	0.27	0/508
1	f	0.18	0/371	0.29	0/508
1	h	0.41	0/371	0.38	0/508
1	j	0.17	0/371	0.26	0/508
1	l	0.19	0/371	0.28	0/508
1	n	0.33	0/371	0.54	1/508 (0.2%)
1	p	0.59	0/371	0.75	2/508 (0.4%)
2	7	0.33	0/439	0.56	0/595
2	9	0.39	0/439	0.70	2/595 (0.3%)
2	a	0.30	0/439	0.41	0/595
2	c	0.14	0/439	0.27	0/595
2	e	0.24	0/439	0.32	0/595
2	g	0.16	0/439	0.27	0/595
2	i	0.20	0/439	0.29	0/595
2	k	0.16	0/439	0.28	0/595
2	m	0.32	0/439	0.50	1/595 (0.2%)
2	o	0.40	0/439	0.74	3/595 (0.5%)
3	C	0.43	1/2864 (0.0%)	0.61	6/3929 (0.2%)
4	H	0.40	1/2065 (0.0%)	0.37	1/2795 (0.0%)
5	L	0.30	0/2261	0.42	1/3097 (0.0%)
6	M	0.36	0/2732	0.45	2/3737 (0.1%)
All	All	0.35	2/18022 (0.0%)	0.49	22/24588 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	54	PRO	N-CD	11.11	1.63	1.47
3	C	27	ALA	CA-C	-5.18	1.46	1.52

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	124	THR	N-CA-C	-11.21	91.79	109.72
2	9	4	PHE	N-CA-C	-8.40	103.22	113.97
2	o	45	GLU	N-CA-C	-8.38	103.00	113.55
5	L	165	TYR	N-CA-C	-7.35	101.51	111.87
3	C	6	PHE	N-CA-C	-7.11	104.48	113.72

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	358	0	338	17	0
1	8	358	0	338	14	0
1	b	358	0	338	16	0
1	d	358	0	338	3	0
1	f	358	0	338	6	0
1	h	358	0	338	9	0
1	j	358	0	338	5	0
1	l	358	0	338	3	0
1	n	358	0	338	5	0
1	p	358	0	338	10	0
2	7	425	0	433	33	0
2	9	425	0	433	40	0
2	a	425	0	433	18	0
2	c	425	0	433	8	0
2	e	425	0	433	5	0
2	g	425	0	433	6	0
2	i	425	0	433	5	0
2	k	425	0	433	1	0
2	m	425	0	433	1	0
2	o	425	0	433	30	0
3	C	2785	0	2630	64	0
4	H	2015	0	1963	20	0
5	L	2172	0	2113	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	M	2634	0	2526	29	0
7	0	66	0	74	14	0
7	7	66	0	74	15	0
7	8	66	0	74	13	0
7	9	66	0	74	10	0
7	L	132	0	148	8	0
7	M	132	0	148	18	0
7	a	66	0	74	5	0
7	b	66	0	74	3	0
7	c	66	0	74	3	0
7	d	66	0	74	5	0
7	e	66	0	74	3	0
7	f	66	0	74	10	0
7	g	66	0	74	3	0
7	h	66	0	74	5	0
7	i	66	0	74	4	0
7	j	66	0	74	5	0
7	k	66	0	74	4	0
7	l	66	0	74	5	0
7	m	66	0	74	9	0
7	n	66	0	74	4	0
7	o	66	0	74	4	0
7	p	66	0	74	10	0
8	0	43	0	69	6	0
8	8	43	0	69	9	0
8	9	43	0	69	7	0
8	M	43	0	69	11	0
8	a	129	0	207	12	0
8	e	43	0	69	2	0
8	f	86	0	138	10	0
8	g	86	0	138	6	0
8	h	43	0	69	5	0
8	i	86	0	138	5	0
8	l	43	0	69	1	0
8	m	43	0	69	3	0
8	n	43	0	69	2	0
8	p	86	0	138	16	0
9	C	129	0	90	12	0
10	L	38	0	47	0	0
10	M	63	0	90	1	0
11	L	130	0	152	25	0
11	M	65	0	76	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	M	1	0	0	0	0
All	All	20306	0	20553	465	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 11.

The worst 5 of 465 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)
3:C:266:CYS:SG	9:C:402:HEM:CAB	2.01	1.46
1:O:45:ARG:HD2	2:G:41:PHE:CE1	1.53	1.44
3:C:266:CYS:SG	9:C:402:HEM:CBB	2.08	1.42
11:L:305:BPH:HBB1	7:M:405:BCL:C20	1.65	1.25
3:C:166:GLY:HA3	3:C:355:VAL:CG2	1.66	1.25

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	0	42/44 (96%)	42 (100%)	0	0	100	100
1	8	42/44 (96%)	35 (83%)	7 (17%)	0	100	100
1	b	42/44 (96%)	42 (100%)	0	0	100	100
1	d	42/44 (96%)	42 (100%)	0	0	100	100
1	f	42/44 (96%)	42 (100%)	0	0	100	100
1	h	42/44 (96%)	42 (100%)	0	0	100	100
1	j	42/44 (96%)	42 (100%)	0	0	100	100
1	l	42/44 (96%)	42 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	n	42/44 (96%)	42 (100%)	0	0	100	100
1	p	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
2	7	49/51 (96%)	43 (88%)	6 (12%)	0	100	100
2	9	49/51 (96%)	45 (92%)	4 (8%)	0	100	100
2	a	49/51 (96%)	47 (96%)	2 (4%)	0	100	100
2	c	49/51 (96%)	49 (100%)	0	0	100	100
2	e	49/51 (96%)	49 (100%)	0	0	100	100
2	g	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
2	i	49/51 (96%)	49 (100%)	0	0	100	100
2	k	49/51 (96%)	49 (100%)	0	0	100	100
2	m	49/51 (96%)	49 (100%)	0	0	100	100
2	o	49/51 (96%)	46 (94%)	3 (6%)	0	100	100
3	C	355/357 (99%)	337 (95%)	17 (5%)	1 (0%)	36	44
4	H	253/255 (99%)	248 (98%)	5 (2%)	0	100	100
5	L	271/273 (99%)	265 (98%)	5 (2%)	1 (0%)	30	36
6	M	323/325 (99%)	318 (98%)	5 (2%)	0	100	100
All	All	2112/2160 (98%)	2054 (97%)	56 (3%)	2 (0%)	49	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	14	PRO
5	L	166	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	0	37/37 (100%)	37 (100%)	0	100	100
1	8	37/37 (100%)	32 (86%)	5 (14%)	4	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	37/37 (100%)	37 (100%)	0	100	100
1	d	37/37 (100%)	37 (100%)	0	100	100
1	f	37/37 (100%)	37 (100%)	0	100	100
1	h	37/37 (100%)	37 (100%)	0	100	100
1	j	37/37 (100%)	37 (100%)	0	100	100
1	l	37/37 (100%)	37 (100%)	0	100	100
1	n	37/37 (100%)	37 (100%)	0	100	100
1	p	37/37 (100%)	36 (97%)	1 (3%)	39	52
2	7	43/43 (100%)	43 (100%)	0	100	100
2	9	43/43 (100%)	43 (100%)	0	100	100
2	a	43/43 (100%)	42 (98%)	1 (2%)	44	57
2	c	43/43 (100%)	42 (98%)	1 (2%)	44	57
2	e	43/43 (100%)	43 (100%)	0	100	100
2	g	43/43 (100%)	43 (100%)	0	100	100
2	i	43/43 (100%)	42 (98%)	1 (2%)	44	57
2	k	43/43 (100%)	43 (100%)	0	100	100
2	m	43/43 (100%)	43 (100%)	0	100	100
2	o	43/43 (100%)	42 (98%)	1 (2%)	44	57
3	C	304/304 (100%)	301 (99%)	3 (1%)	68	77
4	H	213/213 (100%)	212 (100%)	1 (0%)	81	87
5	L	217/217 (100%)	217 (100%)	0	100	100
6	M	266/266 (100%)	263 (99%)	3 (1%)	65	75
All	All	1800/1800 (100%)	1783 (99%)	17 (1%)	68	80

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	i	18	VAL
1	p	45	ARG
3	C	104	VAL
4	H	194	VAL
6	M	180	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
6	M	267	HIS
2	e	40	HIS
2	a	40	HIS
2	e	50	ASN
3	C	223	ASN

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 53 ligands modelled in this entry, 1 is monoatomic - leaving 52 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	j	101	1	69,74,74	0.87	4 (5%)	83,115,115	1.18	11 (13%)
7	BCL	n	101	1	69,74,74	0.80	1 (1%)	83,115,115	1.25	13 (15%)
8	SPN	p	102	-	40,42,42	3.87	19 (47%)	50,52,52	2.52	19 (38%)
7	BCL	L	303	5	69,74,74	0.95	4 (5%)	83,115,115	1.15	11 (13%)
8	SPN	9	101	-	40,42,42	3.91	19 (47%)	50,52,52	2.44	19 (38%)
7	BCL	f	102	1	69,74,74	0.85	2 (2%)	83,115,115	1.18	12 (14%)
8	SPN	g	103	-	40,42,42	3.94	19 (47%)	50,52,52	2.56	18 (36%)
8	SPN	M	406	-	40,42,42	3.93	19 (47%)	50,52,52	2.72	18 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	BPH	M	404	-	59,70,70	1.10	4 (6%)	61,101,101	0.96	4 (6%)
7	BCL	L	301	5	69,74,74	0.90	4 (5%)	83,115,115	1.24	13 (15%)
7	BCL	8	101	-	69,74,74	0.83	1 (1%)	83,115,115	1.34	16 (19%)
8	SPN	e	102	-	40,42,42	3.87	19 (47%)	50,52,52	2.47	21 (42%)
9	HEM	C	402	3	50,50,50	0.76	1 (2%)	66,82,82	1.08	4 (6%)
7	BCL	d	101	1	69,74,74	0.80	1 (1%)	83,115,115	1.26	12 (14%)
8	SPN	f	103	-	40,42,42	3.91	19 (47%)	50,52,52	2.56	18 (36%)
8	SPN	p	103	-	40,42,42	3.93	19 (47%)	50,52,52	2.49	20 (40%)
7	BCL	0	101	1	69,74,74	0.81	1 (1%)	83,115,115	1.23	10 (12%)
8	SPN	a	104	-	40,42,42	3.91	19 (47%)	50,52,52	2.46	20 (40%)
8	SPN	g	102	-	40,42,42	3.89	19 (47%)	50,52,52	2.45	21 (42%)
9	HEM	C	403	3	50,50,50	0.73	1 (2%)	66,82,82	0.63	0
7	BCL	h	101	1	69,74,74	0.84	3 (4%)	83,115,115	1.17	7 (8%)
7	BCL	c	101	2	69,74,74	0.81	2 (2%)	83,115,115	1.21	12 (14%)
7	BCL	M	405	6	69,74,74	0.92	3 (4%)	83,115,115	1.14	9 (10%)
7	BCL	p	101	1	69,74,74	0.82	1 (1%)	83,115,115	1.25	13 (15%)
8	SPN	a	102	-	40,42,42	3.87	19 (47%)	50,52,52	2.46	21 (42%)
8	SPN	m	102	-	40,42,42	3.92	19 (47%)	50,52,52	2.45	20 (40%)
11	BPH	L	304	-	59,70,70	1.12	3 (5%)	61,101,101	0.98	4 (6%)
8	SPN	8	102	-	40,42,42	3.89	19 (47%)	50,52,52	2.48	21 (42%)
7	BCL	m	101	2	69,74,74	0.83	3 (4%)	83,115,115	1.21	11 (13%)
8	SPN	h	102	-	40,42,42	3.89	19 (47%)	50,52,52	2.58	18 (36%)
7	BCL	M	402	6	69,74,74	0.85	2 (2%)	83,115,115	1.25	13 (15%)
10	U10	M	403	-	63,63,63	0.18	0	76,79,79	0.40	1 (1%)
9	HEM	C	401	3	50,50,50	0.76	1 (2%)	66,82,82	0.62	0
7	BCL	o	101	2	69,74,74	0.79	1 (1%)	83,115,115	1.25	11 (13%)
8	SPN	a	103	-	40,42,42	3.93	19 (47%)	50,52,52	2.53	20 (40%)
7	BCL	7	101	2	69,74,74	0.77	1 (1%)	83,115,115	1.30	14 (16%)
8	SPN	i	102	-	40,42,42	3.88	19 (47%)	50,52,52	2.46	21 (42%)
7	BCL	g	101	2	69,74,74	0.83	3 (4%)	83,115,115	1.19	11 (13%)
7	BCL	k	101	2	69,74,74	0.85	3 (4%)	83,115,115	1.20	11 (13%)
7	BCL	l	101	1	69,74,74	0.83	1 (1%)	83,115,115	1.20	9 (10%)
7	BCL	b	101	1	69,74,74	0.80	1 (1%)	83,115,115	1.28	12 (14%)
7	BCL	9	102	2	69,74,74	0.78	2 (2%)	83,115,115	1.29	14 (16%)
8	SPN	i	103	-	40,42,42	3.89	19 (47%)	50,52,52	2.57	18 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	SPN	f	101	-	40,42,42	3.87	19 (47%)	50,52,52	2.46	21 (42%)
10	U10	L	302	-	38,38,63	0.21	0	46,49,79	0.50	1 (2%)
8	SPN	l	102	-	40,42,42	3.87	19 (47%)	50,52,52	2.46	21 (42%)
7	BCL	i	101	2	69,74,74	0.86	4 (5%)	83,115,115	1.19	12 (14%)
11	BPH	L	305	-	59,70,70	1.12	4 (6%)	61,101,101	1.59	11 (18%)
7	BCL	a	101	2	69,74,74	0.82	3 (4%)	83,115,115	1.21	12 (14%)
8	SPN	n	102	-	40,42,42	3.87	19 (47%)	50,52,52	2.44	21 (42%)
7	BCL	e	101	2	69,74,74	0.83	2 (2%)	83,115,115	1.19	12 (14%)
8	SPN	0	102	-	40,42,42	3.90	19 (47%)	50,52,52	2.58	21 (42%)

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	j	101	1	-	19/41/137/137	-
7	BCL	n	101	1	-	22/41/137/137	-
8	SPN	p	102	-	-	27/50/51/51	-
7	BCL	L	303	5	-	20/41/137/137	-
8	SPN	9	101	-	-	22/50/51/51	-
7	BCL	f	102	1	-	18/41/137/137	-
8	SPN	g	103	-	-	20/50/51/51	-
8	SPN	M	406	-	-	19/50/51/51	-
11	BPH	M	404	-	-	10/37/105/105	0/5/6/6
7	BCL	L	301	5	-	15/41/137/137	-
7	BCL	8	101	-	-	23/41/137/137	-
8	SPN	e	102	-	-	20/50/51/51	-
9	HEM	C	402	3	-	4/14/54/54	-
7	BCL	d	101	1	-	22/41/137/137	-
8	SPN	f	103	-	-	20/50/51/51	-
8	SPN	p	103	-	-	21/50/51/51	-
7	BCL	0	101	1	-	22/41/137/137	-
8	SPN	a	104	-	-	21/50/51/51	-
8	SPN	g	102	-	-	19/50/51/51	-
9	HEM	C	403	3	-	4/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	BCL	h	101	1	-	14/41/137/137	-
7	BCL	c	101	2	-	15/41/137/137	-
7	BCL	M	405	6	-	18/41/137/137	-
7	BCL	p	101	1	-	20/41/137/137	-
8	SPN	a	102	-	-	19/50/51/51	-
8	SPN	m	102	-	-	20/50/51/51	-
11	BPH	L	304	-	-	10/37/105/105	0/5/6/6
8	SPN	8	102	-	-	18/50/51/51	-
7	BCL	m	101	2	-	21/41/137/137	-
8	SPN	h	102	-	-	20/50/51/51	-
7	BCL	M	402	6	-	19/41/137/137	-
10	U10	M	403	-	-	14/63/87/87	0/1/1/1
9	HEM	C	401	3	-	5/14/54/54	-
7	BCL	o	101	2	-	21/41/137/137	-
8	SPN	a	103	-	-	20/50/51/51	-
7	BCL	7	101	2	-	21/41/137/137	-
8	SPN	i	102	-	-	19/50/51/51	-
7	BCL	g	101	2	-	17/41/137/137	-
7	BCL	k	101	2	-	16/41/137/137	-
7	BCL	l	101	1	-	19/41/137/137	-
7	BCL	b	101	1	-	21/41/137/137	-
7	BCL	9	102	2	-	22/41/137/137	-
8	SPN	i	103	-	-	21/50/51/51	-
8	SPN	f	101	-	-	20/50/51/51	-
10	U10	L	302	-	-	5/33/57/87	0/1/1/1
8	SPN	l	102	-	-	21/50/51/51	-
7	BCL	i	101	2	-	14/41/137/137	-
11	BPH	L	305	-	-	20/37/105/105	0/5/6/6
7	BCL	a	101	2	-	21/41/137/137	-
8	SPN	n	102	-	-	22/50/51/51	-
7	BCL	e	101	2	-	19/41/137/137	-
8	SPN	0	102	-	-	18/50/51/51	-

The worst 5 of 447 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	a	103	SPN	C3-C4	-12.25	1.32	1.50
8	g	103	SPN	C3-C4	-12.22	1.33	1.50
8	p	103	SPN	C3-C4	-12.19	1.33	1.50
8	M	406	SPN	C3-C4	-12.16	1.33	1.50
8	m	102	SPN	C3-C4	-12.15	1.33	1.50

The worst 5 of 703 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	h	102	SPN	C21-C20-C19	7.09	130.95	112.23
8	f	103	SPN	C21-C20-C19	7.02	130.77	112.23
8	i	103	SPN	C21-C20-C19	6.79	130.15	112.23
8	g	103	SPN	C21-C20-C19	6.69	129.90	112.23
11	L	305	BPH	C1A-C2A-C3A	-6.48	96.68	102.84

There are no chirality outliers.

5 of 938 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	0	101	BCL	C1A-C2A-CAA-CBA
7	0	101	BCL	C2C-C3C-CAC-CBC
7	0	101	BCL	C4C-C3C-CAC-CBC
7	7	101	BCL	C4C-C3C-CAC-CBC
7	7	101	BCL	CBD-CGD-O2D-CED

There are no ring outliers.

50 monomers are involved in 270 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	j	101	BCL	5	0
7	n	101	BCL	4	0
8	p	102	SPN	5	0
7	L	303	BCL	4	0
8	9	101	SPN	7	0
7	f	102	BCL	10	0
8	g	103	SPN	5	0
8	M	406	SPN	11	0
11	M	404	BPH	15	0
7	L	301	BCL	6	0
7	8	101	BCL	13	0
8	e	102	SPN	2	0
9	C	402	HEM	7	0

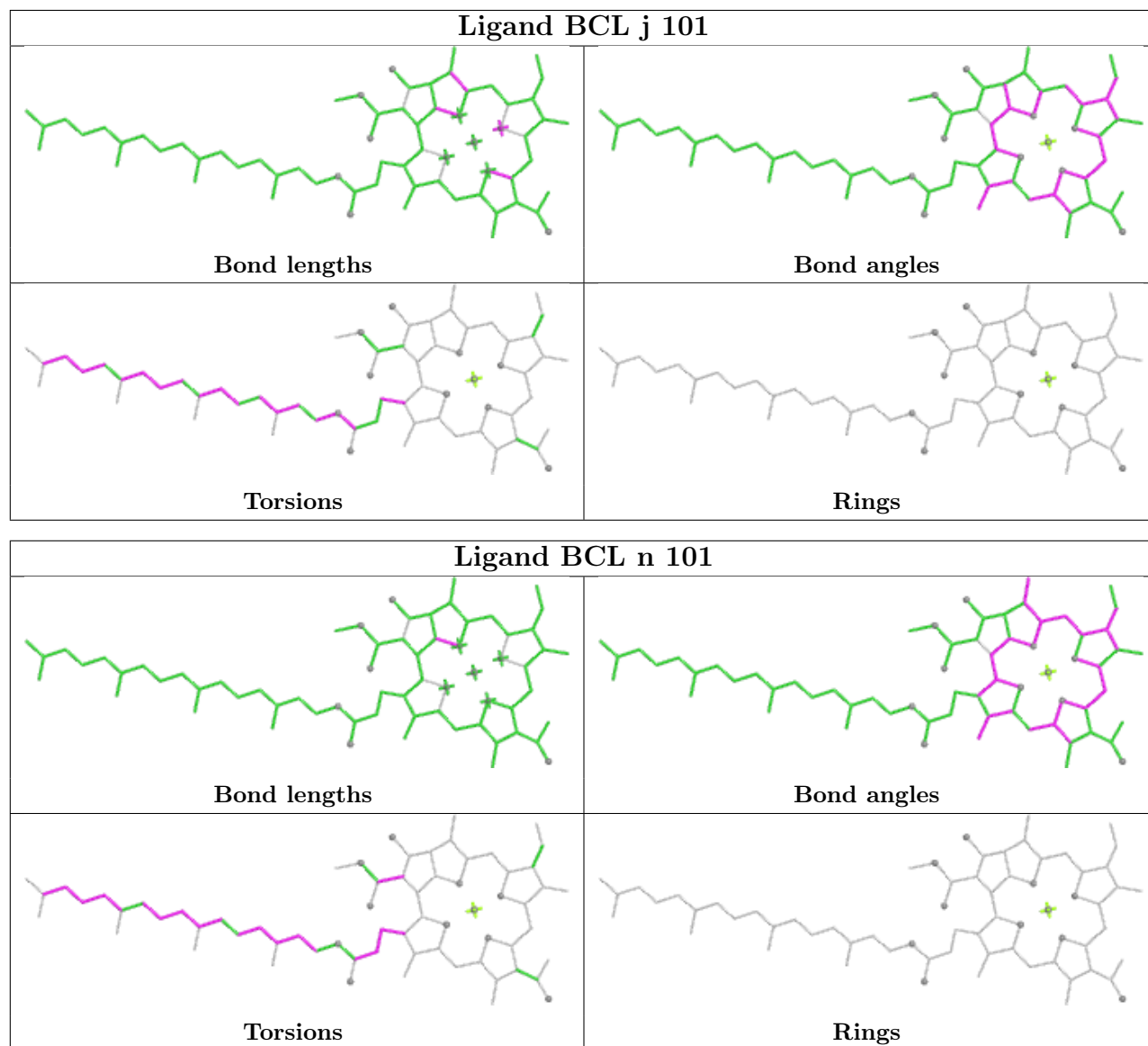
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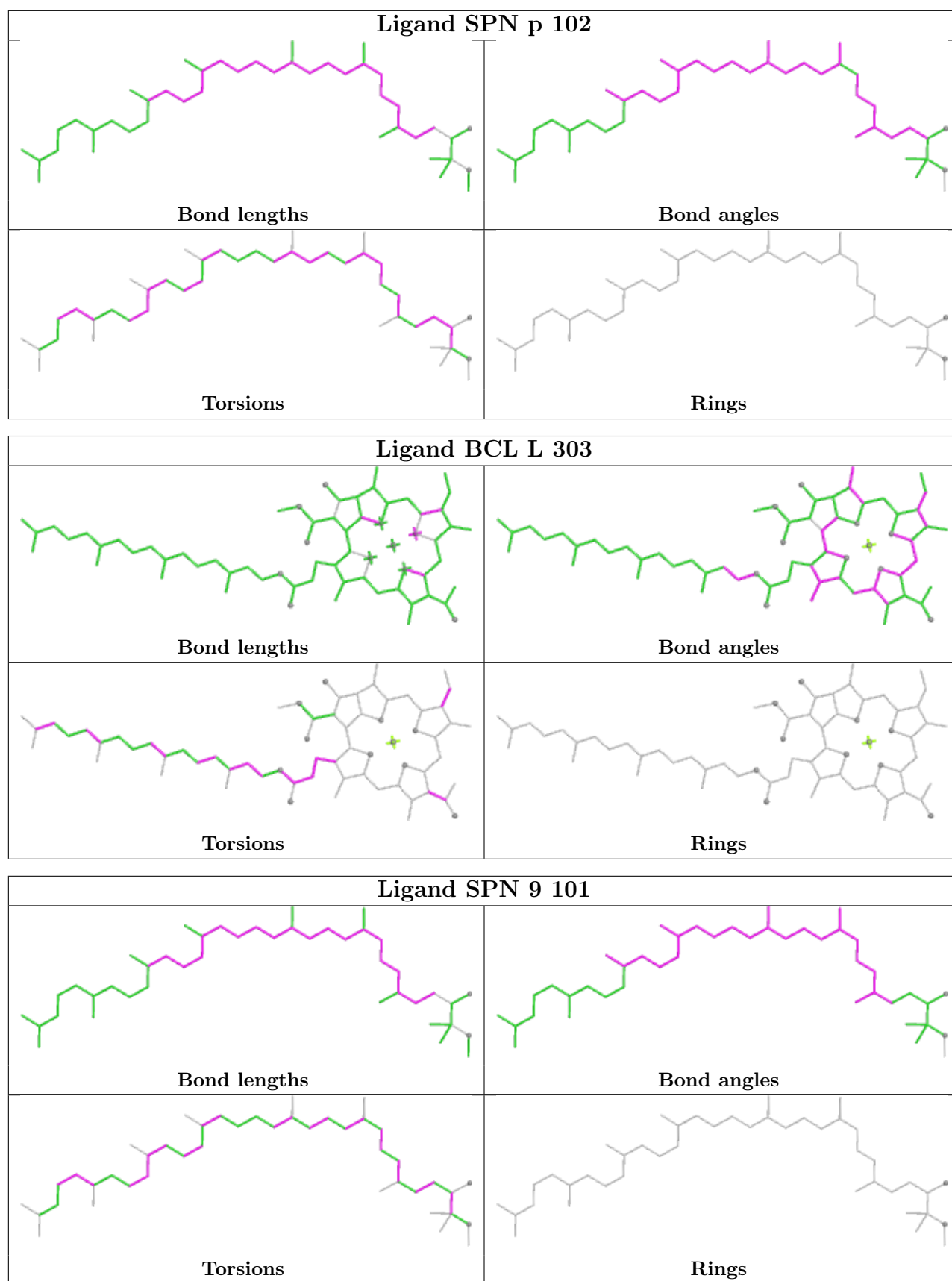
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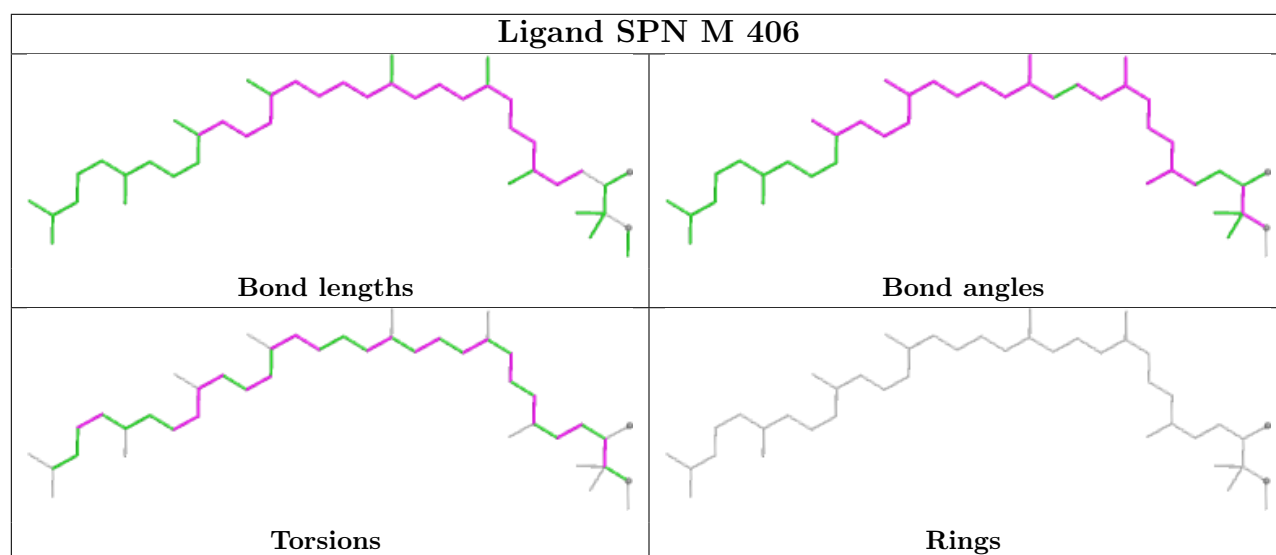
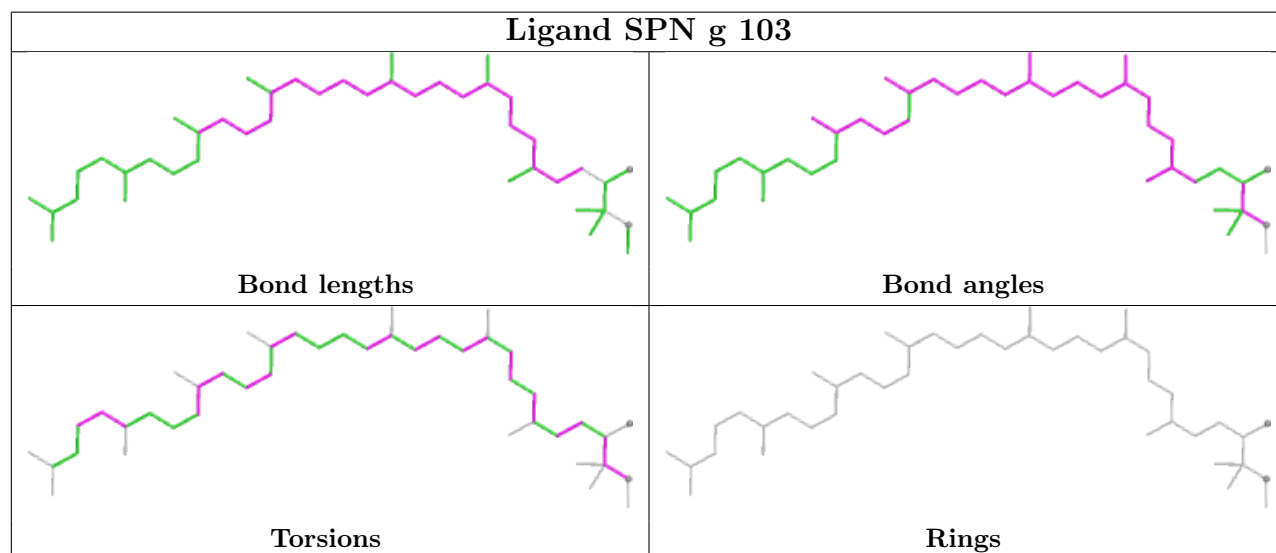
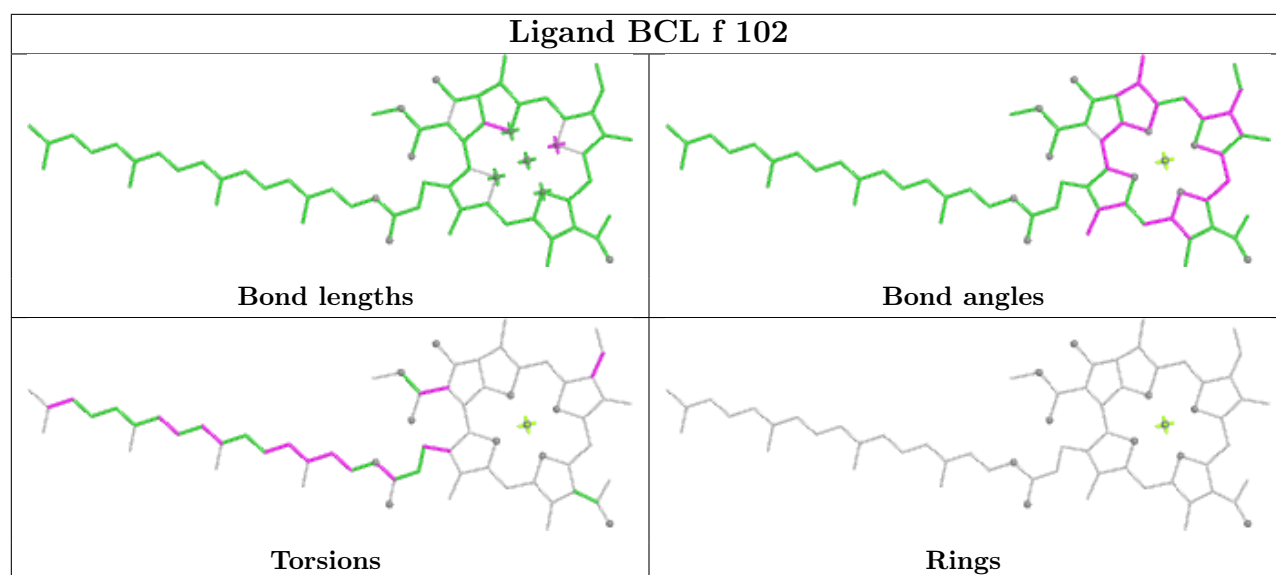
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	d	101	BCL	5	0
8	f	103	SPN	8	0
8	p	103	SPN	11	0
7	0	101	BCL	14	0
8	g	102	SPN	1	0
9	C	403	HEM	2	0
7	h	101	BCL	5	0
7	c	101	BCL	3	0
7	M	405	BCL	11	0
7	p	101	BCL	10	0
8	a	102	SPN	1	0
8	m	102	SPN	3	0
11	L	304	BPH	1	0
8	8	102	SPN	9	0
7	m	101	BCL	9	0
8	h	102	SPN	5	0
7	M	402	BCL	7	0
10	M	403	U10	1	0
9	C	401	HEM	3	0
7	o	101	BCL	4	0
8	a	103	SPN	12	0
7	7	101	BCL	15	0
8	i	102	SPN	2	0
7	g	101	BCL	3	0
7	k	101	BCL	4	0
7	l	101	BCL	5	0
7	b	101	BCL	3	0
7	9	102	BCL	10	0
8	i	103	SPN	3	0
8	f	101	SPN	2	0
8	l	102	SPN	1	0
7	i	101	BCL	4	0
11	L	305	BPH	24	0
7	a	101	BCL	5	0
8	n	102	SPN	2	0
7	e	101	BCL	3	0
8	0	102	SPN	6	0

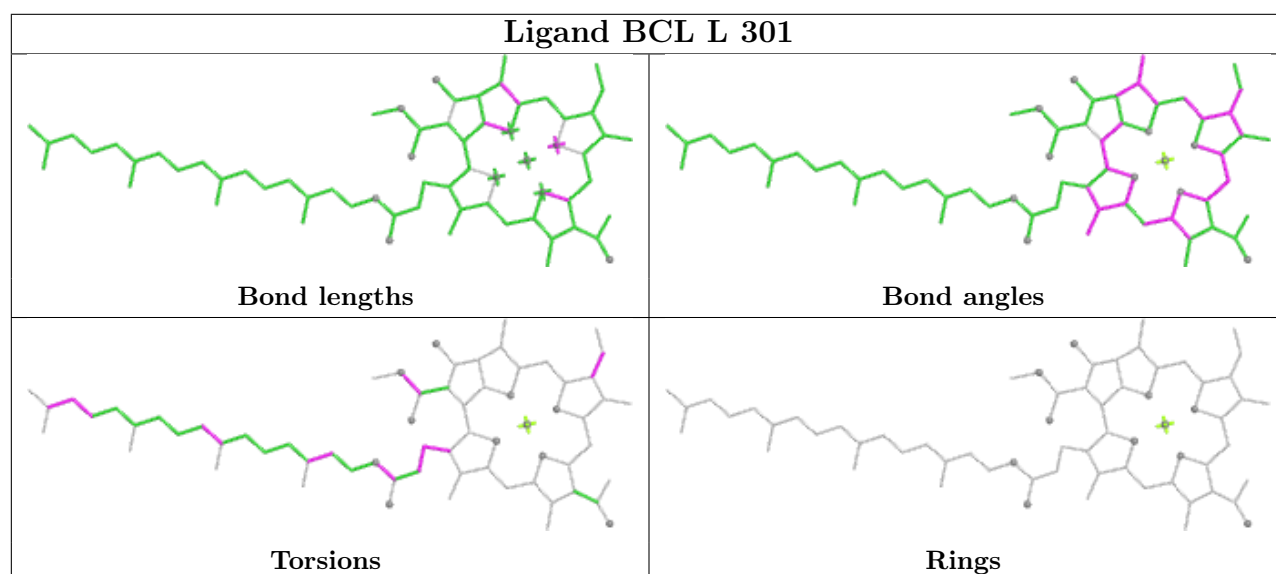
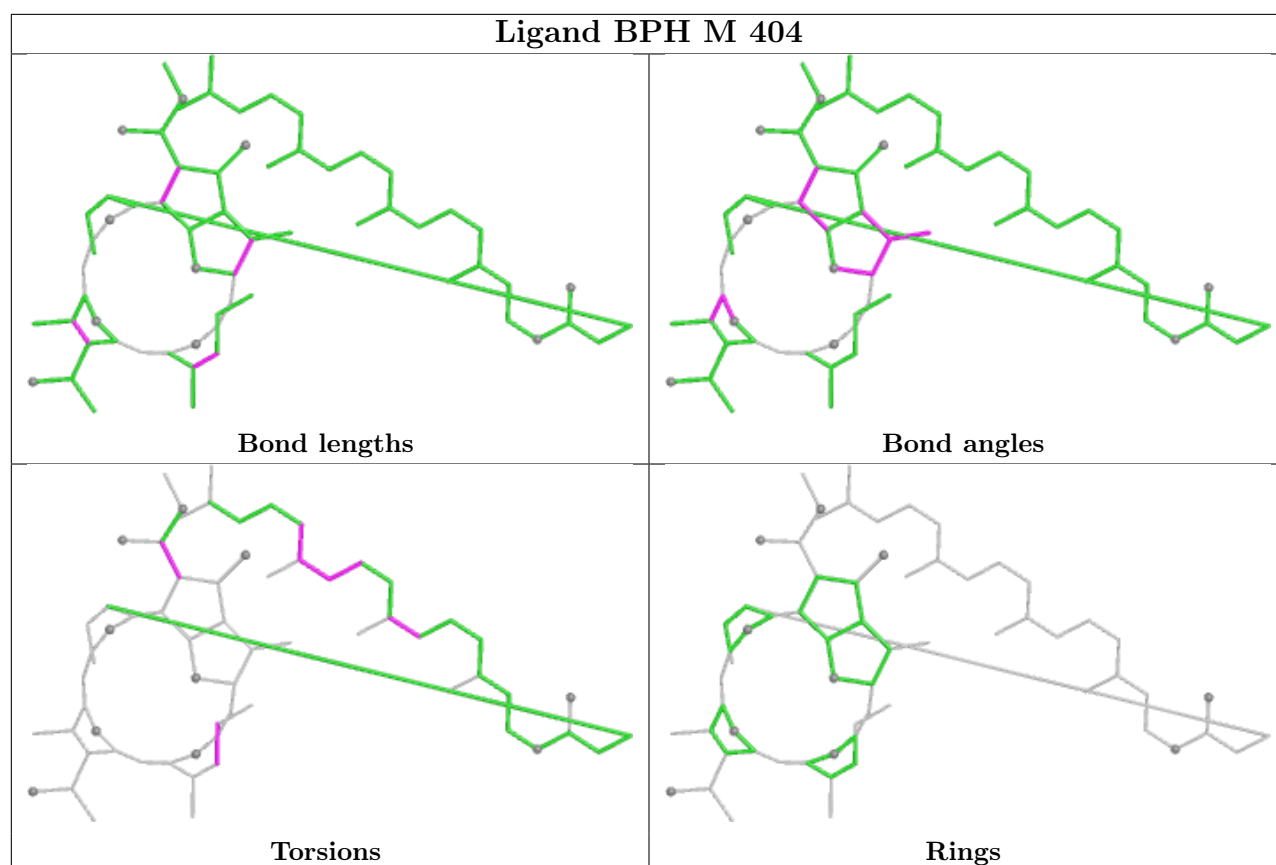
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

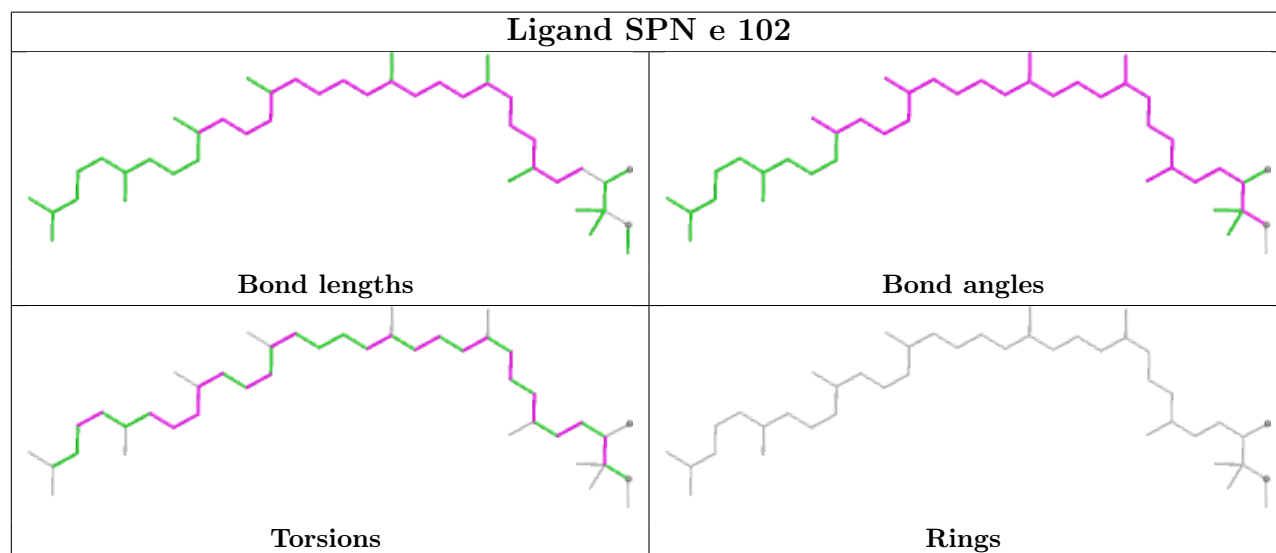
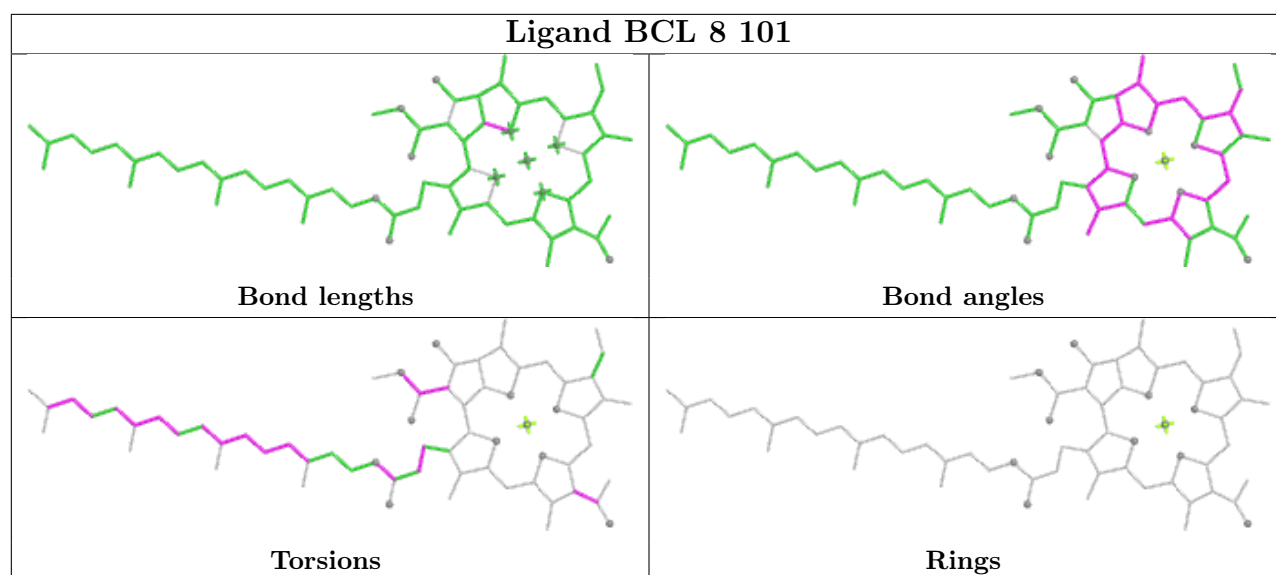
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD 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.

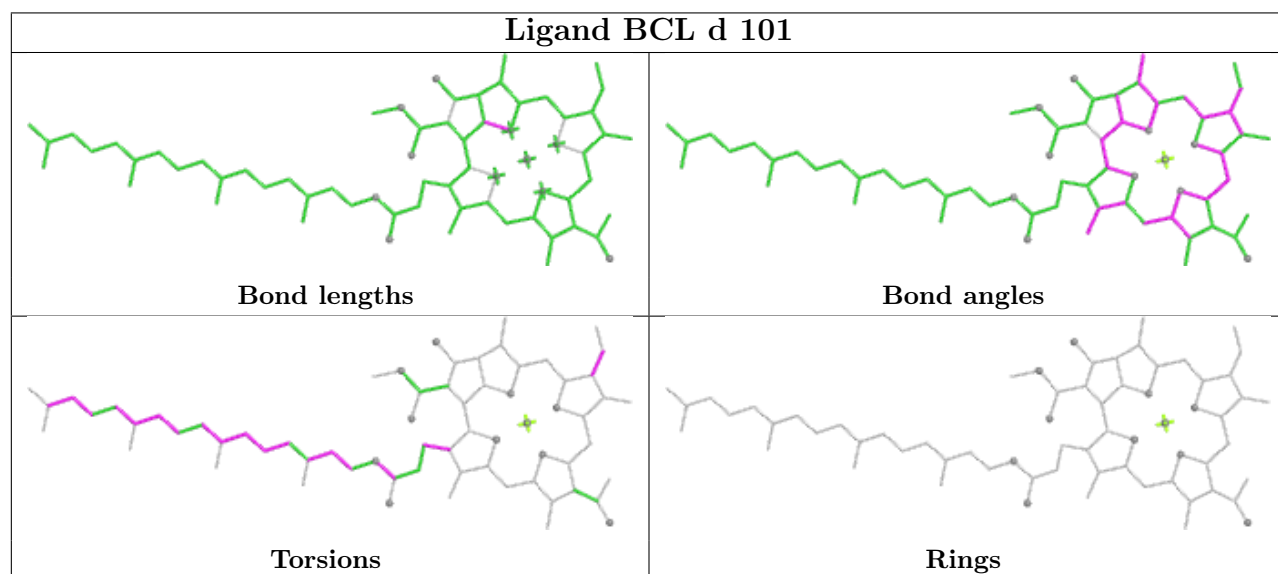
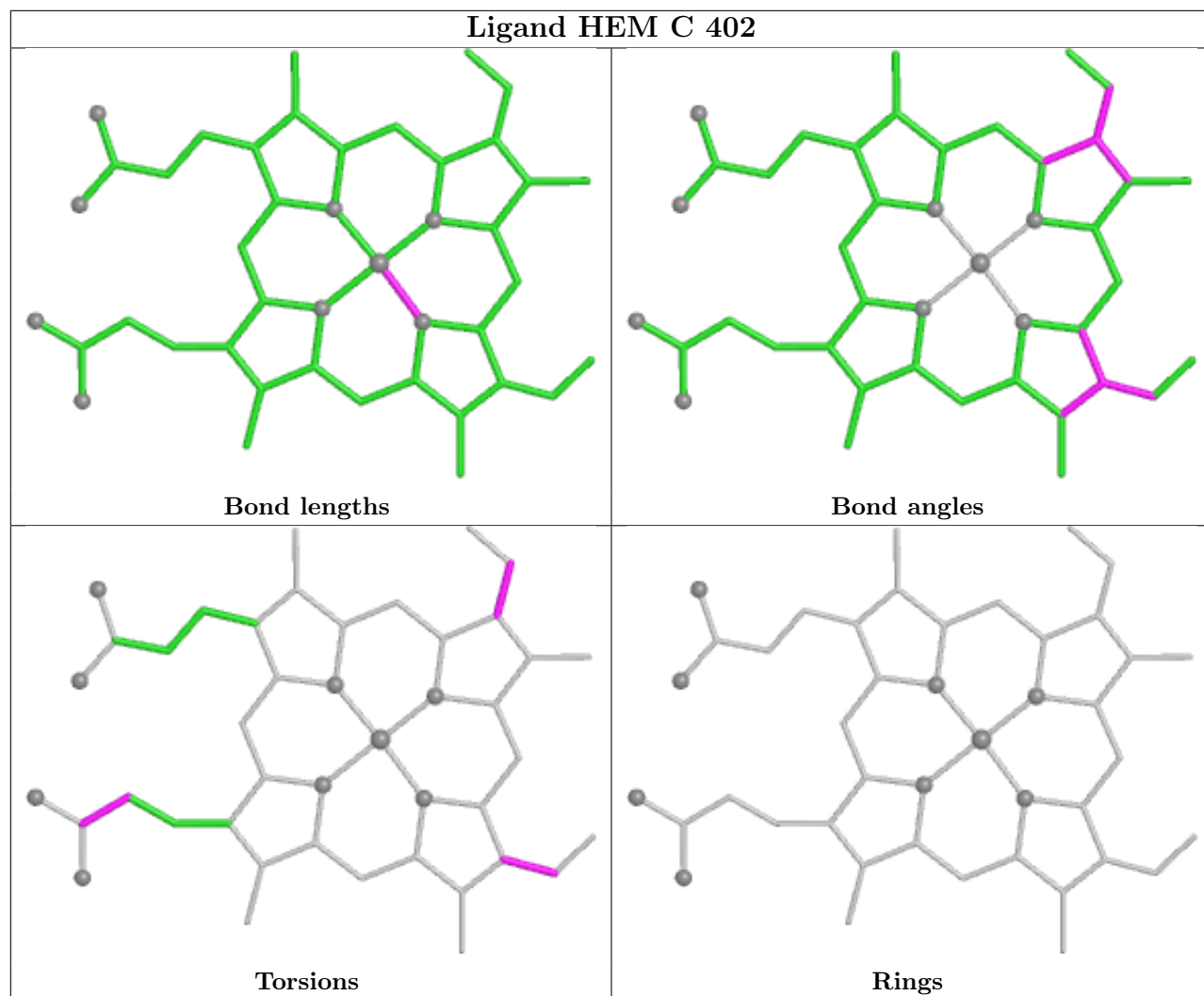


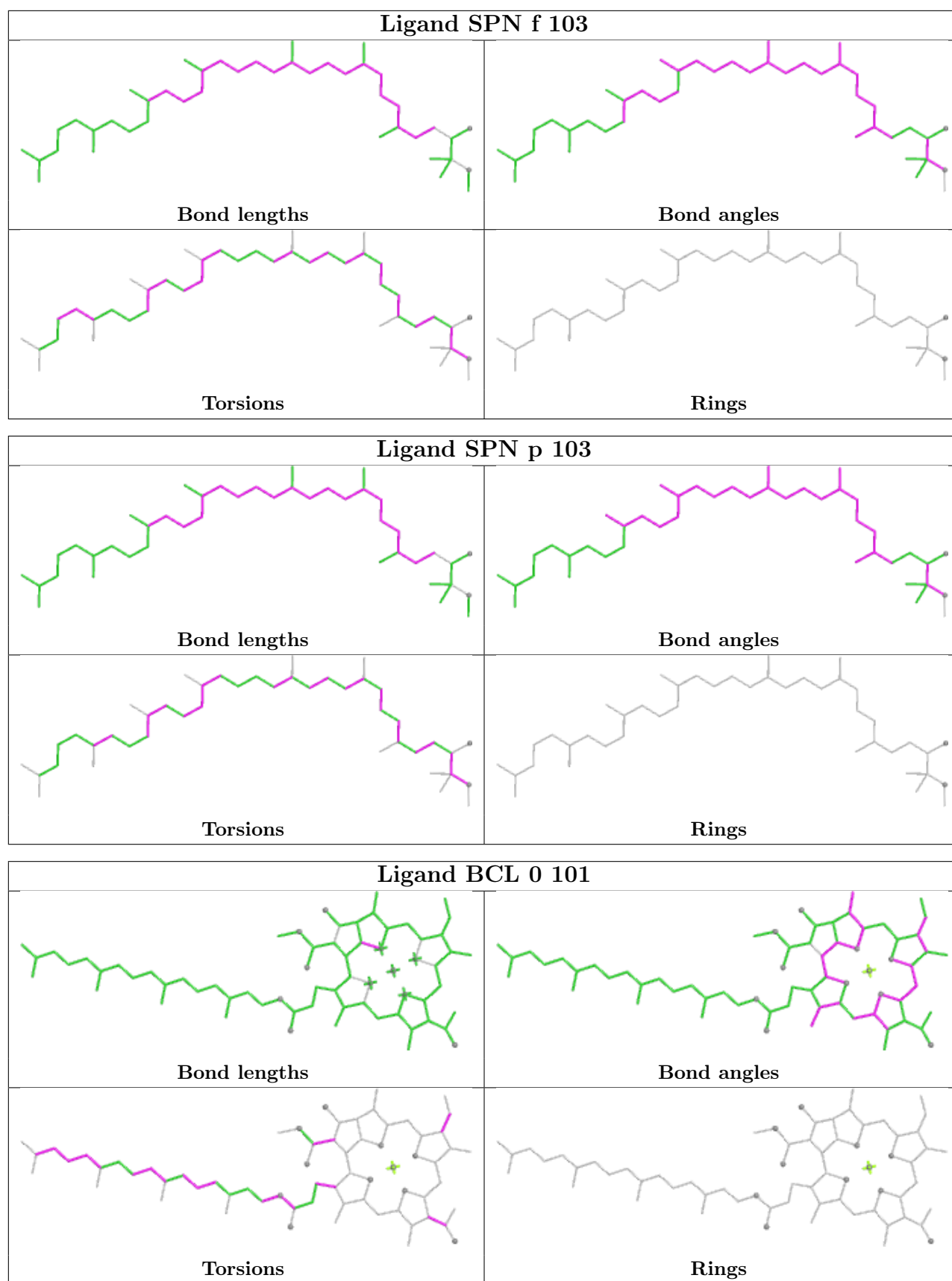


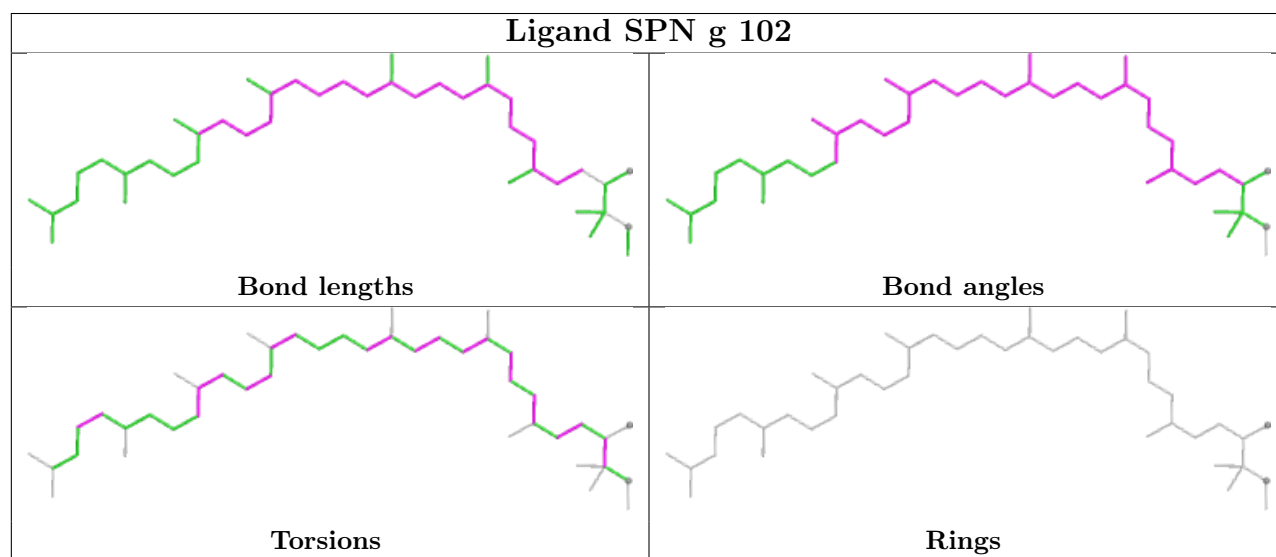
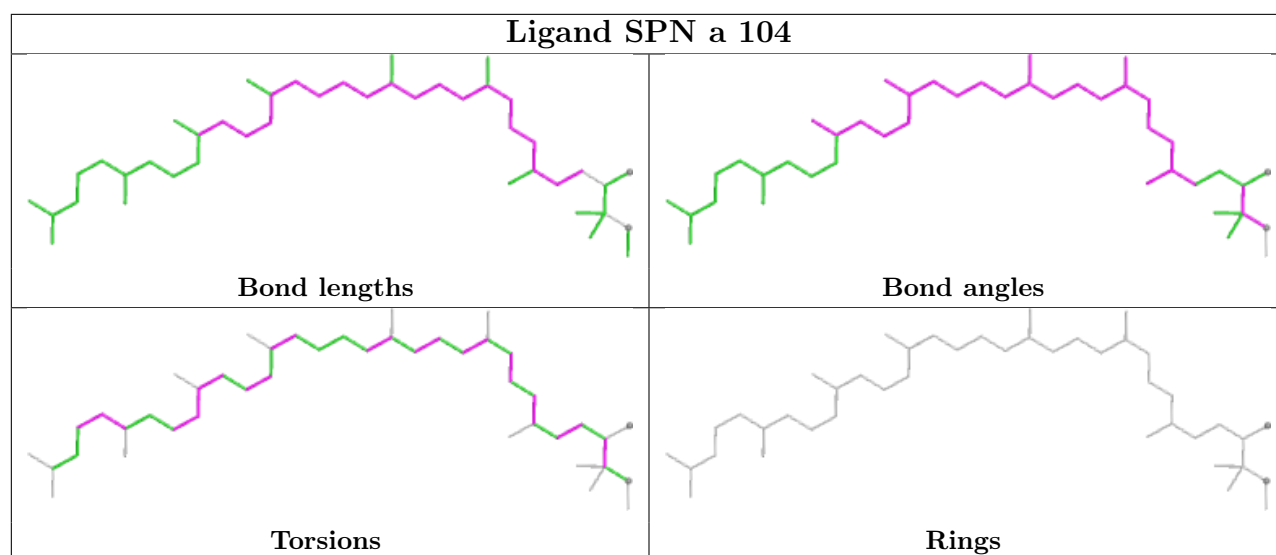


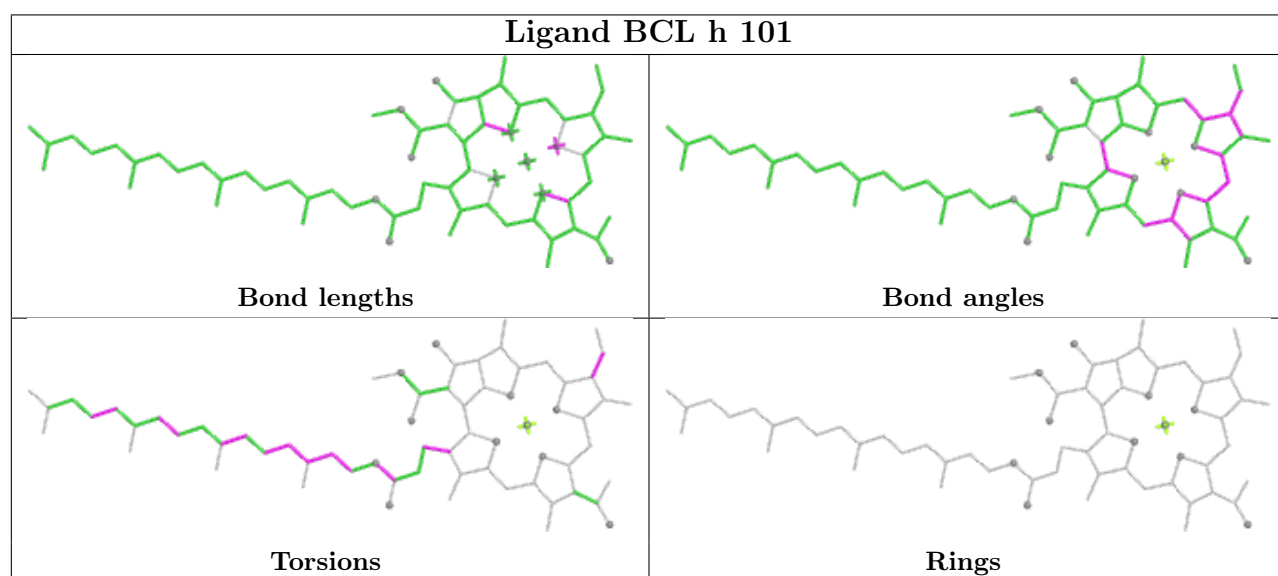
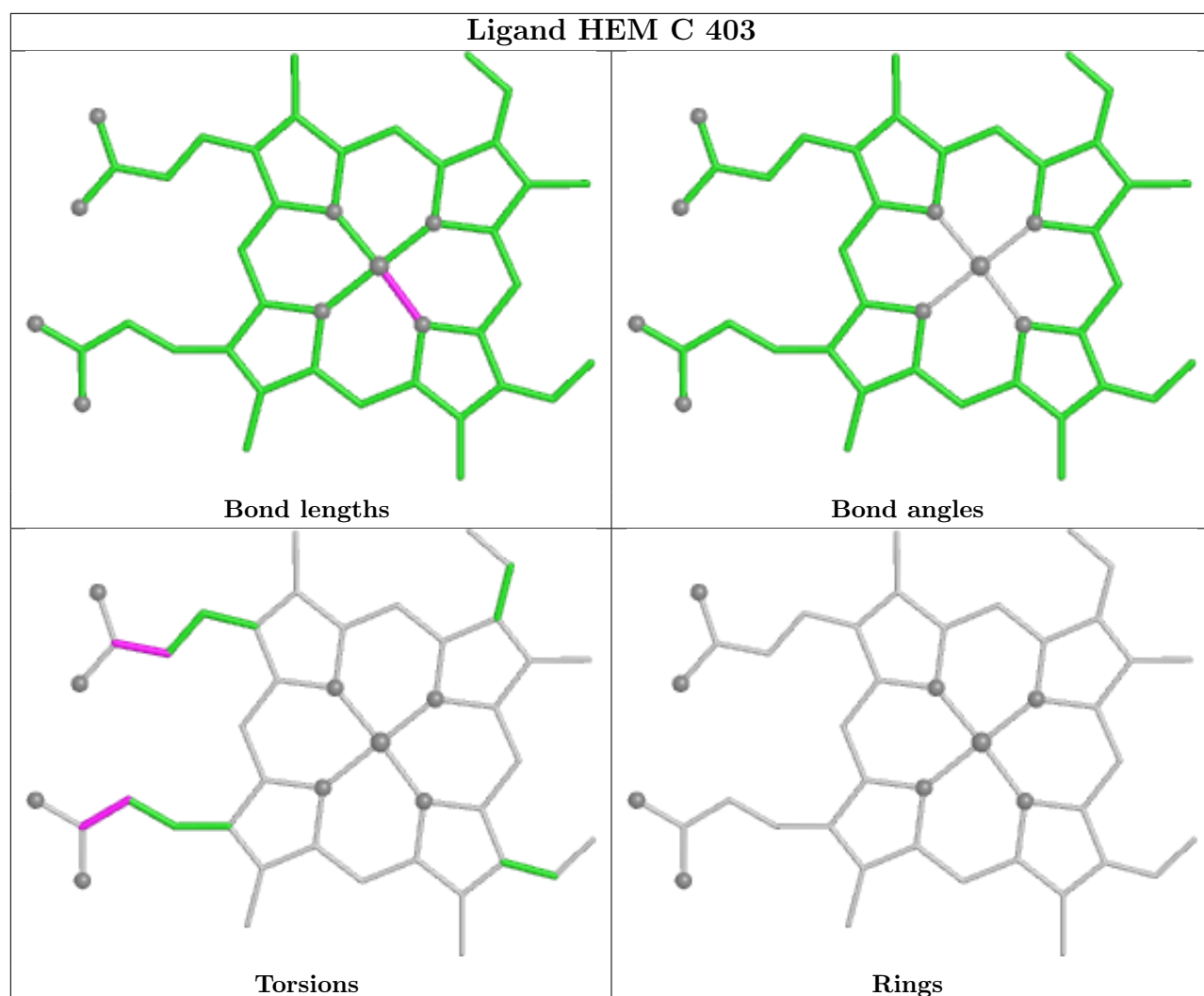


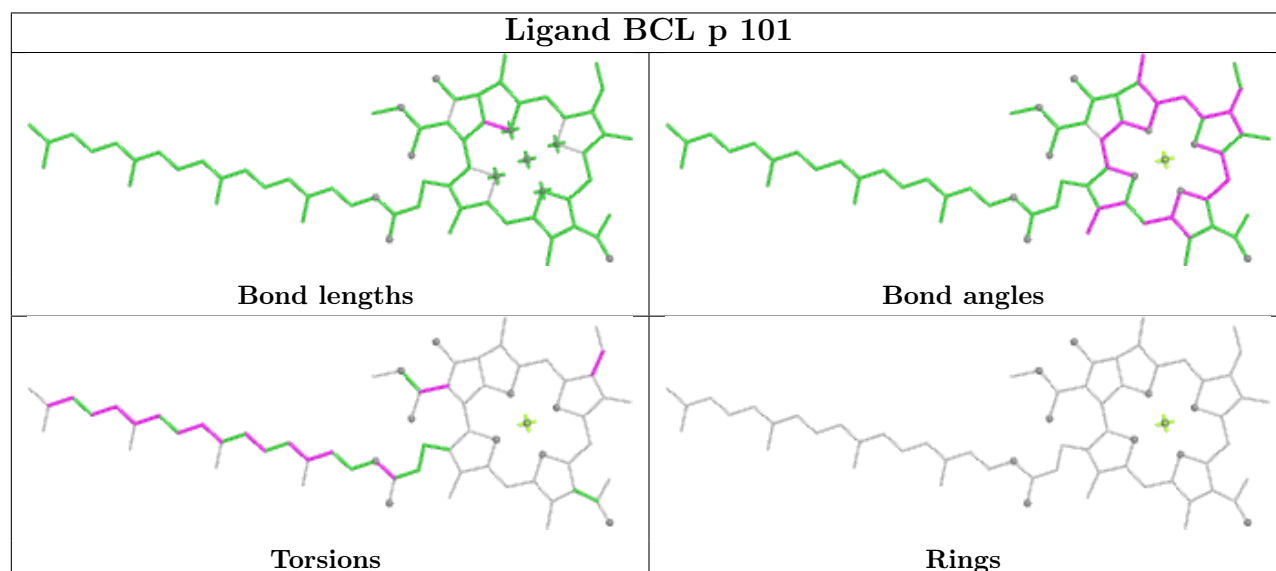
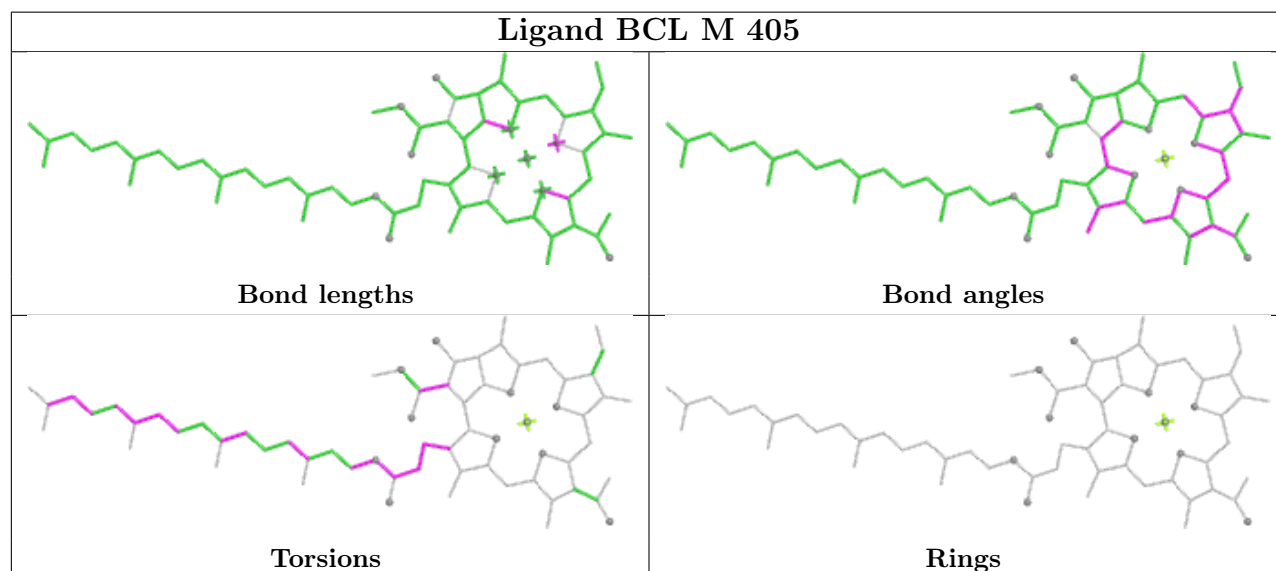
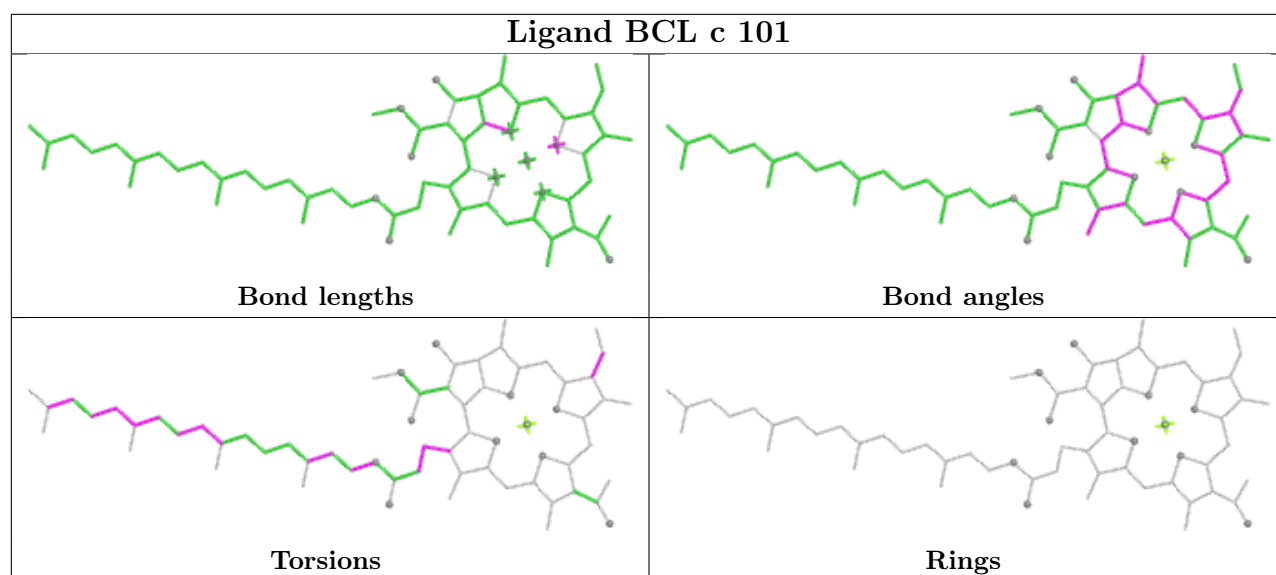


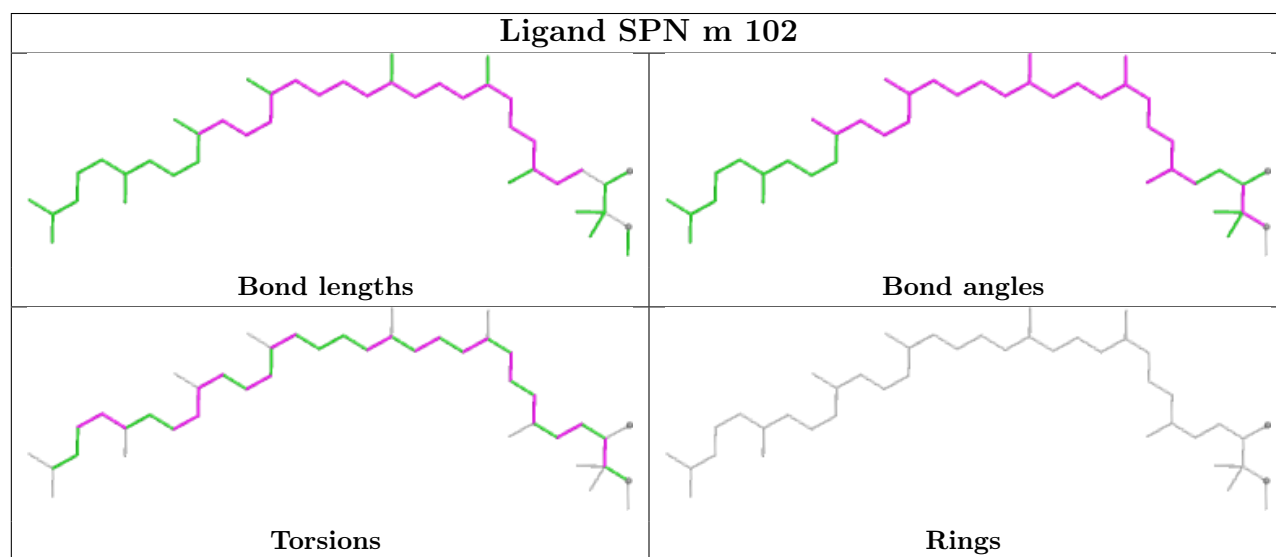
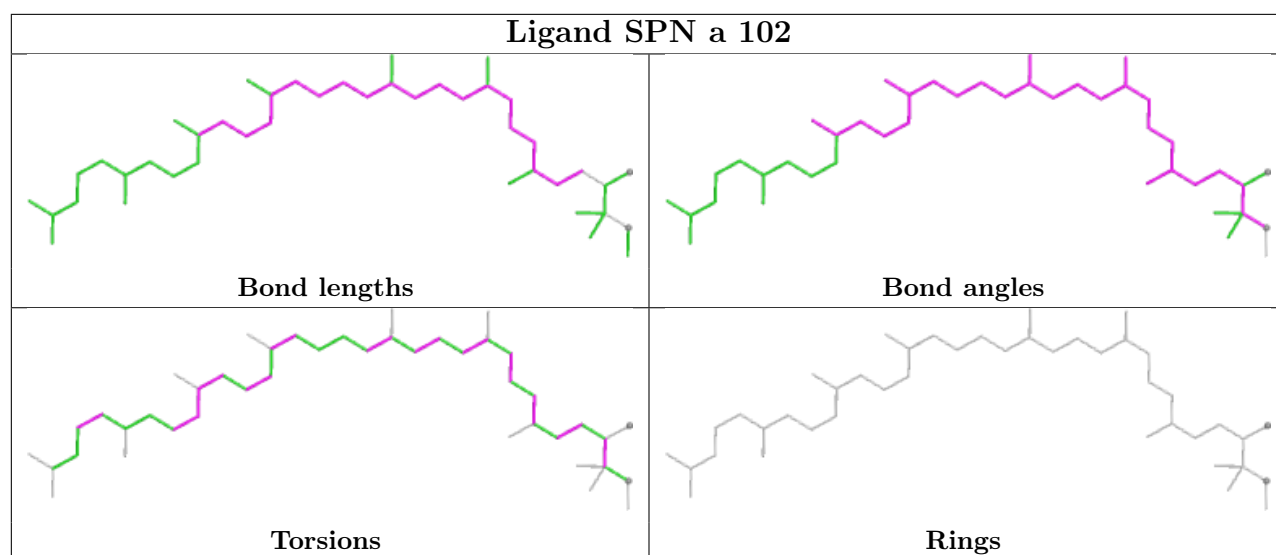


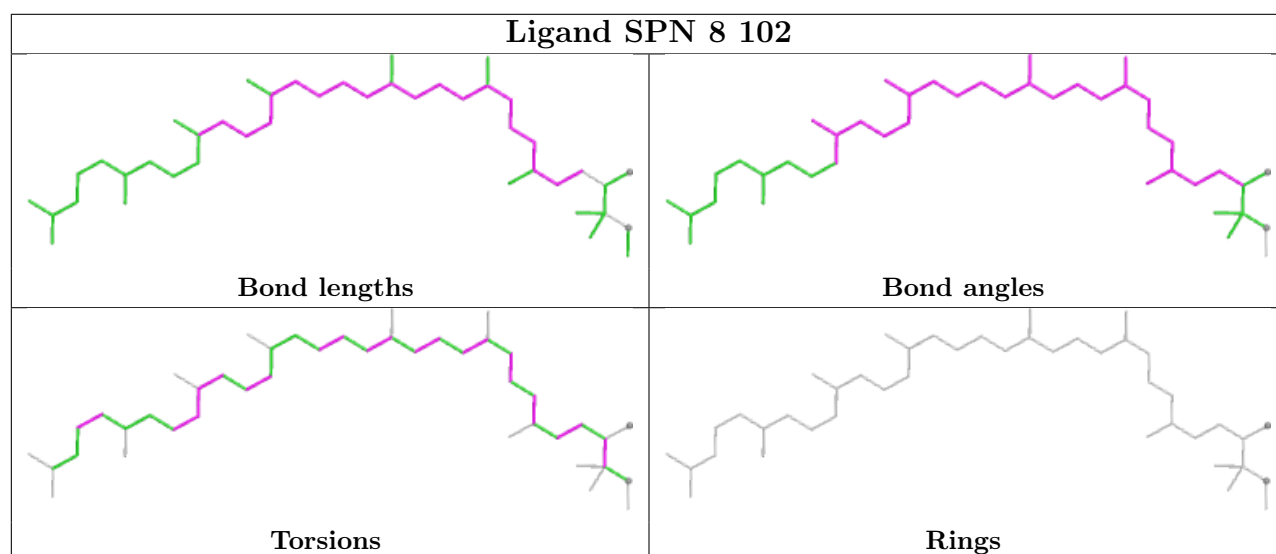
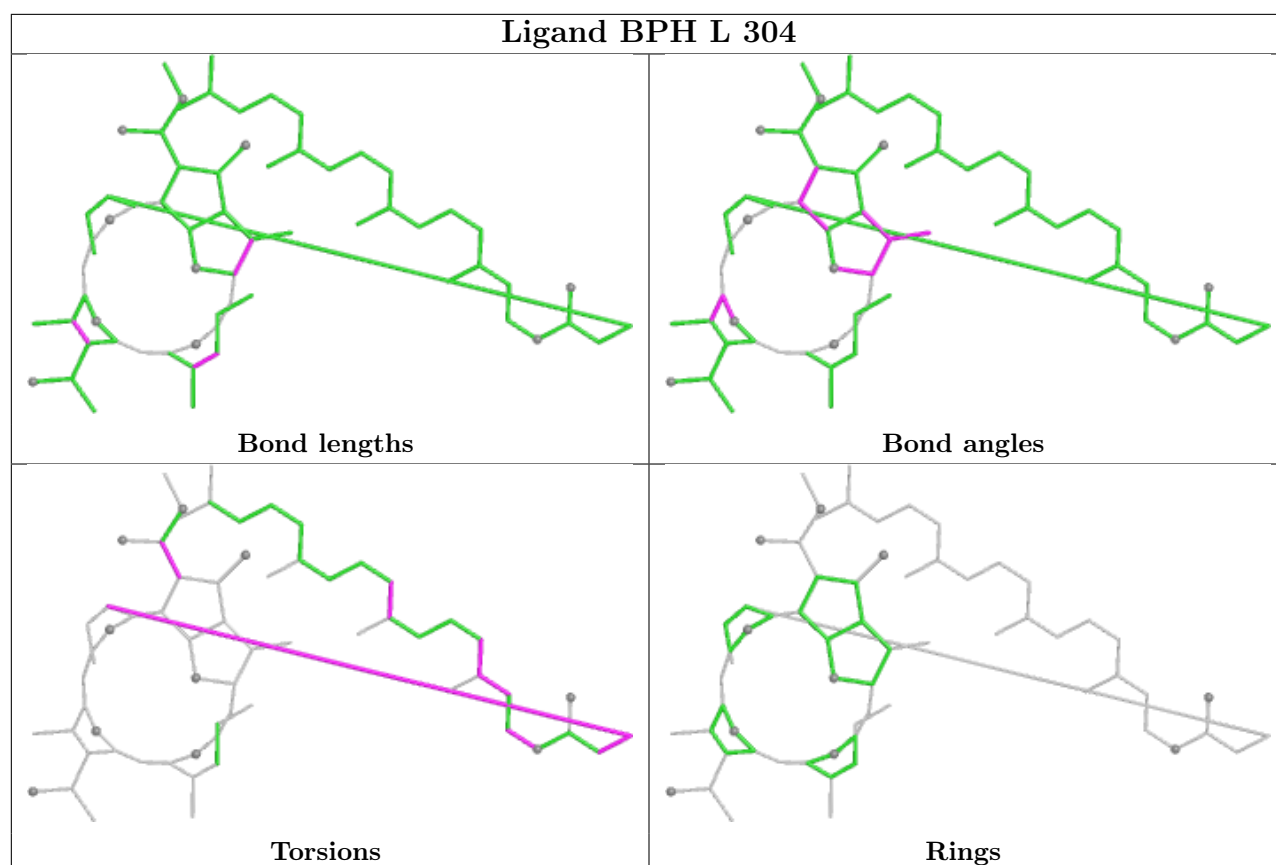


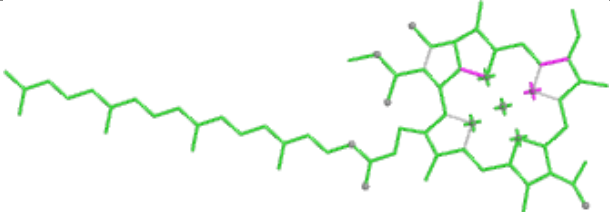
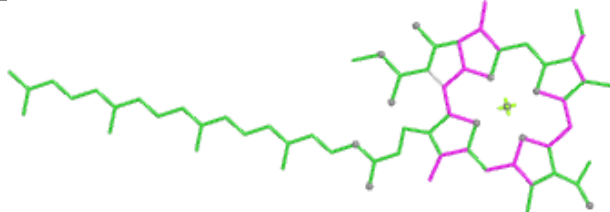
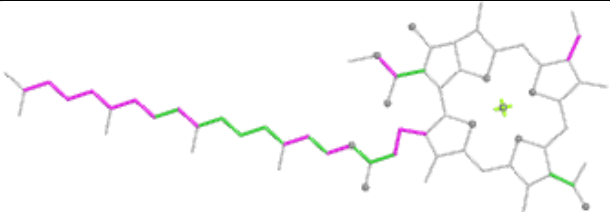
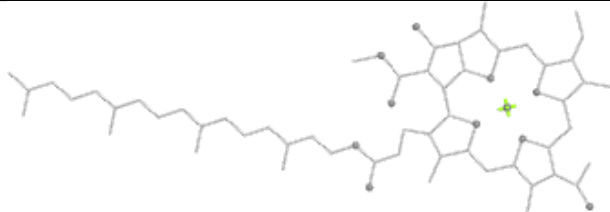
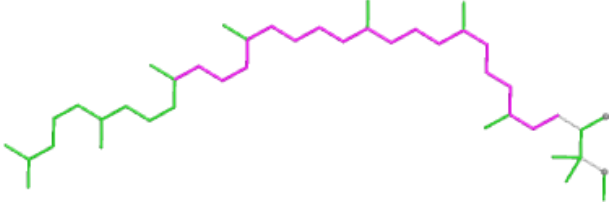
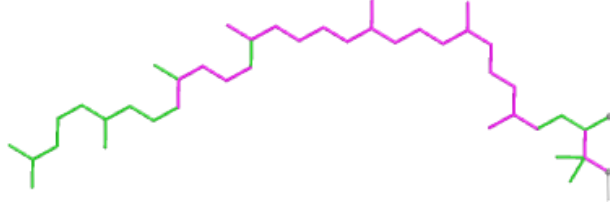
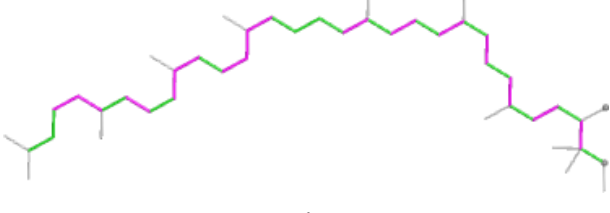
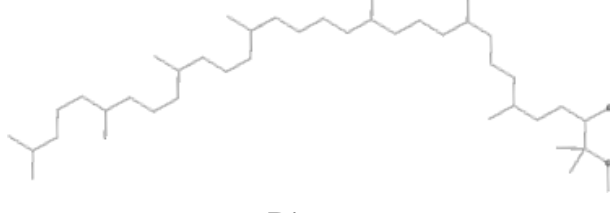
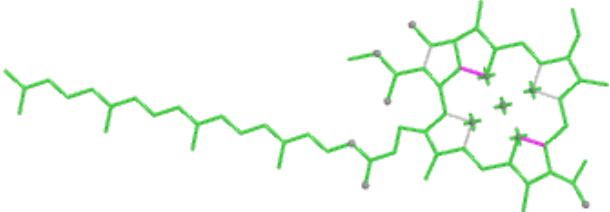
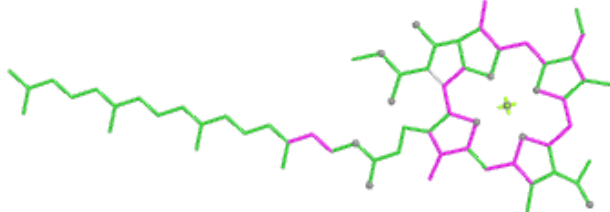
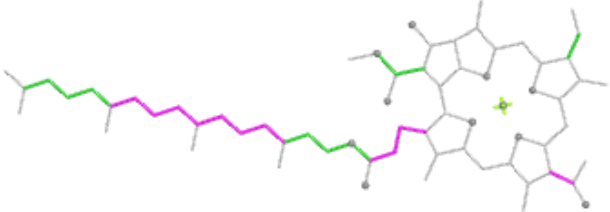
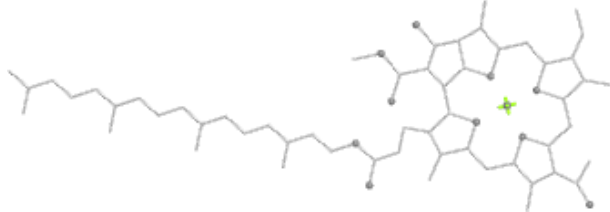


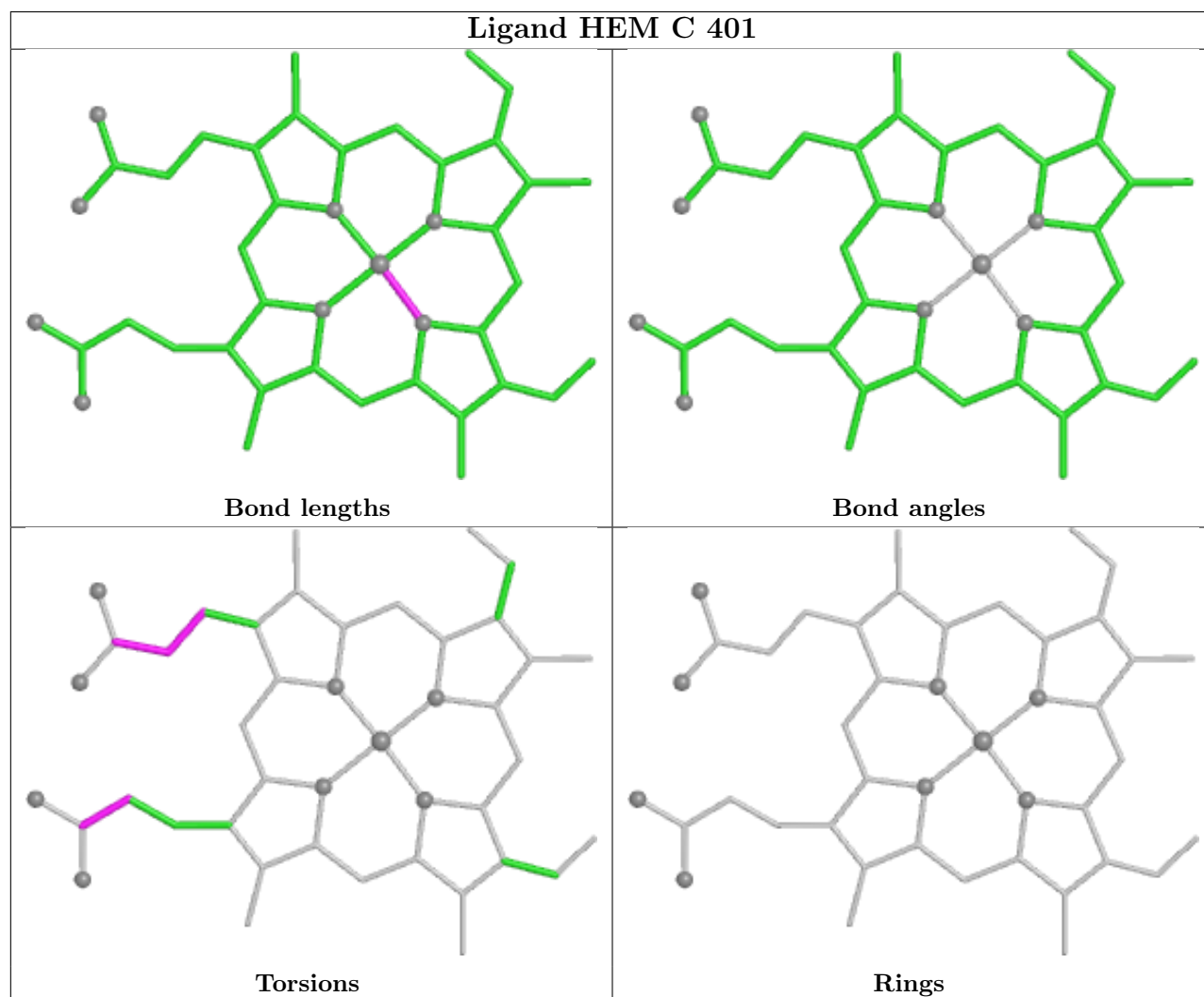
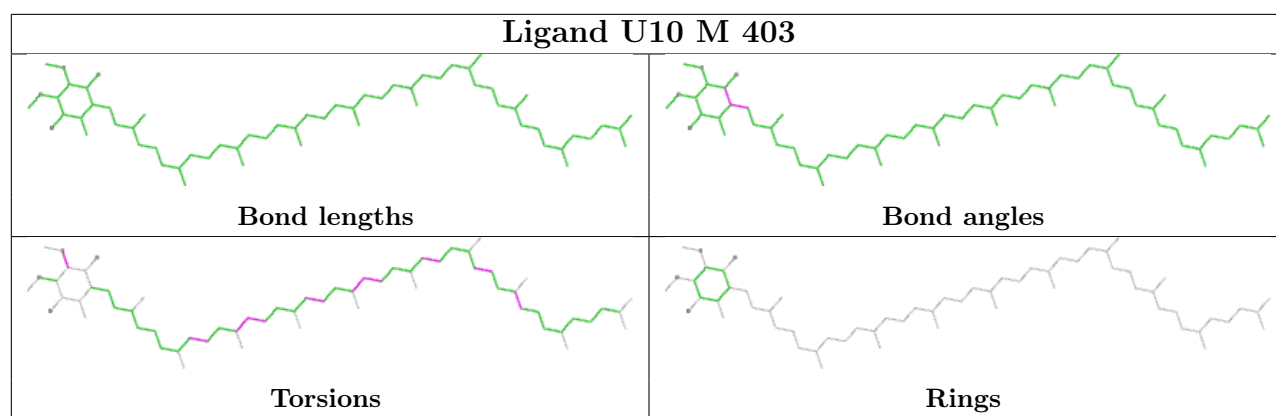


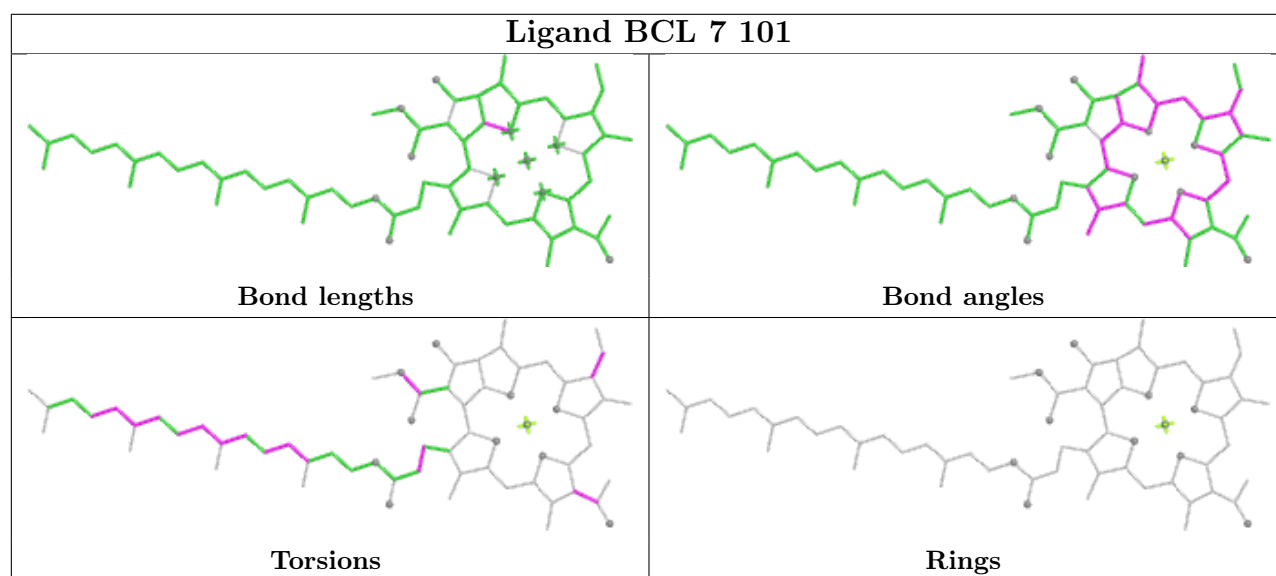
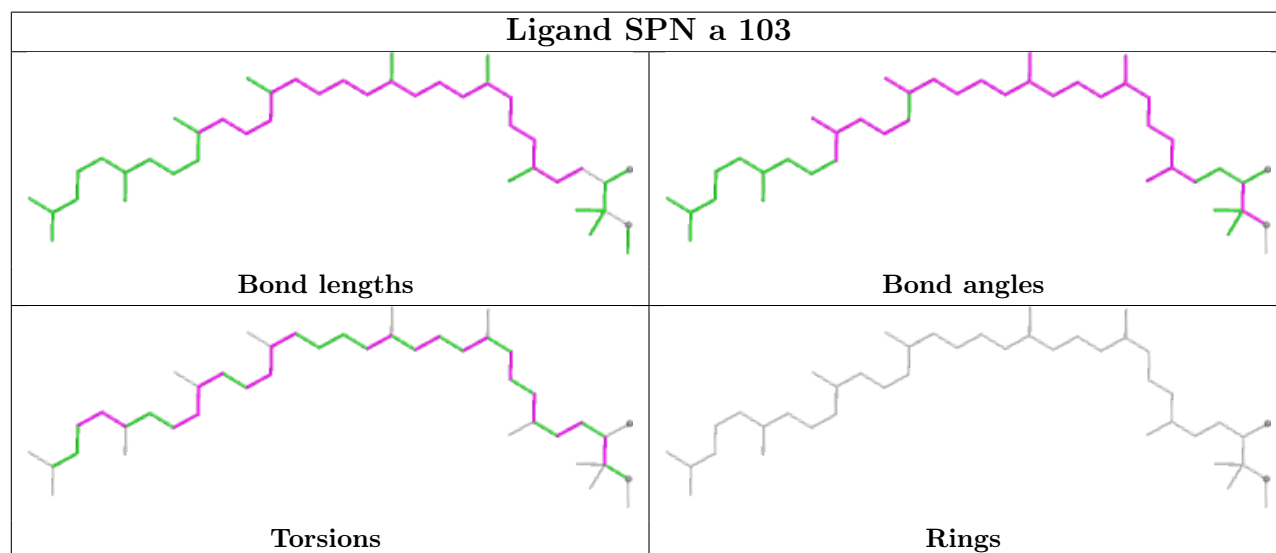
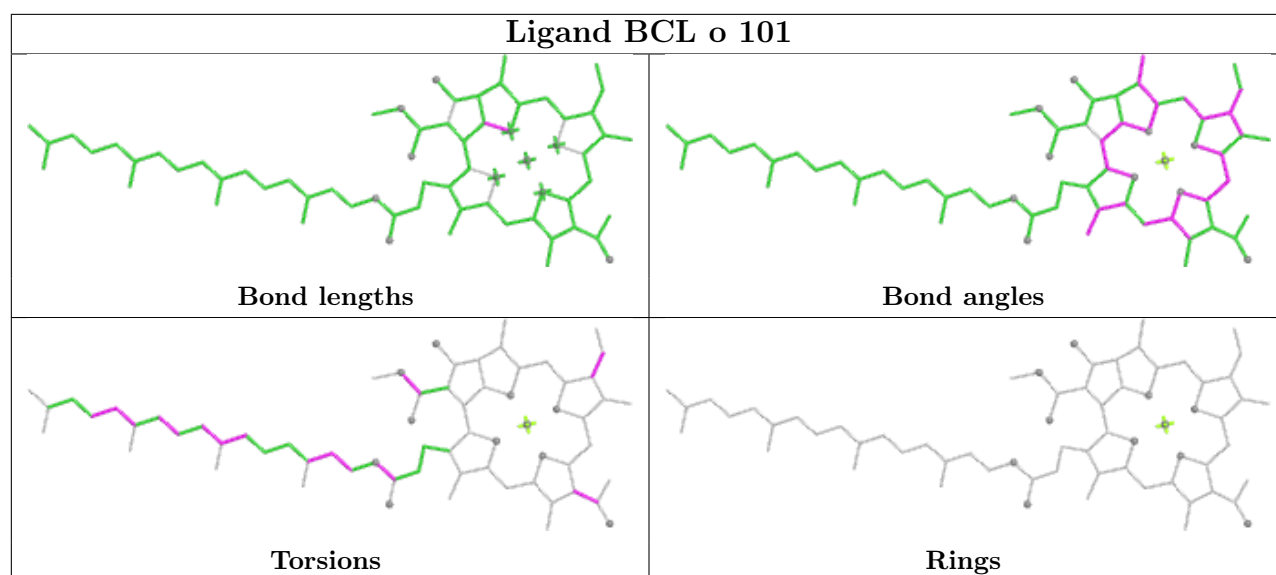


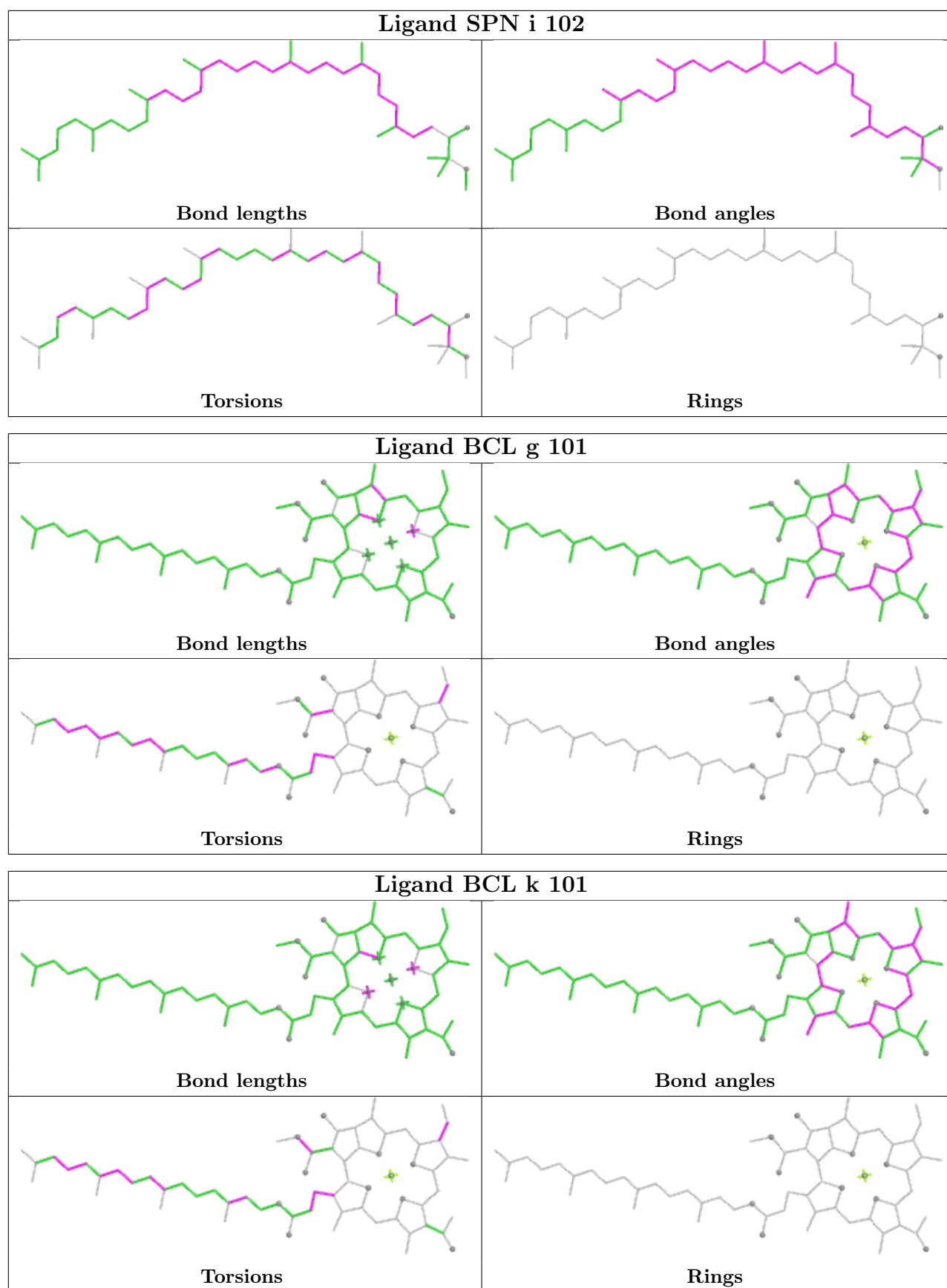


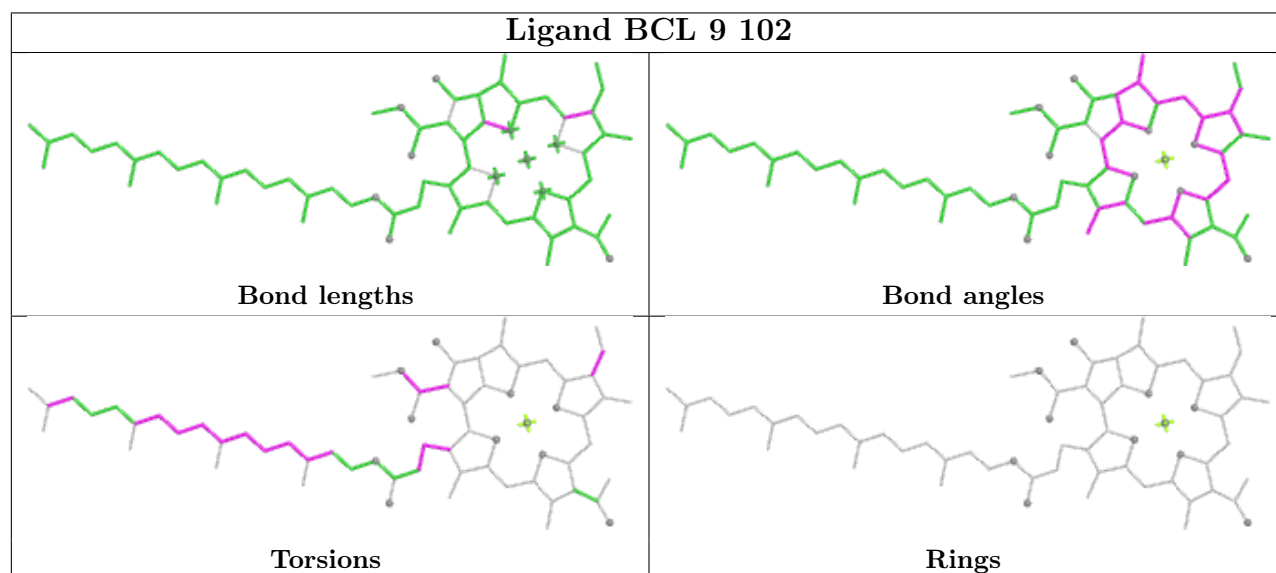
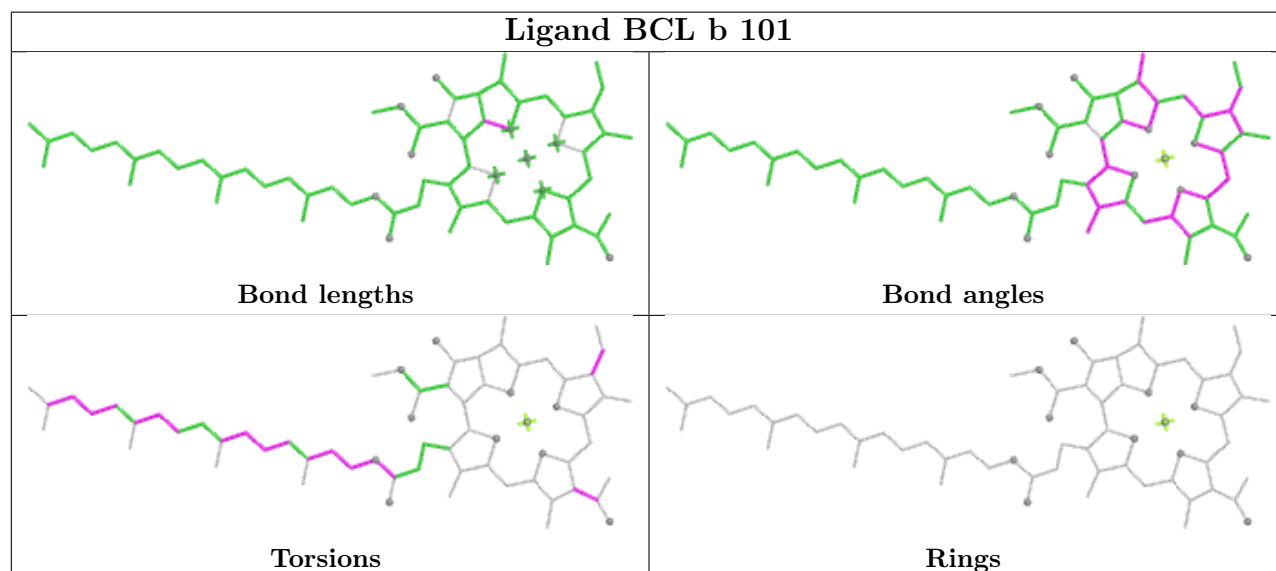
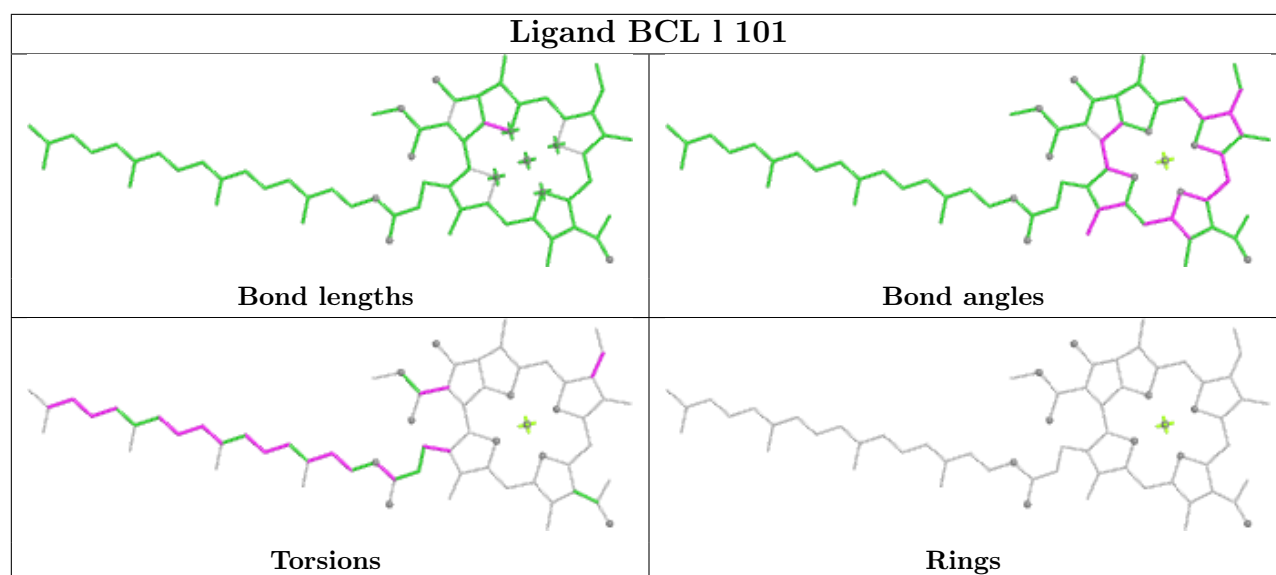


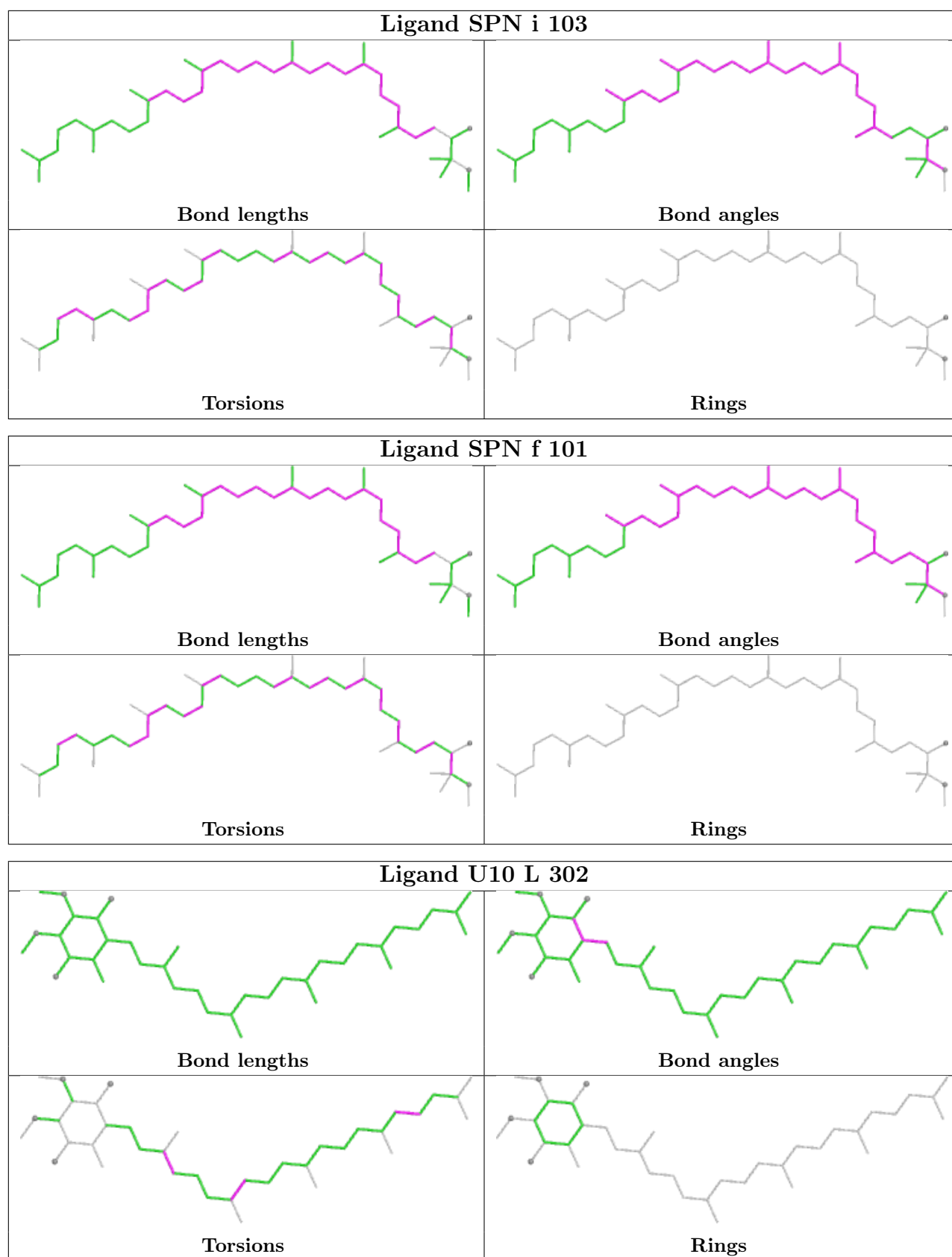
Ligand BCL m 101	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand SPN h 102	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand BCL M 402	
 Bond lengths	 Bond angles
 Torsions	 Rings

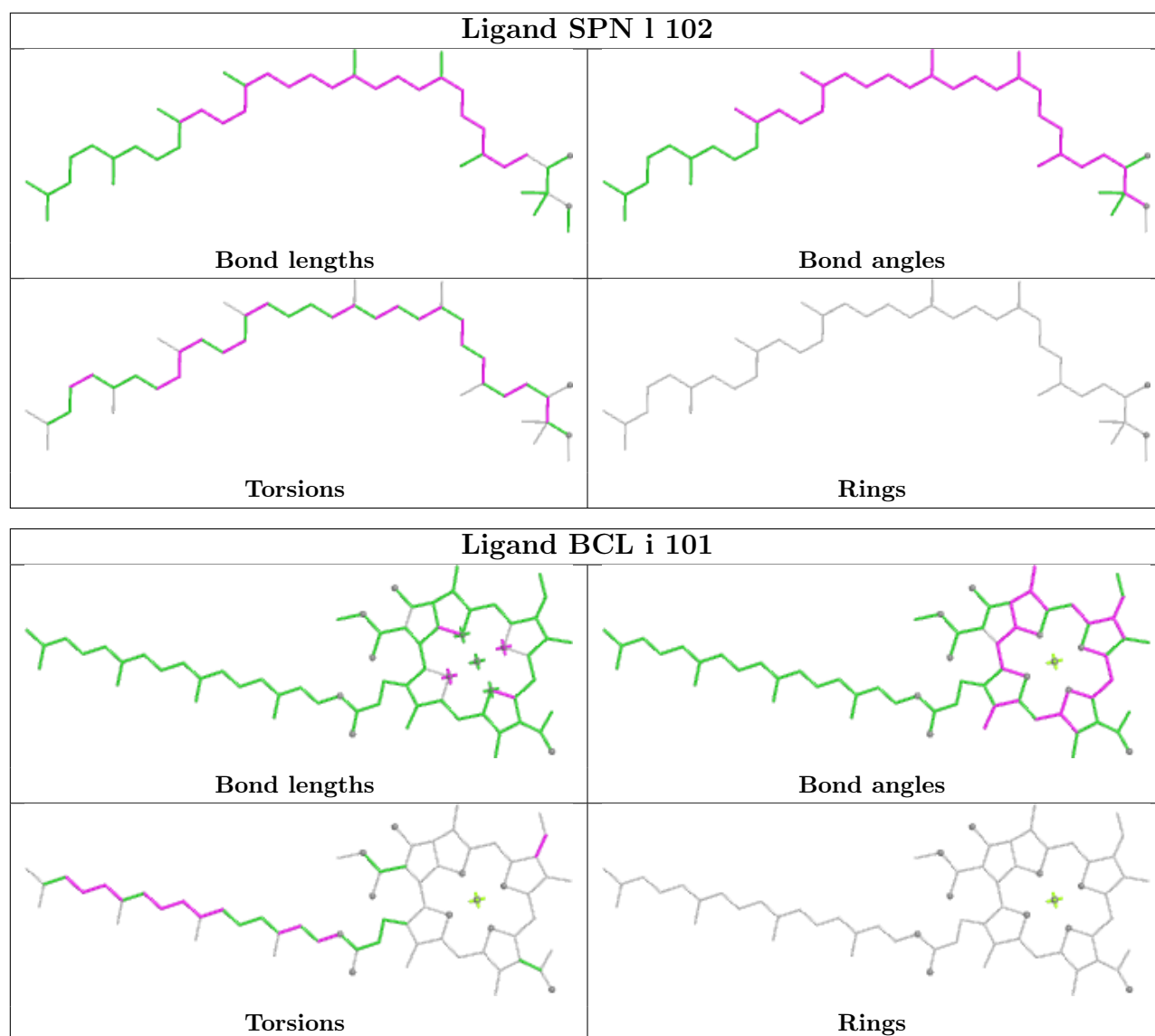


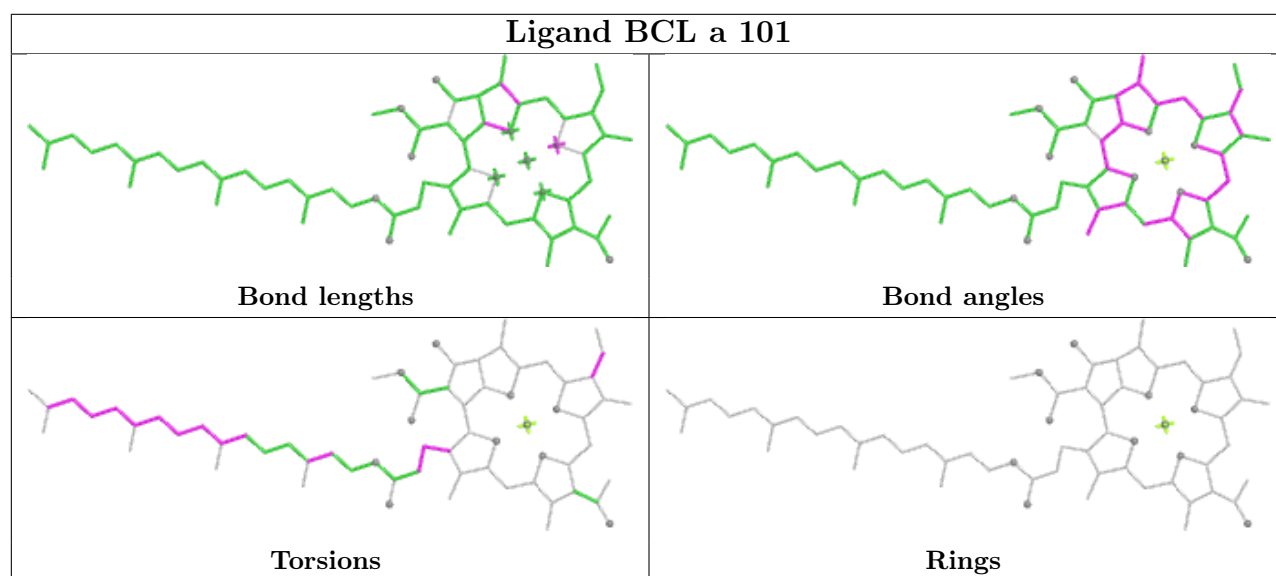
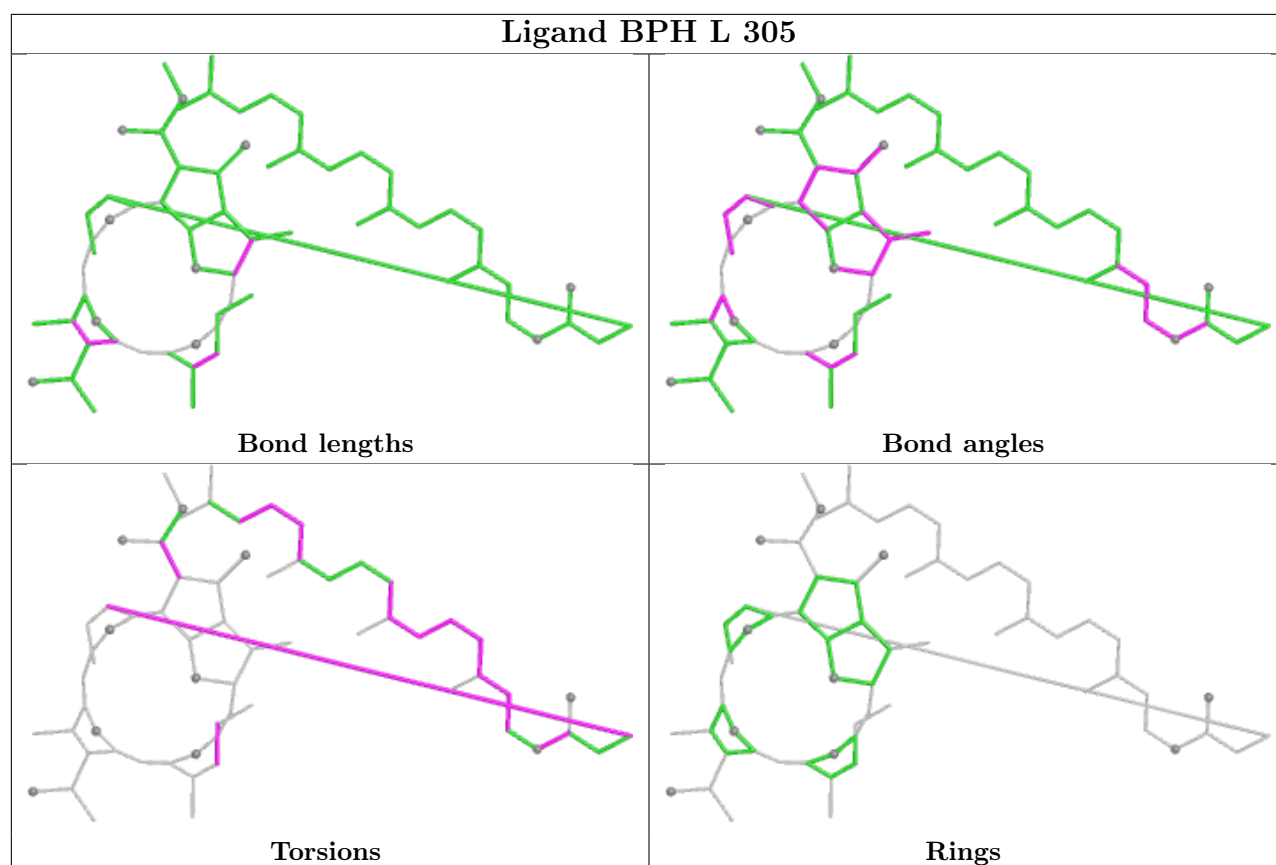


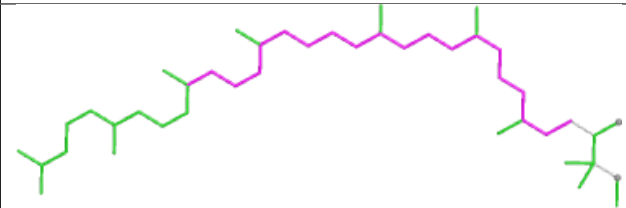
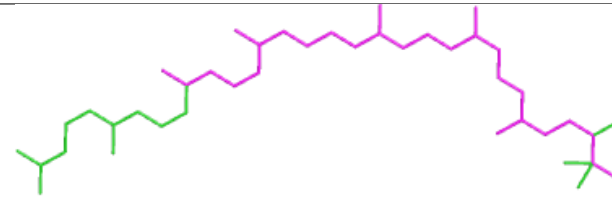
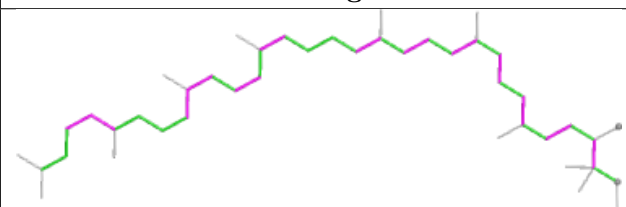
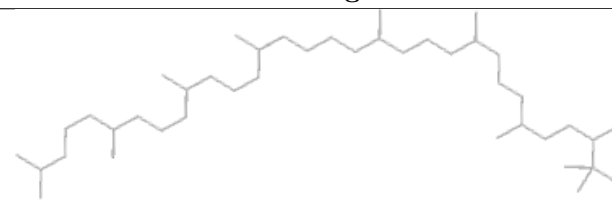


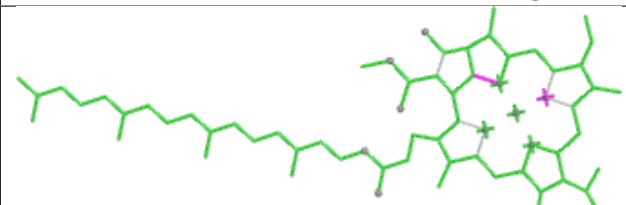
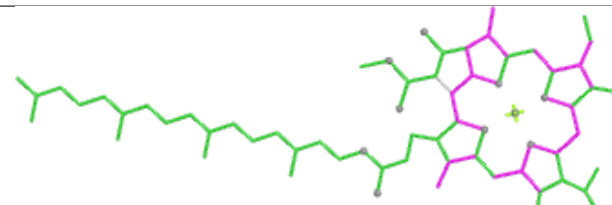
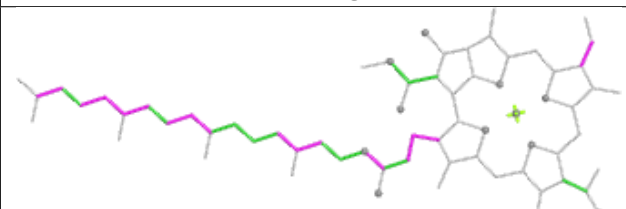
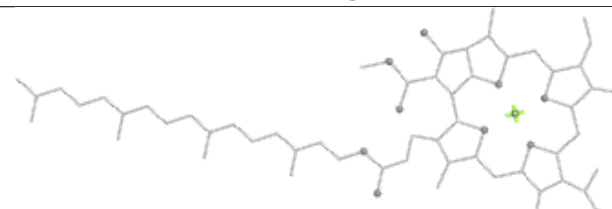


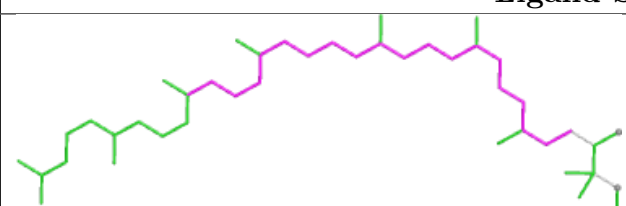
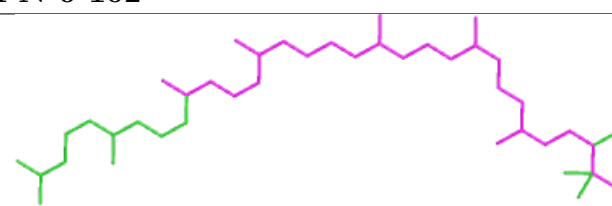
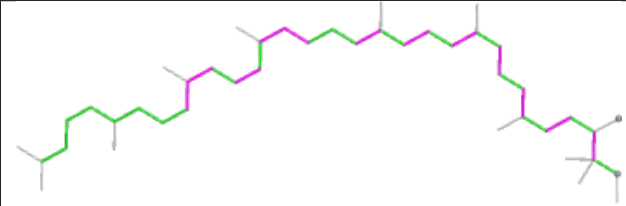
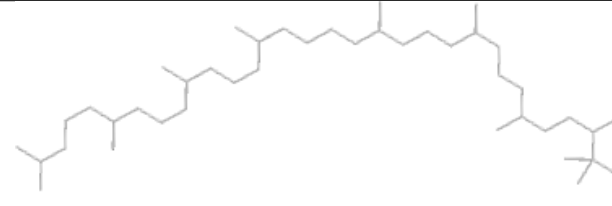






Ligand SPN n 102	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand BCL e 101	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand SPN 0 102	
	
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.

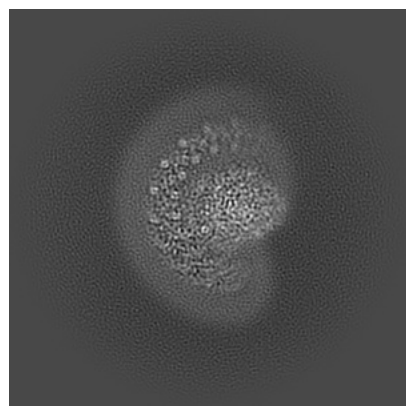
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63381. These allow visual inspection of the internal detail of the map and identification of artifacts.

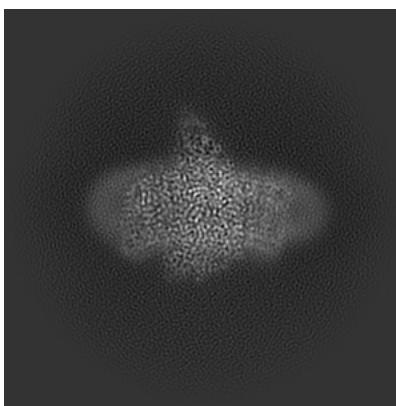
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

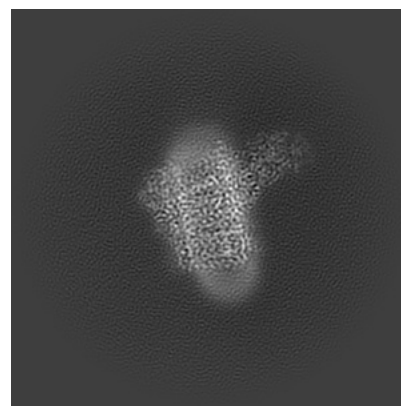
6.1.1 Primary map



X

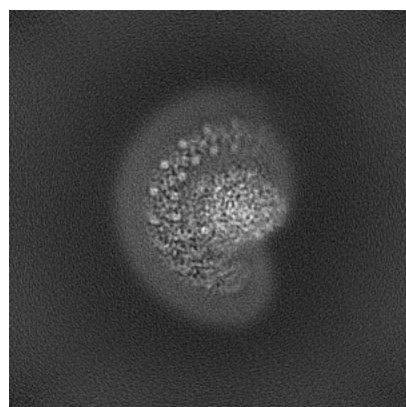


Y

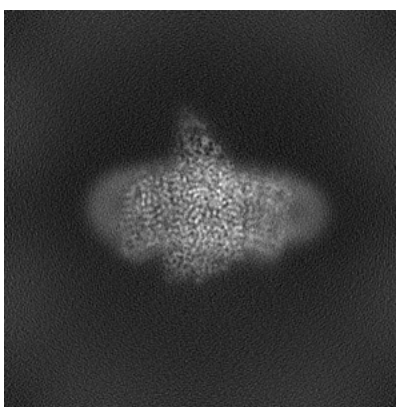


Z

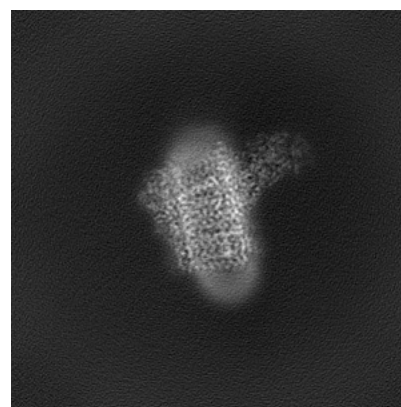
6.1.2 Raw map



X



Y

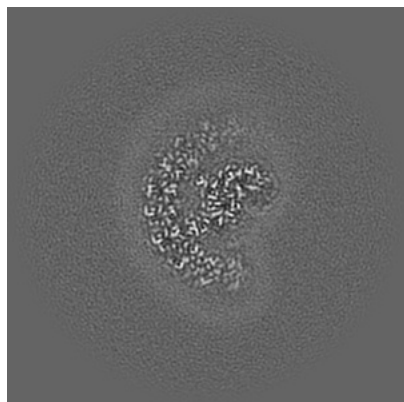


Z

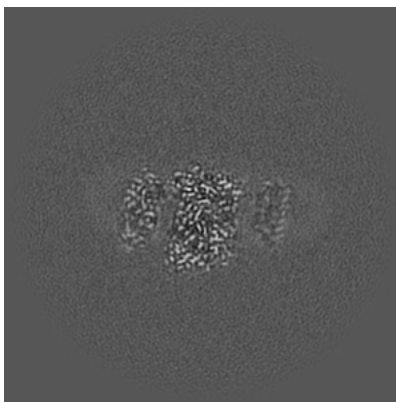
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

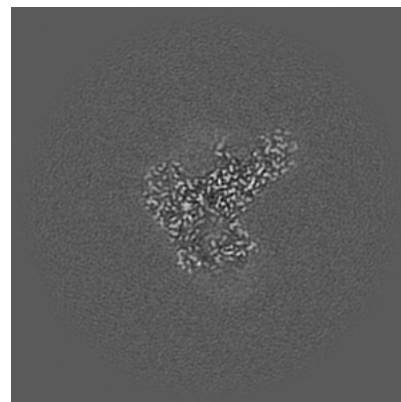
6.2.1 Primary map



X Index: 150

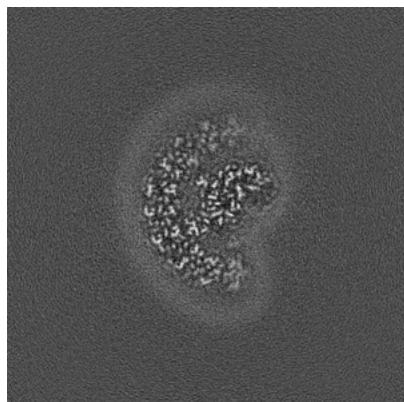


Y Index: 150

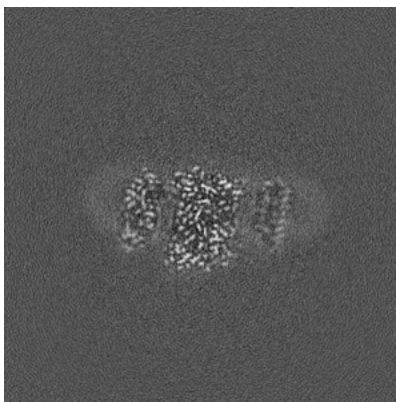


Z Index: 150

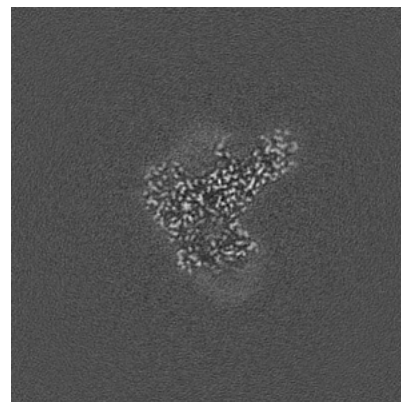
6.2.2 Raw map



X Index: 150



Y Index: 150

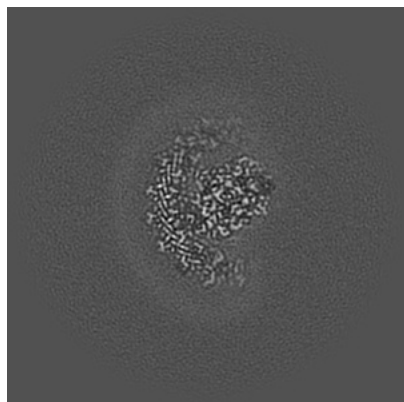


Z Index: 150

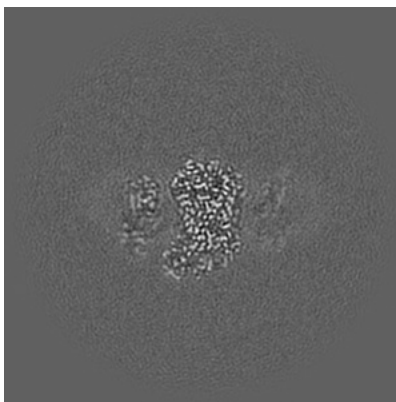
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

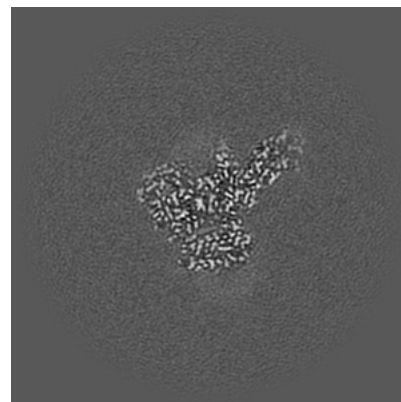
6.3.1 Primary map



X Index: 162

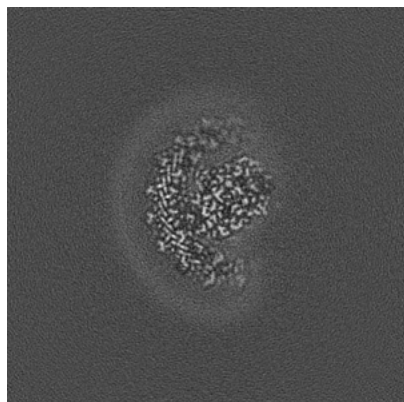


Y Index: 157

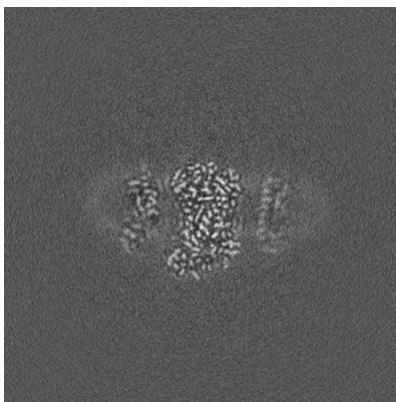


Z Index: 144

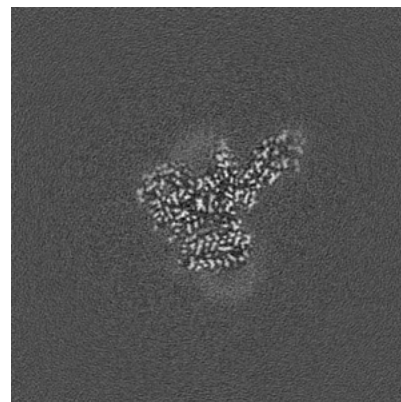
6.3.2 Raw map



X Index: 162



Y Index: 155

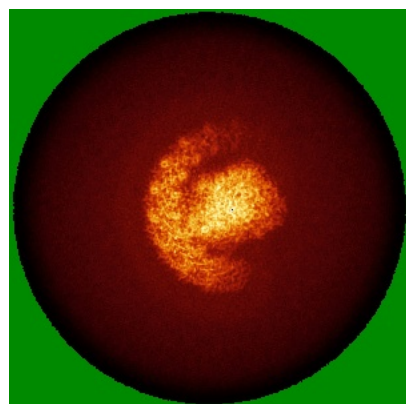


Z Index: 144

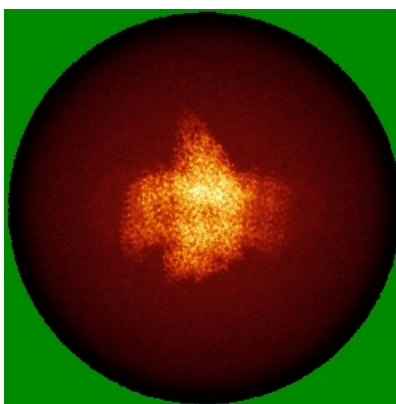
The images above show the largest variance slices of the map in three orthogonal directions.

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

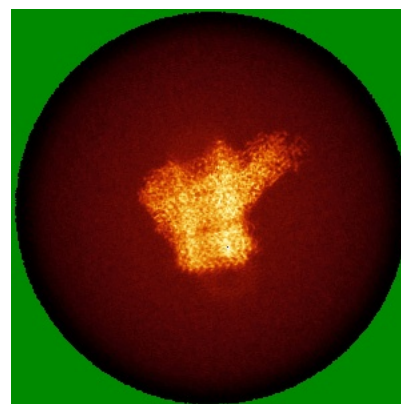
6.4.1 Primary map



X

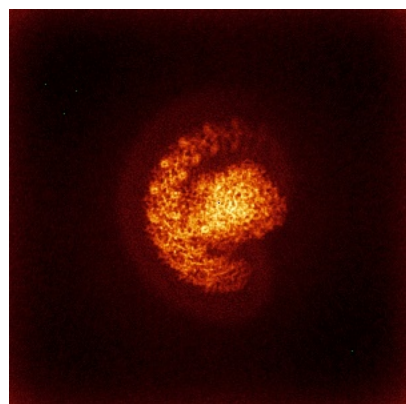


Y

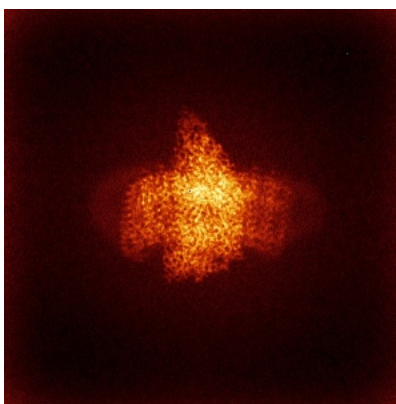


Z

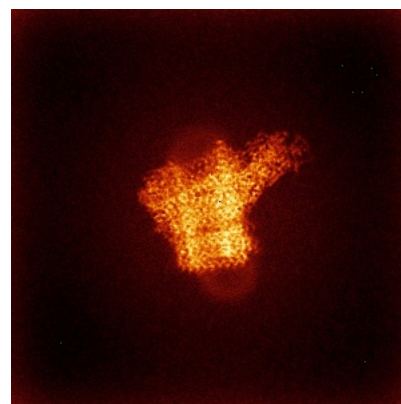
6.4.2 Raw map



X



Y

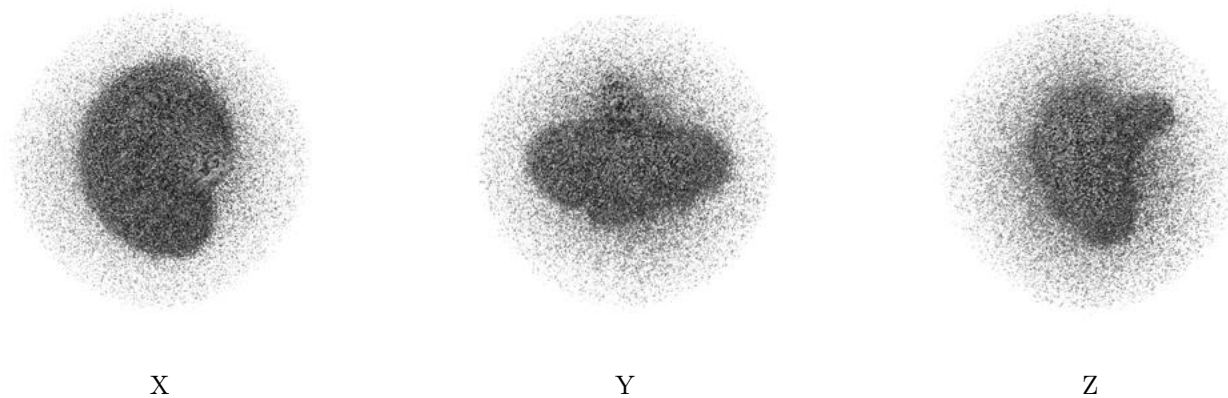


Z

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.

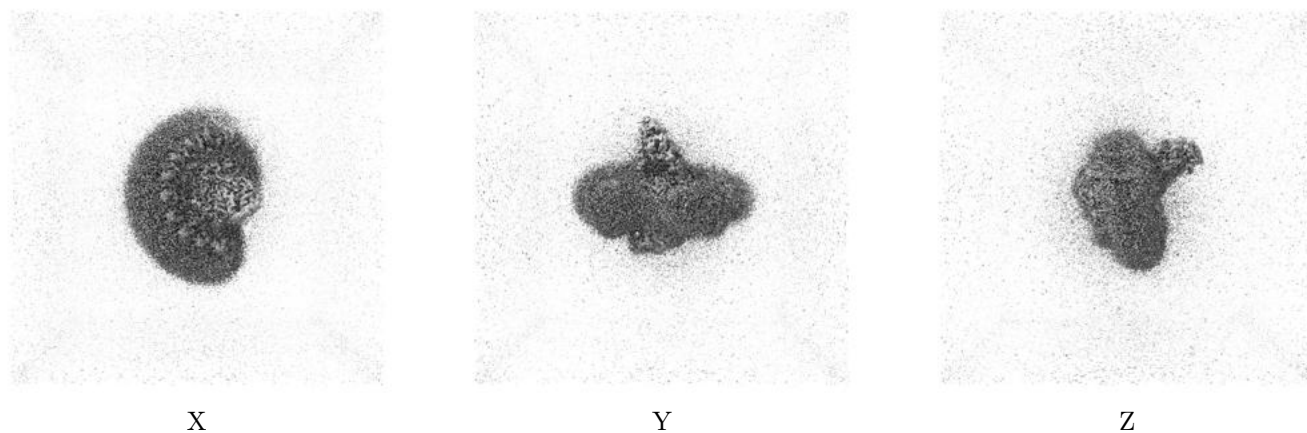
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

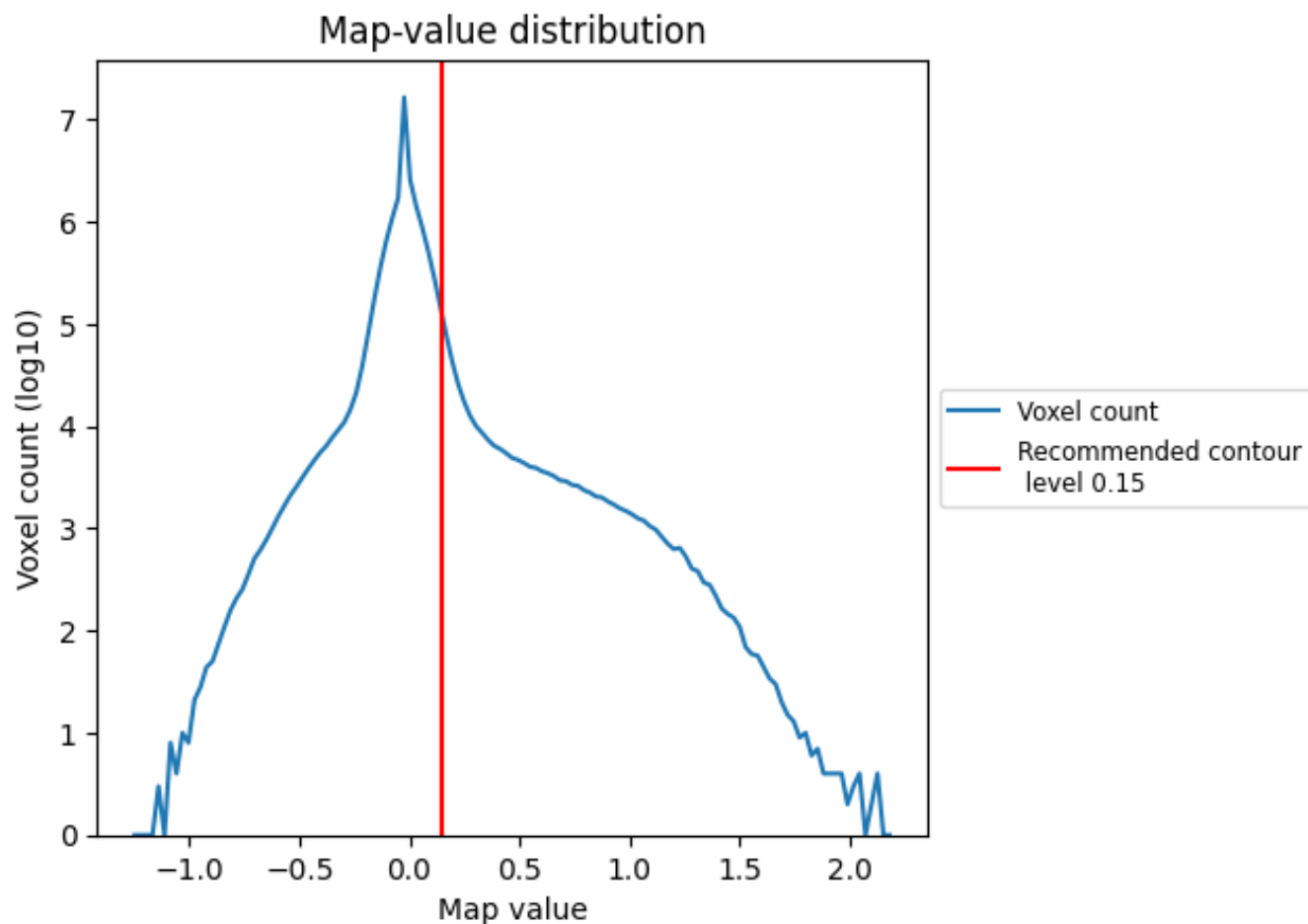
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

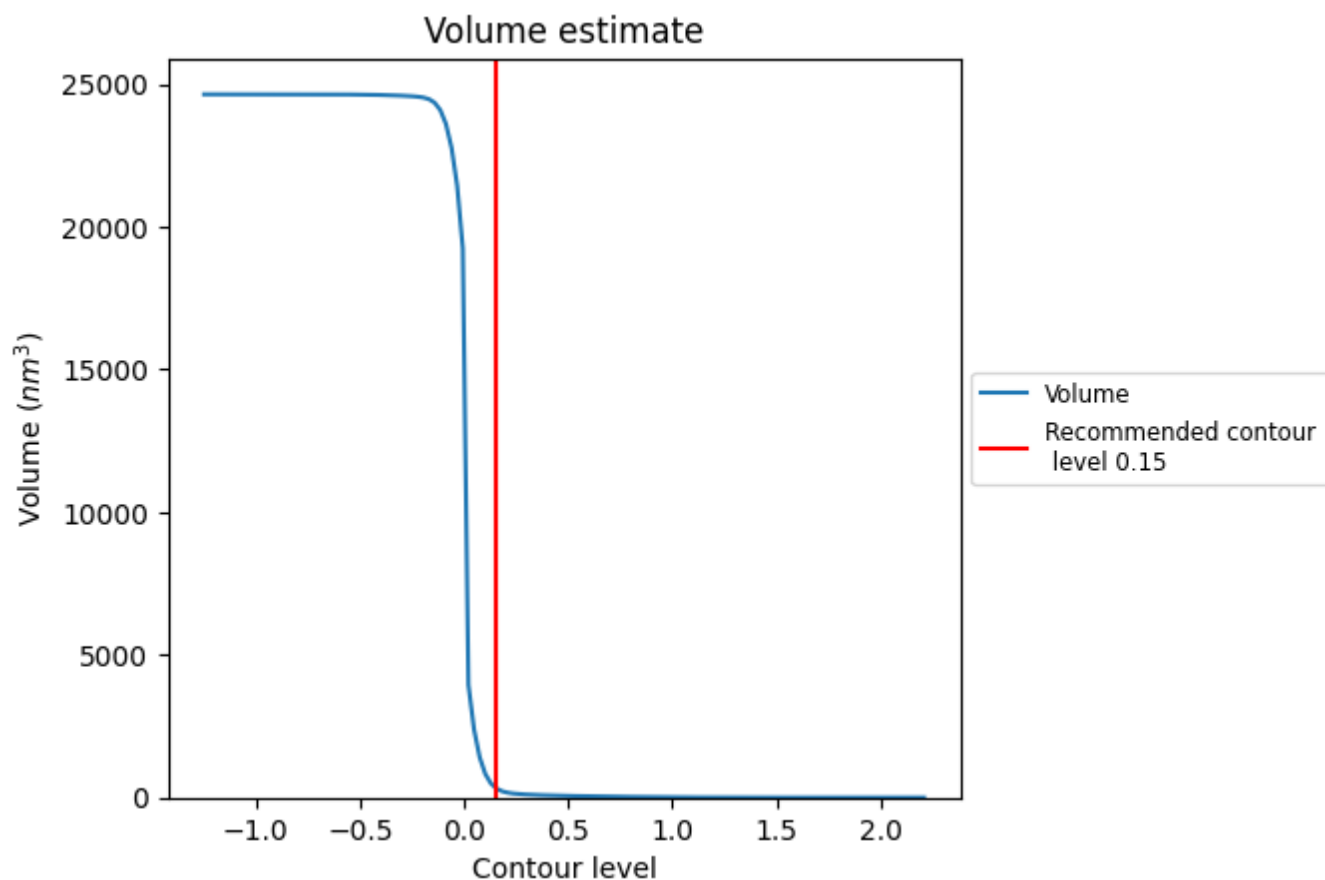
This section contains the results of statistical analysis of the map.

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.

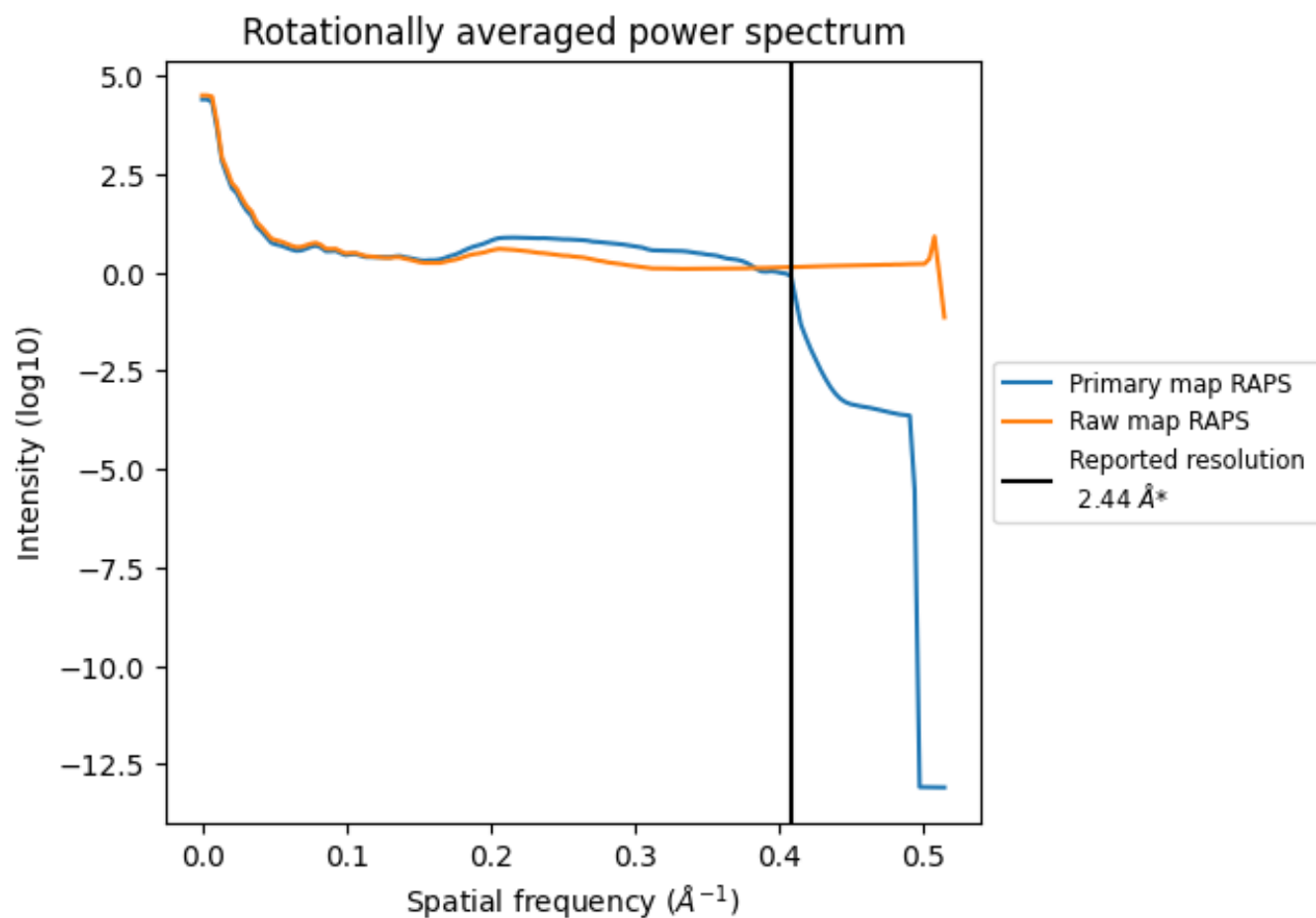
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 350 nm^3 ; this corresponds to an approximate mass of 316 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 ⓘ

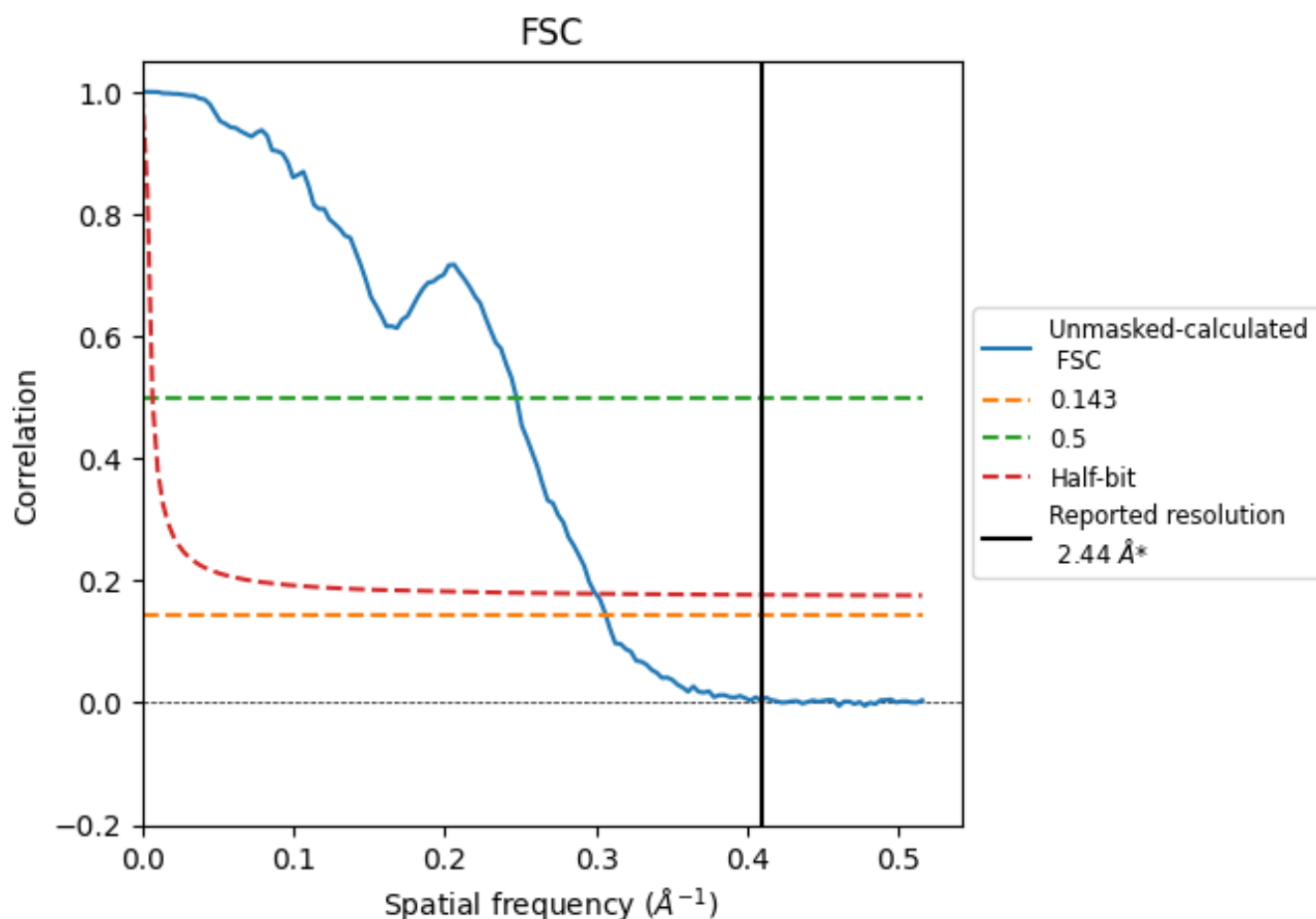


*Reported resolution corresponds to spatial frequency of 0.410 $\text{\AA}^{-1}$

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 0.410 Å⁻¹

8.2 Resolution estimates [i](#)

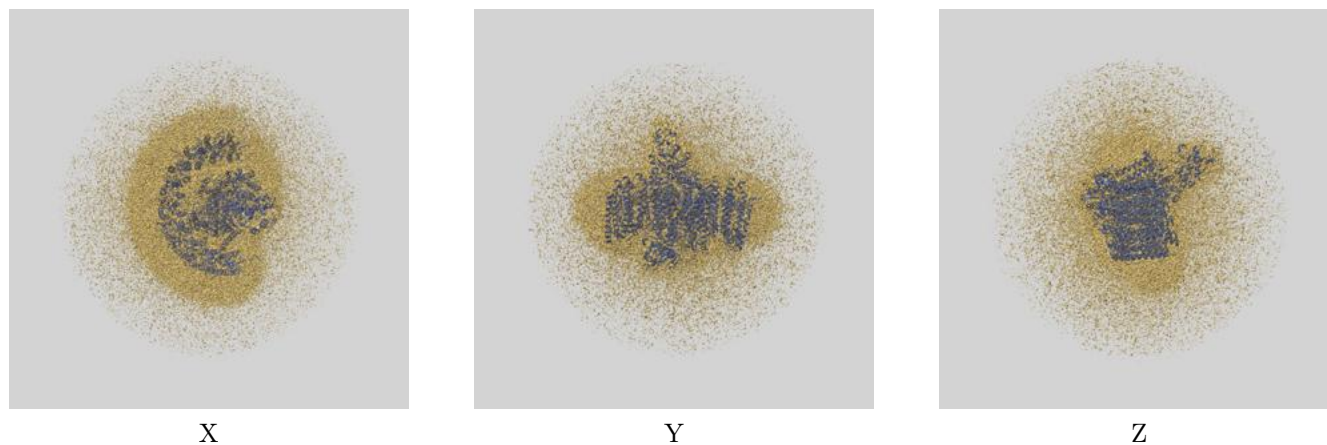
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.26	4.04	3.34

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

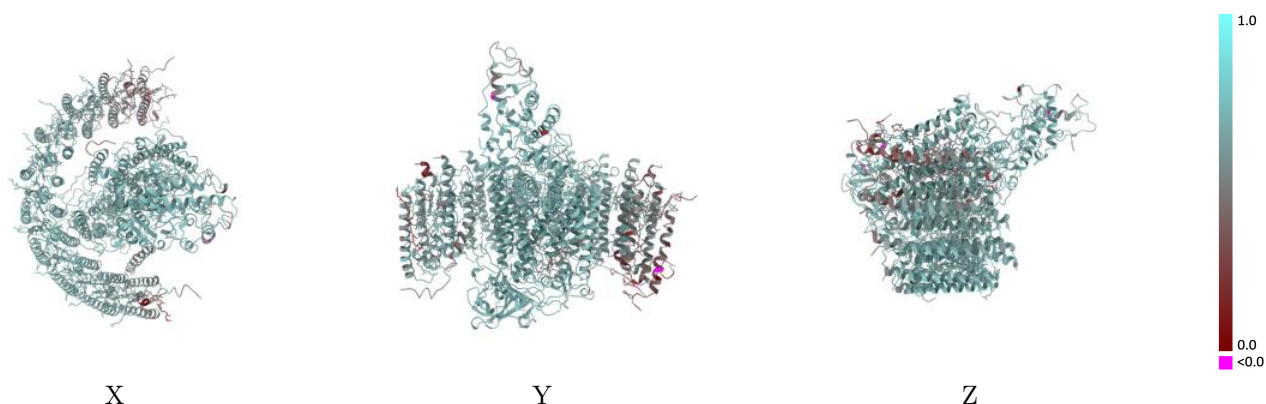
This section contains information regarding the fit between EMDB map EMD-63381 and PDB model 9LTU. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



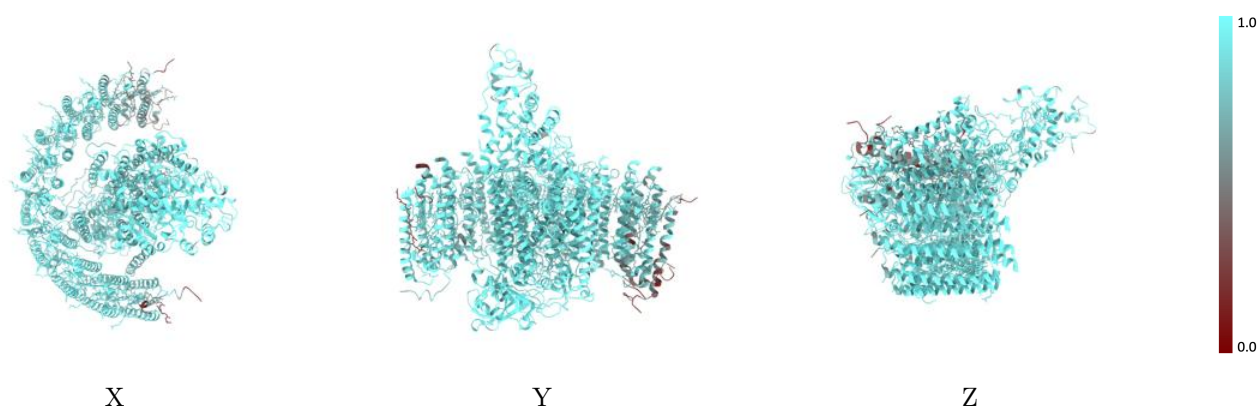
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



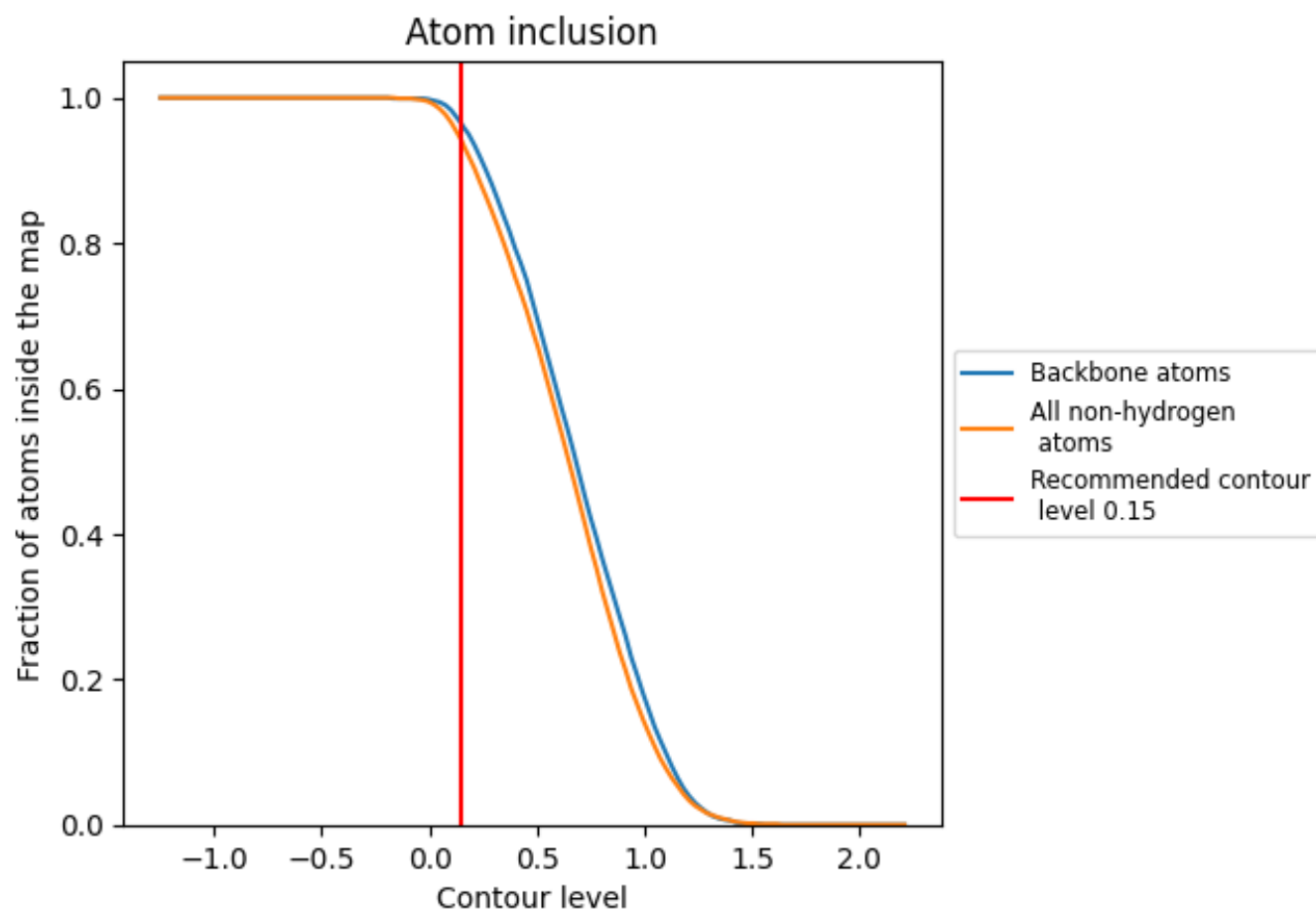
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 94% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9410	0.6270
0	0.8010	0.5040
7	0.6440	0.4020
8	0.5120	0.3630
9	0.8620	0.5190
C	0.9420	0.6210
H	0.9760	0.6510
L	0.9860	0.6730
M	0.9860	0.6730
a	0.9640	0.6200
b	0.9230	0.5750
c	0.9750	0.6400
d	0.9590	0.6350
e	0.9900	0.6750
f	0.9700	0.6550
g	0.9880	0.6760
h	0.9910	0.6640
i	0.9910	0.6800
j	0.9830	0.6580
k	0.9790	0.6620
l	0.9760	0.6580
m	0.9450	0.6210
n	0.9610	0.6280
o	0.8500	0.5610
p	0.8660	0.5430

1.0

0.0

<0.0