



wwPDB EM Validation Summary Report ⓘ

Aug 5, 2026 – 07:57 AM EDT

PDB ID : 7JRG / pdb_00007jrg
EMDB ID : EMD-22445
Title : Plant Mitochondrial complex III2 from Vigna radiata
Authors : Maldonado, M.; Letts, J.A.
Deposited on : 2020-08-12
Resolution : 3.20 Å (reported)
Based on initial models : 6Q9E, 6HU9

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:

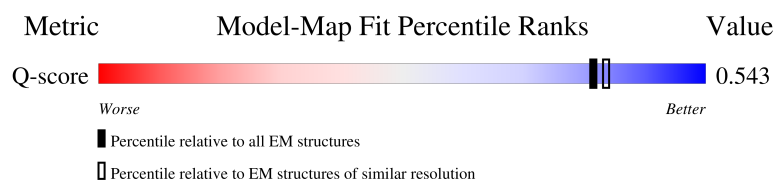
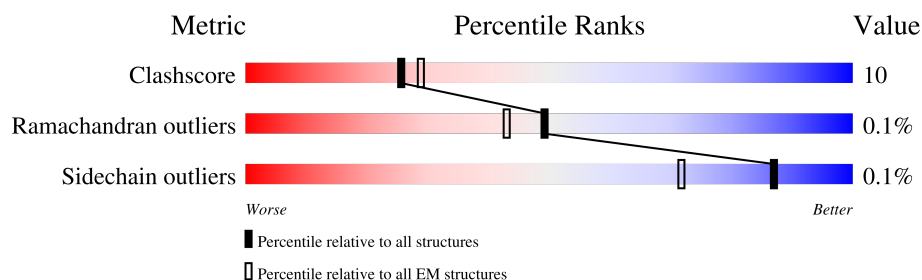
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

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

The reported resolution of this entry is 3.20 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.



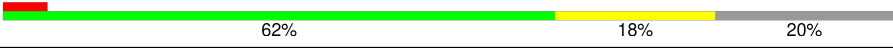
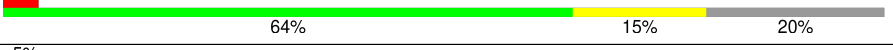
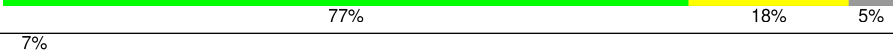
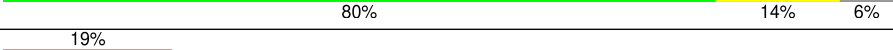
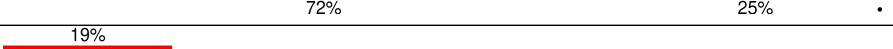
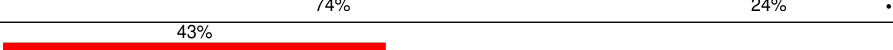
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	A	527	
1	M	527	
2	B	506	
2	N	506	

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Mol	Chain	Length	Quality of chain
3	C	393	
3	O	393	
4	D	306	
4	P	306	
5	E	271	
5	Q	271	
6	F	122	
6	R	122	
7	G	72	
7	S	72	
8	H	69	
8	T	69	
9	J	72	
9	V	72	
10	K	81	
10	W	81	

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
16	HEC	D	501	X	-	-	-
16	HEC	P	501	X	-	-	-

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 32930 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 Mitochondrial-processing peptidase subunit beta, mitochondrial isoform X1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	487	Total	C	N	O	S	0	0
			3838	2409	678	736	15		
1	M	487	Total	C	N	O	S	0	0
			3838	2409	678	736	15		

- Molecule 2 is a protein called Alpha-MPP.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	457	Total	C	N	O	S	0	0
			3471	2196	588	675	12		
2	N	455	Total	C	N	O	S	0	0
			3456	2187	585	672	12		

- Molecule 3 is a protein called COB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	388	Total	C	N	O	S	0	0
			3104	2088	487	515	14		
3	O	388	Total	C	N	O	S	0	0
			3104	2088	487	515	14		

- Molecule 4 is a protein called cytochrome c1-2, heme protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	244	Total	C	N	O	S	0	0
			1910	1214	327	358	11		
4	P	244	Total	C	N	O	S	0	0
			1910	1214	327	358	11		

- Molecule 5 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	77	Total	C	N	O	S	0	0
			597	392	100	104	1		
5	Q	74	Total	C	N	O	S	0	0
			574	375	97	101	1		

- Molecule 6 is a protein called Cytochrome b-c1 complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	116	Total	C	N	O	S	0	0
			965	616	173	172	4		
6	R	115	Total	C	N	O	S	0	0
			959	613	172	170	4		

- Molecule 7 is a protein called cytochrome b-c1 complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	70	Total	C	N	O	S	0	0
			578	382	97	98	1		
7	S	70	Total	C	N	O	S	0	0
			578	382	97	98	1		

- Molecule 8 is a protein called Cytochrome b-c1 complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	65	Total	C	N	O	S	0	0
			536	344	90	96	6		
8	T	64	Total	C	N	O	S	0	0
			527	339	89	93	6		

- Molecule 9 is a protein called cytochrome b-c1 complex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	60	Total	C	N	O	S	0	0
			480	313	83	83	1		
9	V	59	Total	C	N	O	S	0	0
			476	311	82	82	1		

- Molecule 10 is a protein called QCR10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	31	Total	C	N	O	S	0	0
			218	144	35	38	1		

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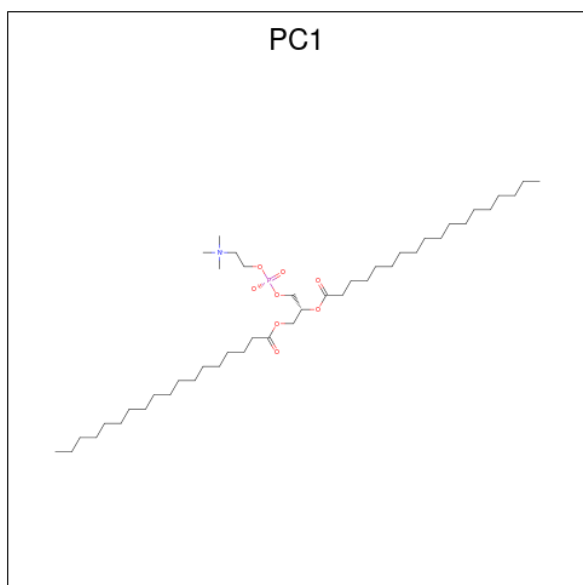
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Mol	Chain	Residues	Atoms					AltConf	Trace
10	W	32	Total	C	N	O	S	0	0
			226	150	36	39	1		

- Molecule 11 is ZINC ION (CCD ID: ZN) (formula: Zn).

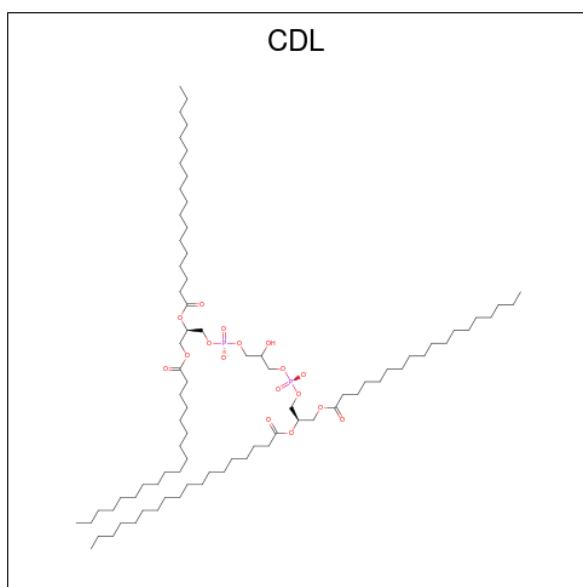
Mol	Chain	Residues	Atoms		AltConf
11	A	1	Total	Zn	0
			1	1	
11	M	1	Total	Zn	0
			1	1	

- Molecule 12 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: C₄₄H₈₈NO₈P).



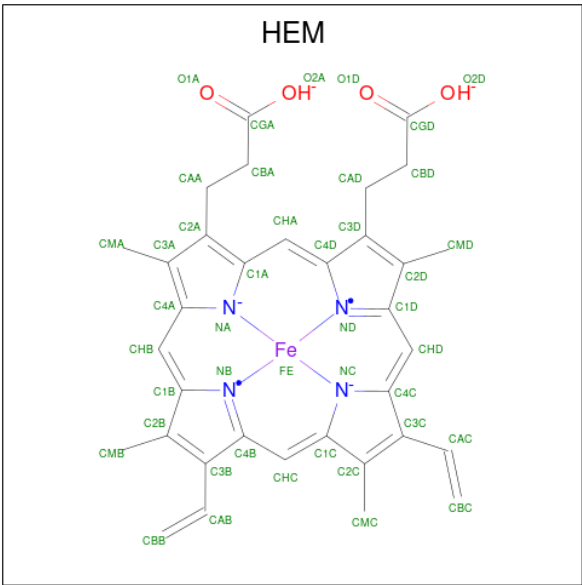
Mol	Chain	Residues	Atoms					AltConf
12	A	1	Total	C	N	O	P	0
			38	28	1	8	1	
12	M	1	Total	C	N	O	P	0
			40	30	1	8	1	
12	S	1	Total	C	N	O	P	0
			38	28	1	8	1	

- Molecule 13 is CARDIOLIPIN (CCD ID: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



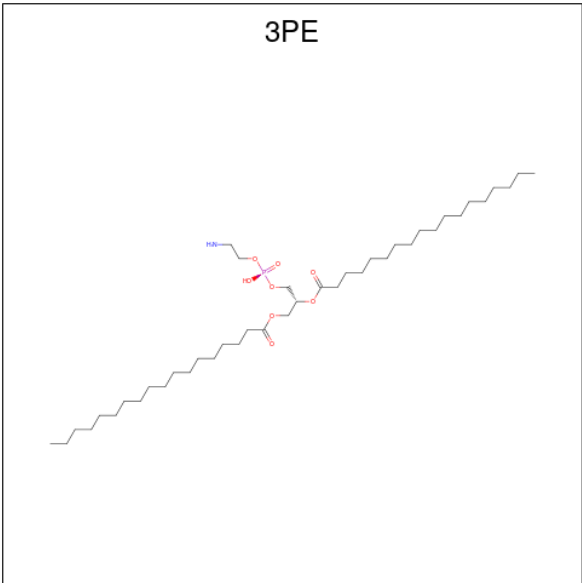
Mol	Chain	Residues	Atoms				AltConf
13	A	1	Total	C	O	P	0
			69	50	17	2	
13	C	1	Total	C	O	P	0
			64	45	17	2	
13	C	1	Total	C	O	P	0
			59	40	17	2	
13	D	1	Total	C	O	P	0
			68	49	17	2	
13	M	1	Total	C	O	P	0
			70	51	17	2	
13	O	1	Total	C	O	P	0
			81	62	17	2	
13	O	1	Total	C	O	P	0
			64	45	17	2	
13	P	1	Total	C	O	P	0
			63	44	17	2	
13	S	1	Total	C	O	P	0
			55	36	17	2	

- Molecule 14 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



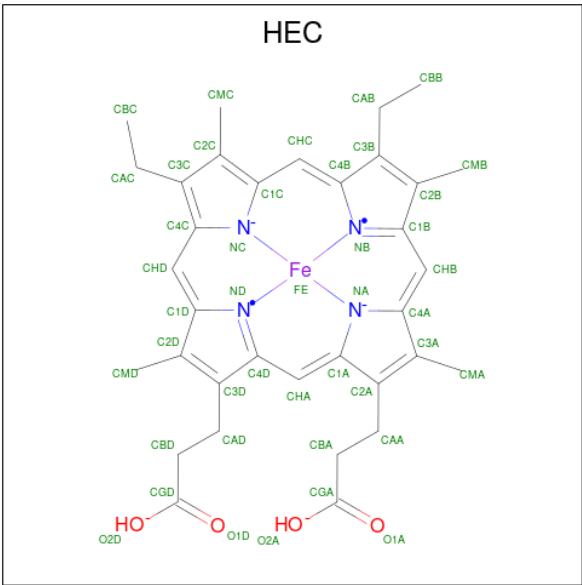
Mol	Chain	Residues	Atoms					AltConf
14	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
14	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
14	O	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
14	O	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 15 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$).

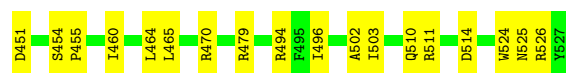


Mol	Chain	Residues	Atoms					AltConf
15	C	1	Total	C	N	O	P	0
			38	28	1	8	1	
15	C	1	Total	C	N	O	P	0
			29	19	1	8	1	
15	C	1	Total	C	N	O	P	0
			45	35	1	8	1	
15	C	1	Total	C	N	O	P	0
			33	23	1	8	1	
15	C	1	Total	C	N	O	P	0
			27	17	1	8	1	
15	C	1	Total	C	N	O	P	0
			34	24	1	8	1	
15	F	1	Total	C	N	O	P	0
			32	22	1	8	1	
15	F	1	Total	C	N	O	P	0
			51	41	1	8	1	
15	G	1	Total	C	N	O	P	0
			37	27	1	8	1	
15	M	1	Total	C	N	O	P	0
			45	35	1	8	1	
15	O	1	Total	C	N	O	P	0
			36	26	1	8	1	
15	O	1	Total	C	N	O	P	0
			30	20	1	8	1	
15	O	1	Total	C	N	O	P	0
			39	29	1	8	1	
15	O	1	Total	C	N	O	P	0
			33	23	1	8	1	
15	O	1	Total	C	N	O	P	0
			51	41	1	8	1	
15	W	1	Total	C	N	O	P	0
			28	18	1	8	1	
15	W	1	Total	C	N	O	P	0
			28	18	1	8	1	

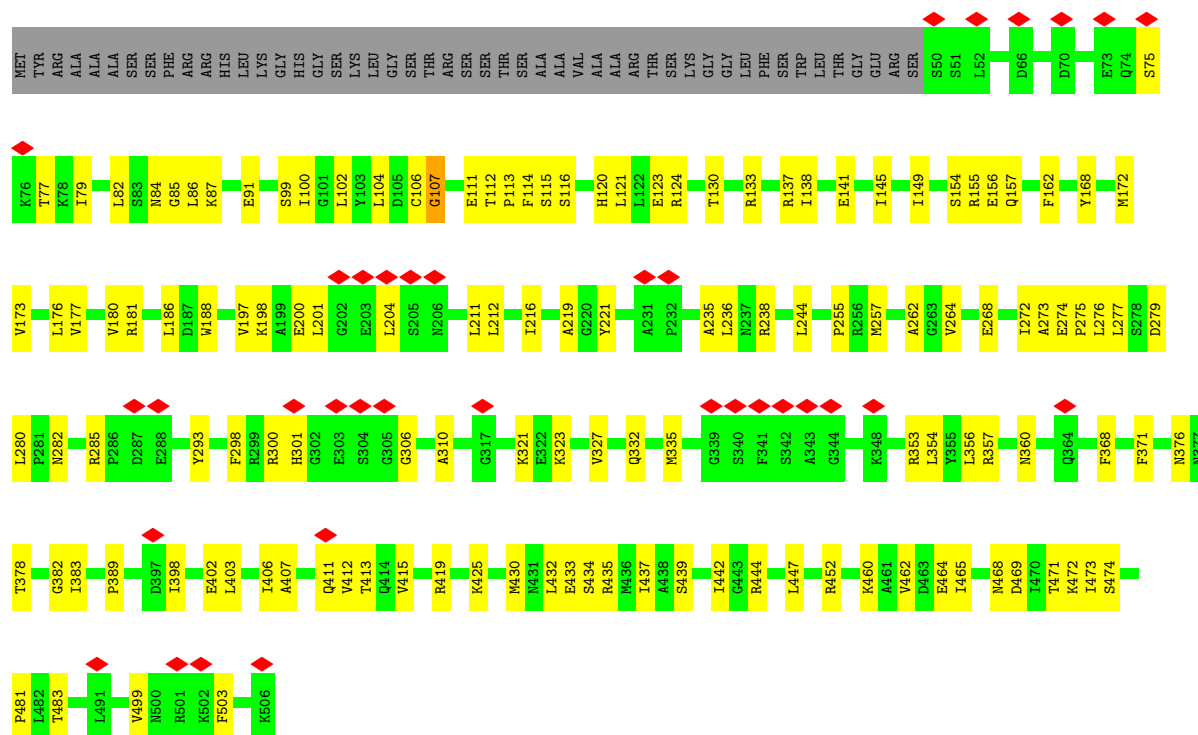
- Molecule 16 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{36}FeN_4O_4$).



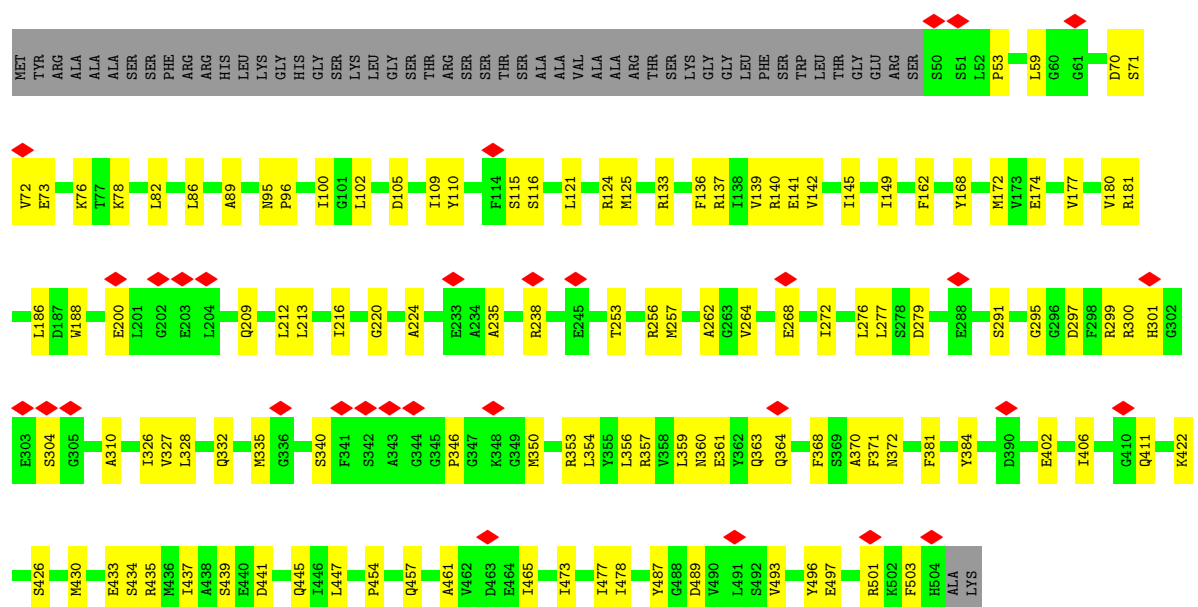
Mol	Chain	Residues	Atoms					AltConf
16	D	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
16	P	1	Total	C	Fe	N	O	0
			43	34	1	4	4	



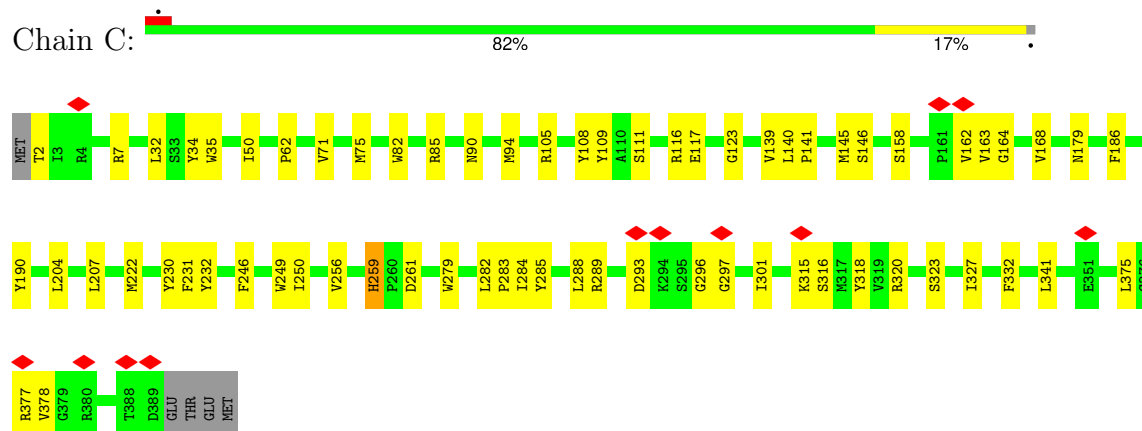
• Molecule 2: Alpha-MPP



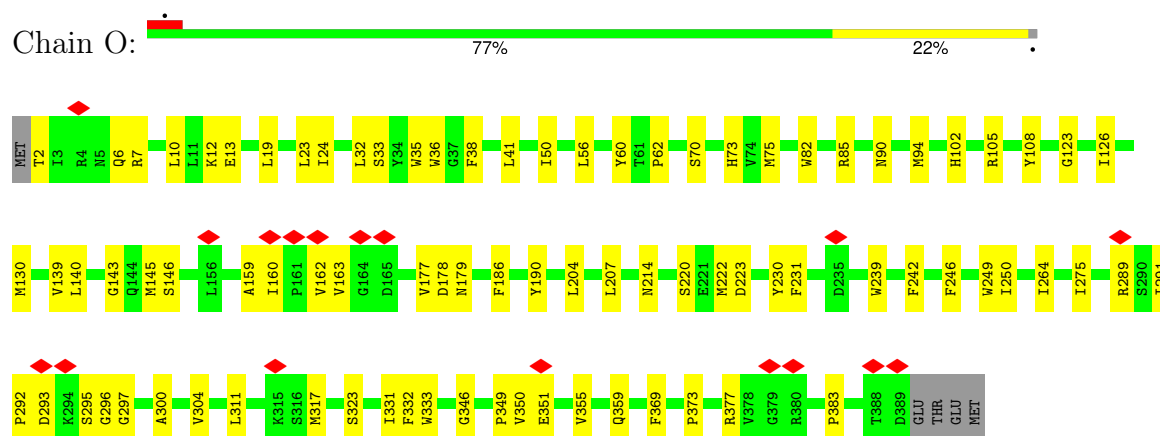
• Molecule 2: Alpha-MPP



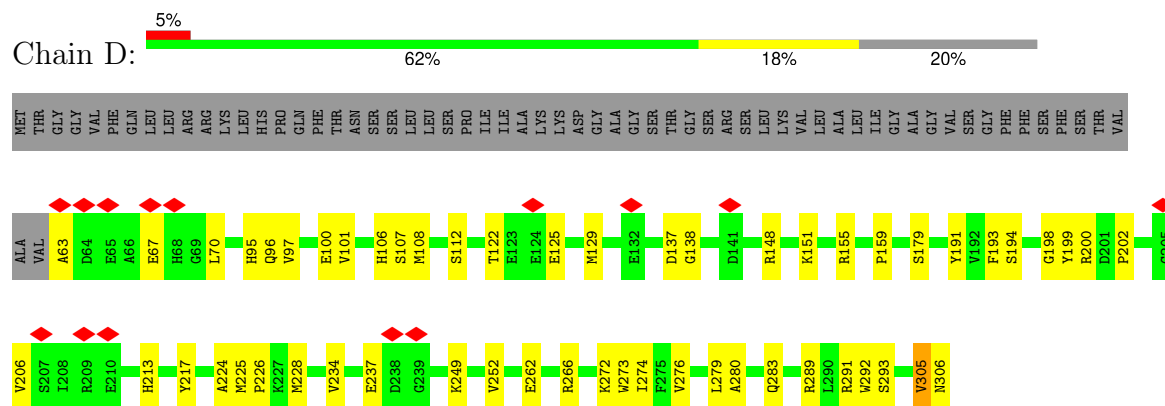
- Molecule 3: COB



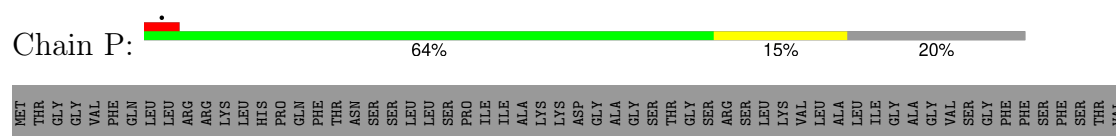
- Molecule 3: COB

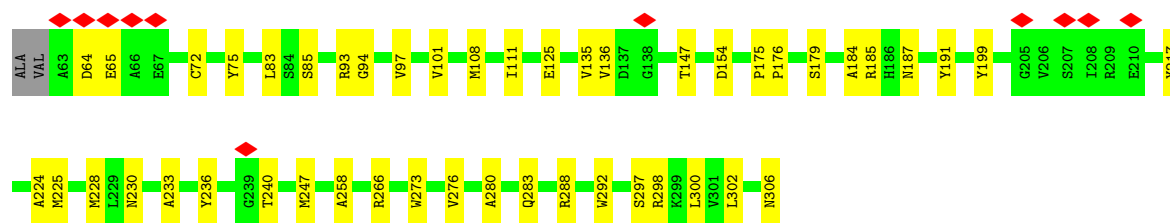


- Molecule 4: cytochrome c1-2, heme protein, mitochondrial

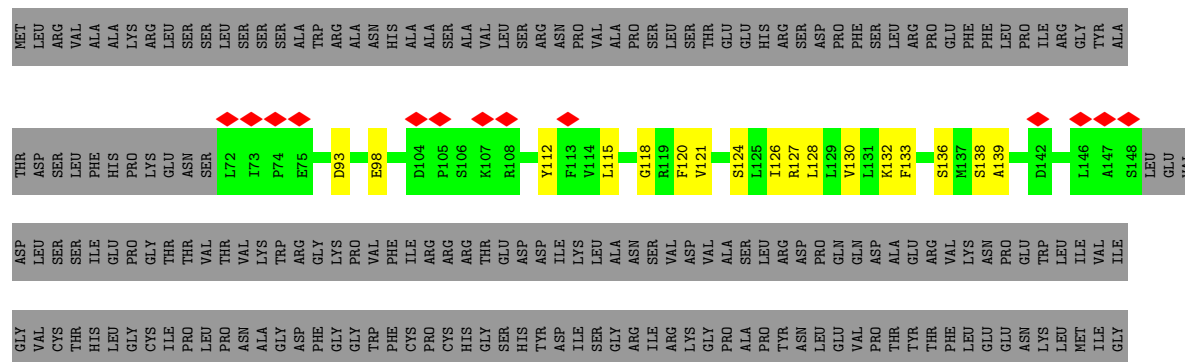


- Molecule 4: cytochrome c1-2, heme protein, mitochondrial

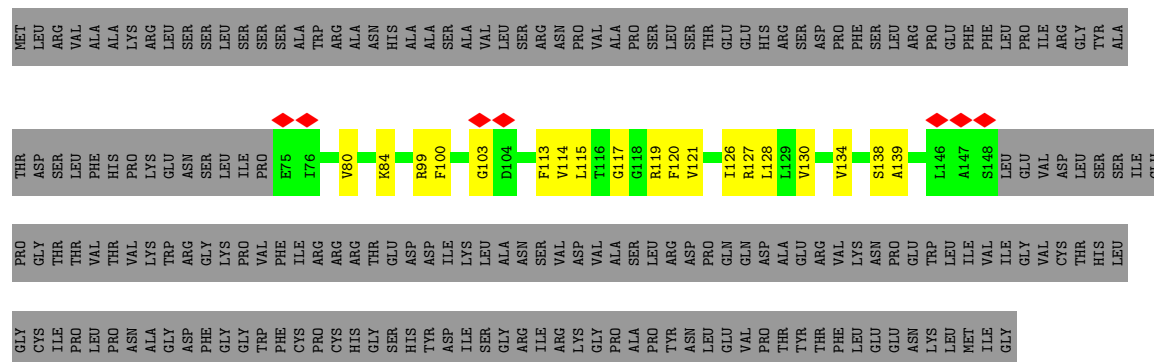




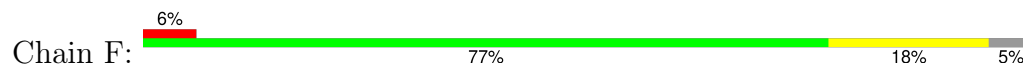
• Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial



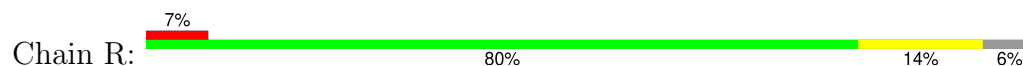
• Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial



• Molecule 6: Cytochrome b-c1 complex subunit 7

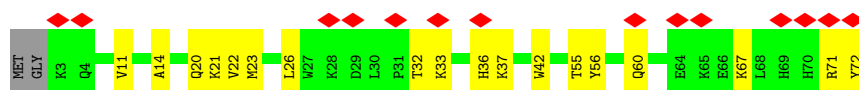


• Molecule 6: Cytochrome b-c1 complex subunit 7

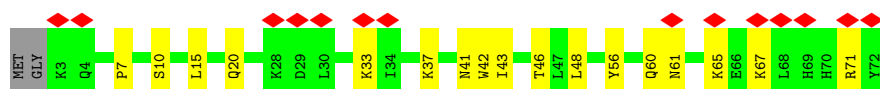
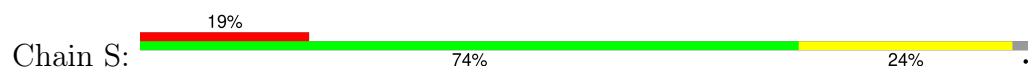




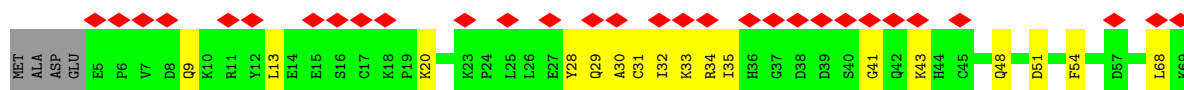
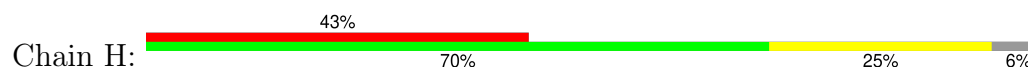
- Molecule 7: cytochrome b-c1 complex subunit 8



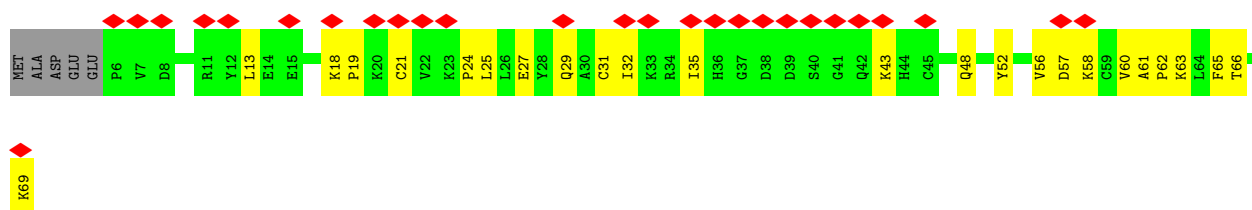
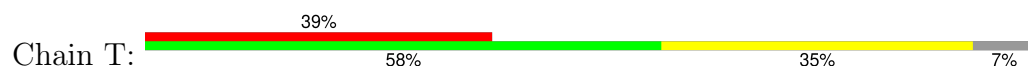
- Molecule 7: cytochrome b-c1 complex subunit 8



- Molecule 8: Cytochrome b-c1 complex subunit 6



- Molecule 8: Cytochrome b-c1 complex subunit 6

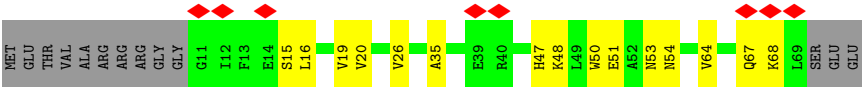


- Molecule 9: cytochrome b-c1 complex subunit 9

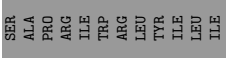
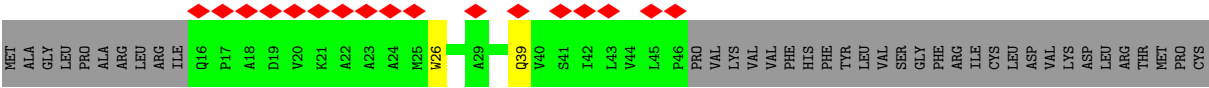


- Molecule 9: cytochrome b-c1 complex subunit 9

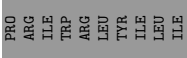
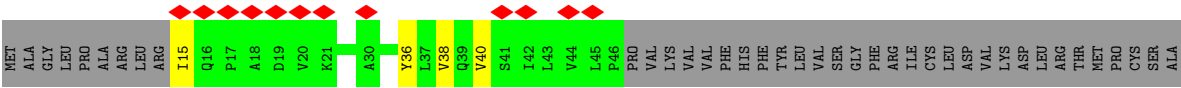
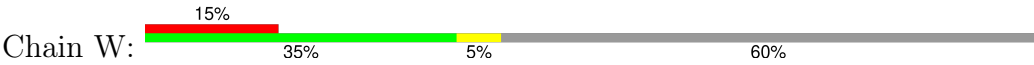




● Molecule 10: QCR10



● Molecule 10: QCR10



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	48111	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 ($e^-/\text{\AA}^2$)	86.4	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	60010	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.820	Depositor
Minimum map value	-0.839	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	426.5984, 426.5984, 426.5984	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8332, 0.8332, 0.8332	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, HEC, CDL, 3PE, PC1, 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	A	0.24	0/3914	0.41	0/5309
1	M	0.24	0/3914	0.41	0/5309
2	B	0.21	0/3541	0.40	1/4803 (0.0%)
2	N	0.22	0/3526	0.41	0/4785
3	C	0.28	0/3220	0.39	0/4413
3	O	0.28	0/3220	0.42	0/4413
4	D	0.23	0/1962	0.37	0/2663
4	P	0.23	0/1962	0.36	0/2663
5	E	0.22	0/612	0.39	0/831
5	Q	0.22	0/588	0.42	0/797
6	F	0.25	0/986	0.37	0/1326
6	R	0.25	0/980	0.38	0/1318
7	G	0.20	0/595	0.36	0/807
7	S	0.19	0/595	0.34	0/807
8	H	0.17	0/550	0.35	0/737
8	T	0.19	0/541	0.45	0/724
9	J	0.19	0/490	0.37	0/660
9	V	0.20	0/486	0.32	0/655
10	K	0.15	0/222	0.33	0/305
10	W	0.18	0/230	0.31	0/316
All	All	0.24	0/32134	0.39	1/43641 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	107	GLY	N-CA-C	5.72	117.62	110.29

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	A	3838	0	3797	73	0
1	M	3838	0	3797	96	0
2	B	3471	0	3471	100	0
2	N	3456	0	3453	92	0
3	C	3104	0	3070	67	0
3	O	3104	0	3070	72	0
4	D	1910	0	1843	48	0
4	P	1910	0	1843	37	0
5	E	597	0	620	17	0
5	Q	574	0	591	17	0
6	F	965	0	982	21	0
6	R	959	0	977	14	0
7	G	578	0	599	18	0
7	S	578	0	599	15	0
8	H	536	0	528	15	0
8	T	527	0	521	19	0
9	J	480	0	486	8	0
9	V	476	0	483	11	0
10	K	218	0	230	2	0
10	W	226	0	241	3	0
11	A	1	0	0	0	0
11	M	1	0	0	0	0
12	A	38	0	50	3	0
12	M	40	0	54	6	0
12	S	38	0	50	2	0
13	A	69	0	85	1	0
13	C	123	0	134	5	0
13	D	68	0	83	2	0
13	M	70	0	87	6	0
13	O	145	0	184	10	0
13	P	63	0	70	2	0
13	S	55	0	54	2	0
14	C	86	0	60	8	0
14	O	86	0	60	9	0
15	C	206	0	259	13	0
15	F	83	0	120	3	0
15	G	37	0	48	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	M	45	0	67	2	0
15	O	189	0	254	5	0
15	W	56	0	60	0	0
16	D	43	0	30	8	0
16	P	43	0	30	3	0
All	All	32930	0	33040	678	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 10.

The worst 5 of 678 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)
1:M:187:PRO:HB3	1:M:291:GLN:HE22	1.40	0.86
4:D:95:HIS:HE1	4:D:129:MET:HE1	1.45	0.80
6:F:16:LEU:HD12	15:F:201:3PE:H352	1.65	0.79
3:C:315:LYS:HE3	3:C:377:ARG:HH21	1.47	0.79
3:O:162:VAL:HG13	3:O:163:VAL:HG13	1.64	0.79

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	A	485/527 (92%)	450 (93%)	35 (7%)	0	100	100
1	M	485/527 (92%)	451 (93%)	34 (7%)	0	100	100
2	B	455/506 (90%)	411 (90%)	42 (9%)	2 (0%)	30	62
2	N	453/506 (90%)	406 (90%)	47 (10%)	0	100	100
3	C	386/393 (98%)	365 (95%)	21 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	O	386/393 (98%)	363 (94%)	23 (6%)	0	100	100
4	D	242/306 (79%)	233 (96%)	9 (4%)	0	100	100
4	P	242/306 (79%)	229 (95%)	13 (5%)	0	100	100
5	E	75/271 (28%)	68 (91%)	7 (9%)	0	100	100
5	Q	72/271 (27%)	66 (92%)	6 (8%)	0	100	100
6	F	114/122 (93%)	111 (97%)	3 (3%)	0	100	100
6	R	113/122 (93%)	109 (96%)	4 (4%)	0	100	100
7	G	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
7	S	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
8	H	63/69 (91%)	59 (94%)	4 (6%)	0	100	100
8	T	62/69 (90%)	55 (89%)	7 (11%)	0	100	100
9	J	58/72 (81%)	54 (93%)	4 (7%)	0	100	100
9	V	57/72 (79%)	55 (96%)	2 (4%)	0	100	100
10	K	29/81 (36%)	25 (86%)	4 (14%)	0	100	100
10	W	30/81 (37%)	28 (93%)	2 (7%)	0	100	100
All	All	3943/4838 (82%)	3671 (93%)	270 (7%)	2 (0%)	49	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	435	ARG
2	B	113	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	A	407/438 (93%)	407 (100%)	0	100	100
1	M	407/438 (93%)	407 (100%)	0	100	100
2	B	378/414 (91%)	378 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	N	377/414 (91%)	377 (100%)	0	100	100
3	C	333/338 (98%)	332 (100%)	1 (0%)	86	88
3	O	333/338 (98%)	333 (100%)	0	100	100
4	D	198/247 (80%)	196 (99%)	2 (1%)	68	80
4	P	198/247 (80%)	198 (100%)	0	100	100
5	E	65/233 (28%)	65 (100%)	0	100	100
5	Q	62/233 (27%)	62 (100%)	0	100	100
6	F	102/107 (95%)	102 (100%)	0	100	100
6	R	101/107 (94%)	101 (100%)	0	100	100
7	G	64/65 (98%)	64 (100%)	0	100	100
7	S	64/65 (98%)	64 (100%)	0	100	100
8	H	60/63 (95%)	60 (100%)	0	100	100
8	T	59/63 (94%)	59 (100%)	0	100	100
9	J	49/59 (83%)	49 (100%)	0	100	100
9	V	49/59 (83%)	49 (100%)	0	100	100
10	K	21/66 (32%)	21 (100%)	0	100	100
10	W	22/66 (33%)	22 (100%)	0	100	100
All	All	3349/4060 (82%)	3346 (100%)	3 (0%)	87	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	259	HIS
4	D	305	VAL
4	D	306	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	158	GLN
1	M	133	ASN
7	S	60	GLN
1	M	66	ASN
2	N	74	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 37 ligands modelled in this entry, 2 are monoatomic - leaving 35 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$
15	3PE	W	101	-	27,27,50	0.40	0	30,32,55	0.41	0
14	HEM	O	403	3	50,50,50	1.37	6 (12%)	67,82,82	1.69	15 (22%)
13	CDL	S	102	-	54,54,99	0.39	0	60,66,111	0.39	0
13	CDL	O	402	-	80,80,99	0.34	0	86,92,111	0.39	0
15	3PE	C	406	-	44,44,50	0.32	0	47,49,55	0.38	0
15	3PE	O	408	-	32,32,50	0.37	0	35,37,55	0.35	0
14	HEM	O	404	3	50,50,50	1.39	7 (14%)	67,82,82	1.63	14 (20%)
16	HEC	P	501	4	50,50,50	1.35	6 (12%)	68,82,82	1.19	4 (5%)
15	3PE	O	401	-	35,35,50	0.36	0	38,40,55	0.41	0
15	3PE	O	405	-	29,29,50	0.38	0	32,34,55	0.34	0
15	3PE	O	409	-	50,50,50	0.30	0	53,55,55	0.33	0
12	PC1	S	101	-	37,37,53	0.34	0	43,45,61	0.36	0
15	3PE	F	202	-	50,50,50	0.30	0	53,55,55	0.31	0
13	CDL	D	502	-	67,67,99	0.36	0	73,79,111	0.36	0
15	3PE	C	405	-	28,28,50	0.40	0	31,33,55	0.41	0
13	CDL	O	406	-	63,63,99	0.37	0	69,75,111	0.42	0
14	HEM	C	403	3	50,50,50	1.37	7 (14%)	67,82,82	1.64	13 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
15	3PE	M	602	-	44,44,50	0.32	0	47,49,55	0.33	0
15	3PE	O	407	-	38,38,50	0.34	0	41,43,55	0.36	0
13	CDL	C	410	-	58,58,99	0.38	0	64,70,111	0.33	0
13	CDL	C	401	-	63,63,99	0.37	0	69,75,111	0.34	0
15	3PE	C	404	-	37,37,50	0.35	0	40,42,55	0.37	0
15	3PE	G	101	-	36,36,50	0.35	0	39,41,55	0.31	0
14	HEM	C	402	3	50,50,50	1.36	7 (14%)	67,82,82	1.69	14 (20%)
15	3PE	W	102	-	27,27,50	0.40	0	30,32,55	0.37	0
15	3PE	C	408	-	26,26,50	0.40	0	29,31,55	0.35	0
15	3PE	C	407	-	32,32,50	0.37	0	35,37,55	0.32	0
13	CDL	M	603	-	69,69,99	0.36	0	75,81,111	0.39	0
13	CDL	A	603	-	68,68,99	0.35	0	74,80,111	0.32	0
13	CDL	P	502	-	62,62,99	0.37	0	68,74,111	0.44	0
16	HEC	D	501	4	50,50,50	1.34	5 (10%)	68,82,82	1.25	5 (7%)
15	3PE	F	201	-	31,31,50	0.39	0	34,36,55	0.55	0
12	PC1	A	602	-	37,37,53	0.35	0	43,45,61	0.29	0
12	PC1	M	604	-	39,39,53	0.34	0	45,47,61	0.39	0
15	3PE	C	409	-	33,33,50	0.37	0	36,38,55	0.34	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
15	3PE	W	101	-	-	7/31/31/54	-
14	HEM	O	403	3	-	10/14/54/54	-
13	CDL	S	102	-	-	13/65/65/110	-
13	CDL	O	402	-	-	16/91/91/110	-
15	3PE	C	406	-	-	13/48/48/54	-
15	3PE	O	408	-	-	7/36/36/54	-
14	HEM	O	404	3	-	9/14/54/54	-
16	HEC	P	501	4	1/1/3/7	2/14/54/54	-
15	3PE	O	401	-	-	13/39/39/54	-
15	3PE	O	405	-	-	5/33/33/54	-
15	3PE	O	409	-	-	5/54/54/54	-
12	PC1	S	101	-	-	7/41/41/57	-
15	3PE	F	202	-	-	11/54/54/54	-
13	CDL	D	502	-	-	18/78/78/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	3PE	C	405	-	-	6/32/32/54	-
13	CDL	O	406	-	-	17/74/74/110	-
14	HEM	C	403	3	-	8/14/54/54	-
15	3PE	M	602	-	-	14/48/48/54	-
15	3PE	O	407	-	-	10/42/42/54	-
13	CDL	C	410	-	-	8/69/69/110	-
13	CDL	C	401	-	-	11/74/74/110	-
15	3PE	C	404	-	-	9/41/41/54	-
15	3PE	G	101	-	-	6/40/40/54	-
14	HEM	C	402	3	-	5/14/54/54	-
15	3PE	W	102	-	-	9/31/31/54	-
15	3PE	C	408	-	-	10/30/30/54	-
15	3PE	C	407	-	-	8/36/36/54	-
13	CDL	M	603	-	-	9/80/80/110	-
13	CDL	A	603	-	-	16/79/79/110	-
13	CDL	P	502	-	-	16/73/73/110	-
16	HEC	D	501	4	1/1/3/7	4/14/54/54	-
15	3PE	F	201	-	-	9/35/35/54	-
12	PC1	A	602	-	-	5/41/41/57	-
12	PC1	M	604	-	-	5/43/43/57	-
15	3PE	C	409	-	-	5/37/37/54	-

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	O	403	HEM	C4D-ND	-3.91	1.33	1.40
14	C	402	HEM	C4D-ND	-3.83	1.33	1.40
14	C	403	HEM	C4D-ND	-3.70	1.33	1.40
14	O	404	HEM	C4D-ND	-3.67	1.33	1.40
16	P	501	HEC	CBC-CAC	-3.52	1.36	1.51

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	O	403	HEM	CHC-C4B-NB	4.88	129.68	124.42
14	C	402	HEM	CHC-C4B-NB	4.82	129.60	124.42
14	C	402	HEM	CHD-C4C-NC	4.46	129.31	124.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	C	402	HEM	CHB-C1B-NB	4.43	129.85	124.37
14	O	404	HEM	CHB-C1B-NB	4.34	129.74	124.37

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
16	D	501	HEC	NA
16	P	501	HEC	NA

5 of 326 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	A	602	PC1	C11-O13-P-O12
12	A	602	PC1	C11-O13-P-O11
12	S	101	PC1	C1-O11-P-O12
12	S	101	PC1	C1-O11-P-O14
12	S	101	PC1	C1-O11-P-O13

There are no ring outliers.

29 monomers are involved in 80 short contacts:

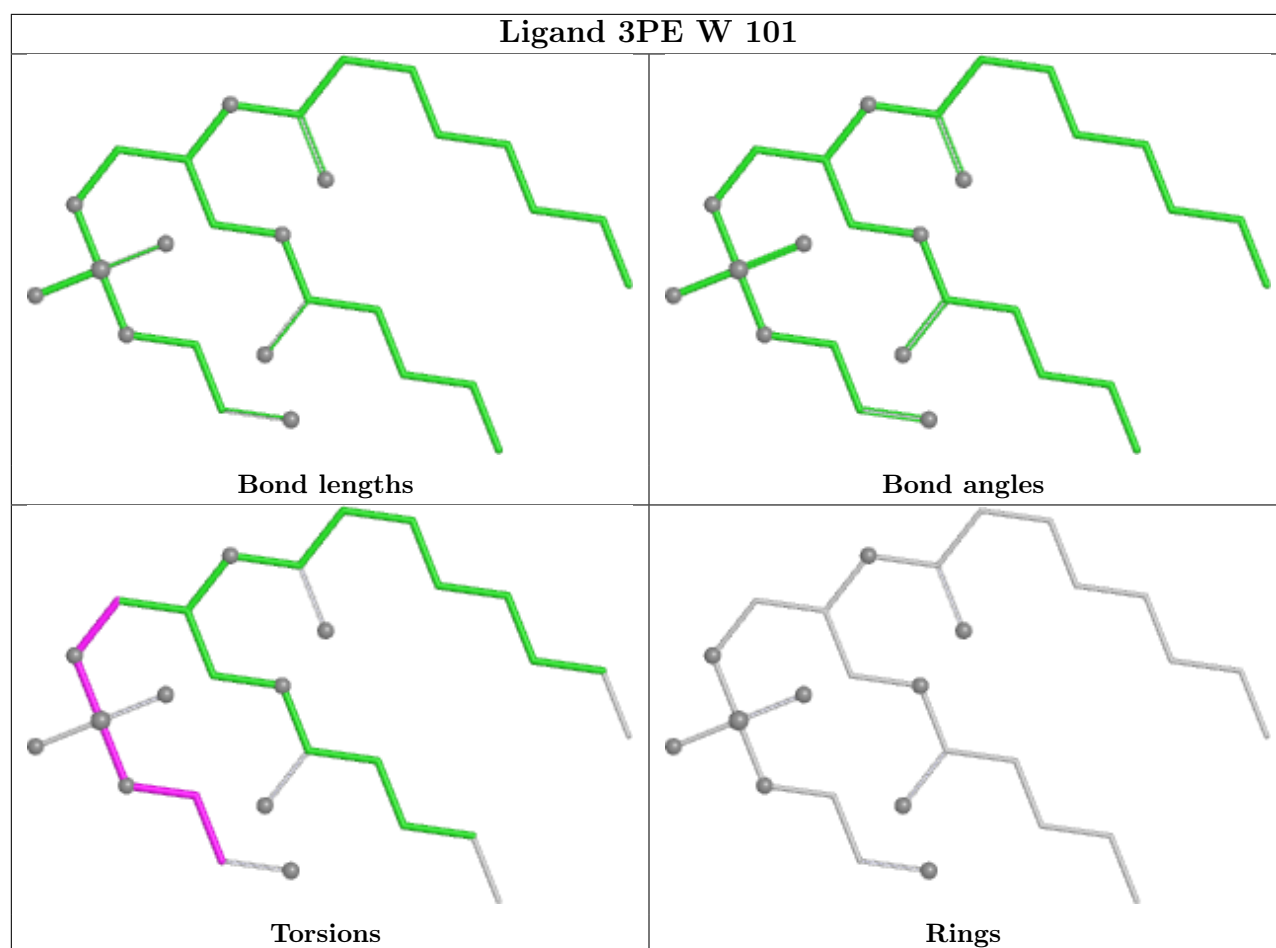
Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	O	403	HEM	3	0
13	S	102	CDL	2	0
13	O	402	CDL	9	0
15	C	406	3PE	4	0
14	O	404	HEM	6	0
16	P	501	HEC	3	0
15	O	401	3PE	1	0
15	O	409	3PE	3	0
12	S	101	PC1	2	0
13	D	502	CDL	2	0
15	C	405	3PE	4	0
13	O	406	CDL	1	0
14	C	403	HEM	5	0
15	M	602	3PE	2	0
15	O	407	3PE	1	0
13	C	410	CDL	2	0
13	C	401	CDL	3	0
15	G	101	3PE	1	0
14	C	402	HEM	3	0
15	C	408	3PE	3	0

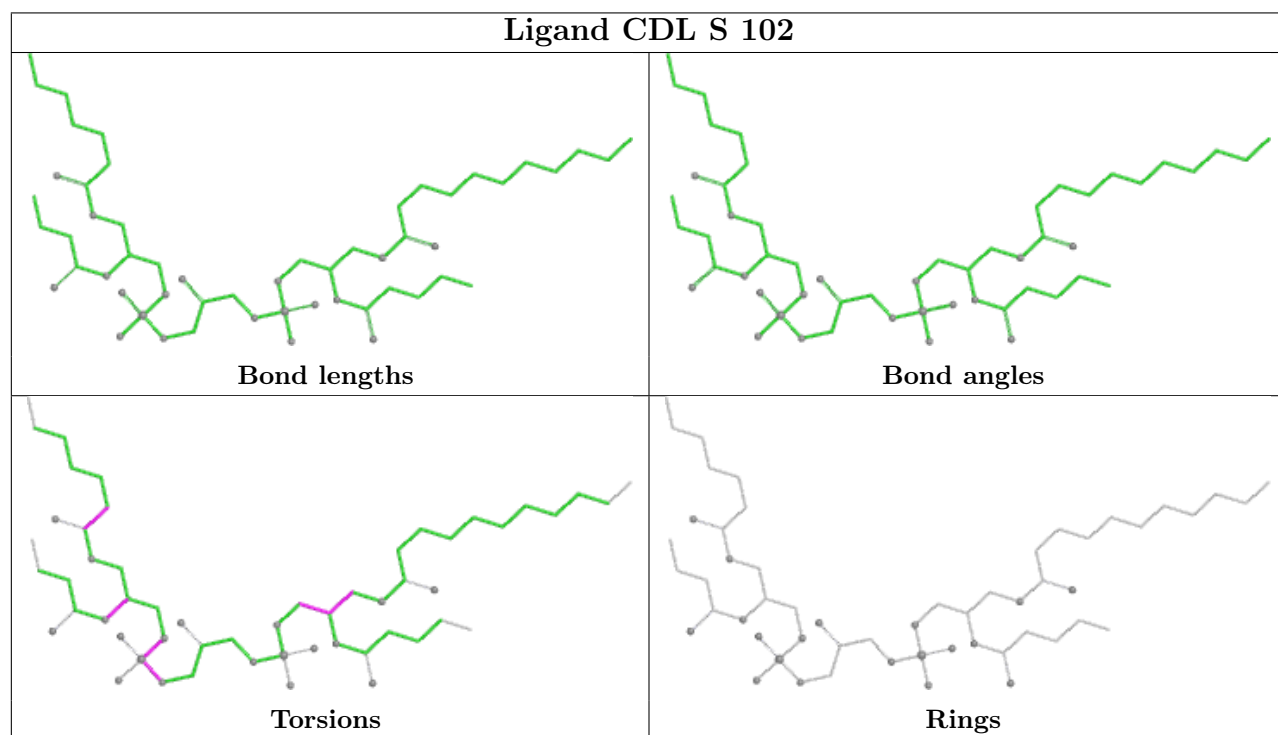
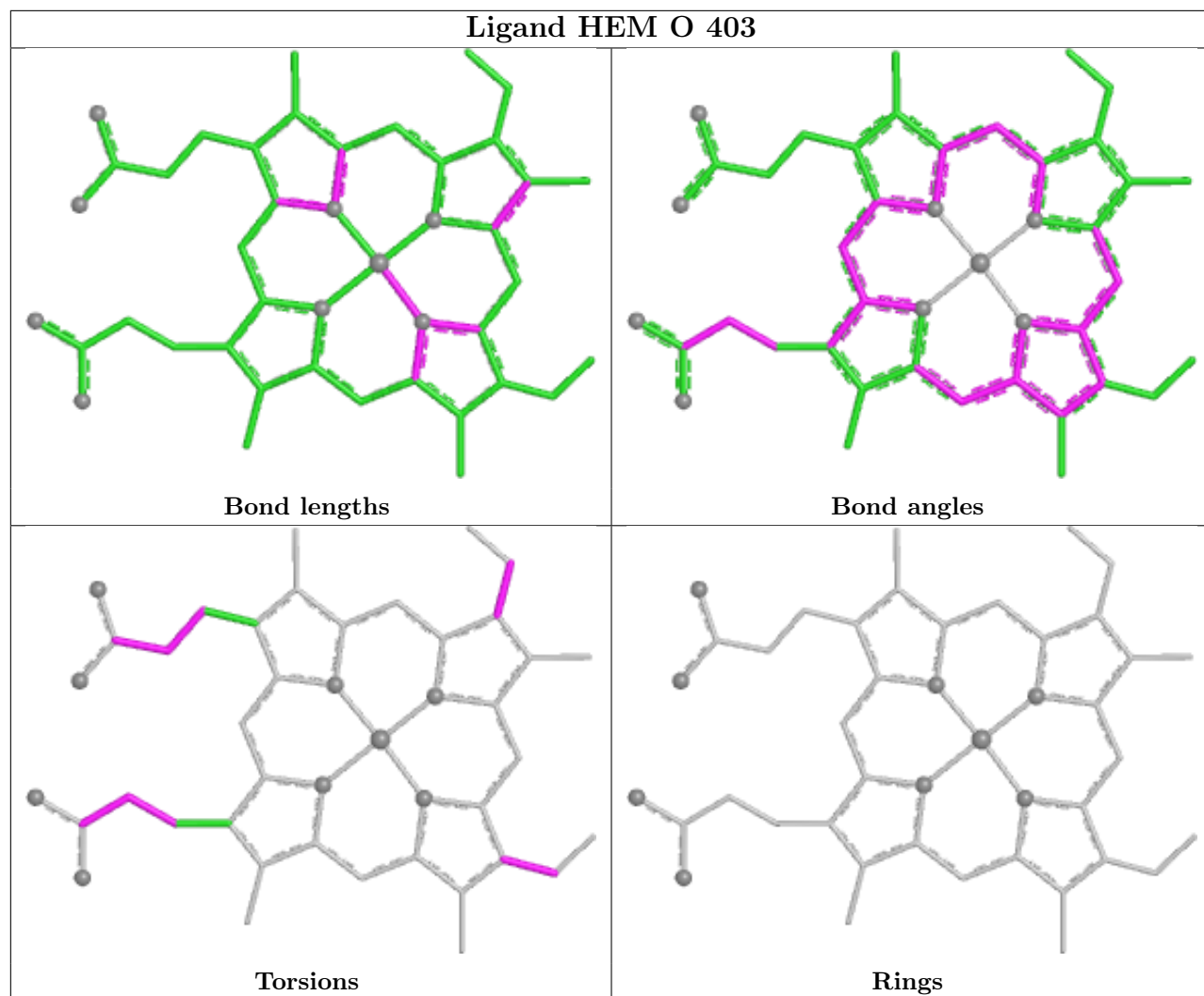
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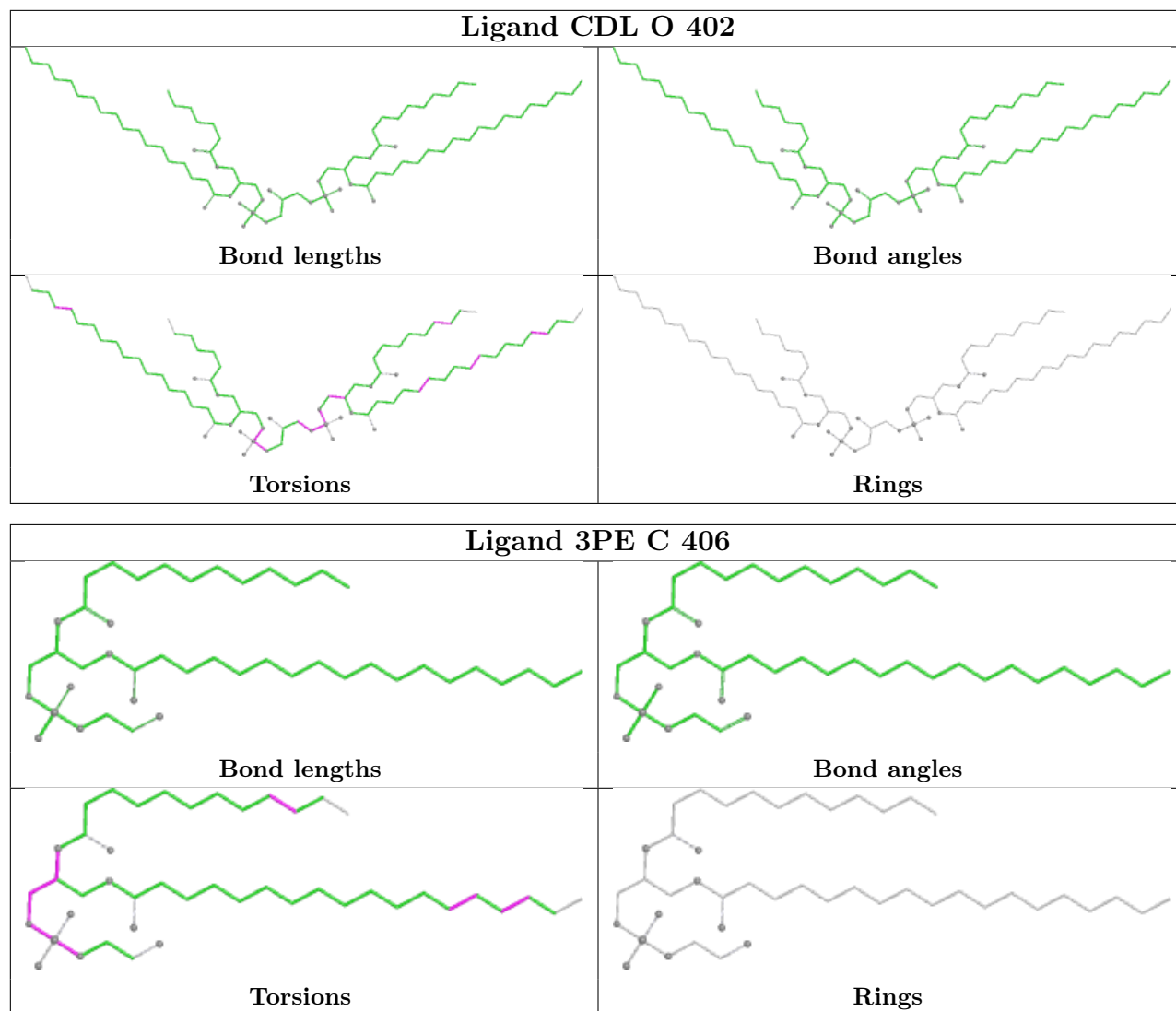
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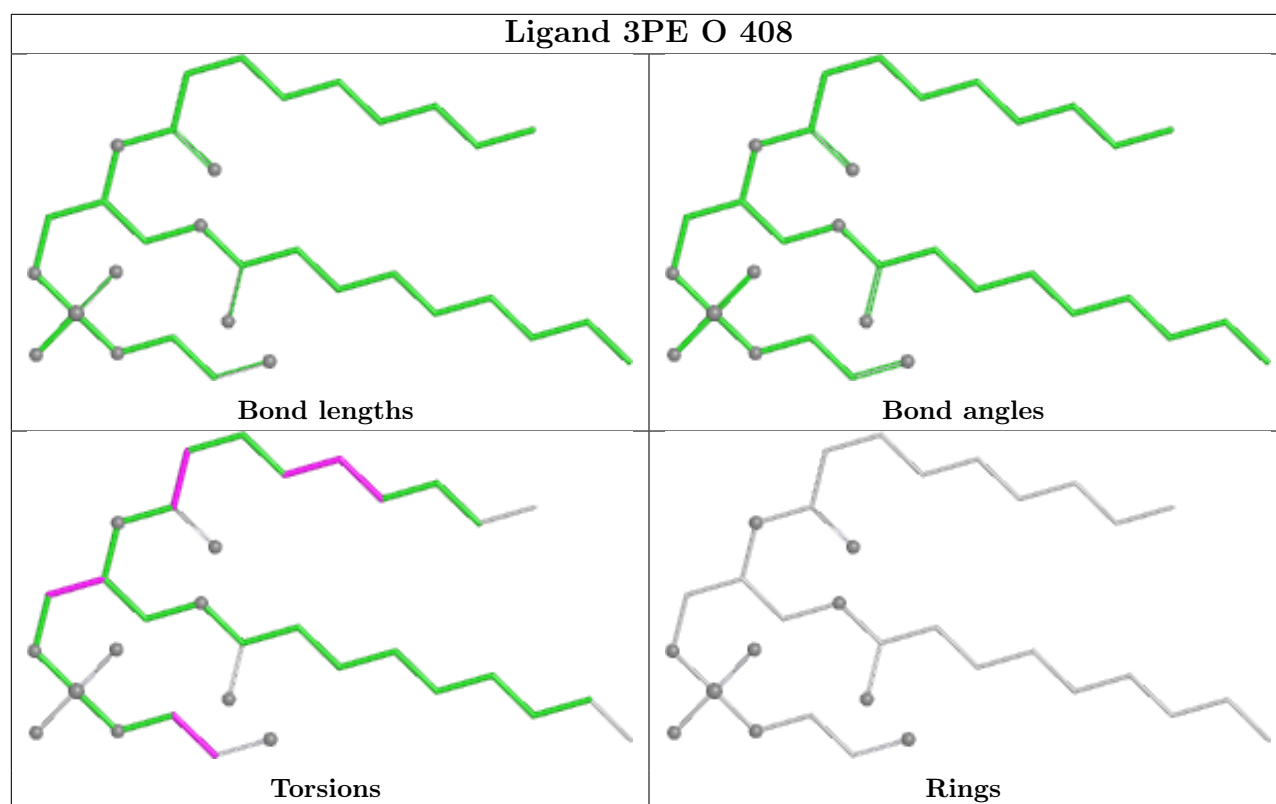
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	C	407	3PE	2	0
13	M	603	CDL	6	0
13	A	603	CDL	1	0
13	P	502	CDL	2	0
16	D	501	HEC	8	0
15	F	201	3PE	3	0
12	A	602	PC1	3	0
12	M	604	PC1	6	0
15	C	409	3PE	1	0

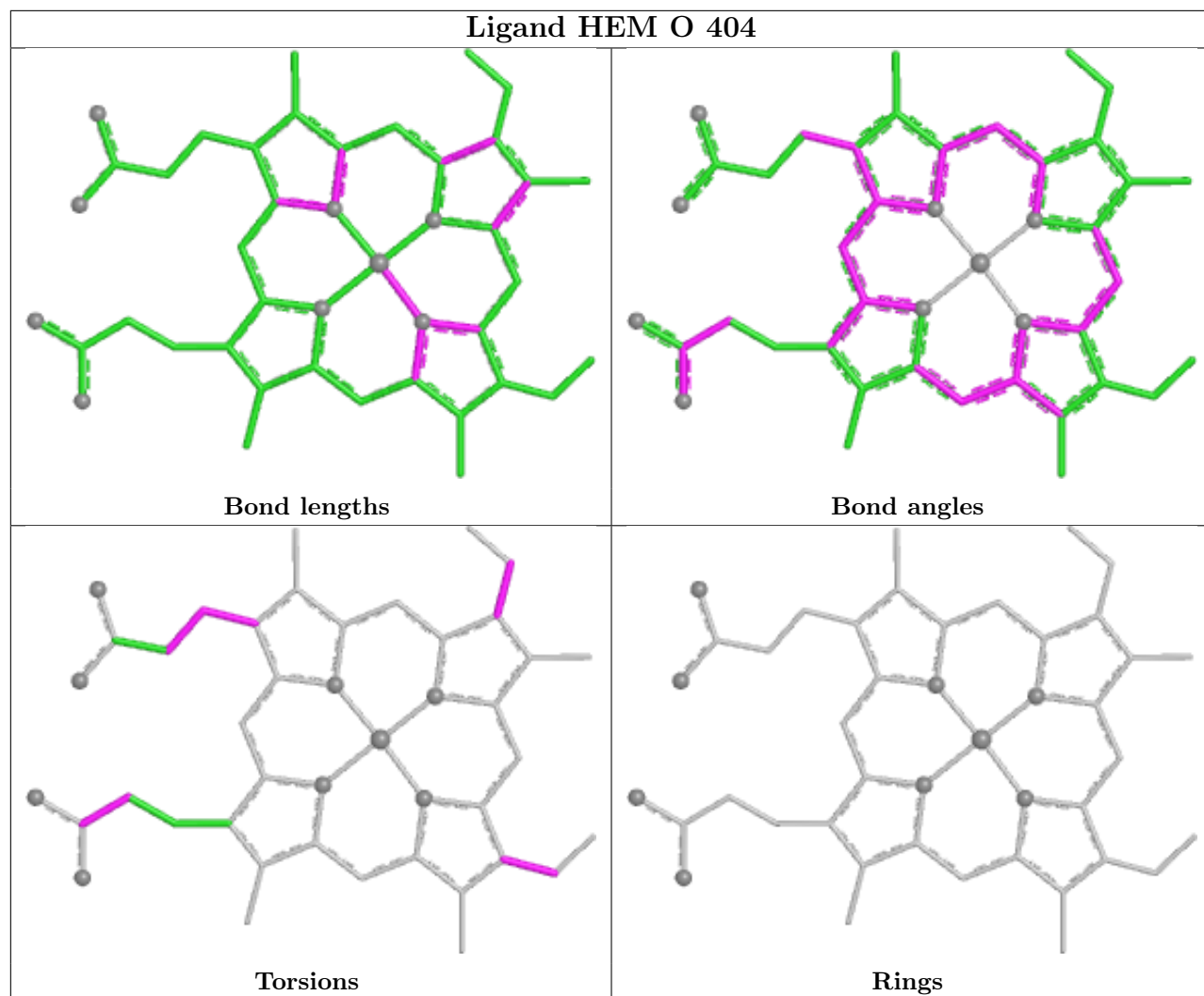
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



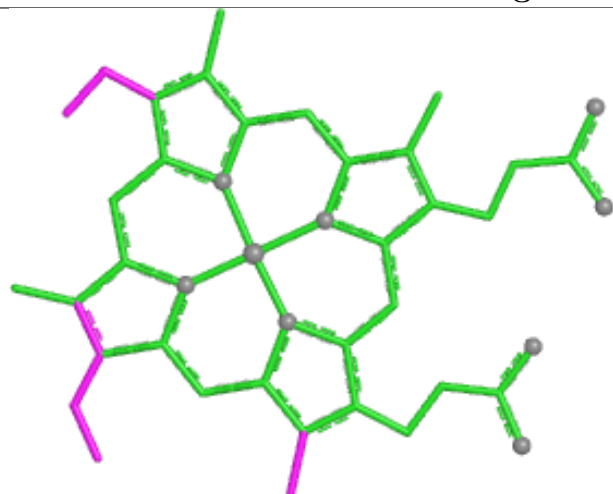




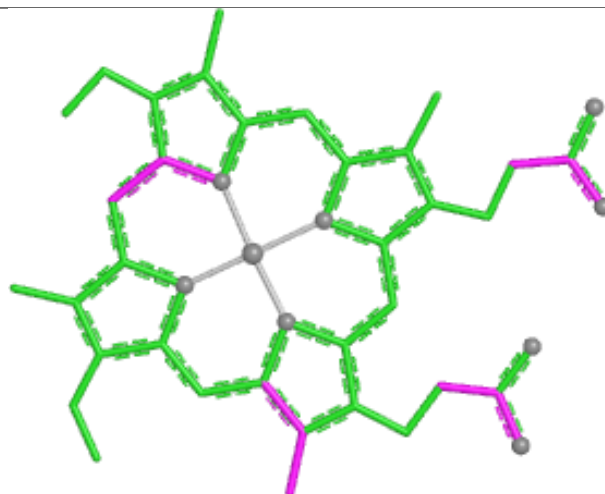




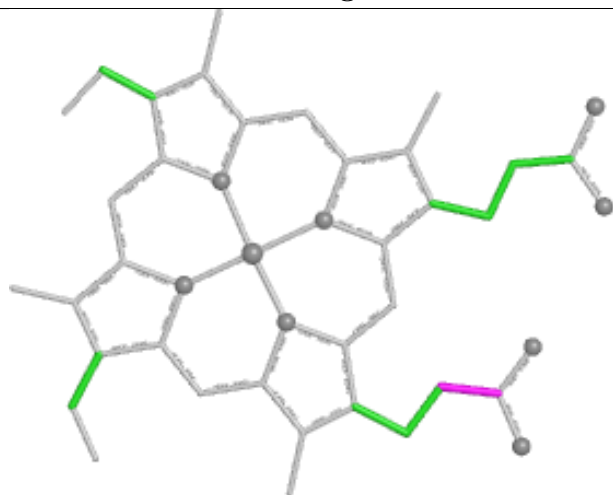
Ligand HEC P 501



Bond lengths



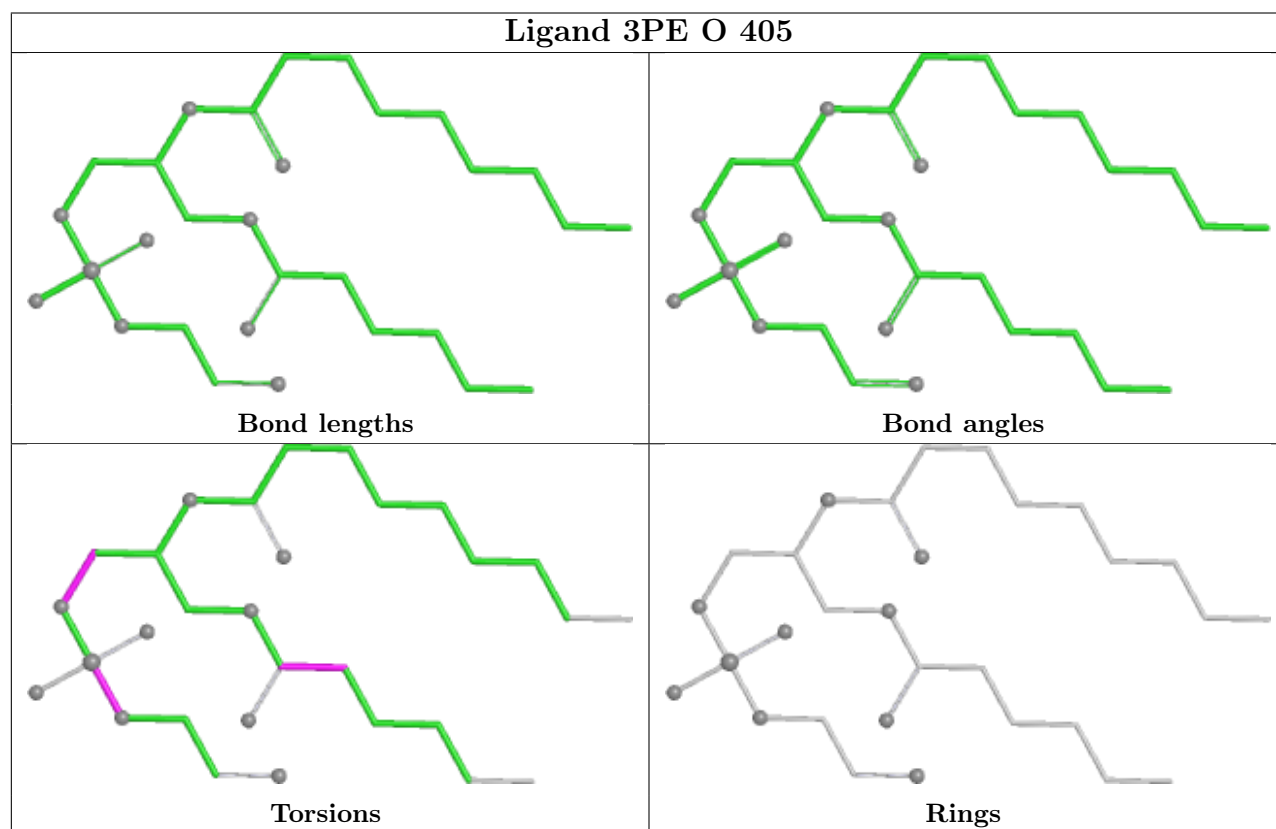
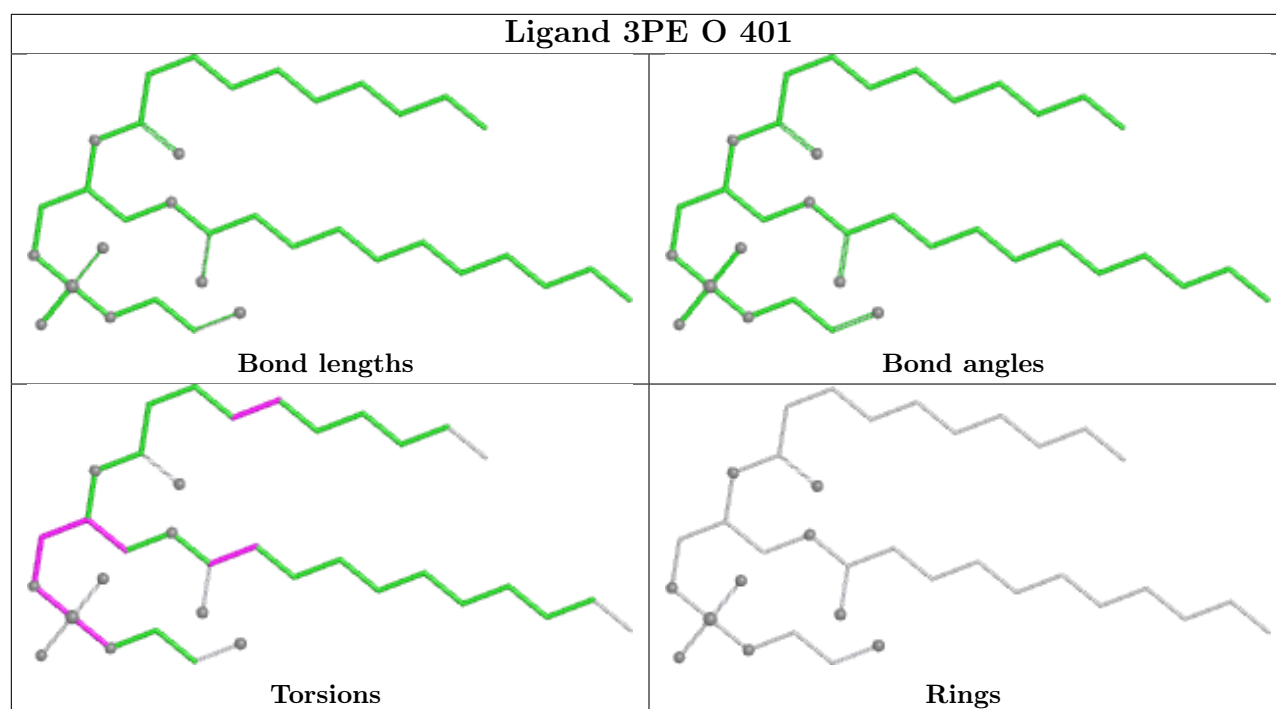
Bond angles

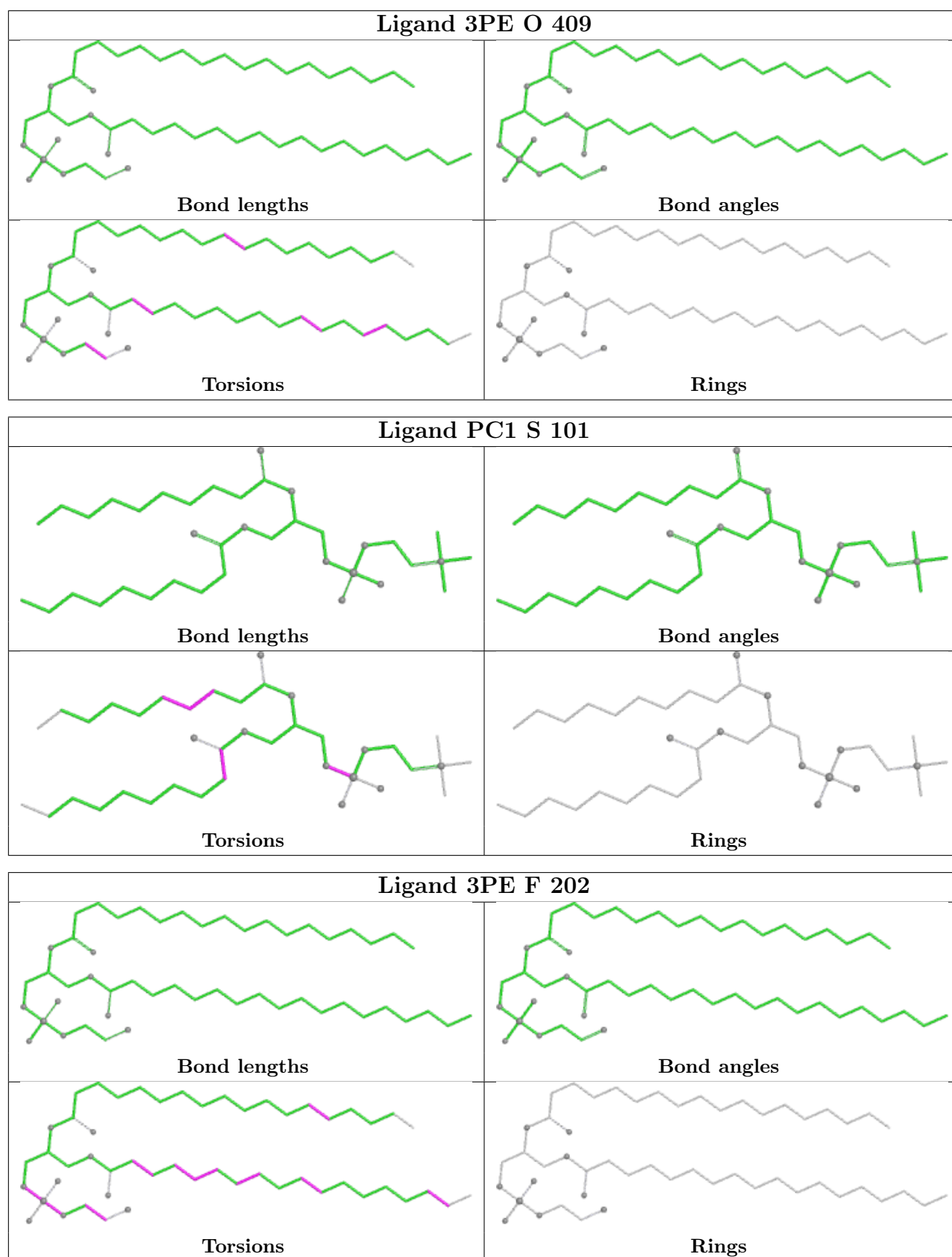


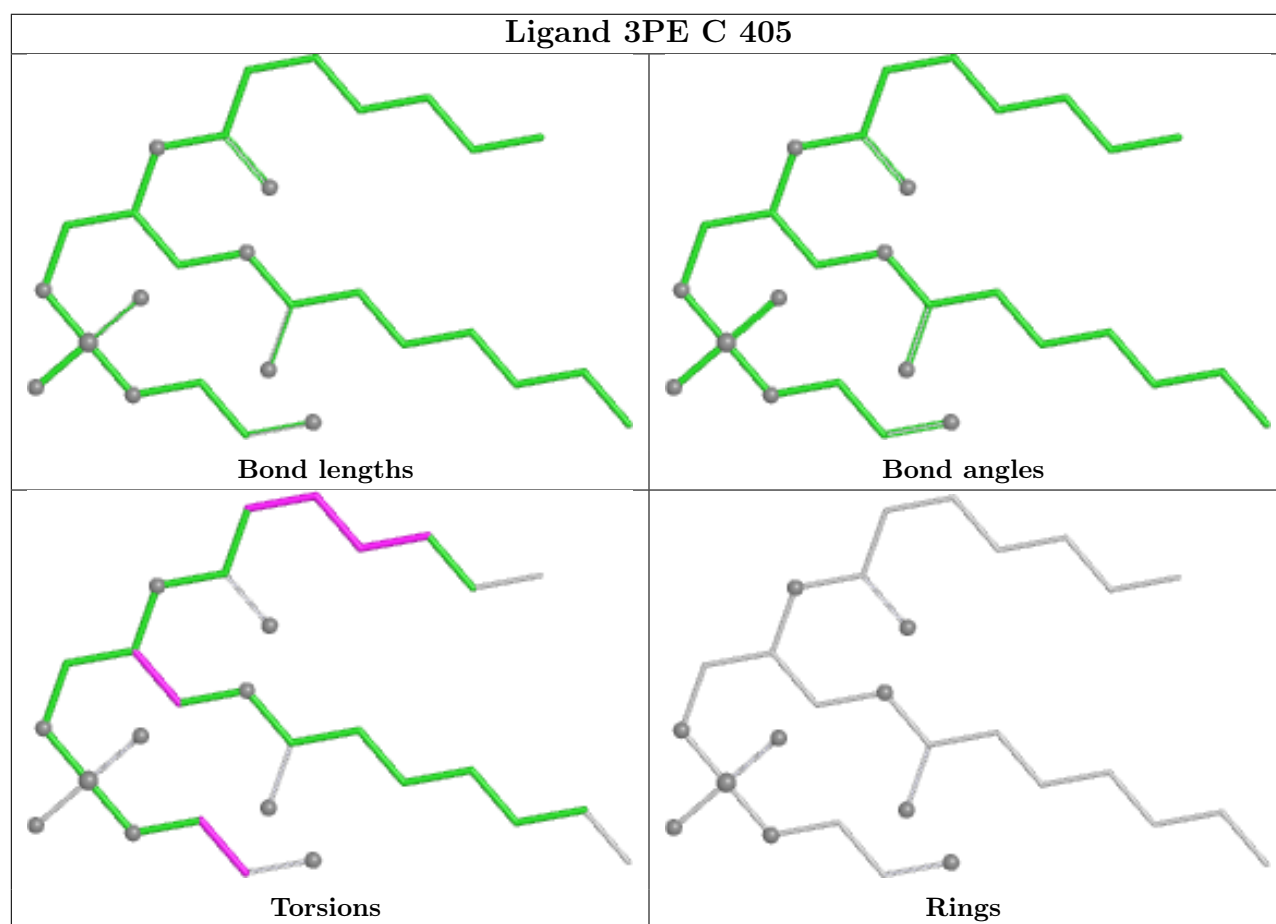
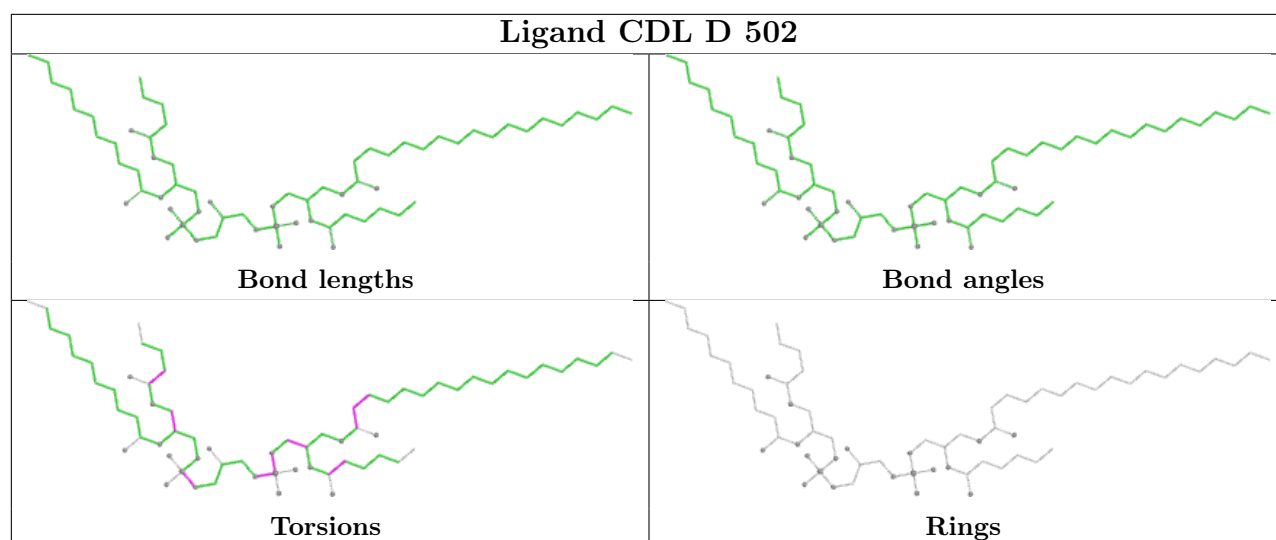
Torsions

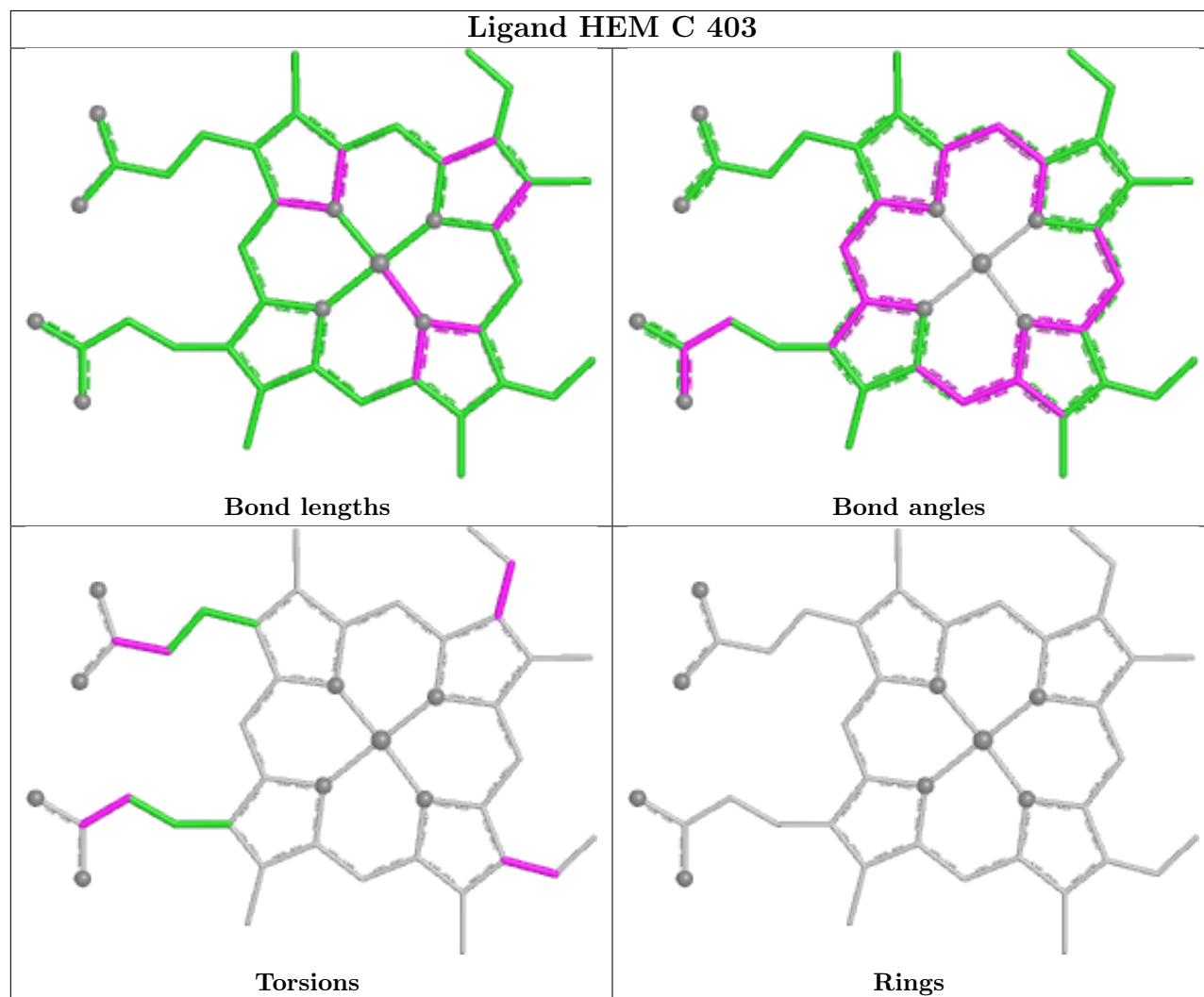
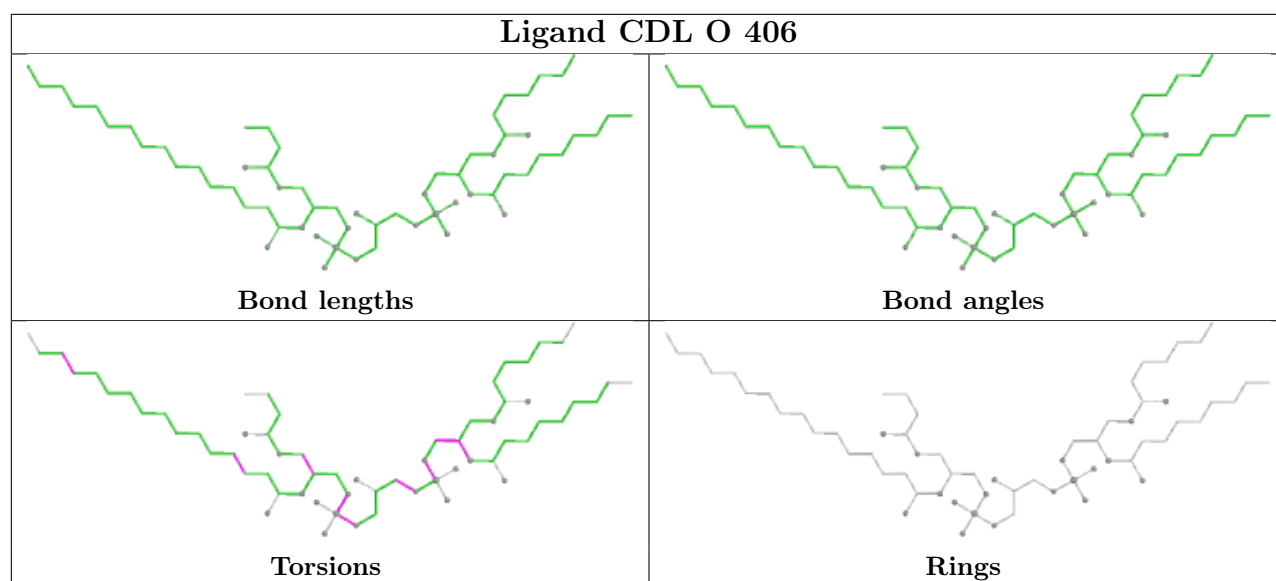


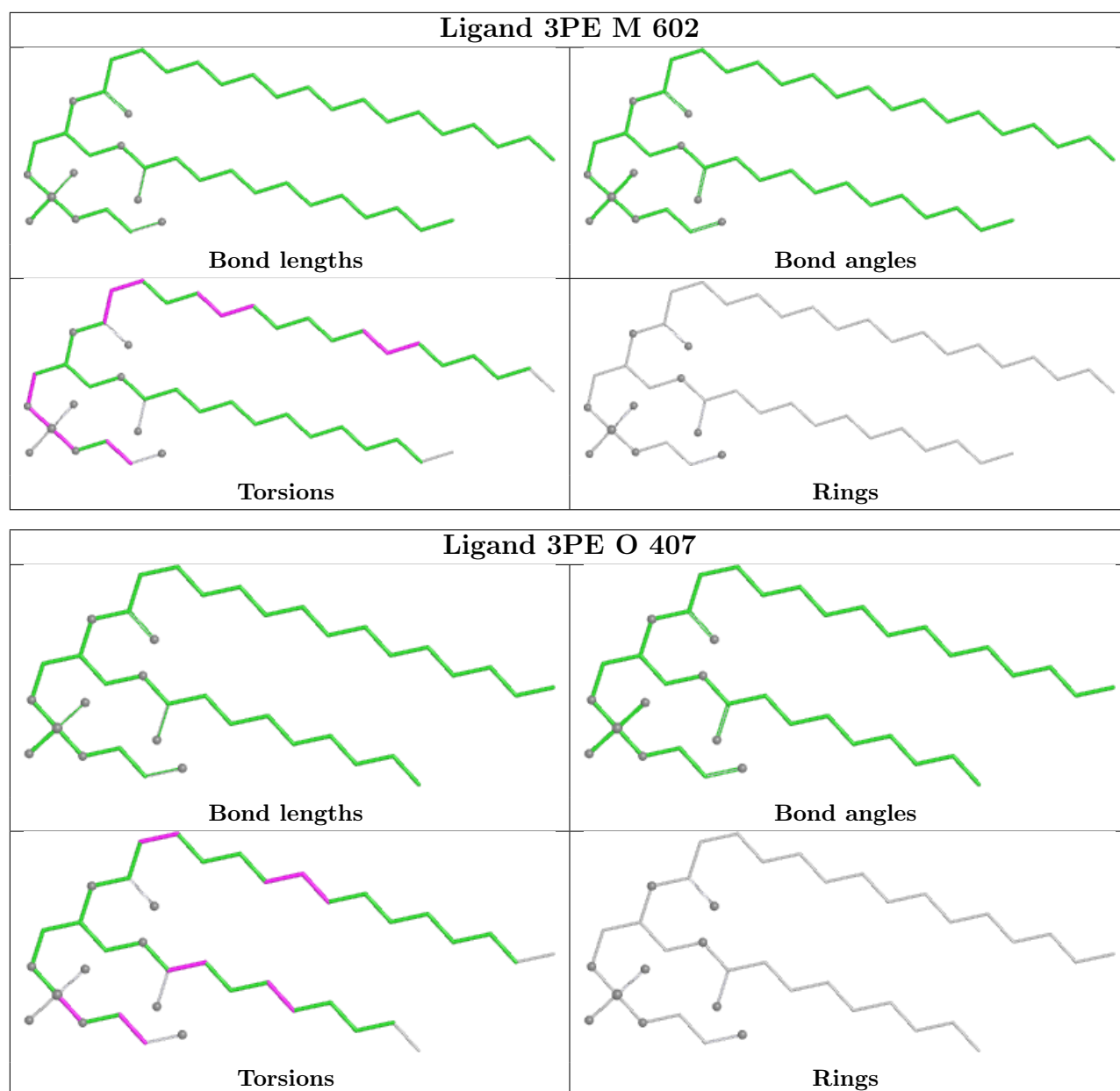
Rings

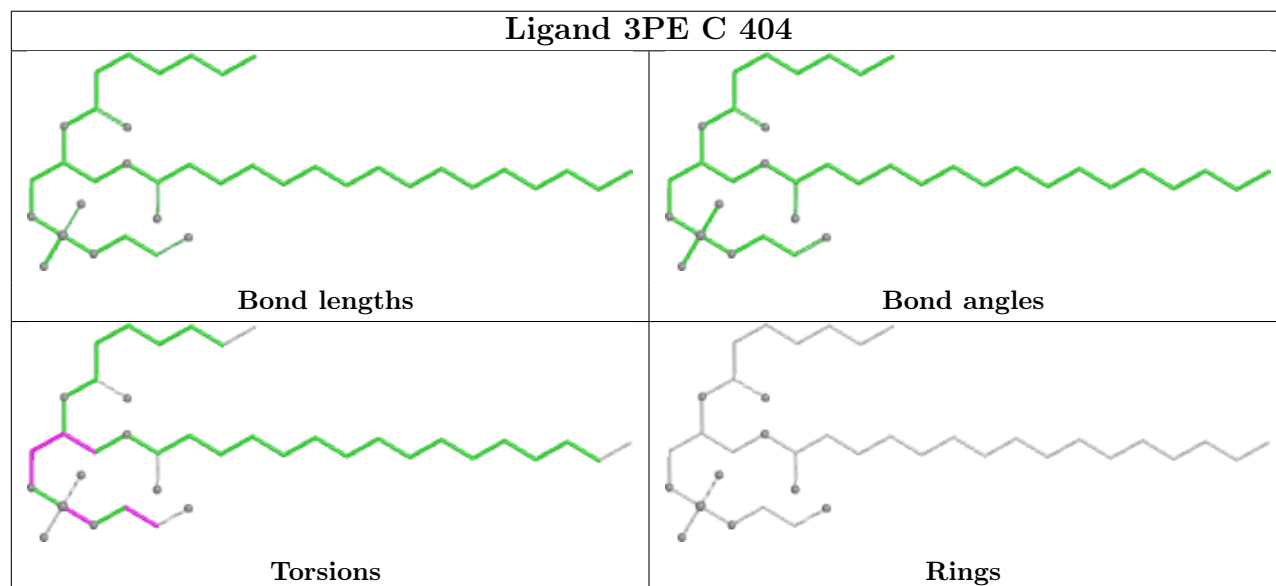
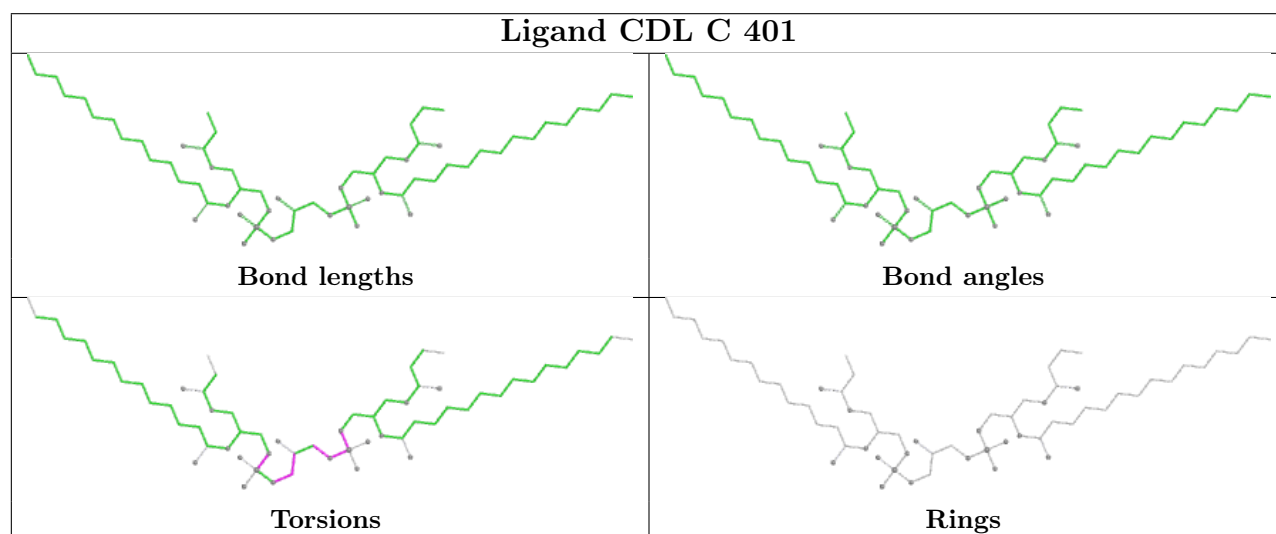
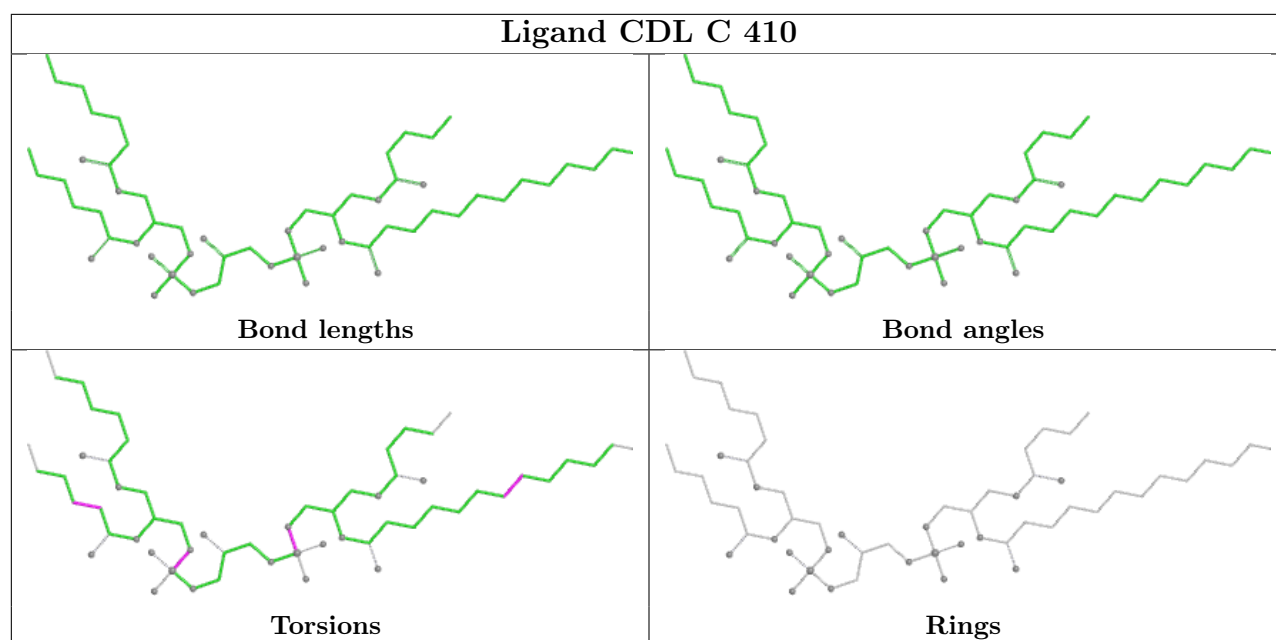


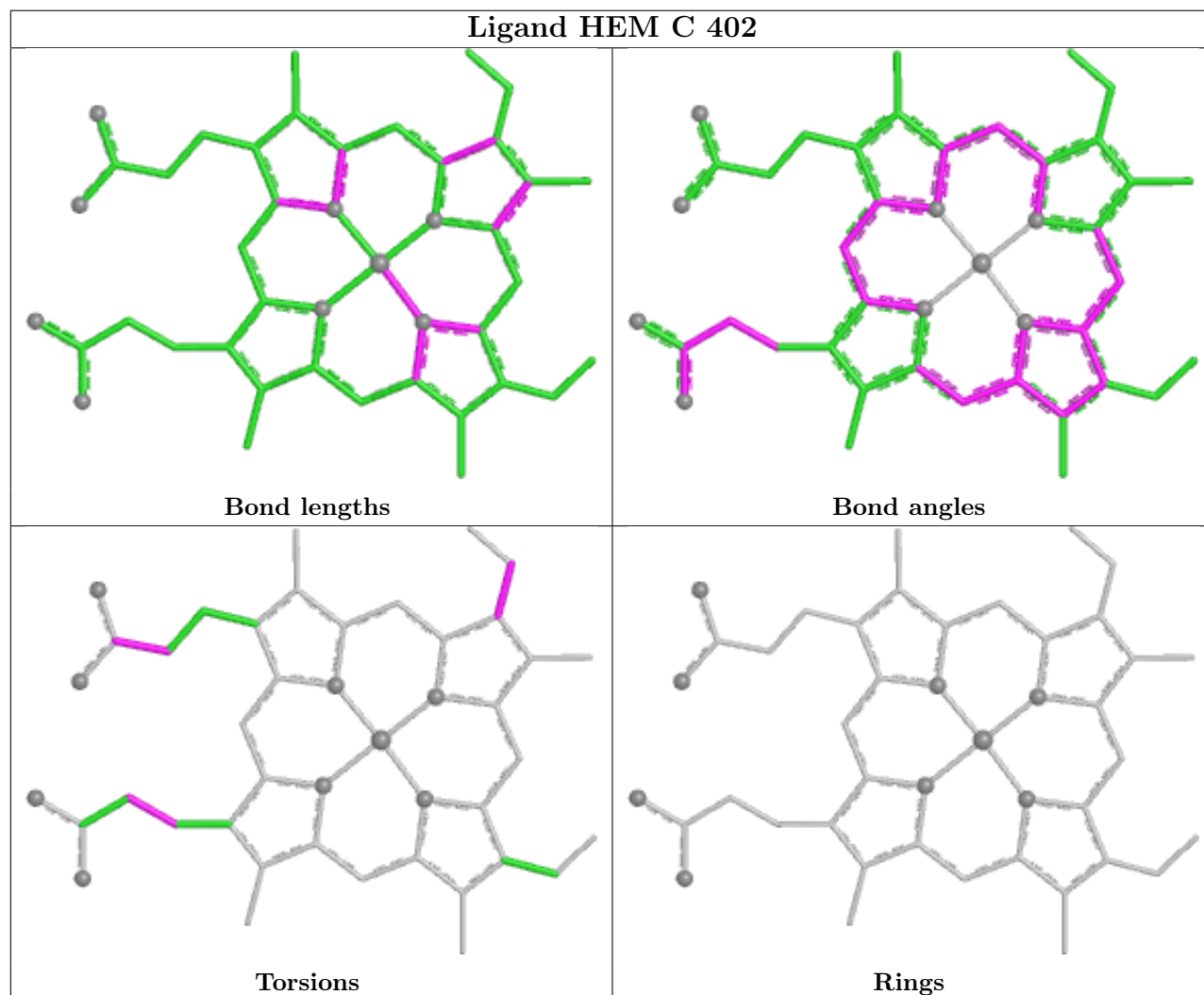
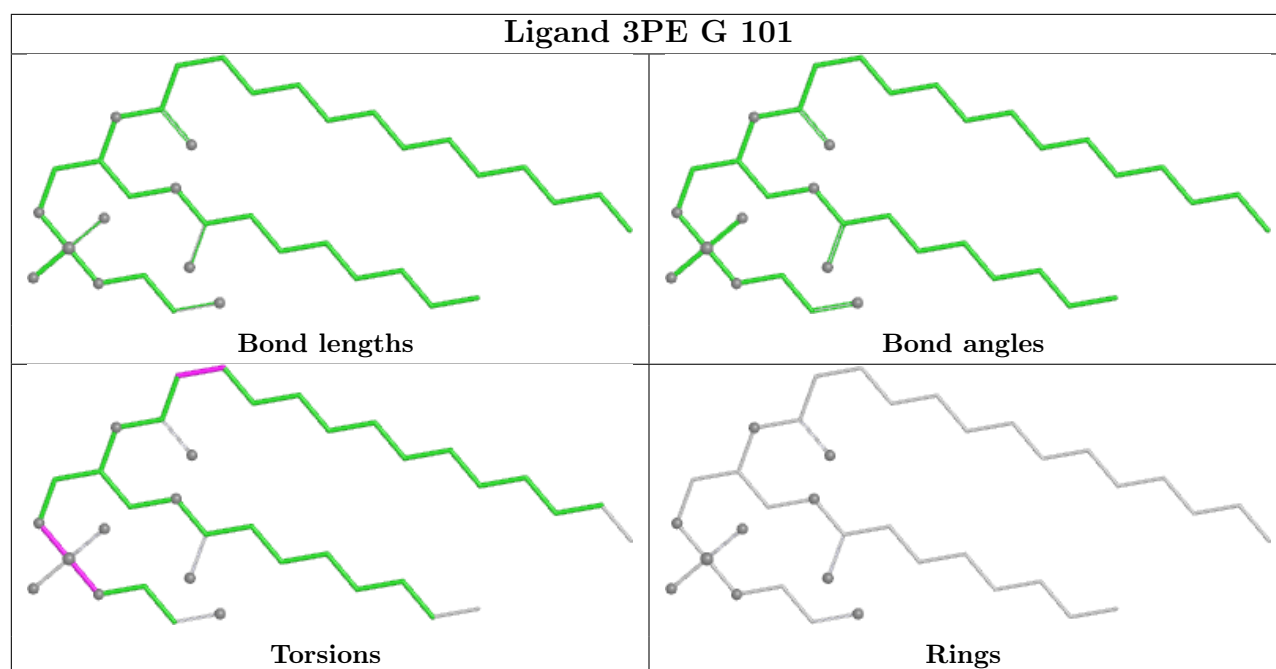


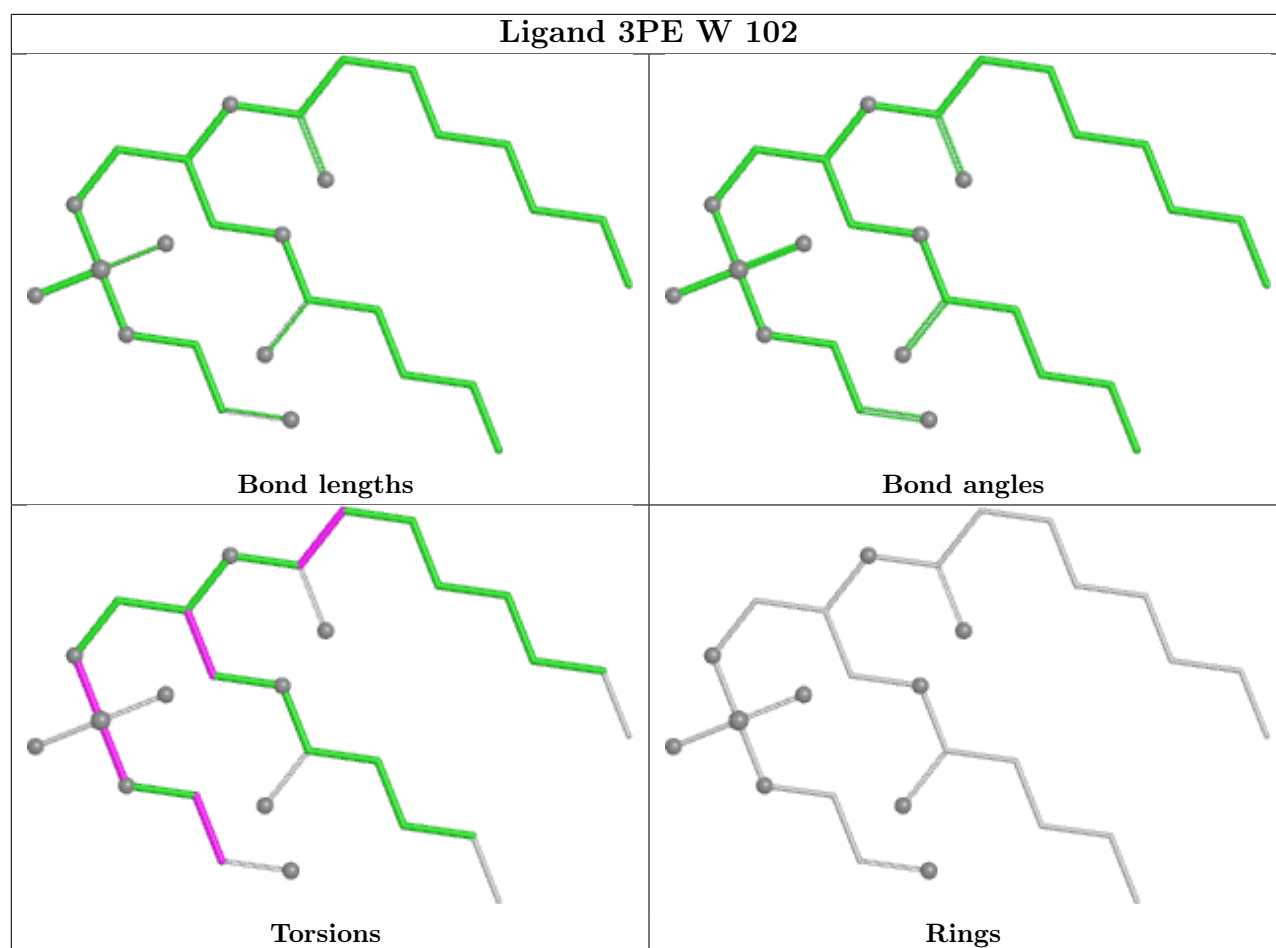


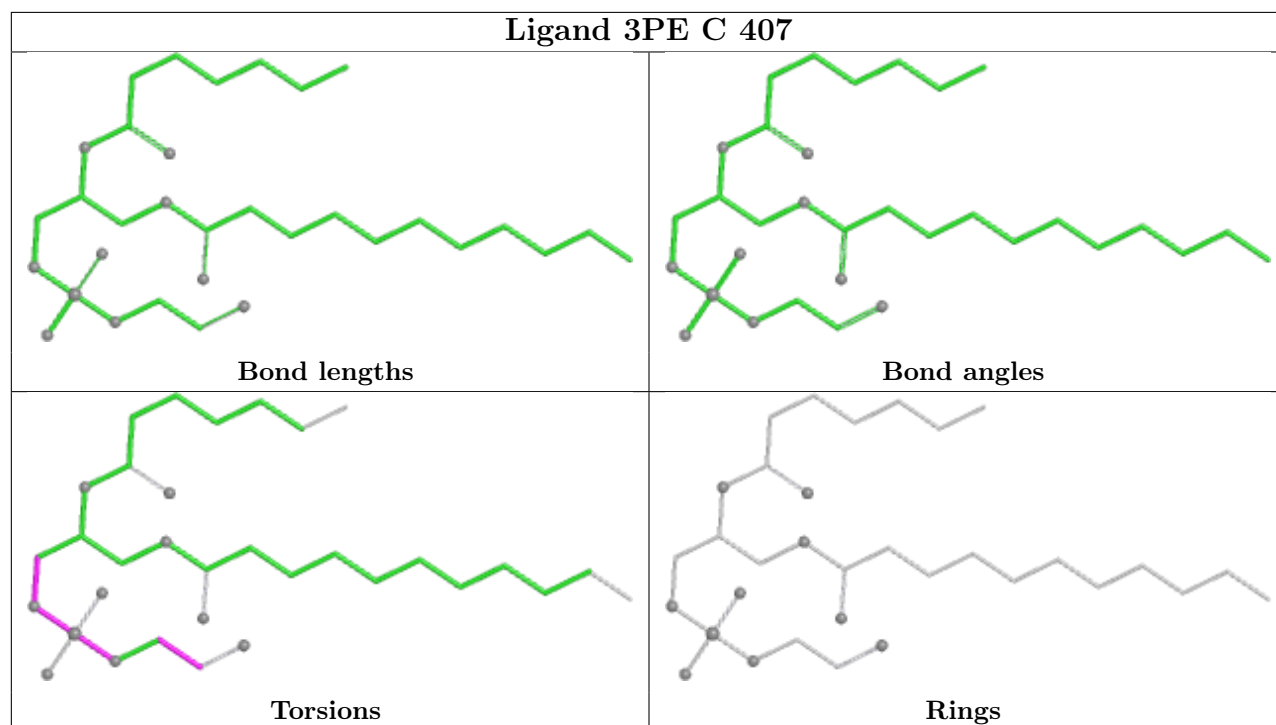
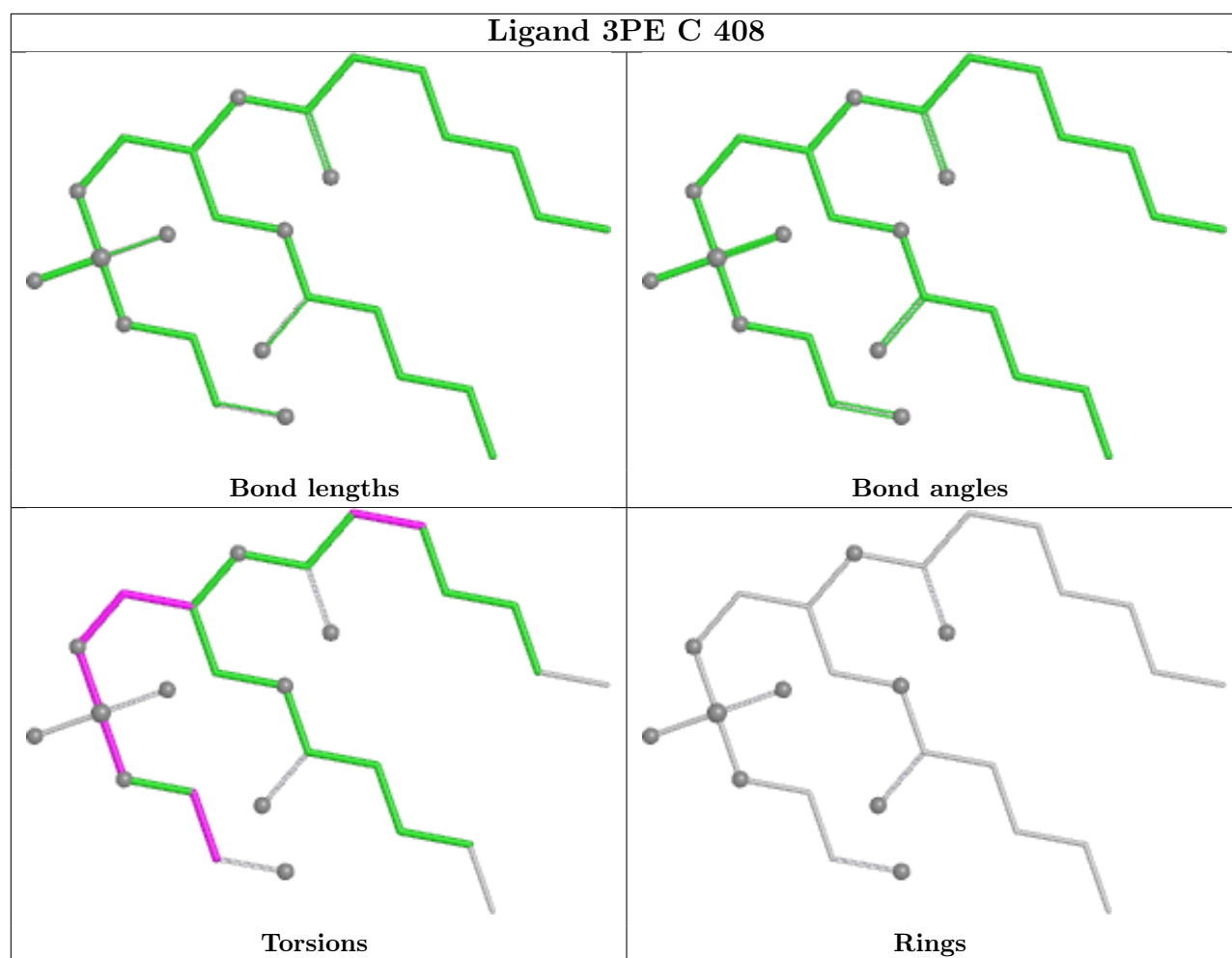


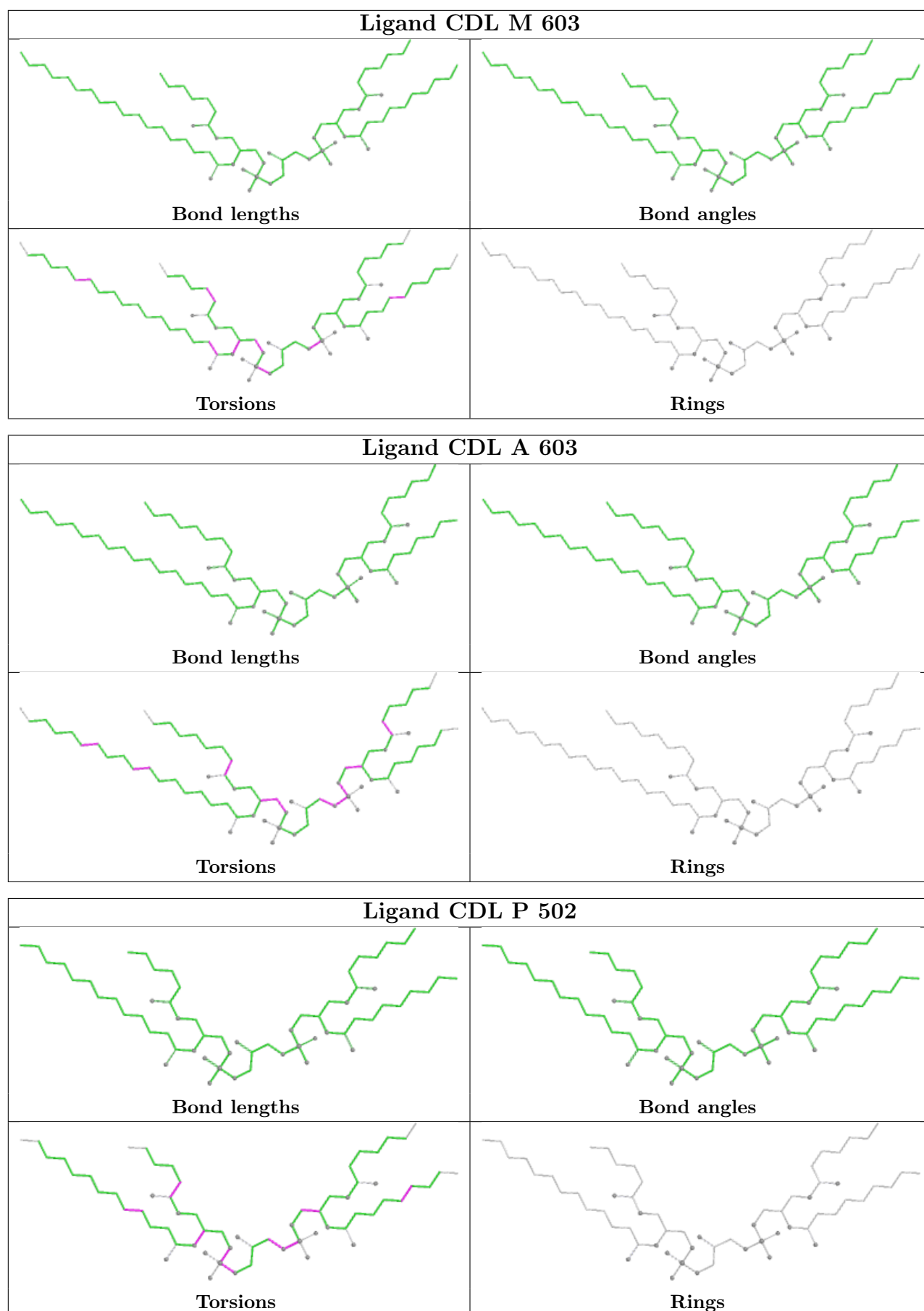


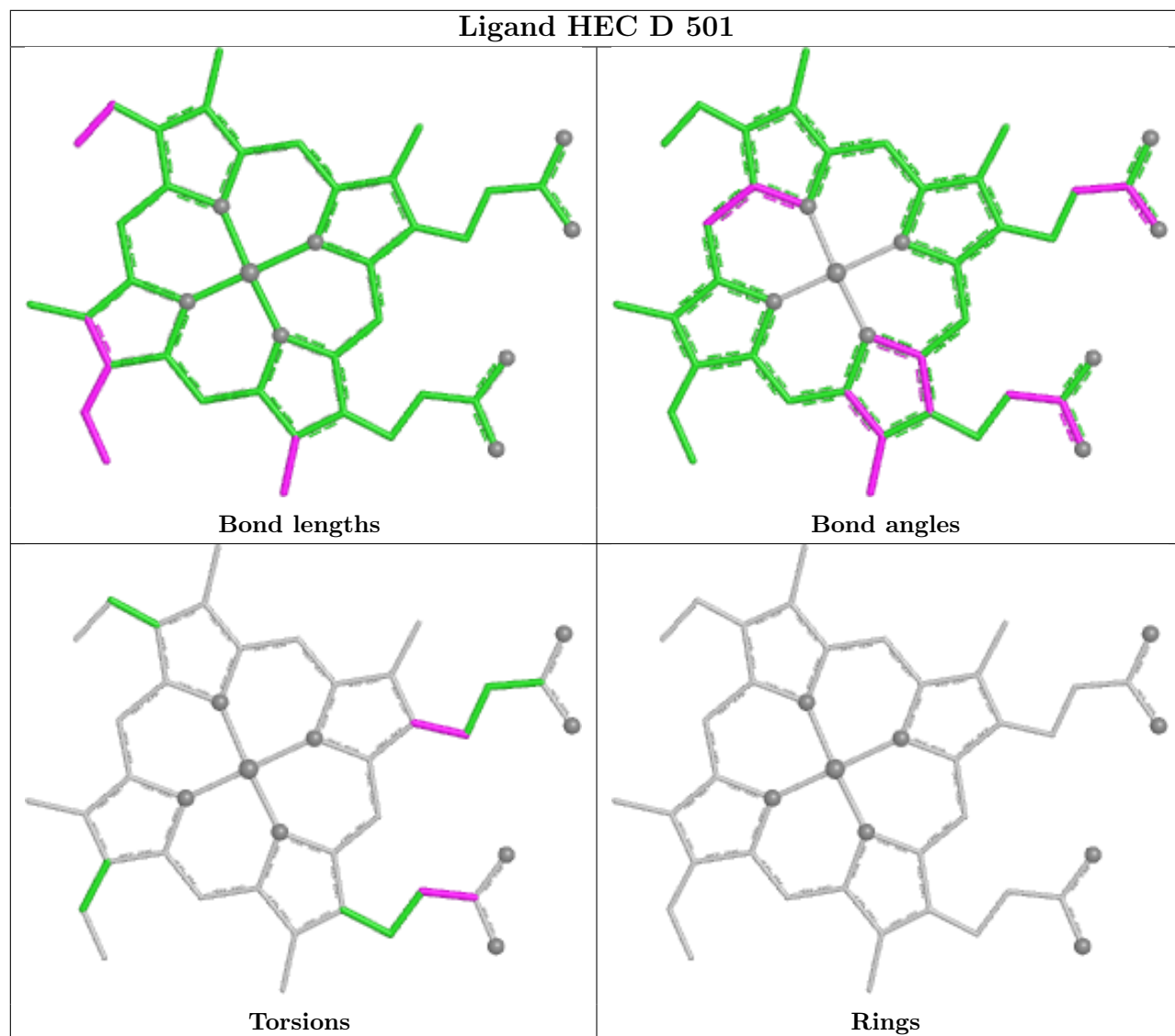


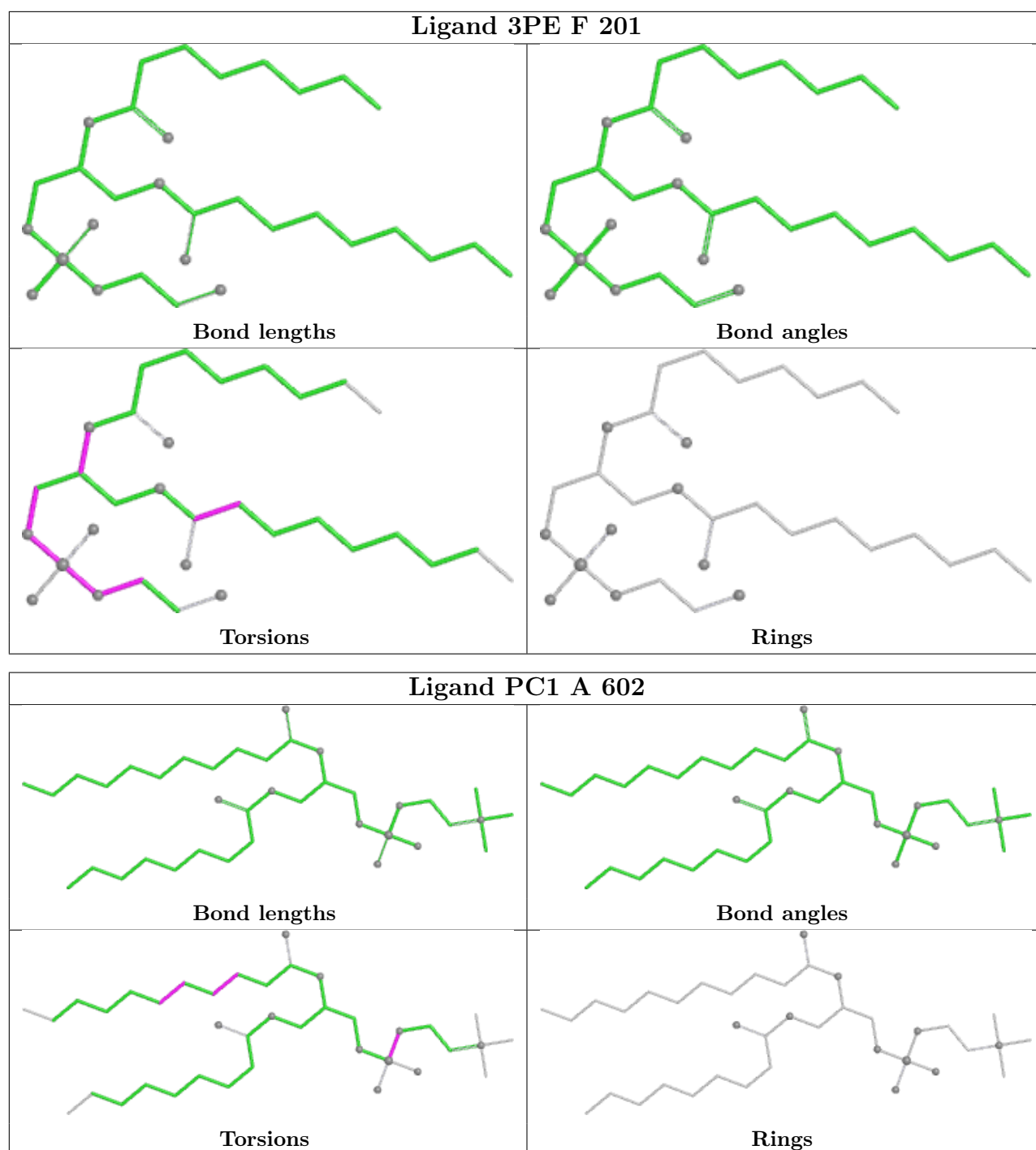


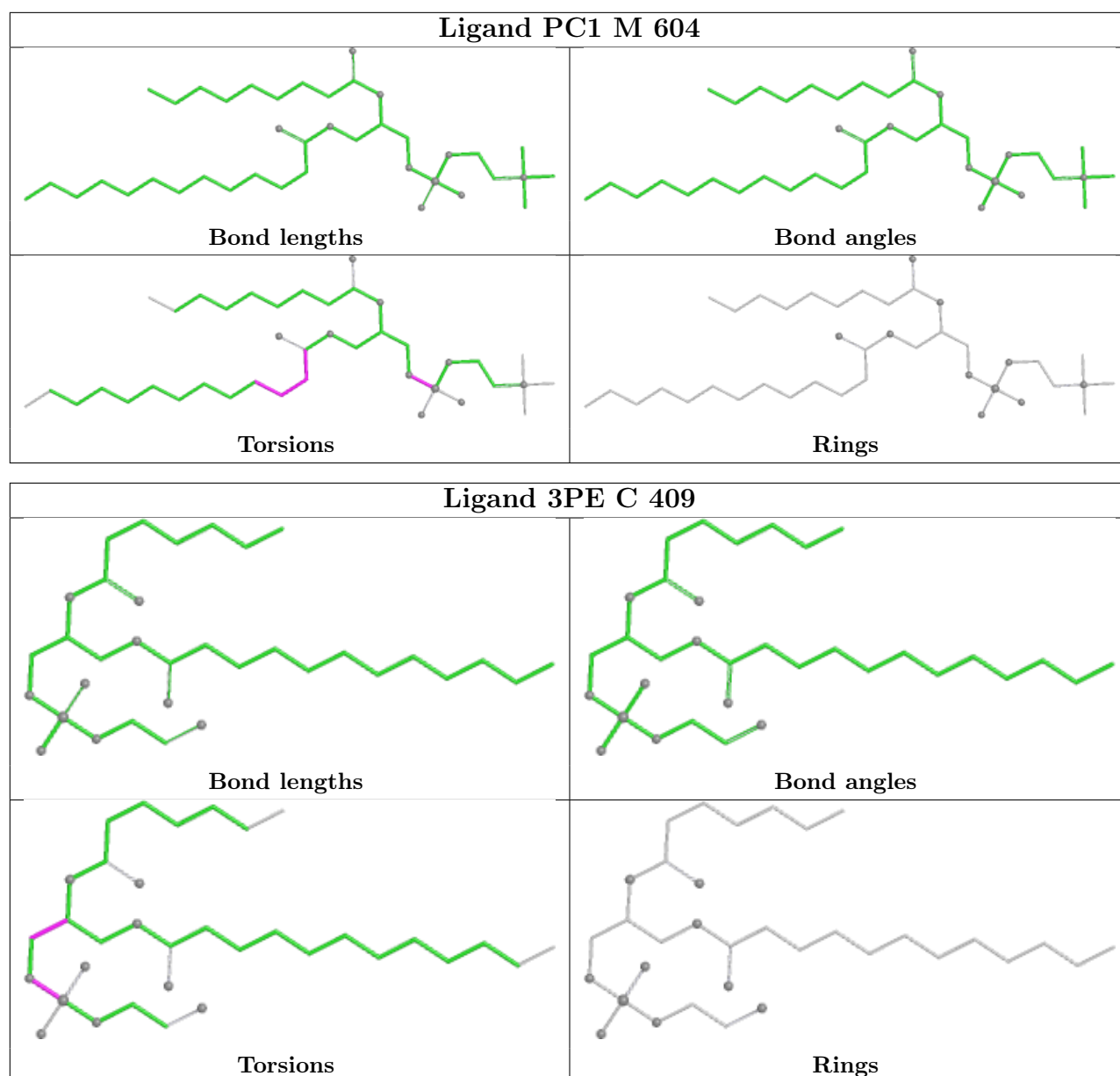












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

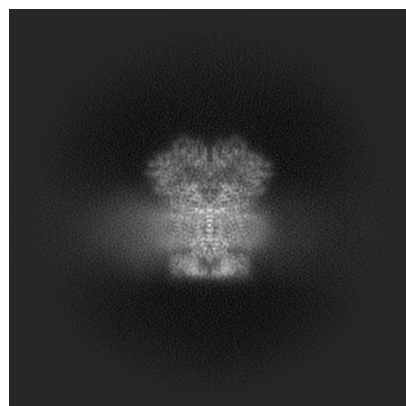
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22445. These allow visual inspection of the internal detail of the map and identification of artifacts.

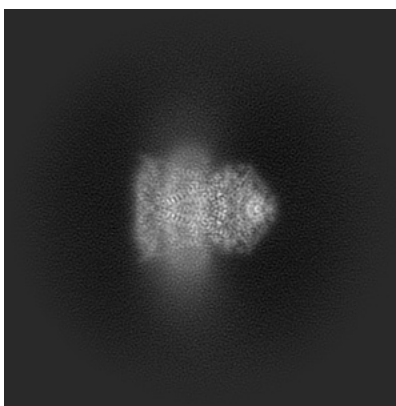
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

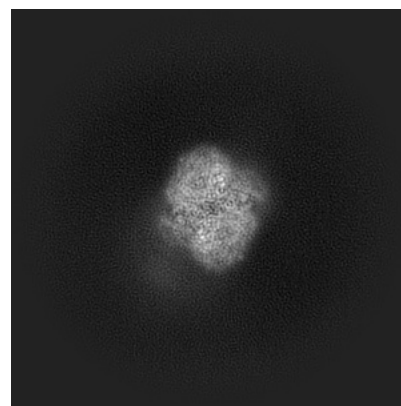
6.1.1 Primary map



X

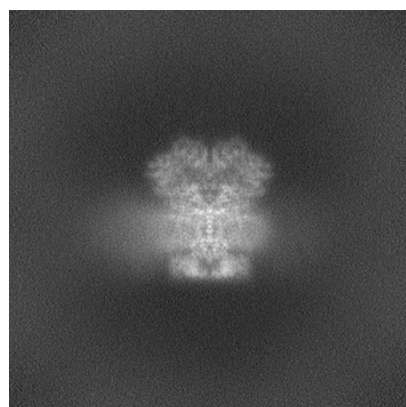


Y

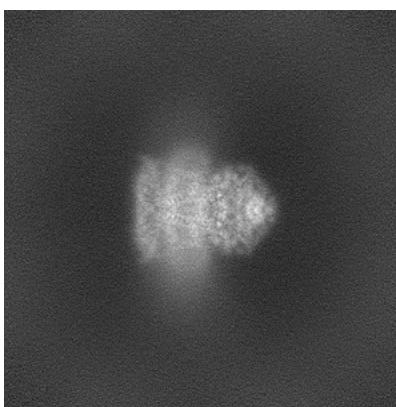


Z

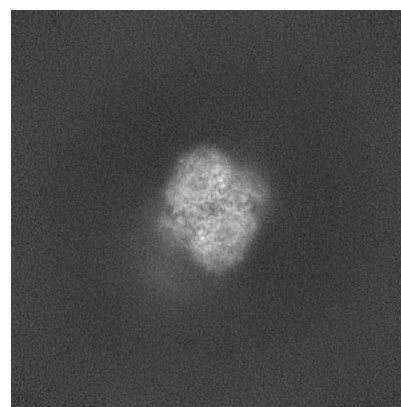
6.1.2 Raw map



X



Y

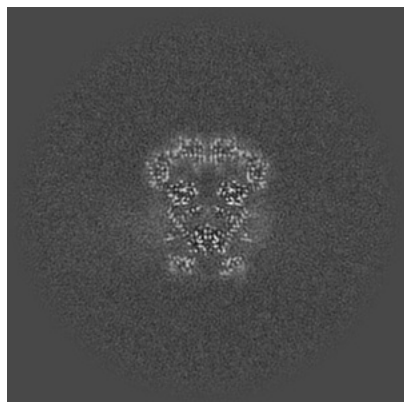


Z

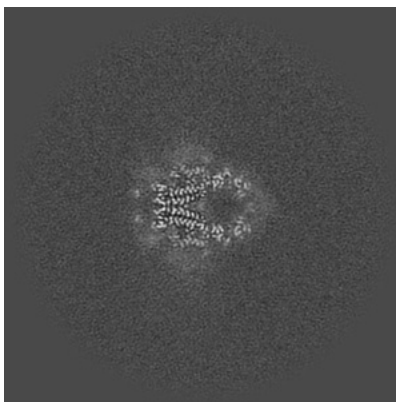
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

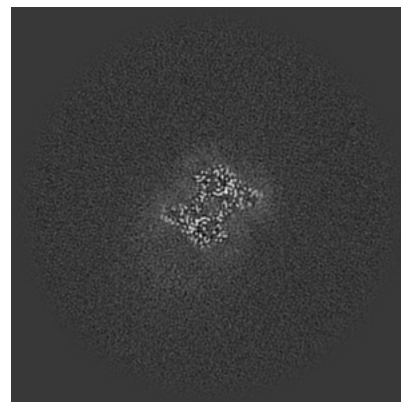
6.2.1 Primary map



X Index: 256

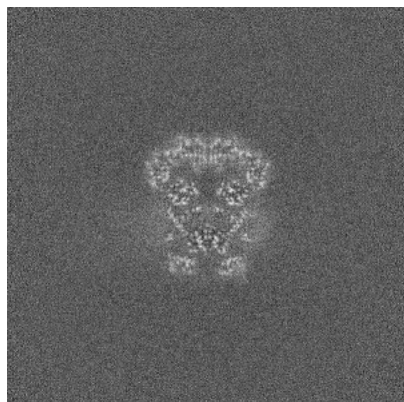


Y Index: 256

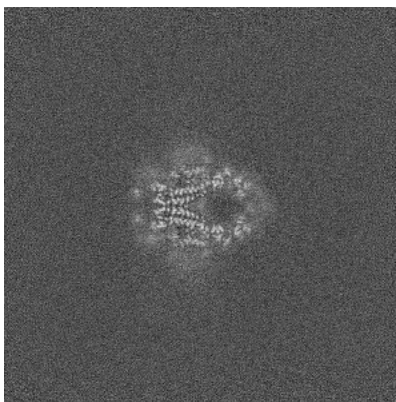


Z Index: 256

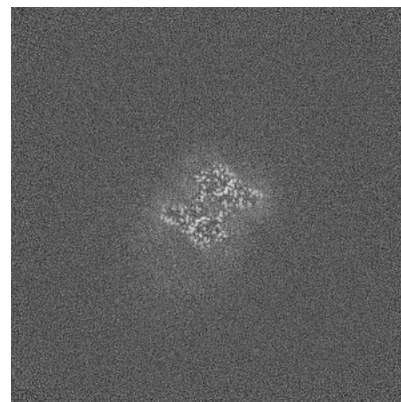
6.2.2 Raw map



X Index: 256



Y Index: 256

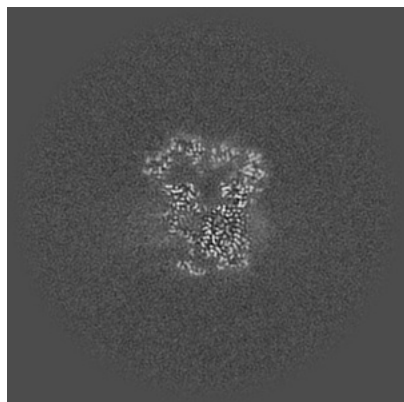


Z Index: 256

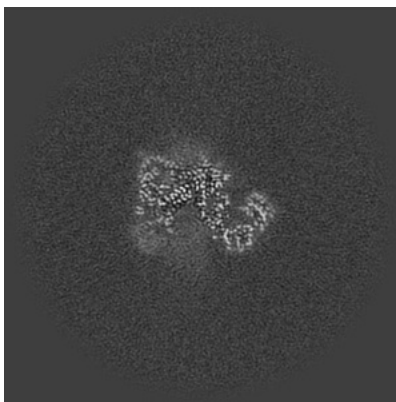
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

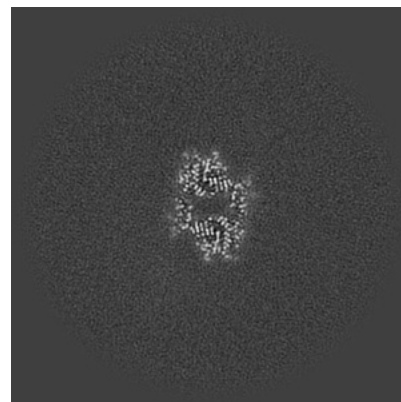
6.3.1 Primary map



X Index: 264

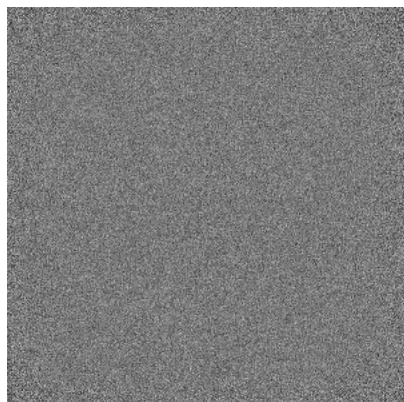


Y Index: 273

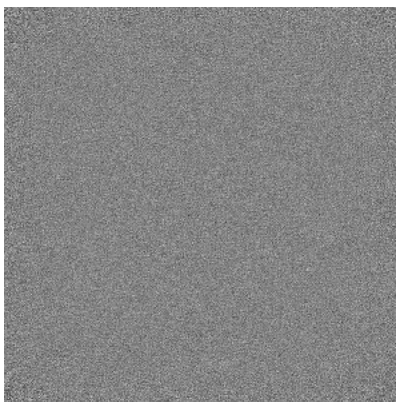


Z Index: 276

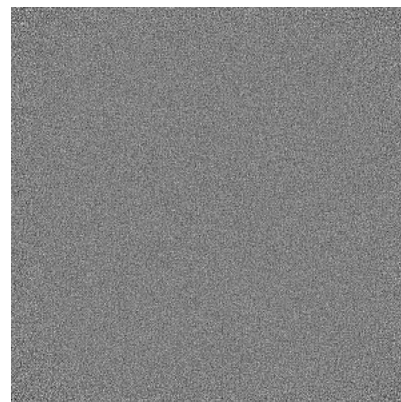
6.3.2 Raw map



X Index: 0



Y Index: 0

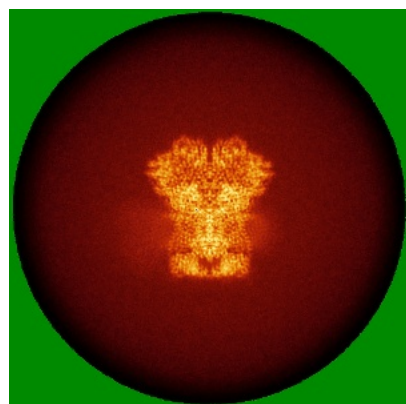


Z Index: 0

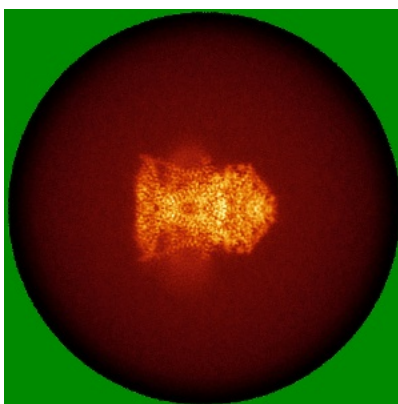
The images above show the largest variance slices of the map in three orthogonal directions.

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

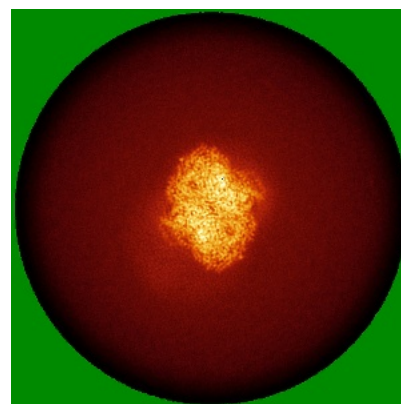
6.4.1 Primary map



X

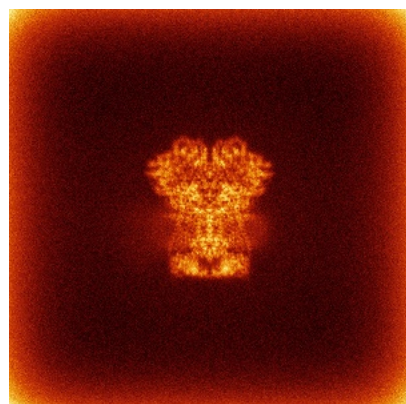


Y

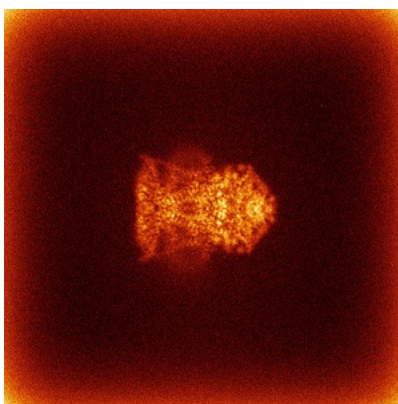


Z

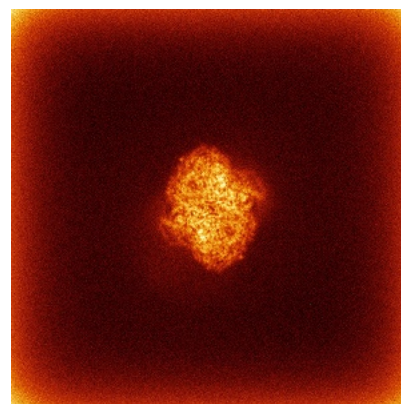
6.4.2 Raw map



X



Y

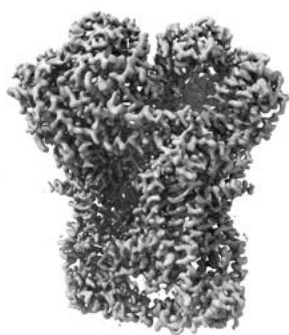


Z

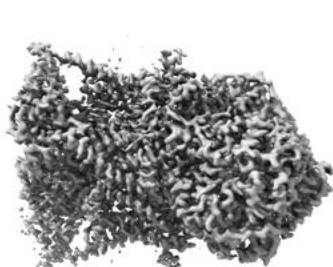
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

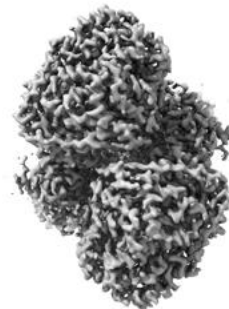
6.5.1 Primary map



X



Y



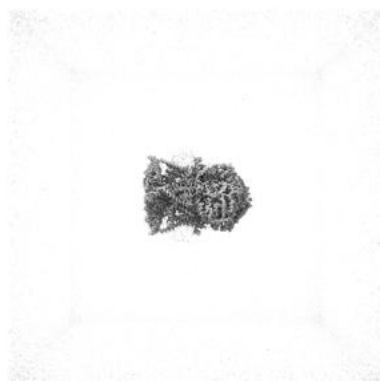
Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

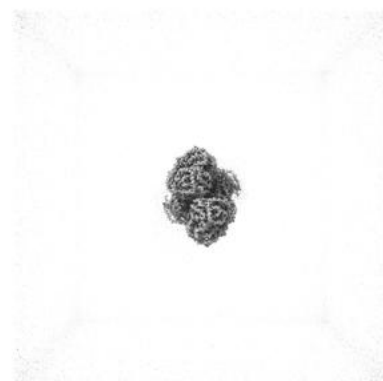
6.5.2 Raw map



X



Y



Z

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.

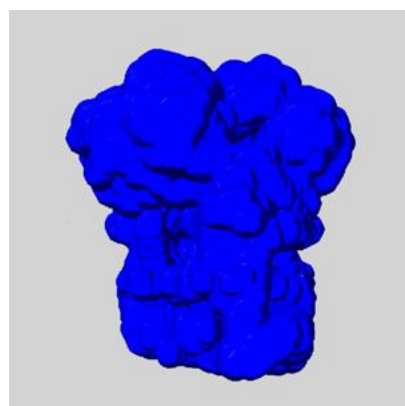
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

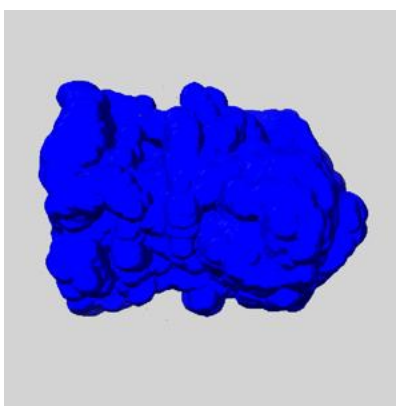
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

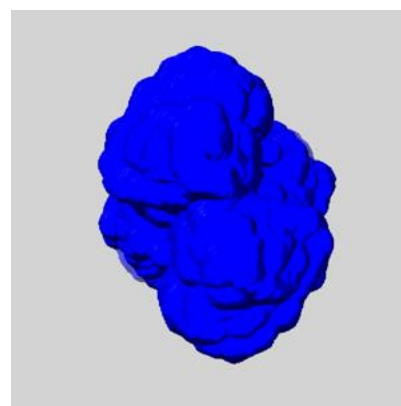
6.6.1 emd_22445_msk_1.map [i](#)



X



Y

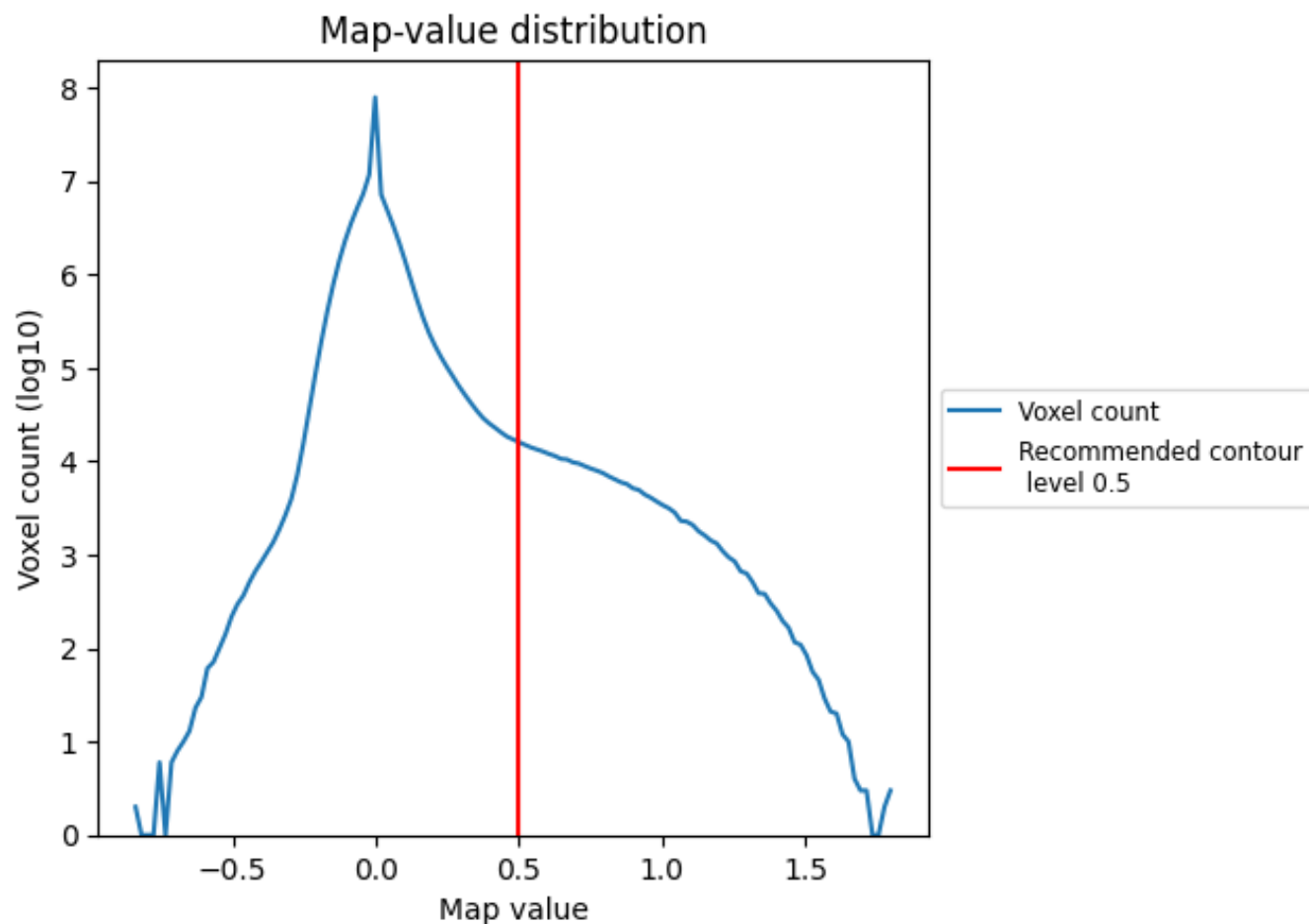


Z

7 Map analysis [i](#)

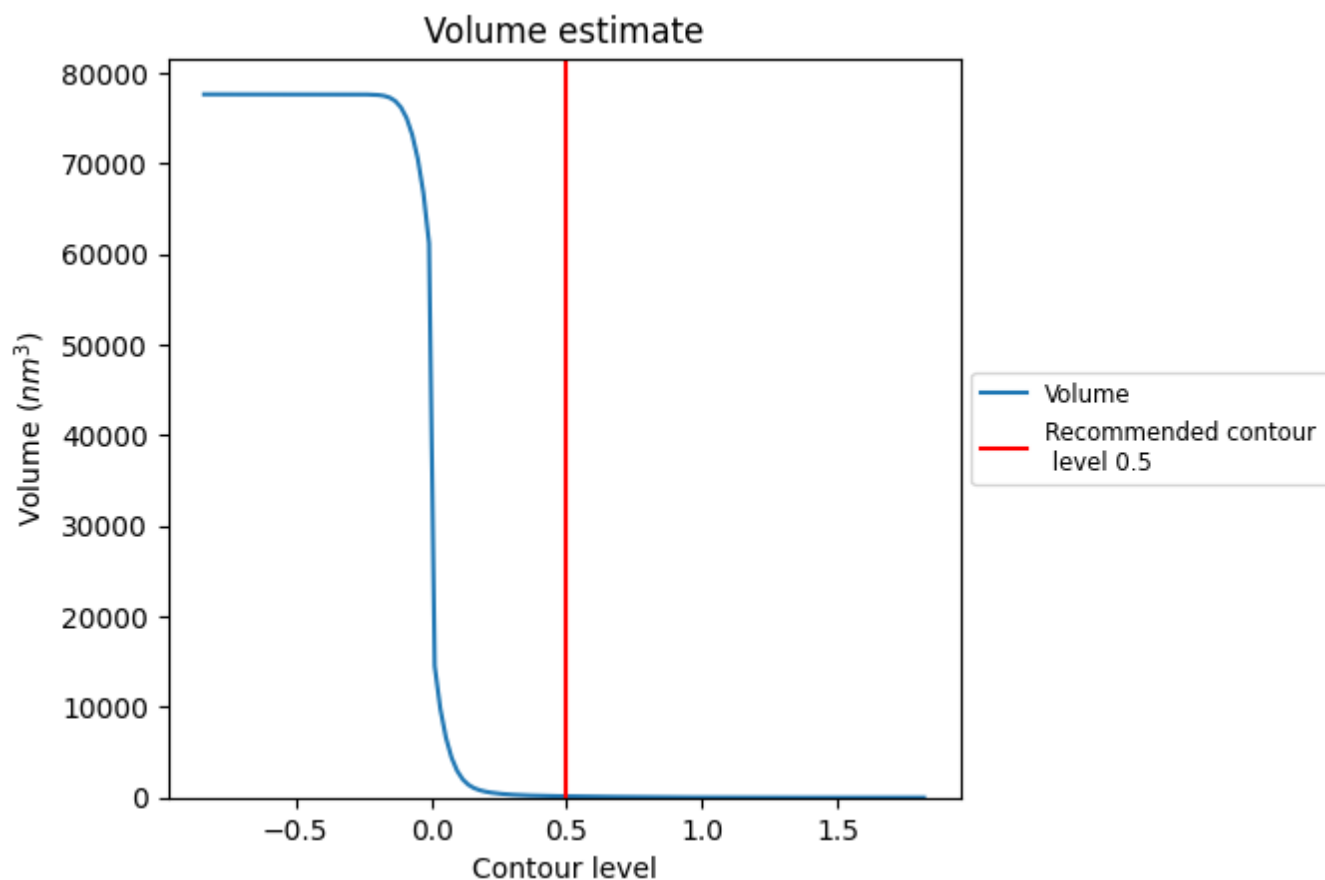
This section contains the results of statistical analysis of the map.

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.

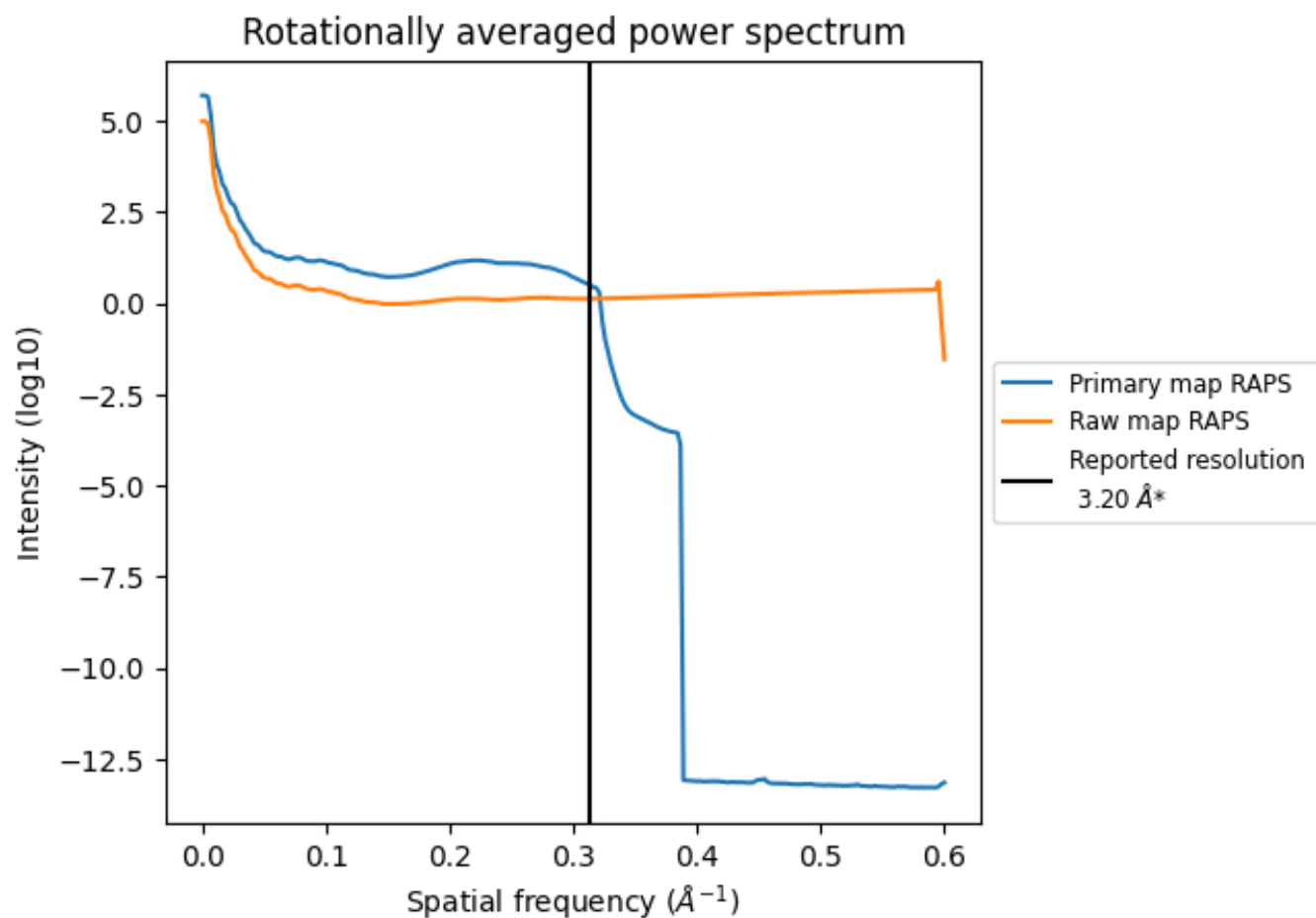
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 142 nm^3 ; this corresponds to an approximate mass of 128 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 ⓘ

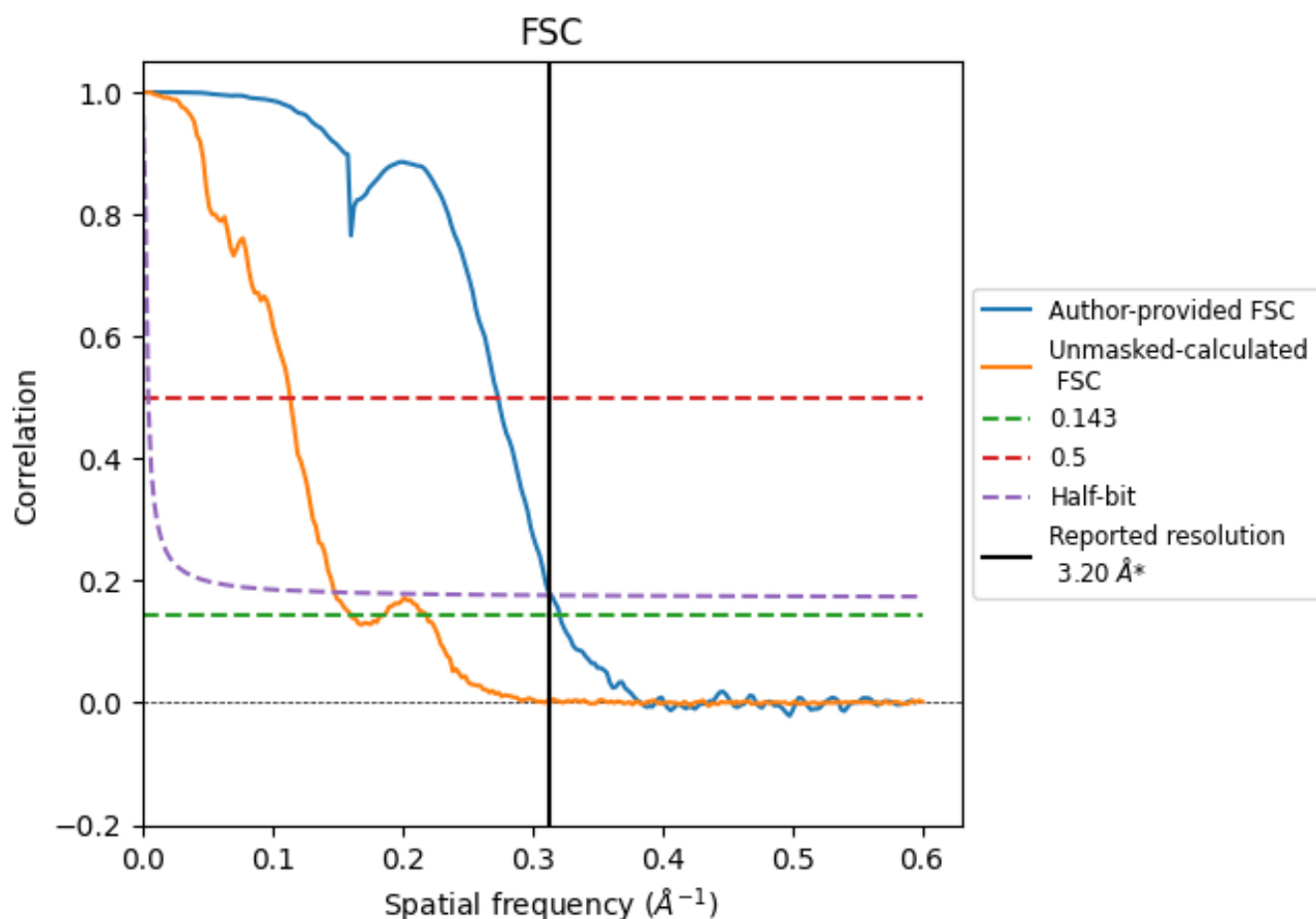


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

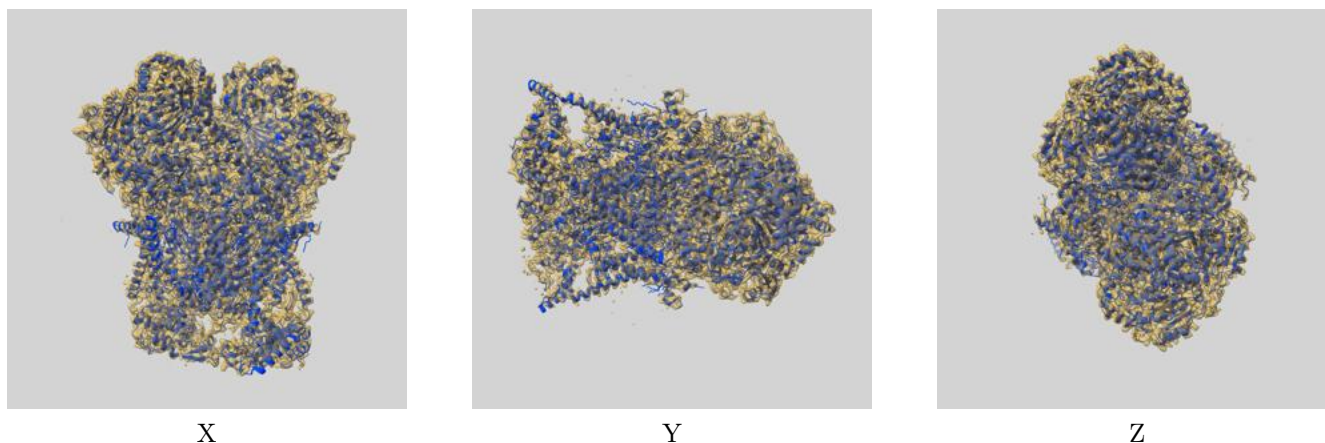
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.11	3.65	3.18
Unmasked-calculated*	6.23	8.79	6.76

*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 6.23 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

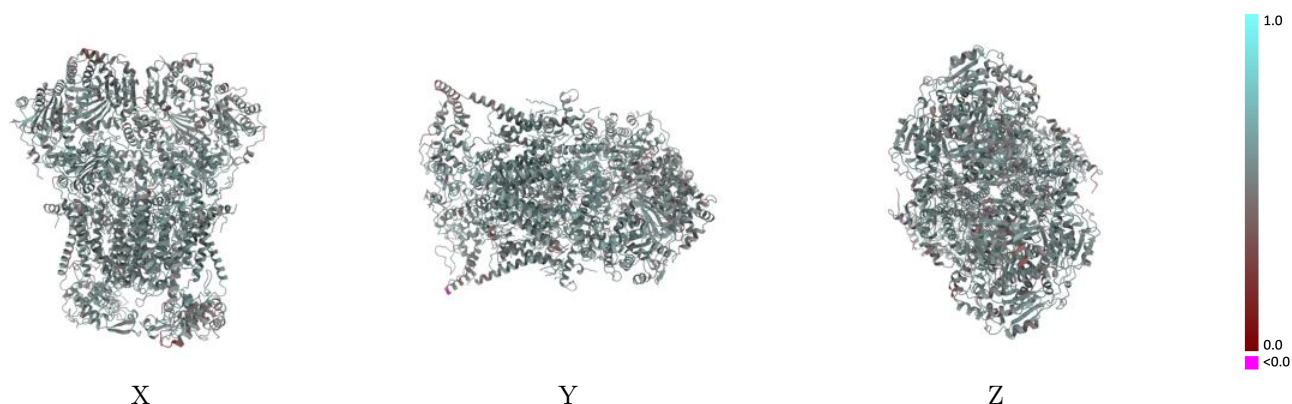
This section contains information regarding the fit between EMDB map EMD-22445 and PDB model 7JRG. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



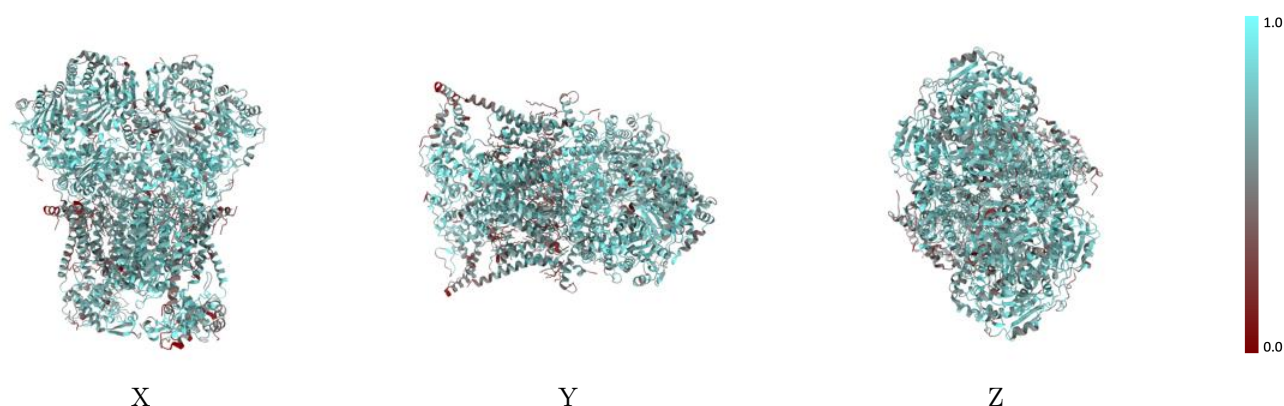
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



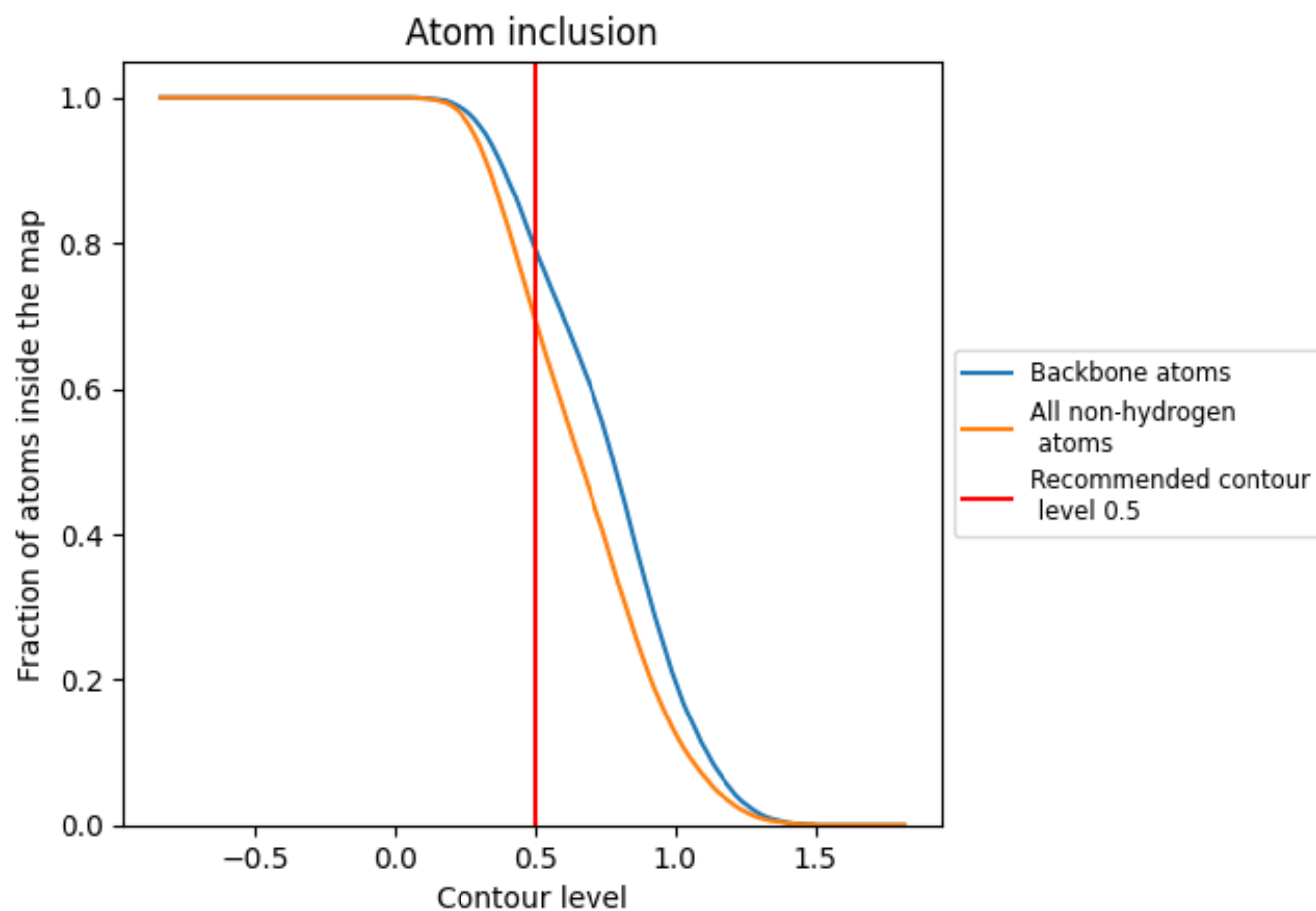
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 70% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6950	 0.5430
A	 0.7400	 0.5500
B	 0.6730	 0.5180
C	 0.7380	 0.5670
D	 0.7240	 0.5520
E	 0.5820	 0.5370
F	 0.7000	 0.5660
G	 0.5430	 0.5240
H	 0.4290	 0.4610
J	 0.5140	 0.5210
K	 0.3840	 0.4960
M	 0.7330	 0.5490
N	 0.6910	 0.5220
O	 0.7460	 0.5690
P	 0.7560	 0.5530
Q	 0.6660	 0.5420
R	 0.7610	 0.5620
S	 0.5390	 0.5330
T	 0.4560	 0.4520
V	 0.6200	 0.5390
W	 0.4710	 0.5040

