



wwPDB EM Validation Summary Report ⓘ

Aug 16, 2025 – 08:03 am BST

PDB ID : 9H8T / pdb_00009h8t
EMDB ID : EMD-51939
Title : Cryo-EM structure of the atovaquone-inhibited Complex III from the *Chloro-
cebus sabaeus* respirasome
Authors : Maclean, A.; Muhleip, A.
Deposited on : 2024-10-29
Resolution : 2.67 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.dev126
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

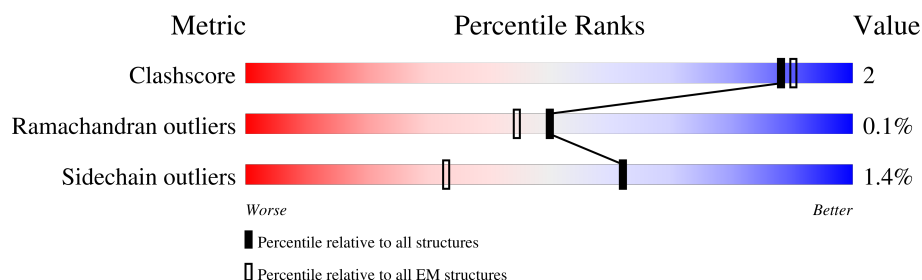
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.67 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	D	325	
1	d	325	
2	A	274	
2	T	274	
2	a	274	
3	G	111	
3	g	111	
4	C	82	

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Mol	Chain	Length	Quality of chain
4	c	82	
5	E	63	
5	e	63	
6	F	91	
6	f	91	
7	K	453	
7	k	453	
8	J	380	
8	j	380	
9	L	480	
9	l	480	
10	H	56	
10	h	56	

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 67324 atoms, of which 33779 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 Cytochrome c1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	D	239	Total	C	H	N	O	S	0	0
			3757	1219	1856	326	341	15		
1	d	239	Total	C	H	N	O	S	0	0
			3757	1219	1856	326	341	15		

- Molecule 2 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	A	196	Total	C	H	N	O	S	0	0
			3044	968	1512	267	289	8		
2	T	77	Total	C	H	N	O	S	0	0
			1142	349	591	102	98	2		
2	a	196	Total	C	H	N	O	S	0	0
			3044	968	1512	267	289	8		

- Molecule 3 is a protein called Cytochrome b-c1 complex subunit 7.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	G	104	Total	C	H	N	O	S	0	0
			1803	580	895	160	166	2		
3	g	104	Total	C	H	N	O	S	0	0
			1803	580	895	160	166	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	43	ASP	GLU	conflict	UNP A0A0D9RJ49
g	43	ASP	GLU	conflict	UNP A0A0D9RJ49

- Molecule 4 is a protein called Cytochrome b-c1 complex subunit 8.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	C	81	Total	C	H	N	O	S	0	0
			1367	439	686	124	117	1		
4	c	81	Total	C	H	N	O	S	0	0
			1367	439	686	124	117	1		

- Molecule 5 is a protein called Complex III subunit 9.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	56	Total	C	H	N	O		0	0
			911	300	458	76	77			
5	e	56	Total	C	H	N	O		0	0
			911	300	458	76	77			

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

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	67	Total	C	H	N	O	S	0	0
			1093	338	539	99	111	6		
6	f	67	Total	C	H	N	O	S	0	0
			1093	338	539	99	111	6		

- Molecule 7 is a protein called Ubiquinol-cytochrome c reductase core protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	K	418	Total	C	H	N	O	S	0	0
			6326	1993	3161	554	610	8		
7	k	418	Total	C	H	N	O	S	0	0
			6326	1993	3161	554	610	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	100	THR	ILE	conflict	UNP A0A0D9R493
K	439	VAL	ALA	conflict	UNP A0A0D9R493
k	100	THR	ILE	conflict	UNP A0A0D9R493
k	439	VAL	ALA	conflict	UNP A0A0D9R493

- Molecule 8 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	J	378	Total	C	H	N	O	S	0	0
			6117	2030	3090	472	507	18		

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Mol	Chain	Residues	Atoms						AltConf	Trace
8	j	378	Total	C	H	N	O	S	0	0
			6117	2030	3090	472	507	18		

- | Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|---------|---------|-------|
| 9 | L | 423 | Total
6533 | C
2075 | H
3231 | N
574 | O
633 | S
20 | 0 | 0 |
| 9 | 1 | 423 | Total
6533 | C
2075 | H
3231 | N
574 | O
633 | S
20 | 0 | 0 |

- | Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|---------|---------|--------|---------|-------|
| 10 | H | 45 | Total
748 | C
251 | H
374 | N
65 | O
57 | S
1 | 0 | 0 |
| 10 | h | 45 | Total
748 | C
251 | H
374 | N
65 | O
57 | S
1 | 0 | 0 |

-
- The chemical structure of HEC (Hydroxyethylchlorin) is shown. It features a central iron atom (Fe) coordinated by four nitrogen atoms (N) in a porphyrin-like ring. The structure includes various side chains and a central hydroxyl group (OH). The atoms are labeled with green and red text, and the bonds are colored green and red.

Mol	Chain	Residues	Atoms						AltConf
11	D	1	Total	C	Fe	H	N	O	0
			75	34	1	32	4	4	



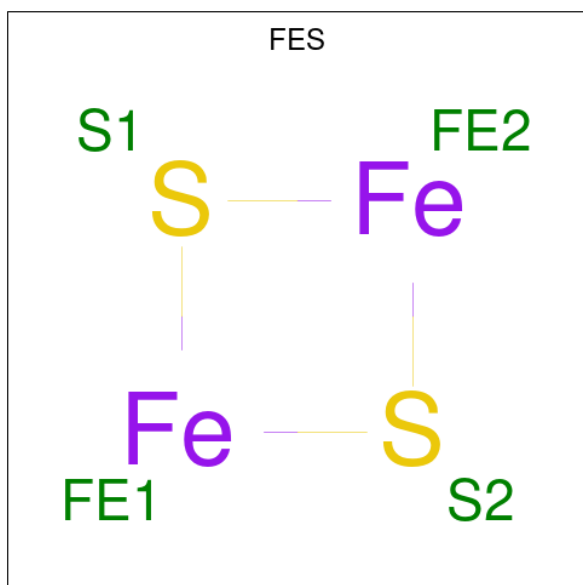
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Mol	Chain	Residues	Atoms						AltConf
11	d	1	Total	C	Fe	H	N	O	0
			75	34	1	32	4	4	

- Molecule 12 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
12	D	1	Total	Zn	0
			1	1	
12	d	1	Total	Zn	0
			1	1	

- Molecule 13 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



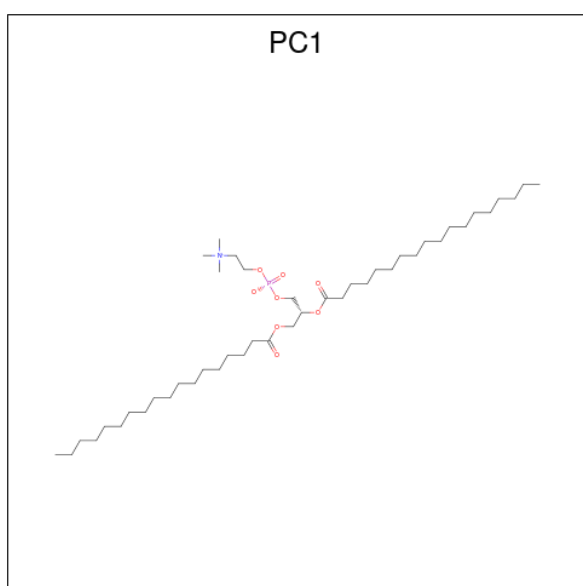
Mol	Chain	Residues	Atoms			AltConf
13	A	1	Total	Fe	S	0
			4	2	2	
13	a	1	Total	Fe	S	0
			4	2	2	

- Molecule 14 is CARDIOLIPIN (CCD ID: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



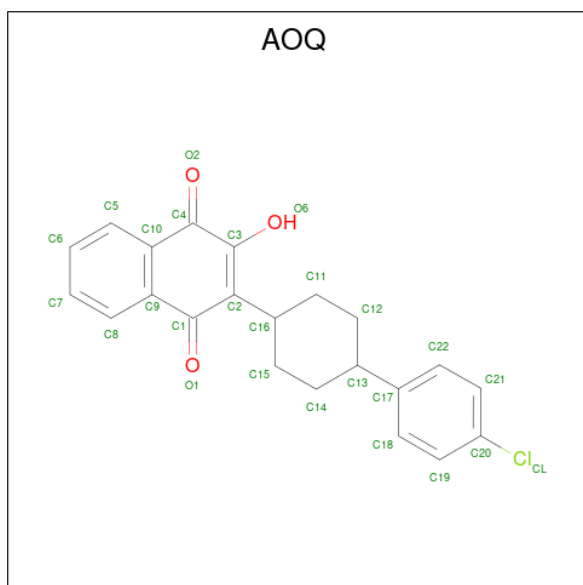
Mol	Chain	Residues	Atoms					AltConf
14	C	1	Total	C	H	O	P	0
			256	81	156	17	2	
14	L	1	Total	C	H	O	P	0
			256	81	156	17	2	
14	c	1	Total	C	H	O	P	0
			256	81	156	17	2	
14	l	1	Total	C	H	O	P	0
			256	81	156	17	2	

- Molecule 15 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$).



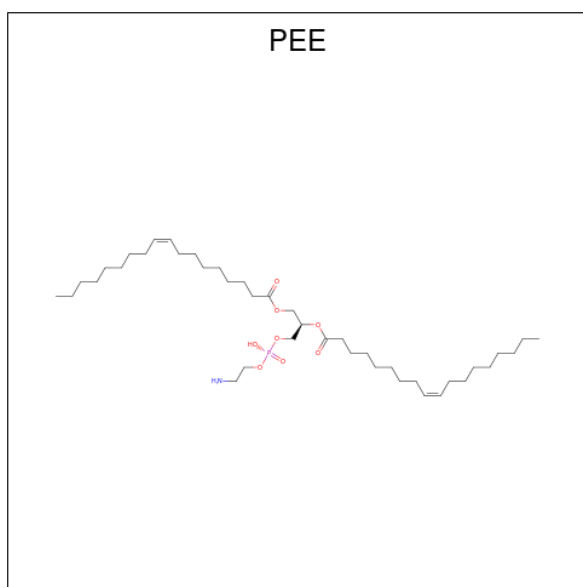
Mol	Chain	Residues	Atoms						AltConf
15	E	1	Total 142	C 44	H 88	N 1	O 8	P 1	0
15	e	1	Total 142	C 44	H 88	N 1	O 8	P 1	0

- Molecule 16 is 2-[trans-4-(4-chlorophenyl)cyclohexyl]-3-hydroxynaphthalene-1,4-dione (CCD ID: AOQ) (formula: $C_{22}H_{19}ClO_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
16	J	1	Total	C	Cl	H	O	0
			44	22	1	18	3	
16	j	1	Total	C	Cl	H	O	0
			44	22	1	18	3	

- Molecule 17 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: $C_{41}H_{78}NO_8P$).



Mol	Chain	Residues	Atoms						AltConf
17	J	1	Total	C	H	N	O	P	0
			134	41	83	1	8	1	
17	J	1	Total	C	H	N	O	P	0
			134	41	83	1	8	1	
17	L	1	Total	C	H	N	O	P	0
			134	41	83	1	8	1	
17	j	1	Total	C	H	N	O	P	0
			134	41	83	1	8	1	
17	j	1	Total	C	H	N	O	P	0
			134	41	83	1	8	1	
17	l	1	Total	C	H	N	O	P	0
			134	41	83	1	8	1	

- Molecule 18 is 2-[4-(4-CHLOROPHENYL)CYCLOHEXYLIDENE]-3,4-DIHYDROXY-1 (2H)-NAPHTHALENONE (CCD ID: AFI) (formula: C₂₂H₁₉ClO₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
18	J	1	Total 45	C 22	Cl 1	H 19	O 3	0
18	j	1	Total 45	C 22	Cl 1	H 19	O 3	0

- Molecule 19 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $\text{C}_{34}\text{H}_{32}\text{FeN}_4\text{O}_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
19	J	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0

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Mol	Chain	Residues	Atoms						AltConf
19	J	1	Total	C	Fe	H	N	O	0
			73	34	1	30	4	4	
19	j	1	Total	C	Fe	H	N	O	0
			73	34	1	30	4	4	
19	j	1	Total	C	Fe	H	N	O	0
			73	34	1	30	4	4	

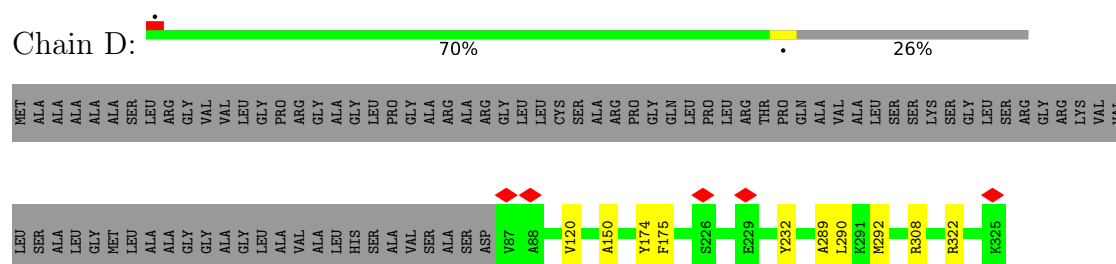
- Molecule 20 is water.

Mol	Chain	Residues	Atoms			AltConf
20	J	7	Total	H	O	0
			21	14	7	
20	j	7	Total	H	O	0
			21	14	7	

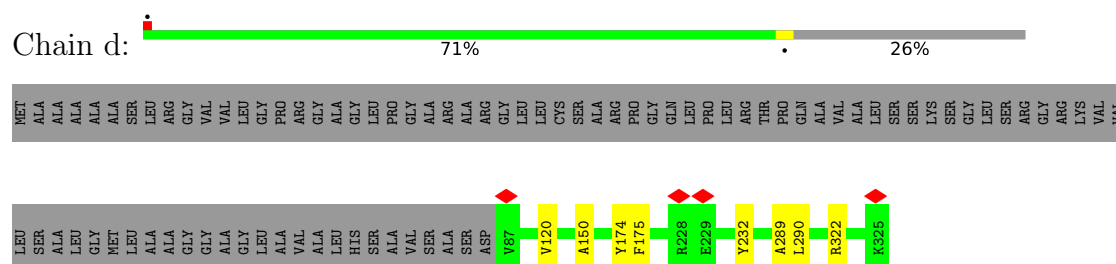
3 Residue-property plots

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.

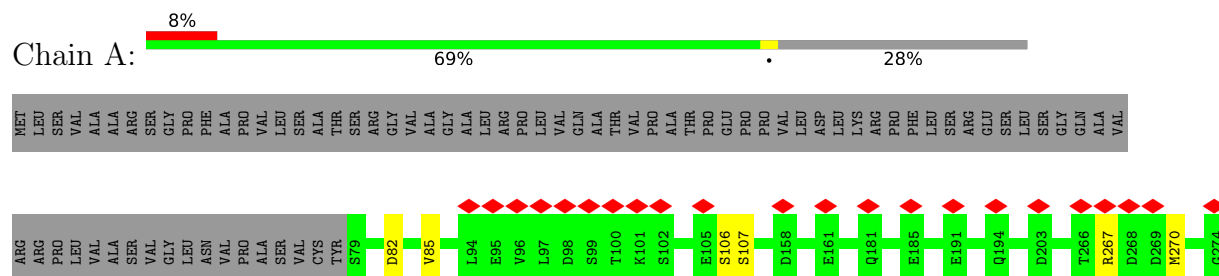
- Molecule 1: Cytochrome c1



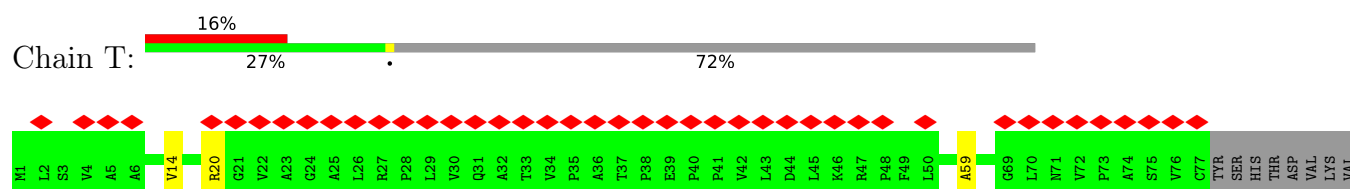
- Molecule 1: Cytochrome c1



- Molecule 2: Cytochrome b-c1 complex subunit Rieske, mitochondrial

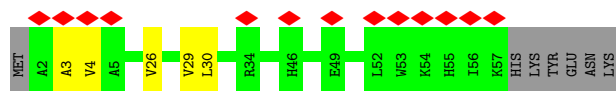
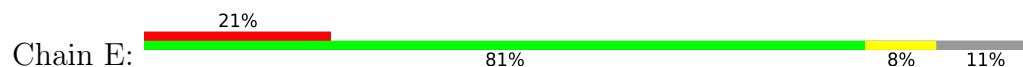


- Molecule 2: Cytochrome b-c1 complex subunit Rieske, mitochondrial

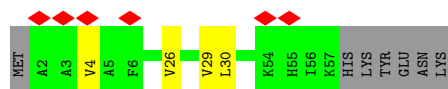
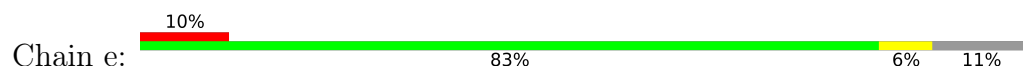




- Molecule 5: Complex III subunit 9



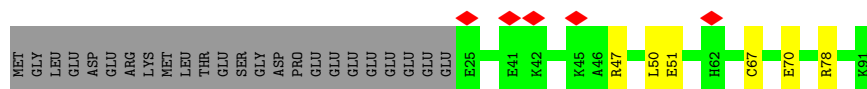
- Molecule 5: Complex III subunit 9



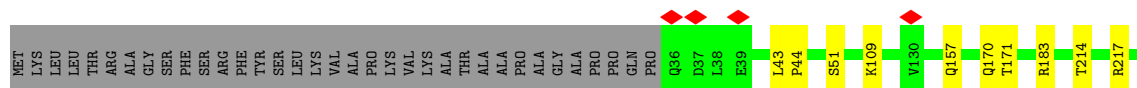
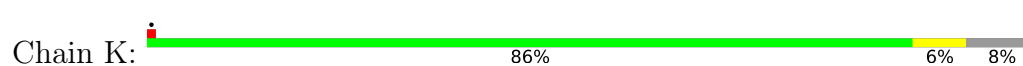
- Molecule 6: Cytochrome b-c1 complex subunit 6



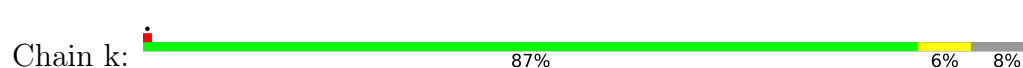
- Molecule 6: Cytochrome b-c1 complex subunit 6

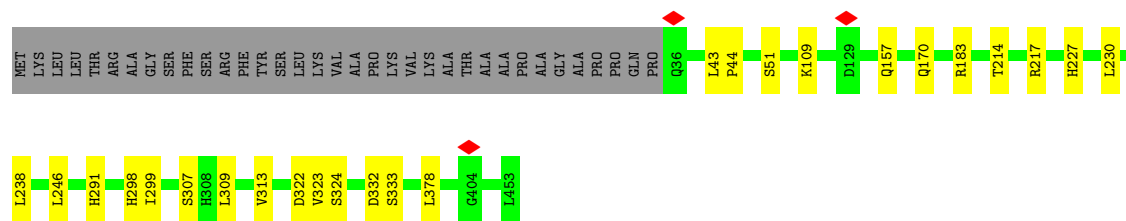


- Molecule 7: Ubiquinol-cytochrome c reductase core protein 2

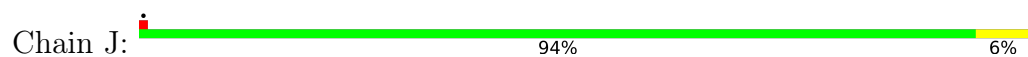


- Molecule 7: Ubiquinol-cytochrome c reductase core protein 2

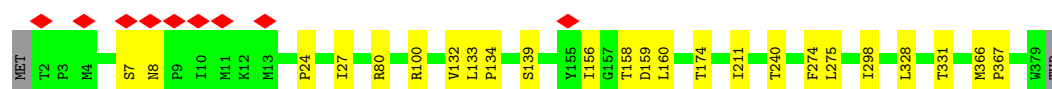
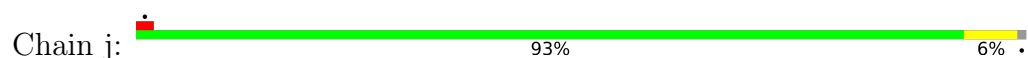




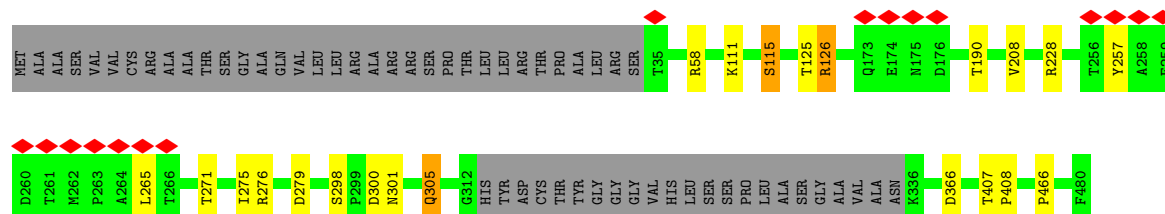
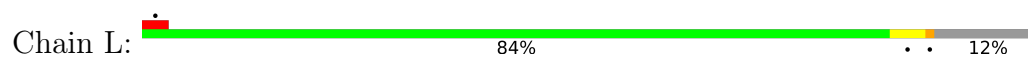
- Molecule 8: Cytochrome b



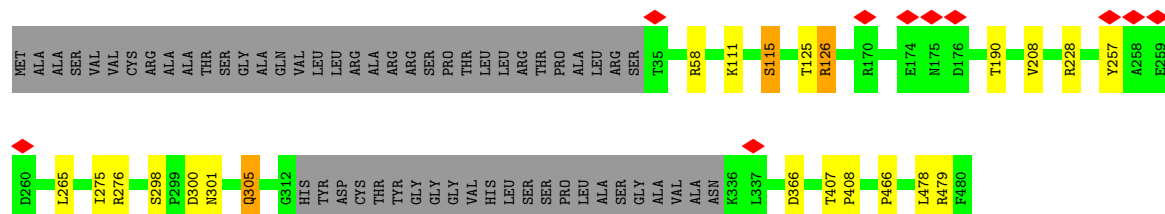
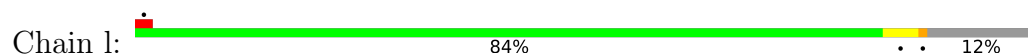
- Molecule 8: Cytochrome b



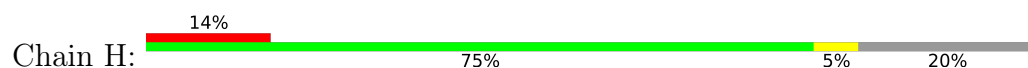
- Molecule 9: Ubiquinol-cytochrome c reductase core protein 1

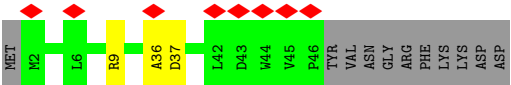


- Molecule 9: Ubiquinol-cytochrome c reductase core protein 1

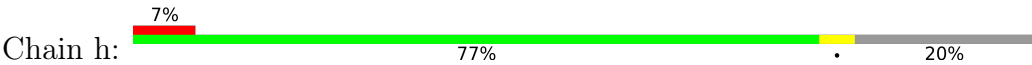


- Molecule 10: UQCRB





• Molecule 10: UQCRB



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	637526	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 ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	8.553	Depositor
Minimum map value	-4.276	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.155	Depositor
Recommended contour level	0.8	Depositor
Map size (Å)	592.482, 592.482, 592.482	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.98747, 0.98747, 0.98747	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEE, CDL, PC1, AOQ, FES, HEM, ZN, AFI, HEC

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	D	0.21	0/1961	0.47	0/2662
1	d	0.21	0/1961	0.47	0/2662
2	A	0.20	0/1567	0.48	0/2124
2	T	0.19	0/562	0.41	0/770
2	a	0.21	0/1567	0.48	0/2124
3	G	0.29	0/929	0.52	0/1245
3	g	0.29	0/929	0.52	0/1245
4	C	0.23	0/699	0.51	0/941
4	c	0.24	0/699	0.52	0/941
5	E	0.22	0/464	0.53	0/626
5	e	0.22	0/464	0.54	0/626
6	F	0.19	0/560	0.47	0/750
6	f	0.19	0/560	0.47	0/750
7	K	0.22	0/3221	0.54	0/4366
7	k	0.22	0/3221	0.54	0/4366
8	J	0.25	0/3128	0.52	0/4281
8	j	0.25	0/3128	0.52	0/4281
9	L	0.24	0/3370	0.54	0/4571
9	l	0.24	0/3370	0.54	0/4571
10	H	0.24	0/389	0.51	0/535
10	h	0.24	0/389	0.51	0/535
All	All	0.23	0/33138	0.52	0/44972

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	K	0	1
7	k	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	L	0	2
9	l	0	2
All	All	0	6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	K	183	ARG	Sidechain
9	L	228	ARG	Sidechain
9	L	276	ARG	Sidechain
7	k	183	ARG	Sidechain
9	l	228	ARG	Sidechain

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	D	1901	1856	1853	5	0
1	d	1901	1856	1853	3	0
2	A	1532	1512	1508	4	0
2	T	551	591	591	2	0
2	a	1532	1512	1508	7	0
3	G	908	895	894	4	0
3	g	908	895	894	5	0
4	C	681	686	685	6	0
4	c	681	686	685	4	0
5	E	453	458	457	4	0
5	e	453	458	457	2	0
6	F	554	539	538	3	0
6	f	554	539	538	3	0
7	K	3165	3161	3157	13	0
7	k	3165	3161	3157	11	0
8	J	3027	3090	3088	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	j	3027	3090	3088	11	0
9	L	3302	3231	3227	11	0
9	l	3302	3231	3227	11	0
10	H	374	374	373	2	0
10	h	374	374	373	1	0
11	D	43	32	30	0	0
11	d	43	32	30	0	0
12	D	1	0	0	0	0
12	d	1	0	0	0	0
13	A	4	0	0	0	0
13	a	4	0	0	0	0
14	C	100	156	156	0	0
14	L	100	156	156	0	0
14	c	100	156	156	0	0
14	l	100	156	156	1	0
15	E	54	88	88	1	0
15	e	54	88	88	1	0
16	J	26	18	18	1	0
16	j	26	18	18	1	0
17	J	102	166	164	0	0
17	L	51	83	82	0	0
17	j	102	166	164	0	0
17	l	51	83	82	0	0
18	J	26	19	17	0	0
18	j	26	19	17	0	0
19	J	86	60	60	8	0
19	j	86	60	60	9	0
20	J	7	14	0	0	0
20	j	7	14	0	1	0
All	All	33545	33779	33693	124	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 2.

The worst 5 of 124 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)
19:j:406:HEM:O2D	20:j:501:HOH:O	2.05	0.75
19:J:405:HEM:HBC2	19:J:405:HEM:HHD	1.70	0.74
19:j:405:HEM:HBC2	19:j:405:HEM:HHD	1.70	0.74
2:T:59:ALA:N	7:k:322:ASP:OD2	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:7:SER:OG	8:J:8:ASN:ND2	2.22	0.68

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	D	237/325 (73%)	223 (94%)	13 (6%)	1 (0%)	30	52
1	d	237/325 (73%)	223 (94%)	13 (6%)	1 (0%)	30	52
2	A	194/274 (71%)	180 (93%)	13 (7%)	1 (0%)	25	46
2	T	75/274 (27%)	72 (96%)	3 (4%)	0	100	100
2	a	194/274 (71%)	180 (93%)	13 (7%)	1 (0%)	25	46
3	G	102/111 (92%)	99 (97%)	3 (3%)	0	100	100
3	g	102/111 (92%)	99 (97%)	3 (3%)	0	100	100
4	C	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
4	c	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
5	E	54/63 (86%)	51 (94%)	3 (6%)	0	100	100
5	e	54/63 (86%)	51 (94%)	3 (6%)	0	100	100
6	F	65/91 (71%)	63 (97%)	2 (3%)	0	100	100
6	f	65/91 (71%)	63 (97%)	2 (3%)	0	100	100
7	K	416/453 (92%)	404 (97%)	12 (3%)	0	100	100
7	k	416/453 (92%)	404 (97%)	12 (3%)	0	100	100
8	J	376/380 (99%)	354 (94%)	22 (6%)	0	100	100
8	j	376/380 (99%)	354 (94%)	22 (6%)	0	100	100
9	L	419/480 (87%)	404 (96%)	15 (4%)	0	100	100
9	l	419/480 (87%)	404 (96%)	15 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	H	43/56 (77%)	41 (95%)	2 (5%)	0	100	100
10	h	43/56 (77%)	41 (95%)	2 (5%)	0	100	100
All	All	4045/4904 (82%)	3856 (95%)	185 (5%)	4 (0%)	50	71

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	150	ALA
1	d	150	ALA
2	A	82	ASP
2	a	82	ASP

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	D	203/257 (79%)	201 (99%)	2 (1%)	73	88
1	d	203/257 (79%)	201 (99%)	2 (1%)	73	88
2	A	167/229 (73%)	167 (100%)	0	100	100
2	T	61/229 (27%)	60 (98%)	1 (2%)	58	80
2	a	167/229 (73%)	167 (100%)	0	100	100
3	G	94/98 (96%)	94 (100%)	0	100	100
3	g	94/98 (96%)	94 (100%)	0	100	100
4	C	74/75 (99%)	74 (100%)	0	100	100
4	c	74/75 (99%)	74 (100%)	0	100	100
5	E	46/53 (87%)	45 (98%)	1 (2%)	47	73
5	e	46/53 (87%)	45 (98%)	1 (2%)	47	73
6	F	64/86 (74%)	62 (97%)	2 (3%)	35	61
6	f	64/86 (74%)	62 (97%)	2 (3%)	35	61
7	K	335/361 (93%)	329 (98%)	6 (2%)	54	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	k	335/361 (93%)	329 (98%)	6 (2%)	54	78
8	J	340/342 (99%)	336 (99%)	4 (1%)	67	85
8	j	340/342 (99%)	336 (99%)	4 (1%)	67	85
9	L	354/396 (89%)	345 (98%)	9 (2%)	42	69
9	l	354/396 (89%)	345 (98%)	9 (2%)	42	69
10	H	36/46 (78%)	36 (100%)	0	100	100
10	h	36/46 (78%)	36 (100%)	0	100	100
All	All	3487/4115 (85%)	3438 (99%)	49 (1%)	62	82

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	f	50	LEU
7	k	307	SER
6	f	78	ARG
7	k	214	THR
8	j	174	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
2	T	31	GLN
9	l	188	HIS
6	f	84	HIS
9	l	375	GLN
8	j	255	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 2 are monoatomic - leaving 24 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
19	HEM	J	406	8	41,50,50	1.44	4 (9%)	45,82,82	1.34	6 (13%)
14	CDL	c	101	-	99,99,99	0.31	0	105,111,111	0.28	0
17	PEE	j	402	-	50,50,50	0.76	2 (4%)	53,55,55	0.45	0
11	HEC	D	401	1	32,50,50	2.29	3 (9%)	24,82,82	1.53	1 (4%)
19	HEM	j	406	8	41,50,50	1.43	4 (9%)	45,82,82	1.34	6 (13%)
14	CDL	L	501	-	99,99,99	0.31	0	105,111,111	0.33	0
13	FES	A	300	2	0,4,4	-	-	-	-	-
14	CDL	C	101	-	99,99,99	0.31	0	105,111,111	0.28	0
13	FES	a	300	2	0,4,4	-	-	-	-	-
16	AOQ	J	401	-	29,29,29	0.18	0	40,42,42	0.30	0
18	AFI	j	404	-	29,29,29	3.85	7 (24%)	38,42,42	1.83	6 (15%)
15	PC1	E	101	-	53,53,53	0.28	0	59,61,61	0.27	0
11	HEC	d	401	1	32,50,50	2.28	3 (9%)	24,82,82	1.54	1 (4%)
14	CDL	l	501	-	99,99,99	0.31	0	105,111,111	0.33	0
17	PEE	l	502	-	50,50,50	0.76	2 (4%)	53,55,55	0.44	0
18	AFI	J	404	-	29,29,29	3.87	7 (24%)	38,42,42	1.82	6 (15%)
19	HEM	j	405	8	41,50,50	1.51	3 (7%)	45,82,82	1.30	4 (8%)
17	PEE	j	403	-	50,50,50	0.77	2 (4%)	53,55,55	0.47	0
17	PEE	J	402	-	50,50,50	0.76	2 (4%)	53,55,55	0.45	0
19	HEM	J	405	8	41,50,50	1.50	3 (7%)	45,82,82	1.30	4 (8%)
16	AOQ	j	401	-	29,29,29	0.18	0	40,42,42	0.29	0
17	PEE	J	403	-	50,50,50	0.76	2 (4%)	53,55,55	0.47	0
17	PEE	L	502	-	50,50,50	0.77	2 (4%)	53,55,55	0.44	0
15	PC1	e	101	-	53,53,53	0.28	0	59,61,61	0.27	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
19	HEM	J	406	8	-	4/12/54/54	-
14	CDL	c	101	-	-	14/110/110/110	-
17	PEE	j	402	-	-	16/54/54/54	-
11	HEC	D	401	1	-	0/10/54/54	-
19	HEM	j	406	8	-	4/12/54/54	-
14	CDL	L	501	-	-	26/110/110/110	-
13	FES	A	300	2	-	-	0/1/1/1
14	CDL	C	101	-	-	14/110/110/110	-
13	FES	a	300	2	-	-	0/1/1/1
16	AOQ	J	401	-	-	2/8/38/38	0/4/4/4
18	AFI	j	404	-	-	6/8/38/38	0/4/4/4
15	PC1	E	101	-	-	14/57/57/57	-
11	HEC	d	401	1	-	0/10/54/54	-
14	CDL	l	501	-	-	26/110/110/110	-
17	PEE	l	502	-	-	18/54/54/54	-
18	AFI	J	404	-	-	6/8/38/38	0/4/4/4
19	HEM	j	405	8	-	2/12/54/54	-
17	PEE	j	403	-	-	14/54/54/54	-
17	PEE	J	402	-	-	16/54/54/54	-
19	HEM	J	405	8	-	2/12/54/54	-
16	AOQ	j	401	-	-	2/8/38/38	0/4/4/4
17	PEE	J	403	-	-	14/54/54/54	-
17	PEE	L	502	-	-	18/54/54/54	-
15	PC1	e	101	-	-	14/57/57/57	-

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	J	404	AFI	C3-C4	18.18	1.53	1.36
18	j	404	AFI	C3-C4	18.09	1.53	1.36
11	D	401	HEC	C2B-C3B	-7.07	1.33	1.40
11	d	401	HEC	C2B-C3B	-7.02	1.33	1.40
11	D	401	HEC	C3C-C2C	-6.72	1.33	1.40

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	J	404	AFI	C15-C16-C2	-5.84	113.17	123.06
18	j	404	AFI	C15-C16-C2	-5.83	113.19	123.06
18	j	404	AFI	C11-C16-C2	-5.82	113.20	123.06
18	J	404	AFI	C11-C16-C2	-5.82	113.21	123.06
11	d	401	HEC	CMB-C2B-C3B	-4.47	120.56	125.82

There are no chirality outliers.

5 of 232 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	C	101	CDL	CA3-OA5-PA1-OA4
14	C	101	CDL	CB3-OB5-PB2-OB2
14	L	501	CDL	O1-C1-CA2-OA2
14	L	501	CDL	OB5-CB3-CB4-OB6
14	L	501	CDL	OB7-CB5-OB6-CB4

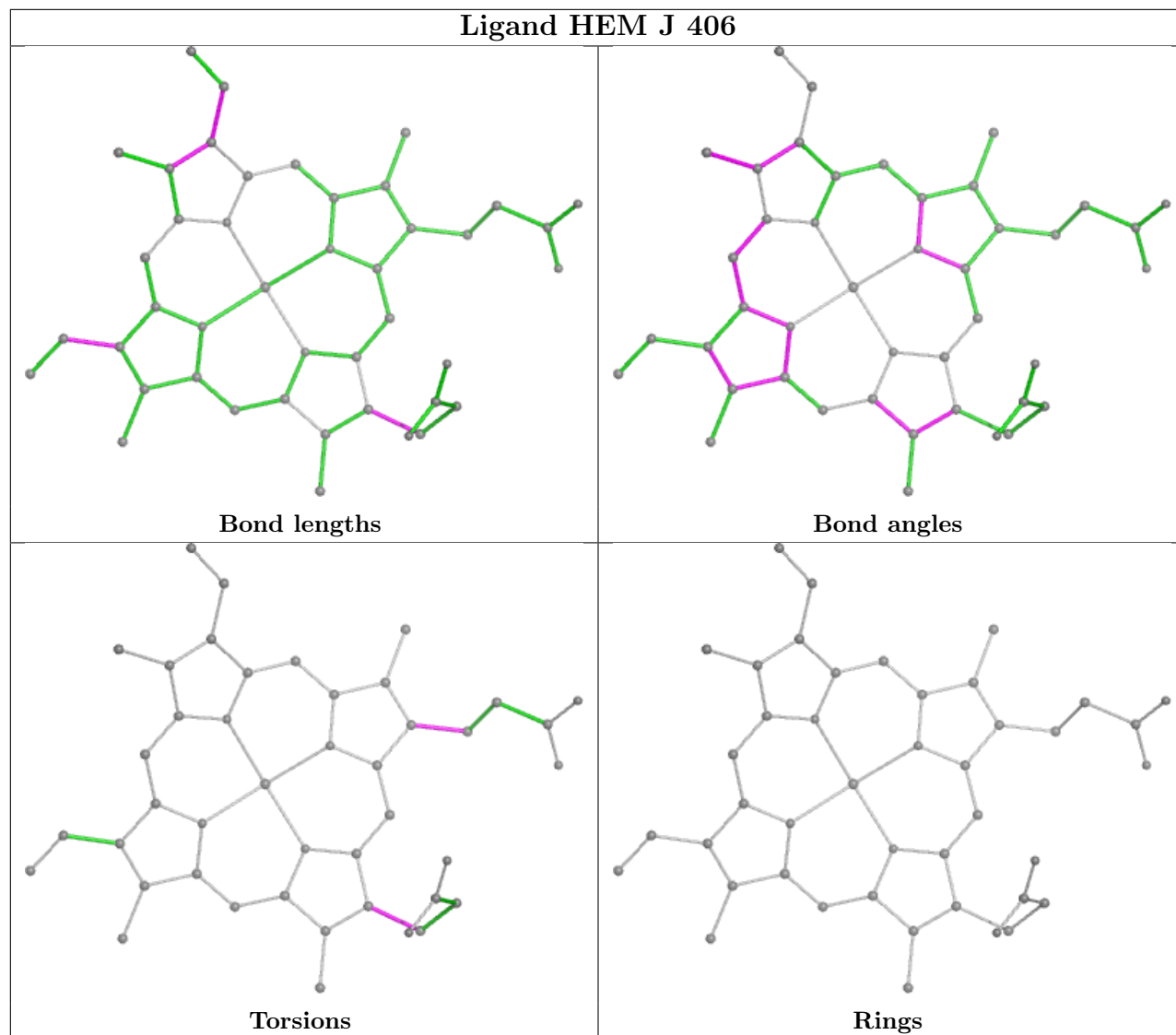
There are no ring outliers.

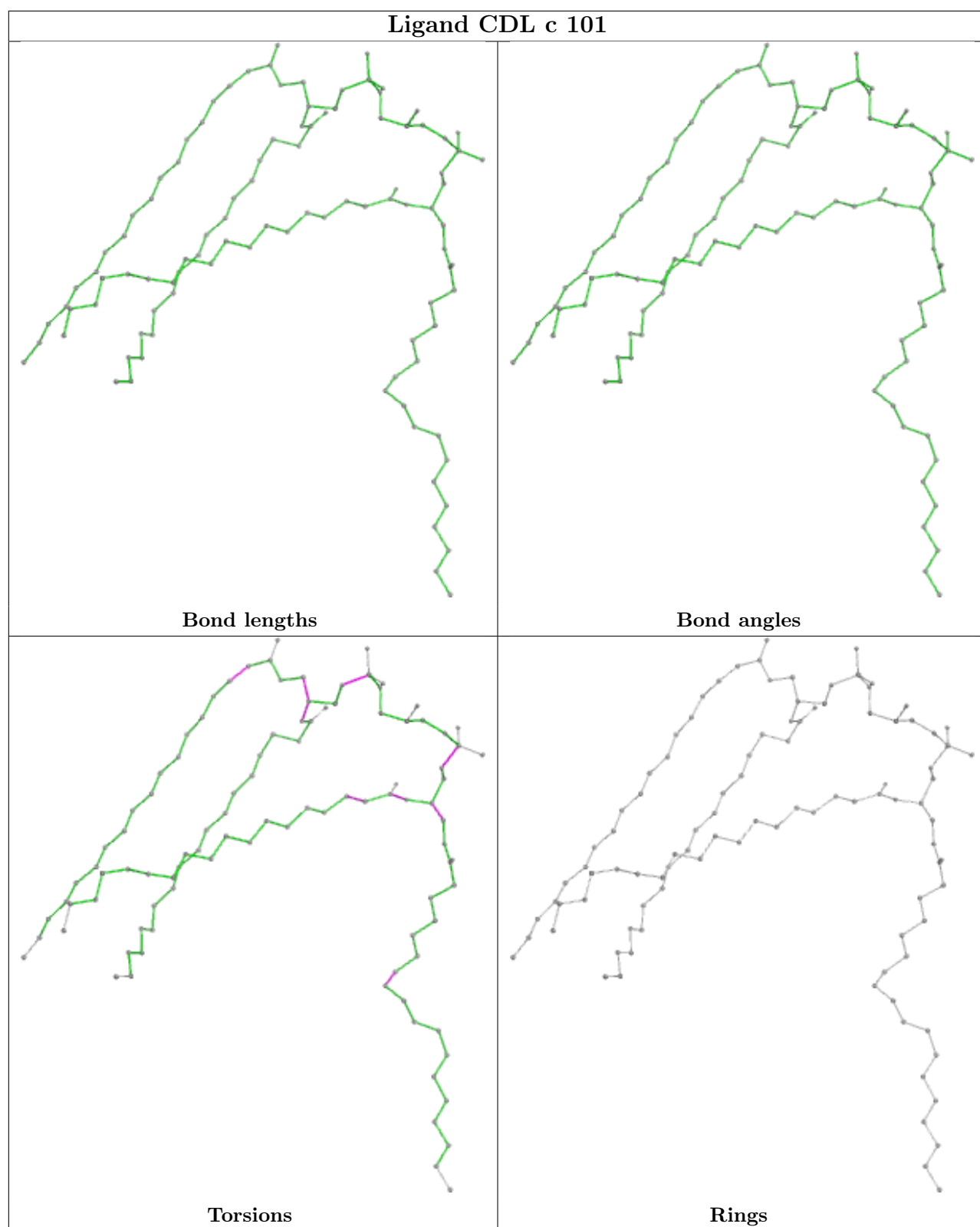
9 monomers are involved in 22 short contacts:

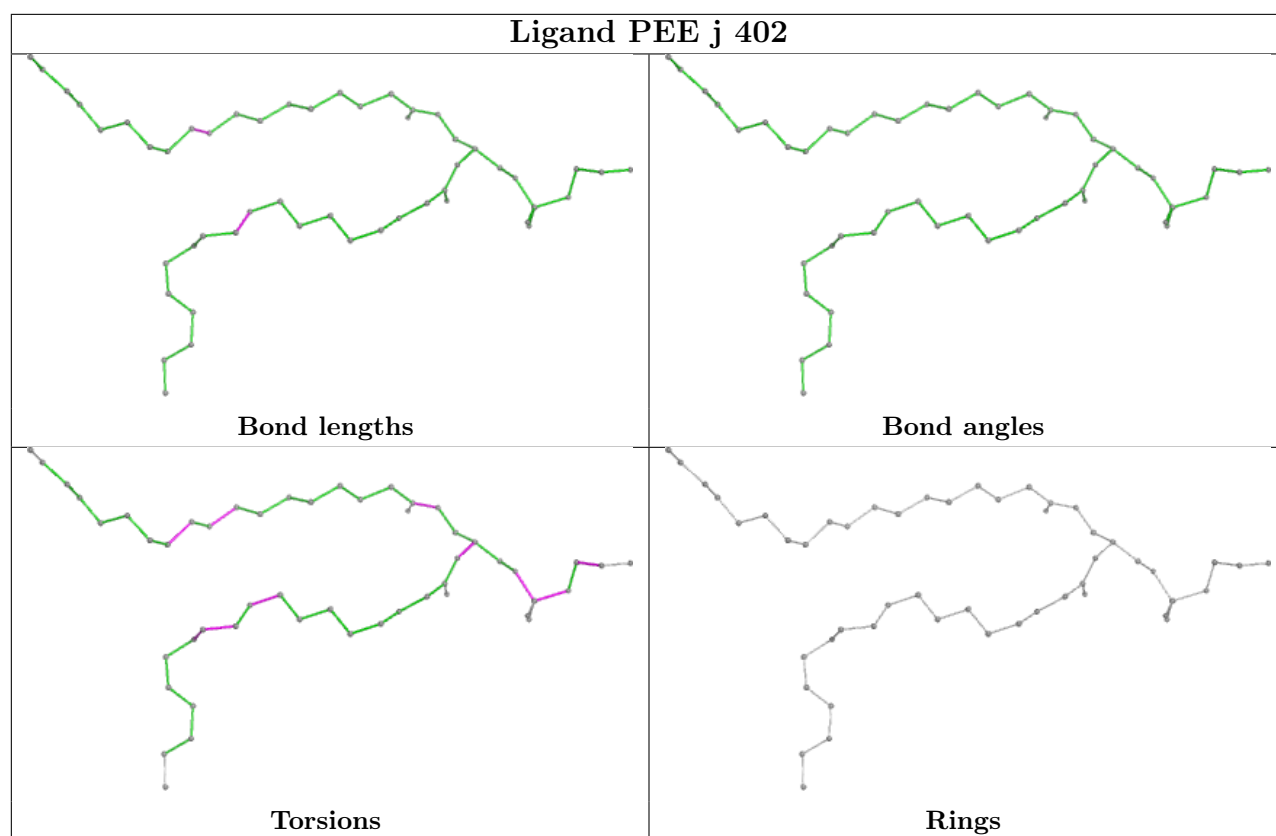
Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	J	406	HEM	5	0
19	j	406	HEM	6	0
16	J	401	AOQ	1	0
15	E	101	PC1	1	0
14	l	501	CDL	1	0
19	j	405	HEM	3	0
19	J	405	HEM	3	0
16	j	401	AOQ	1	0
15	e	101	PC1	1	0

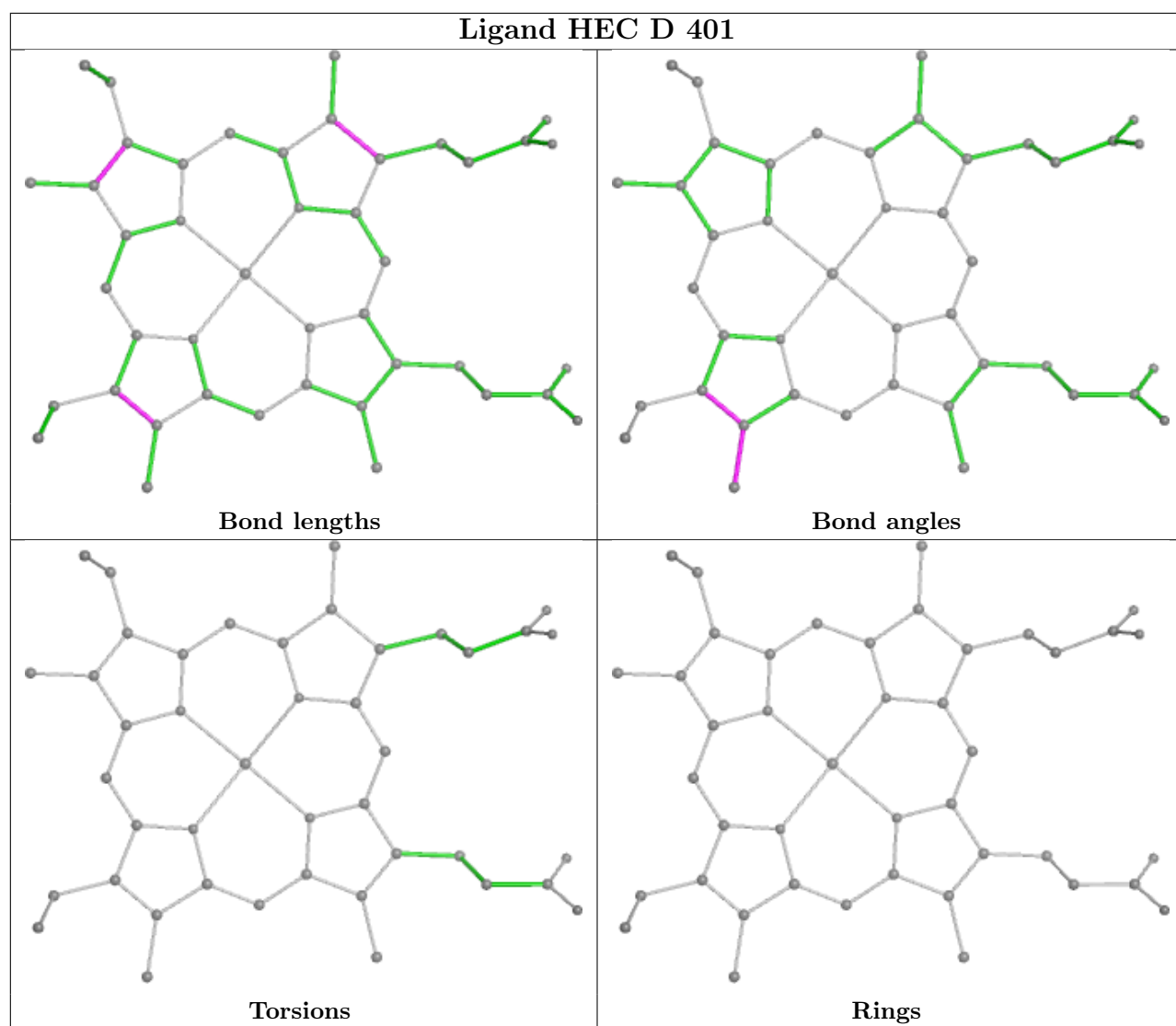
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

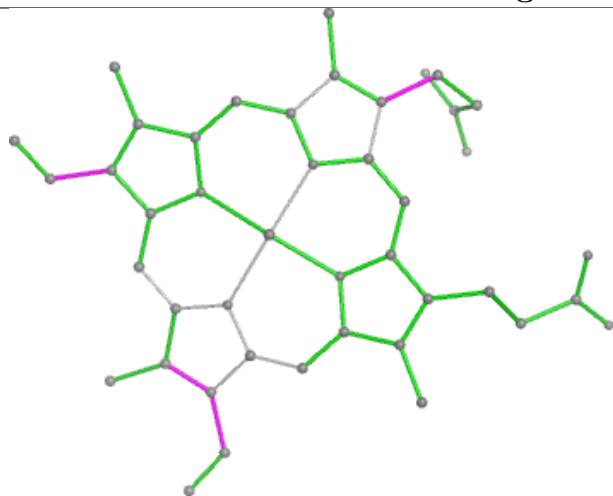




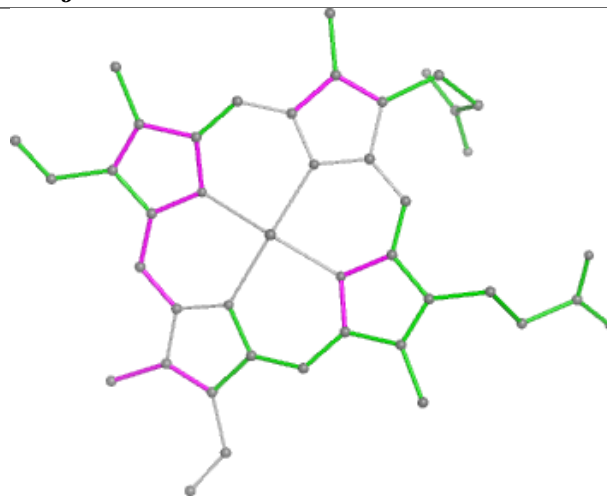




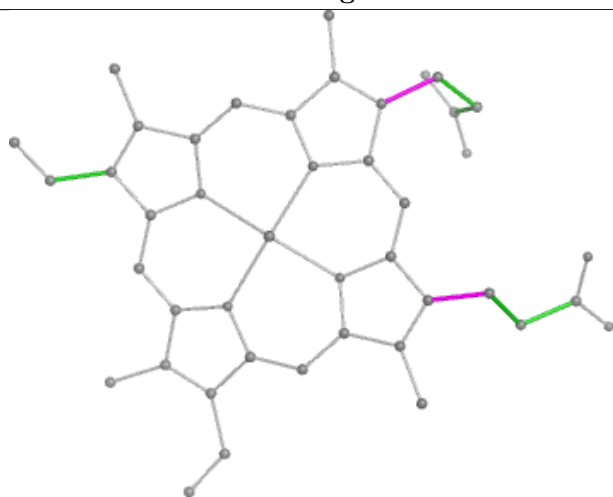
Ligand HEM j 406



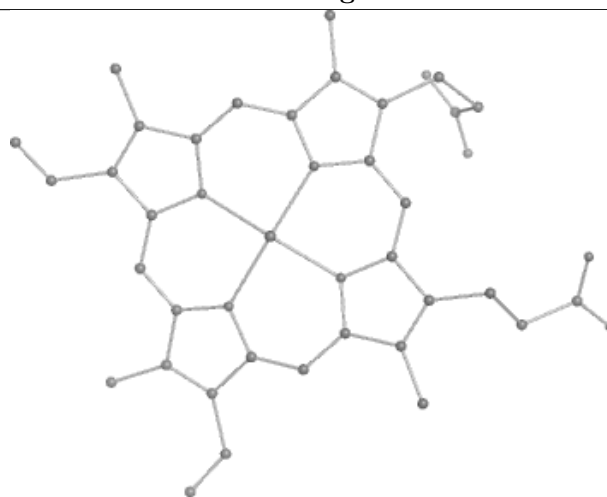
Bond lengths



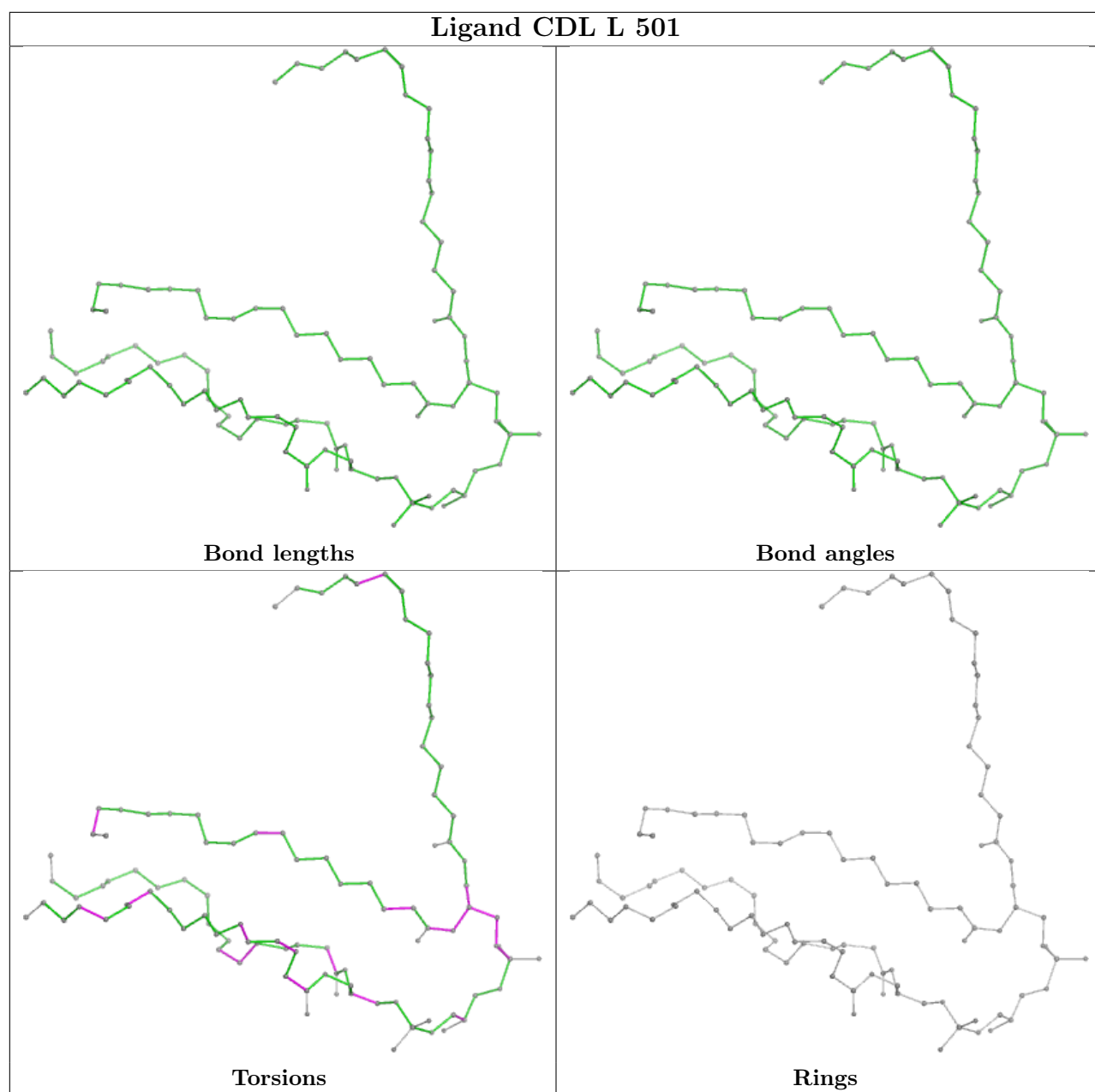
Bond angles

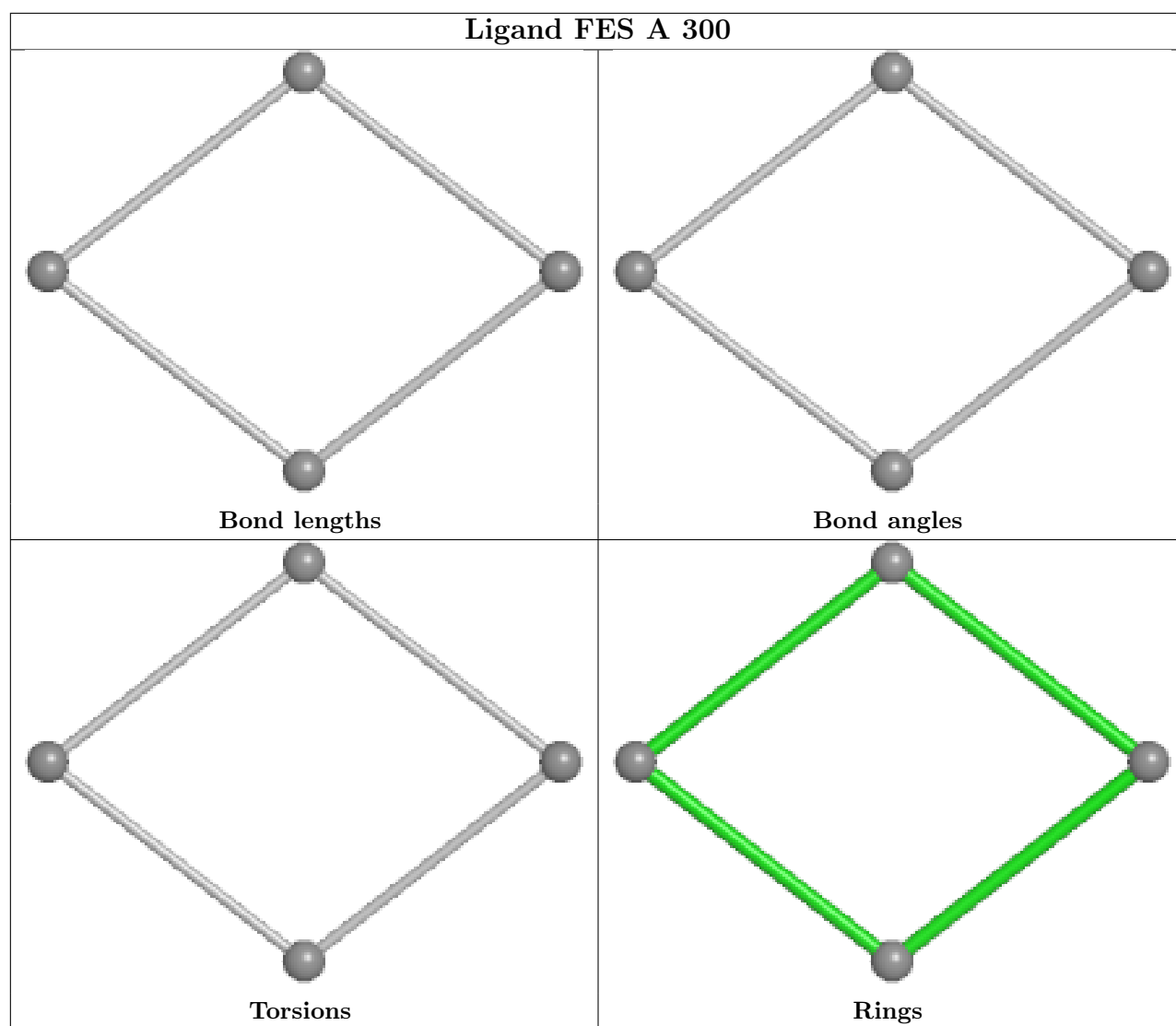


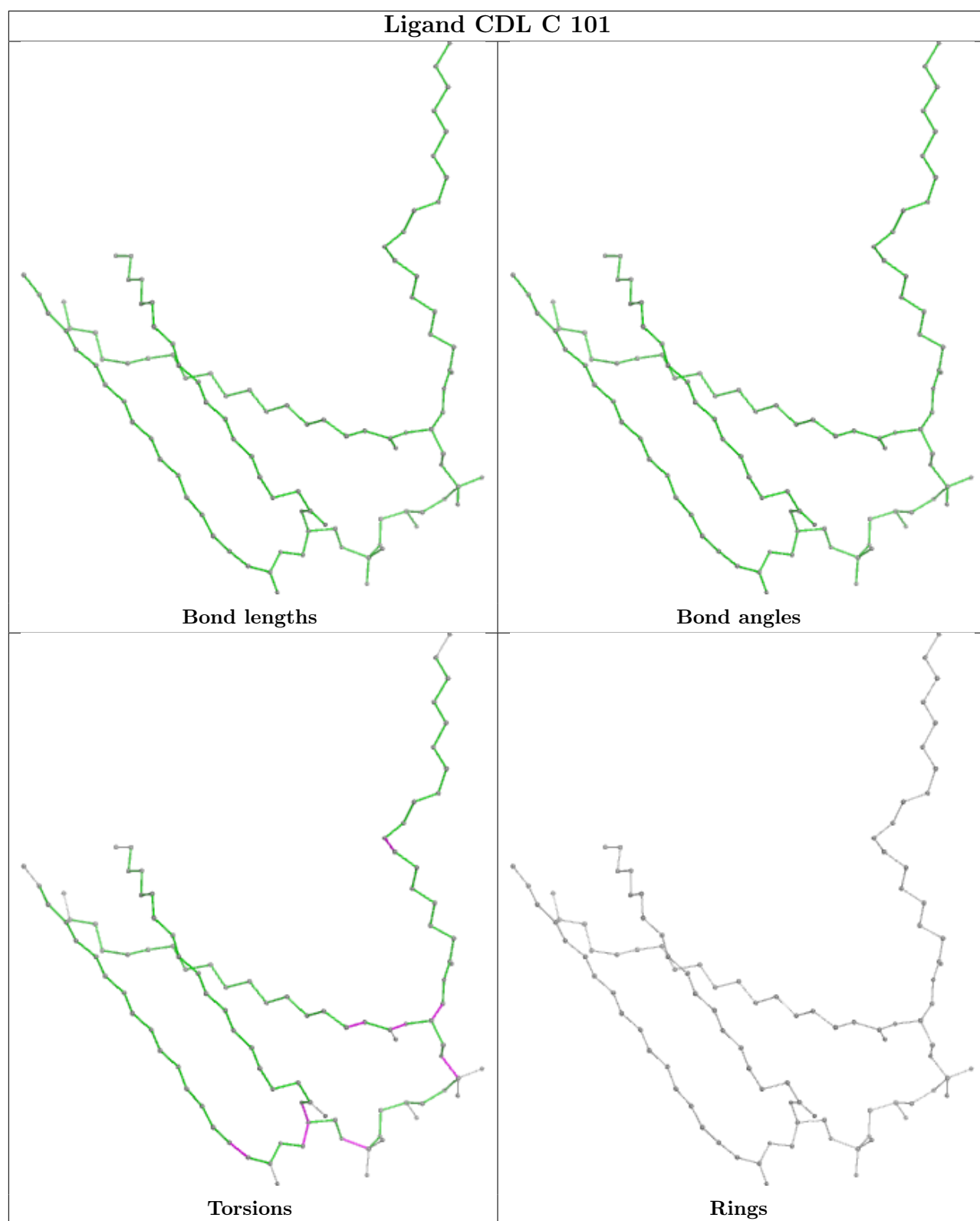
Torsions

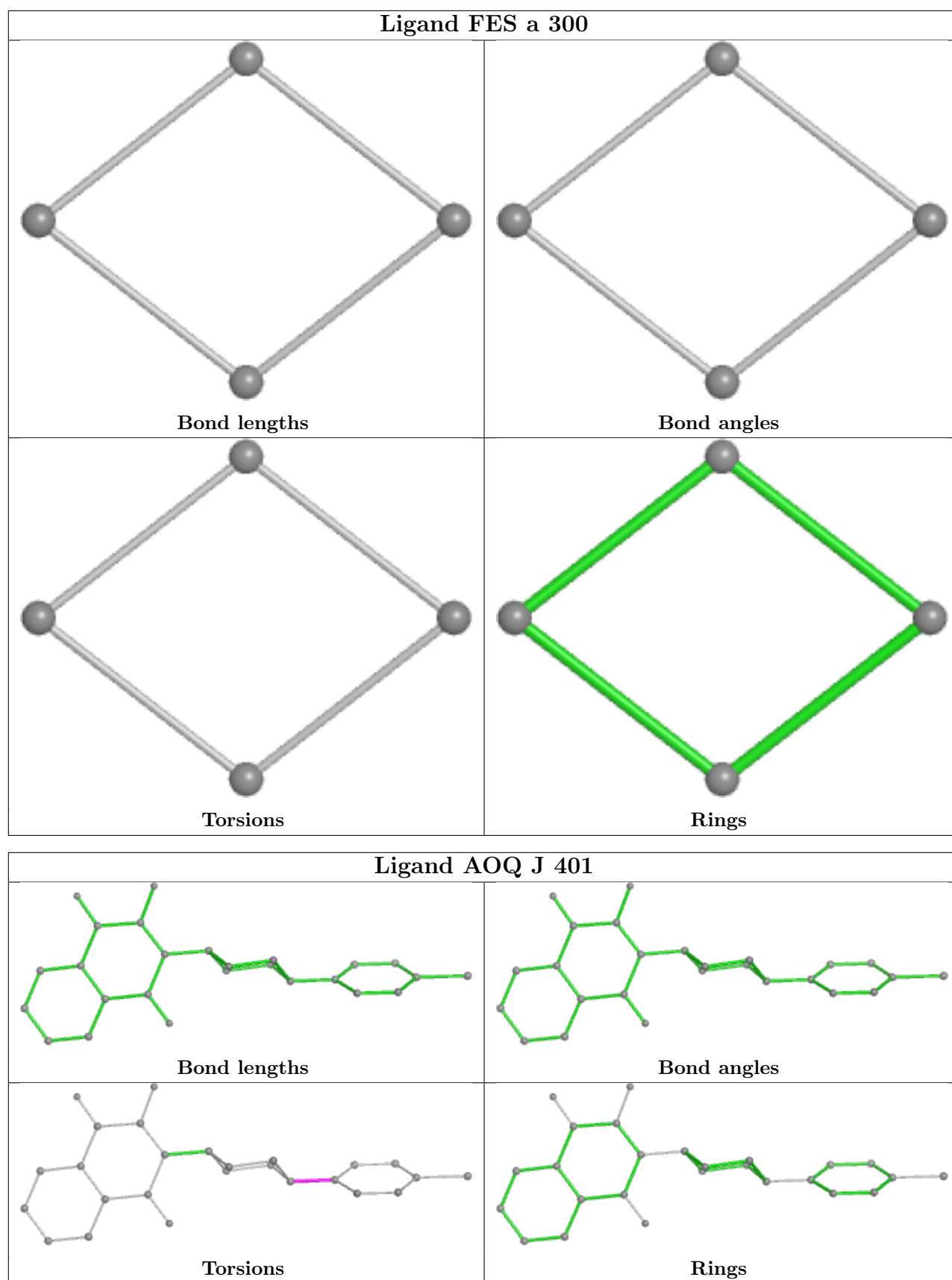


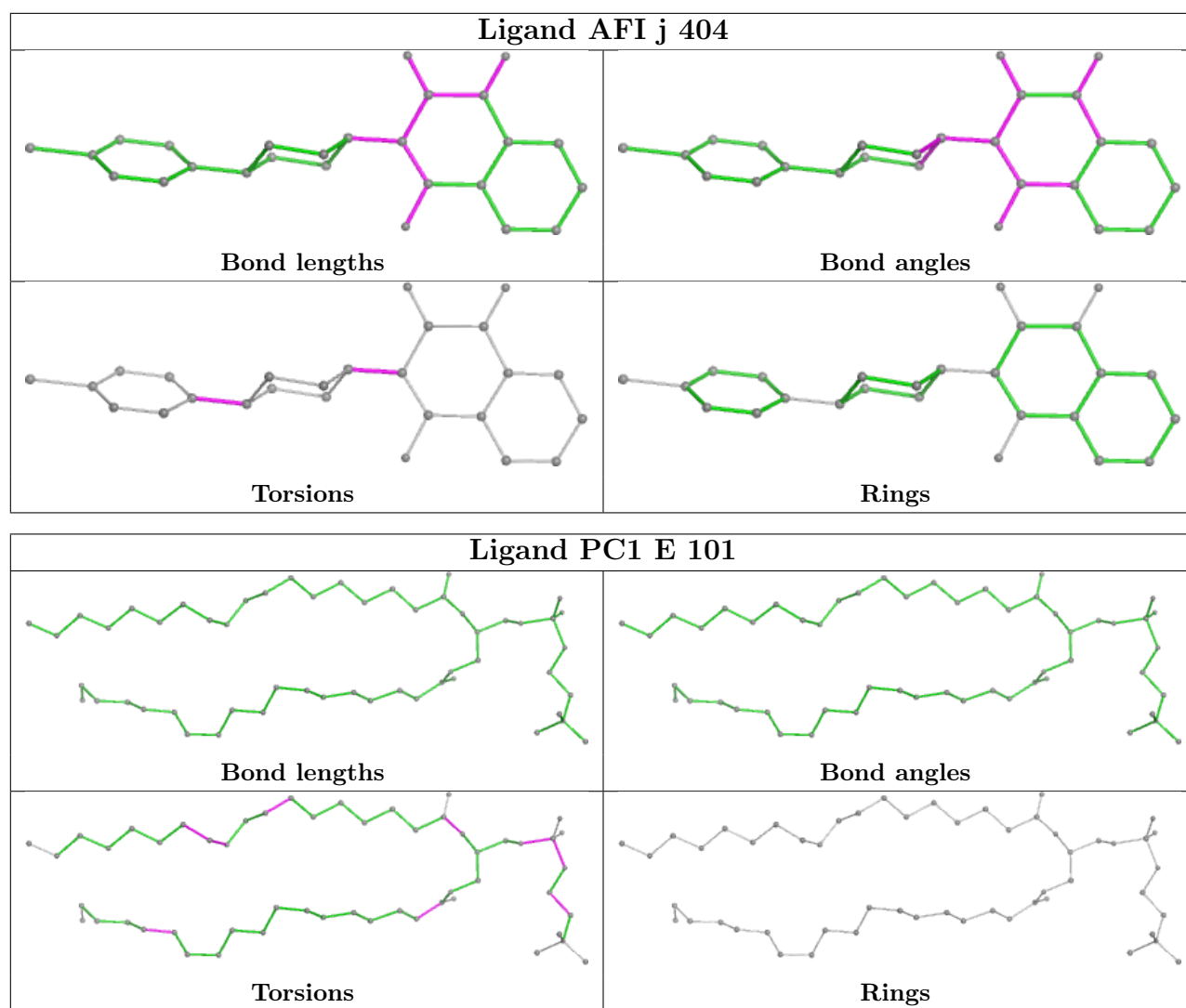
Rings



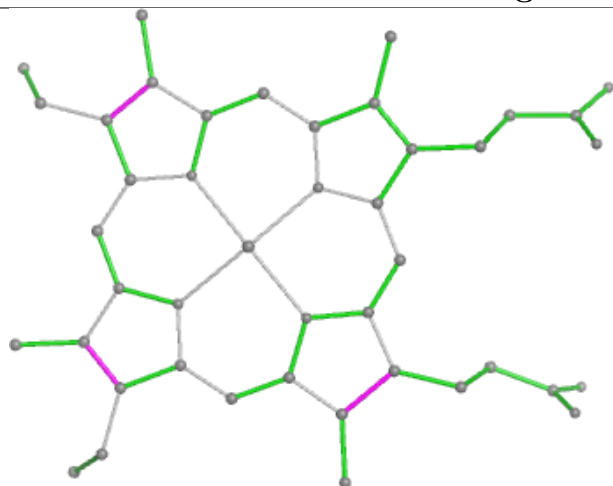




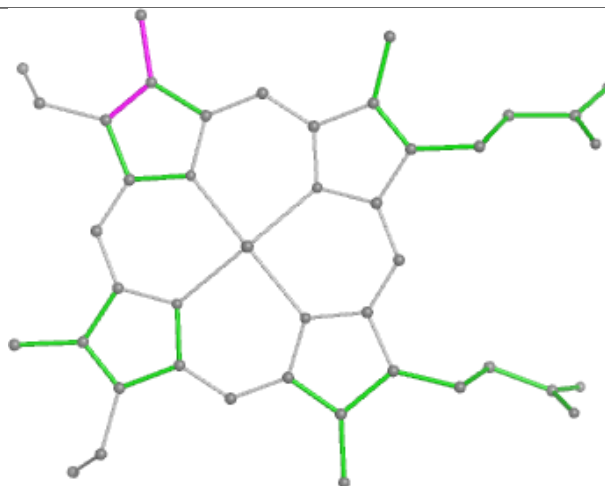




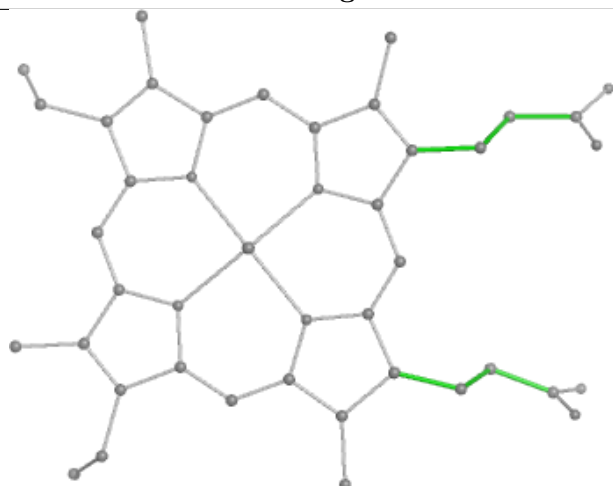
Ligand HEC d 401



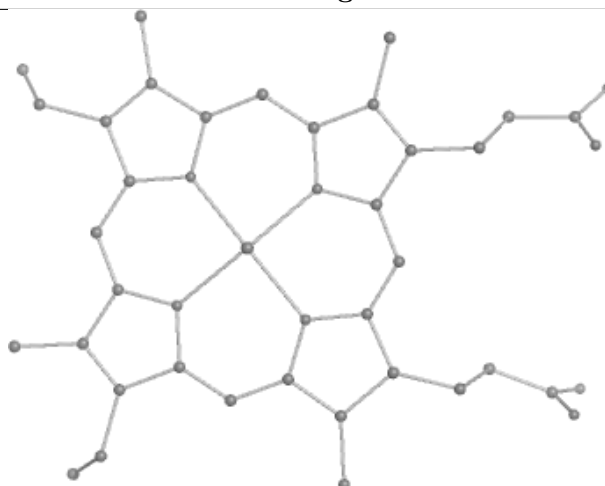
Bond lengths



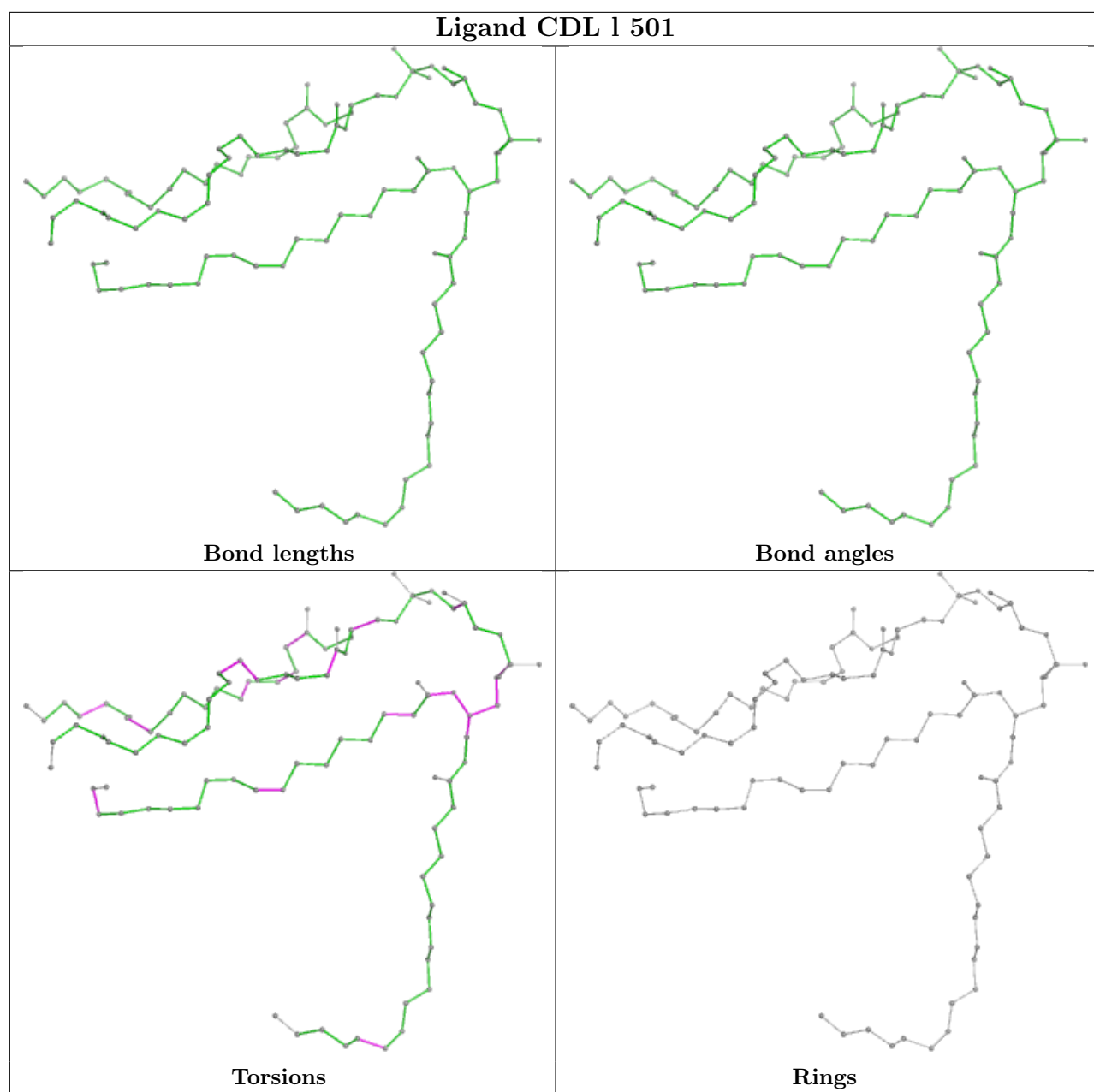
Bond angles

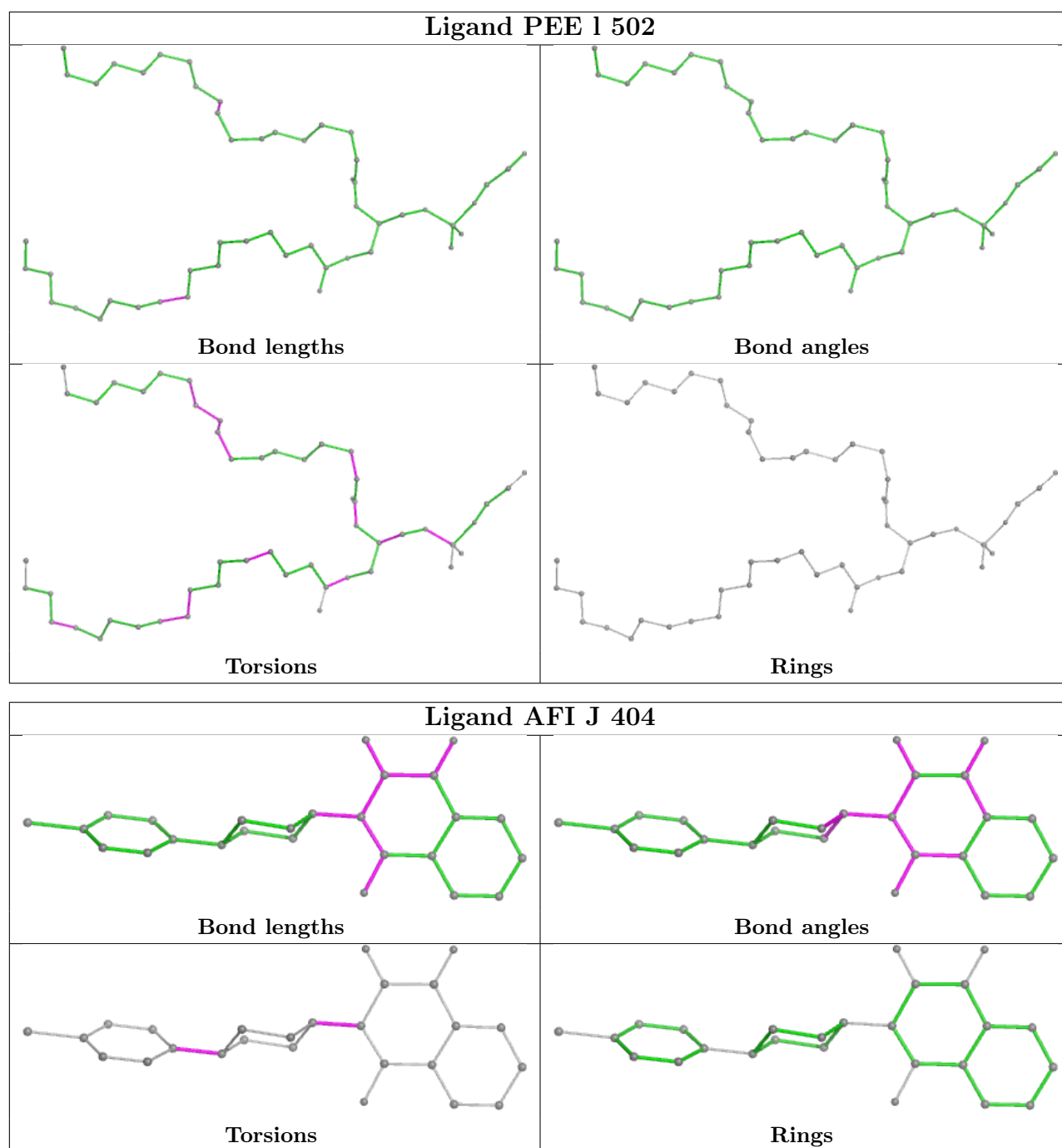


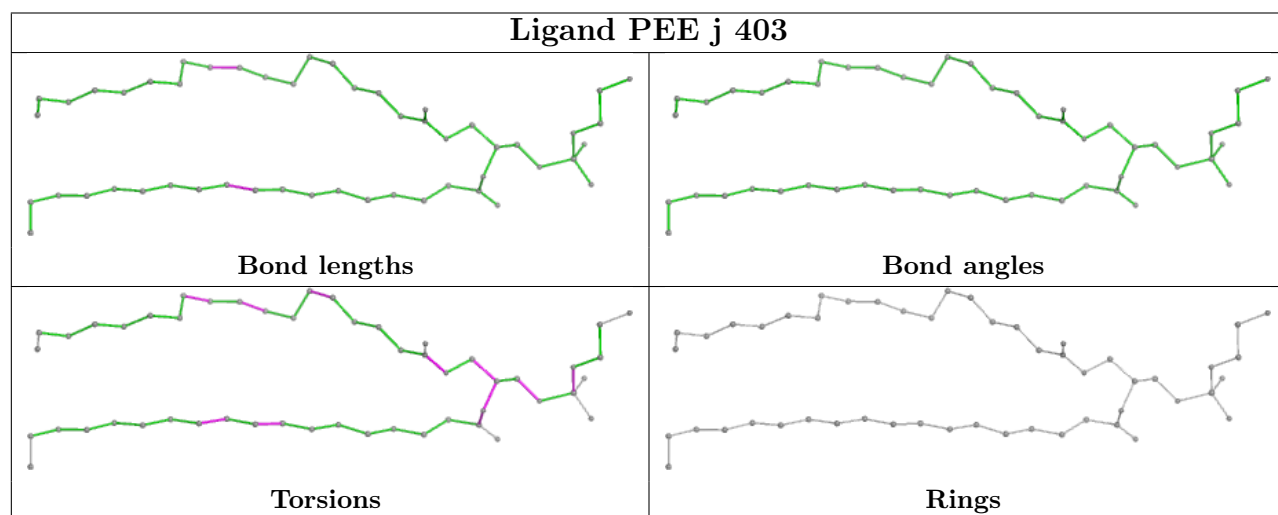
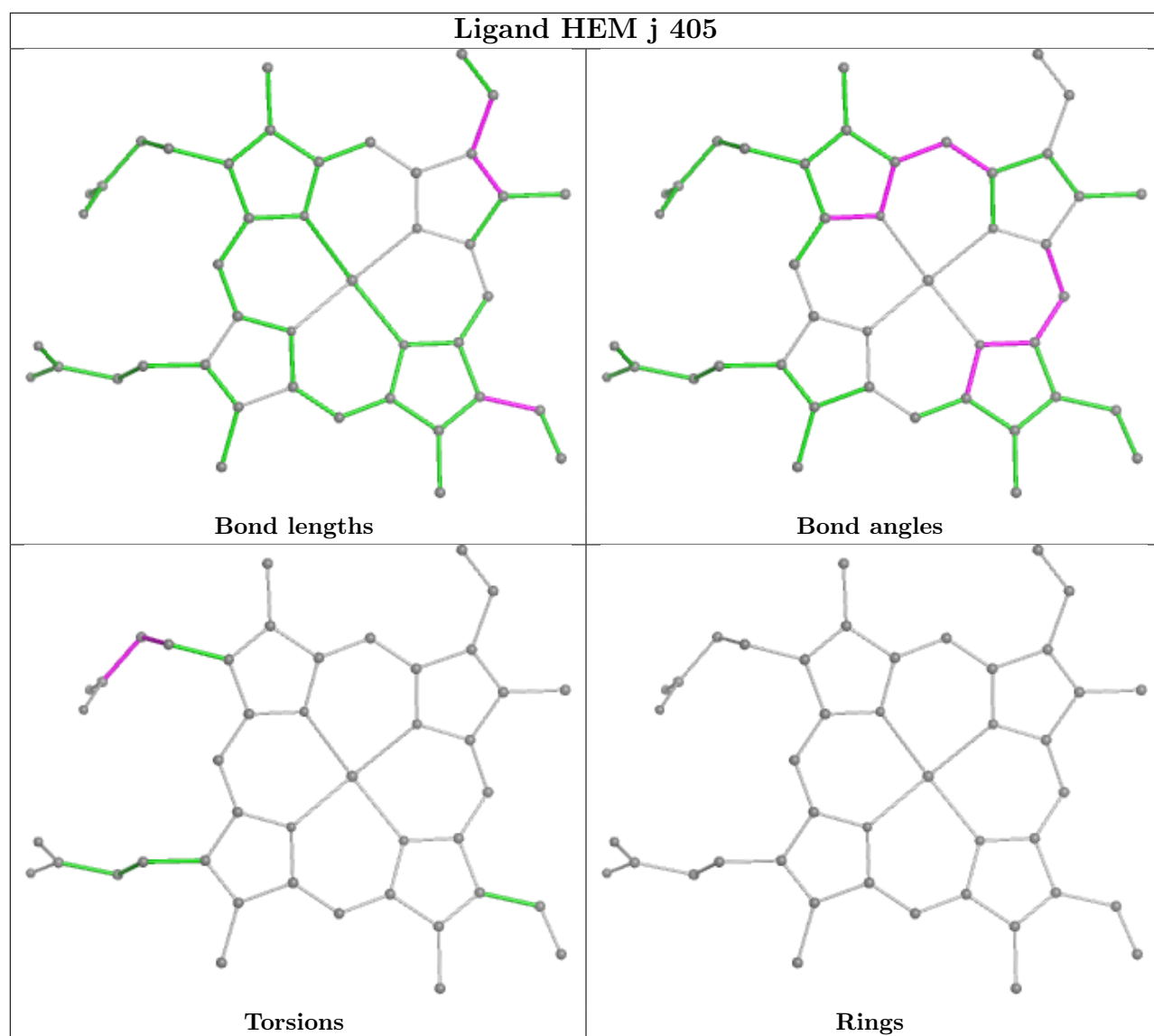
Torsions

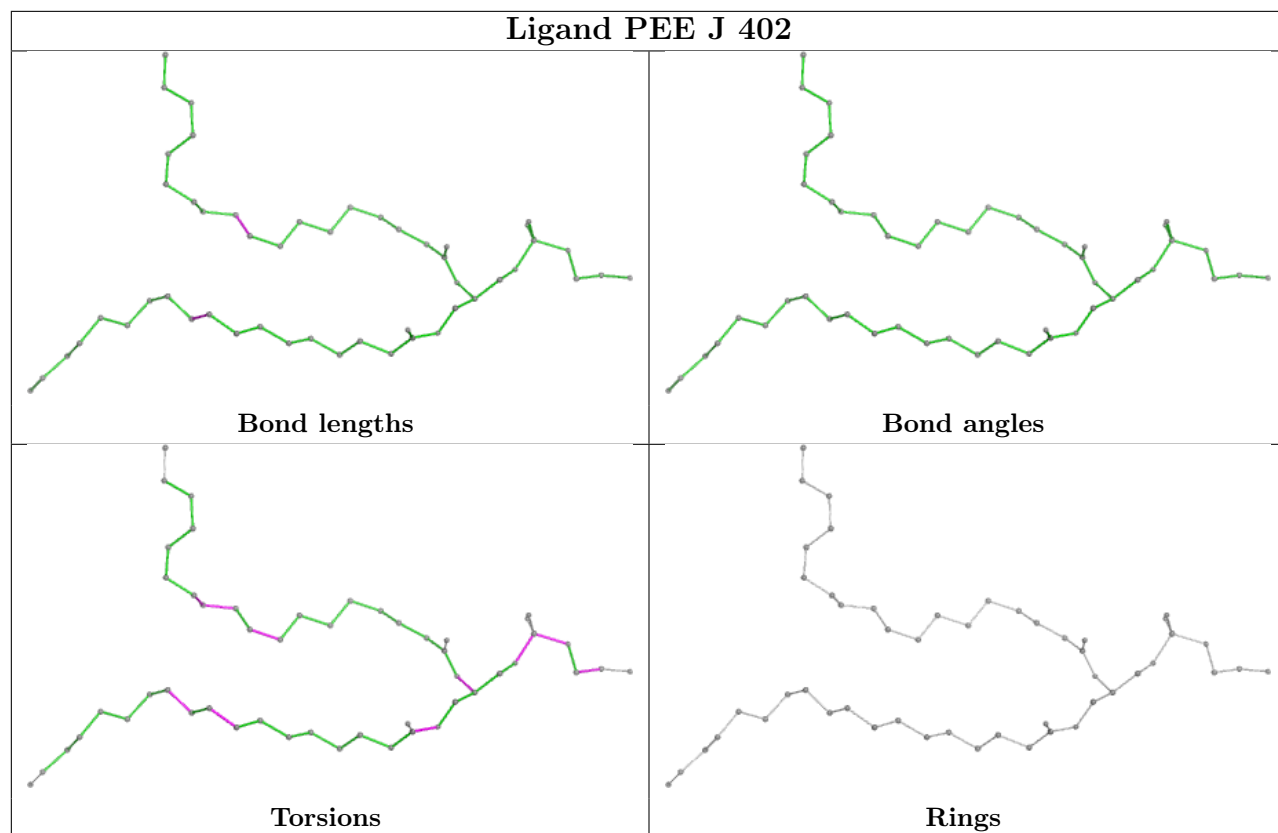


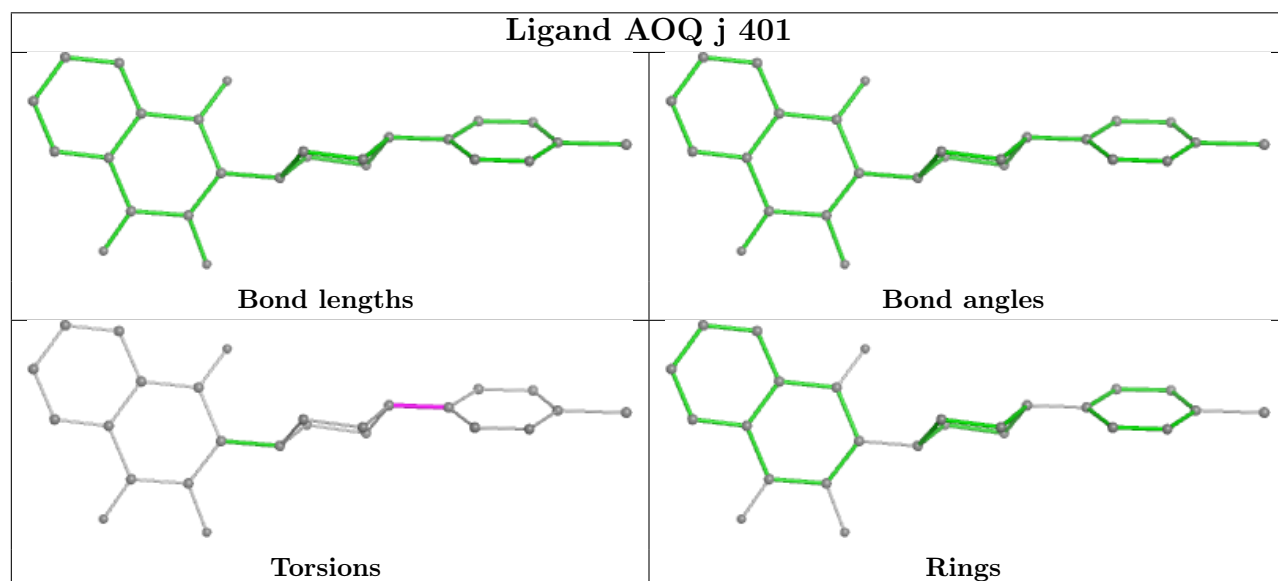
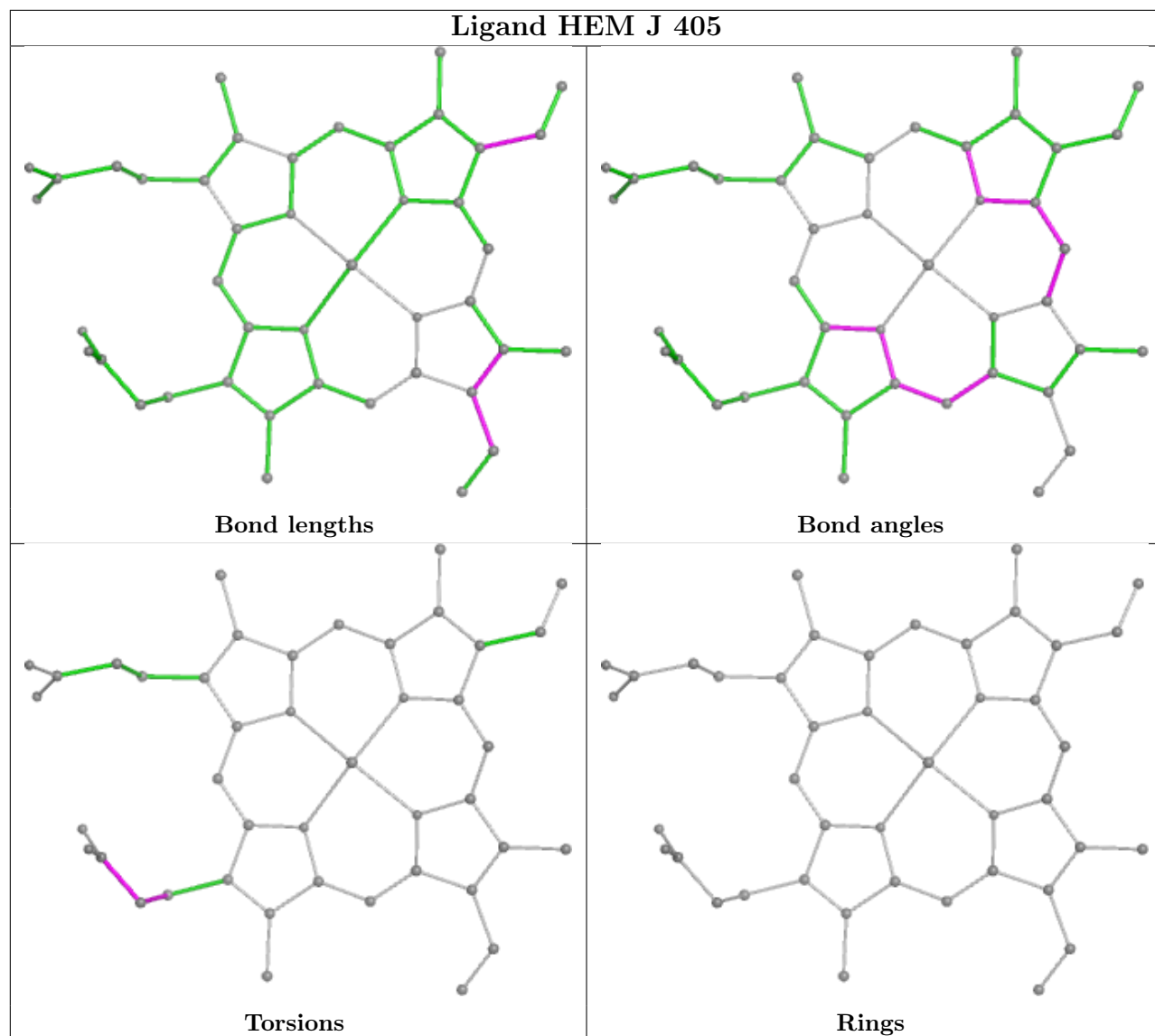
Rings

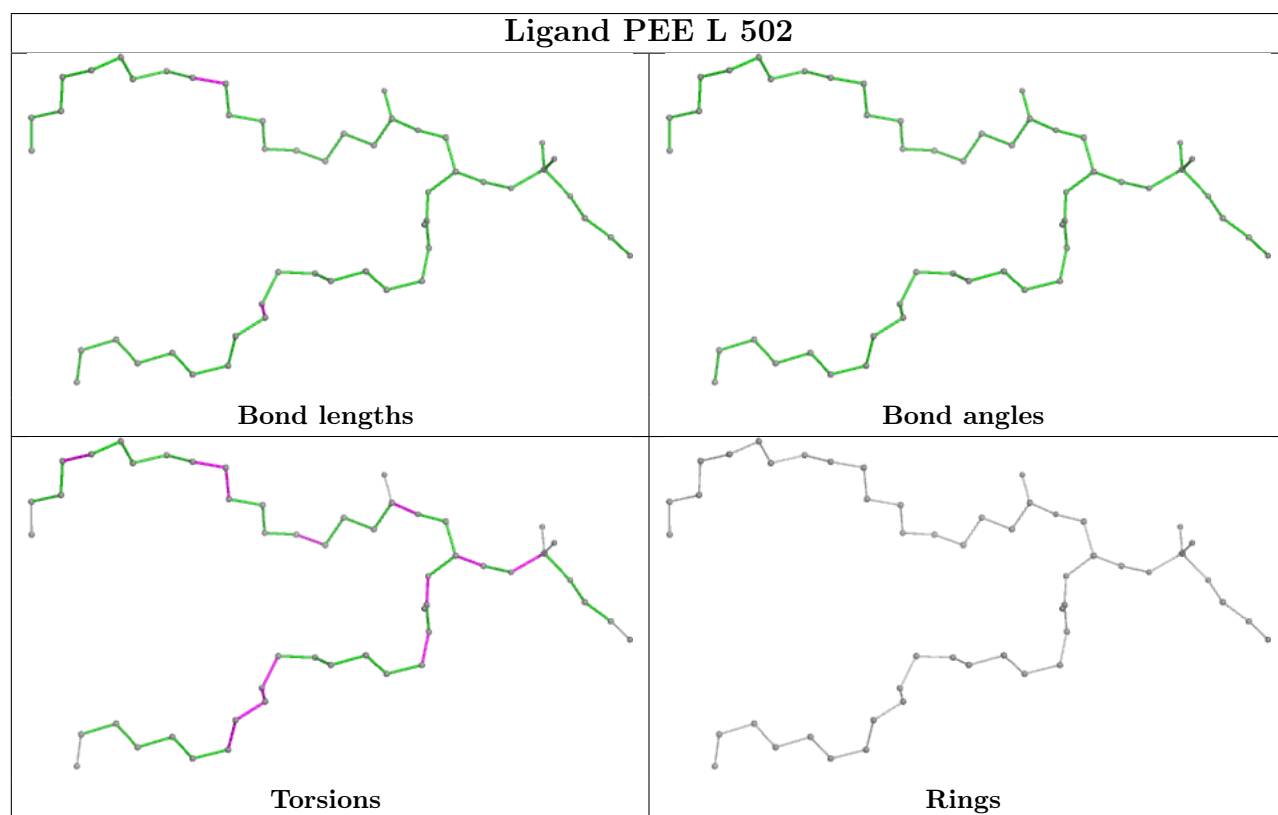
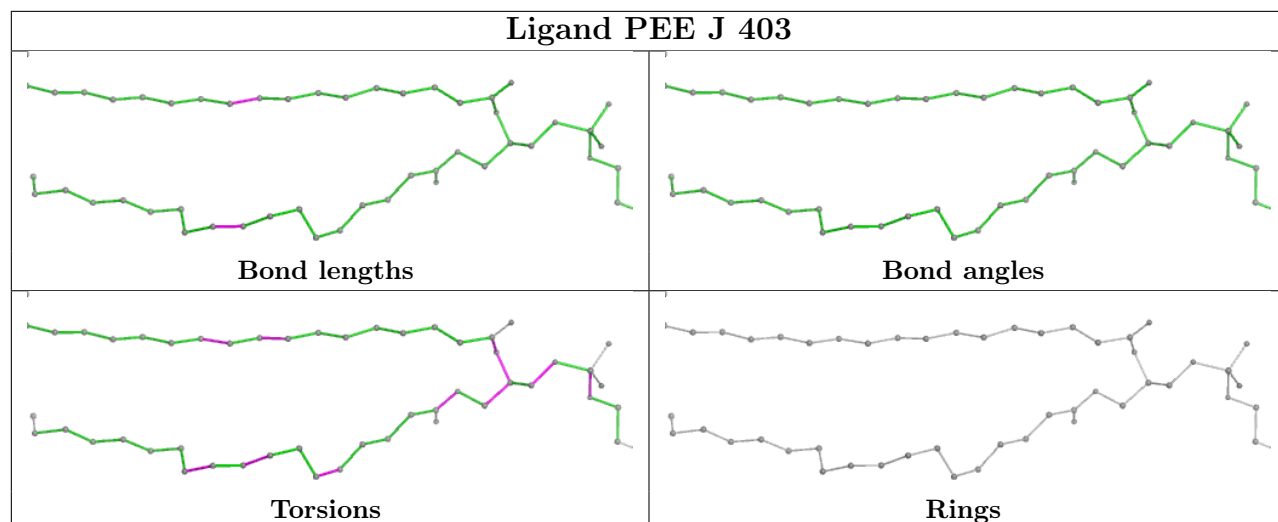


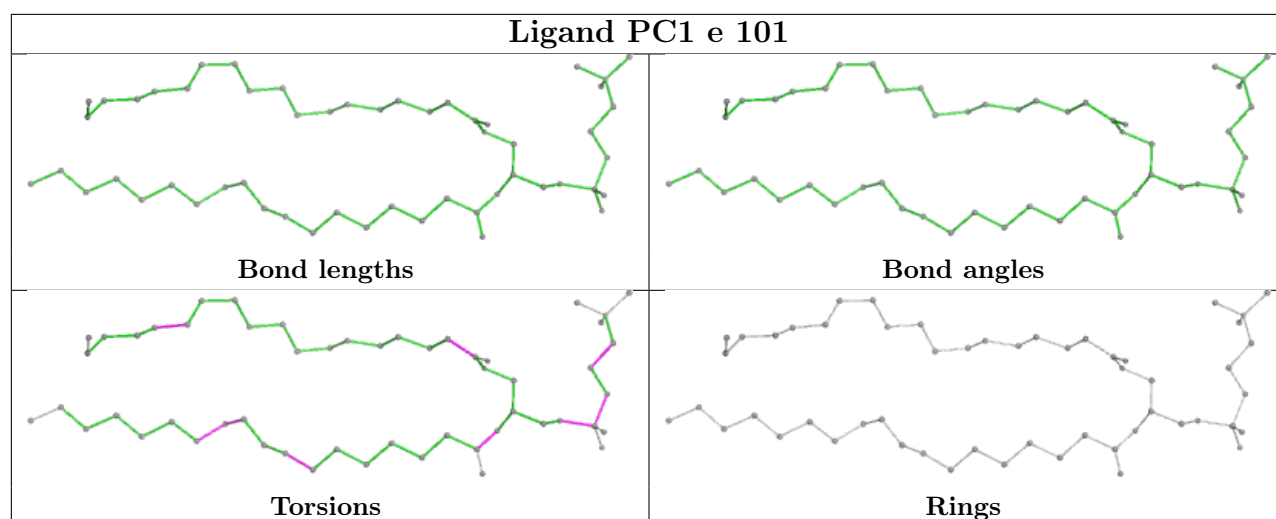












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

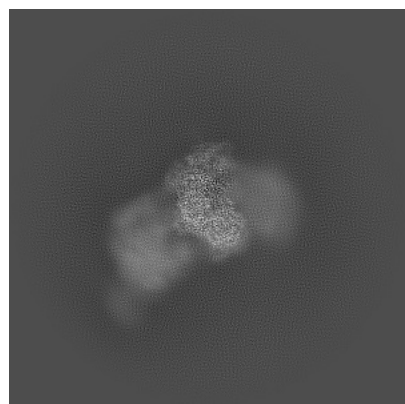
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51939. These allow visual inspection of the internal detail of the map and identification of artifacts.

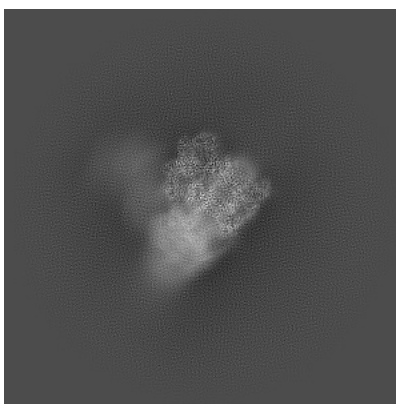
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

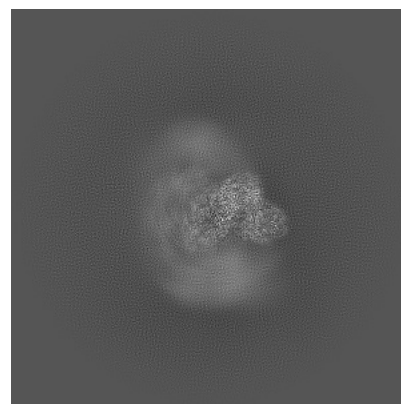
6.1.1 Primary map



X

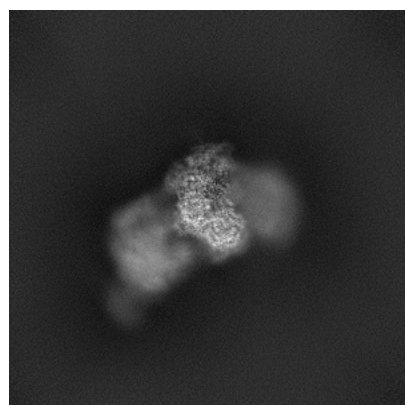


Y

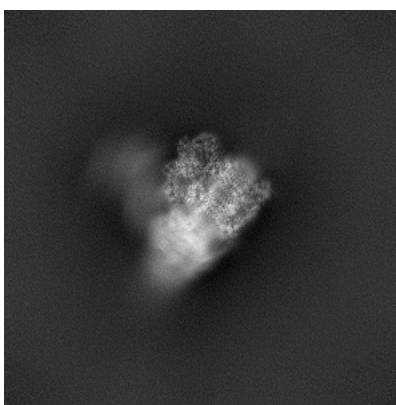


Z

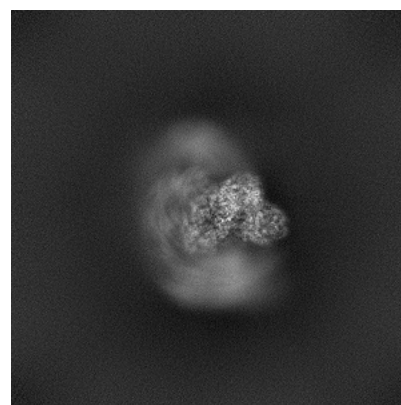
6.1.2 Raw map



X



Y

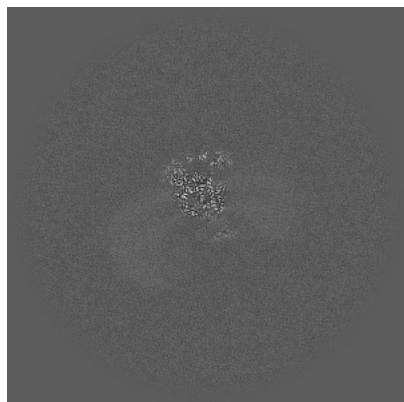


Z

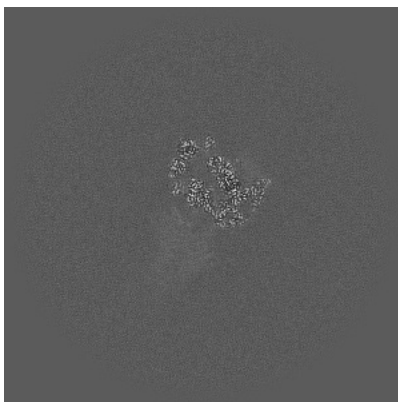
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

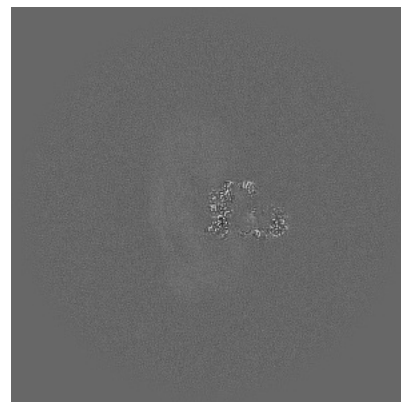
6.2.1 Primary map



X Index: 300

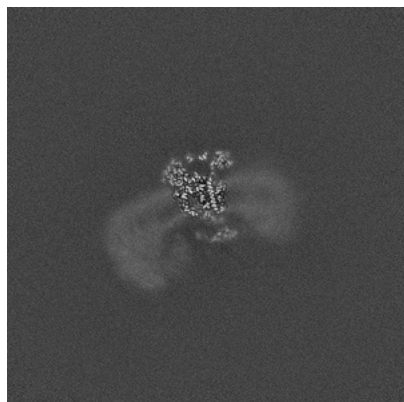


Y Index: 300

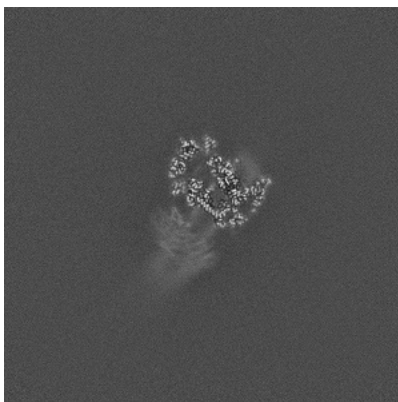


Z Index: 300

6.2.2 Raw map



X Index: 300



Y Index: 300

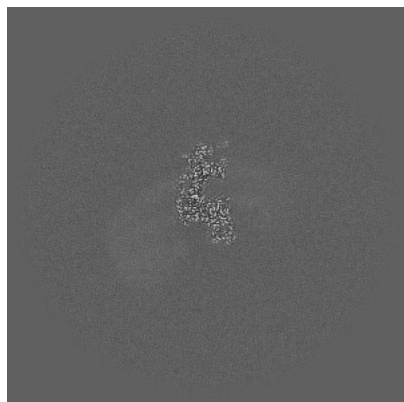


Z Index: 300

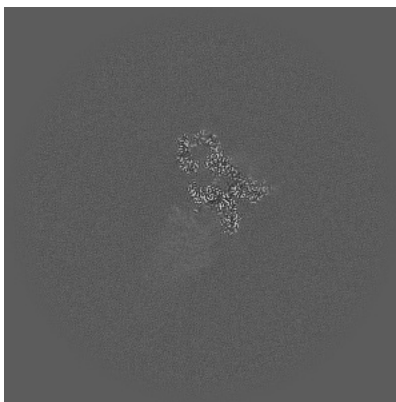
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

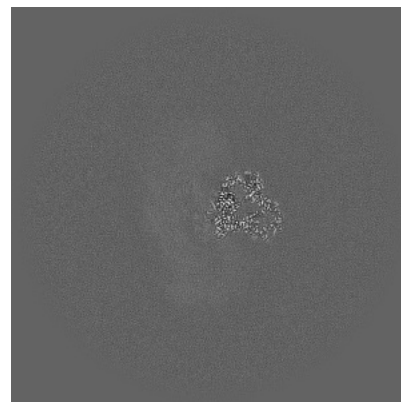
6.3.1 Primary map



X Index: 317



Y Index: 286

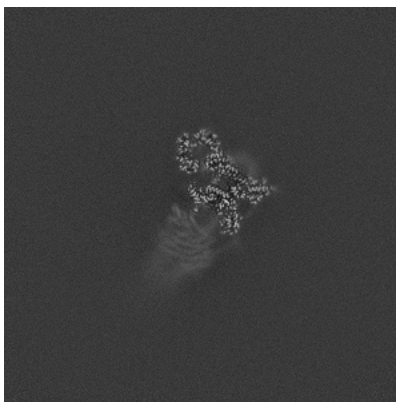


Z Index: 284

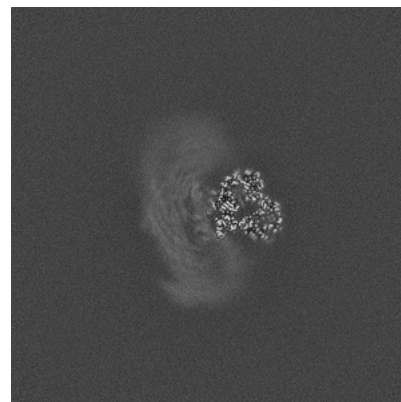
6.3.2 Raw map



X Index: 317



Y Index: 286

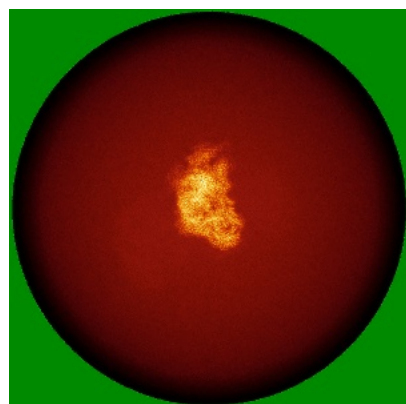


Z Index: 283

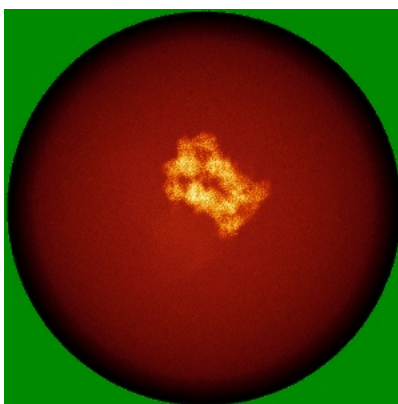
The images above show the largest variance slices of the map in three orthogonal directions.

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

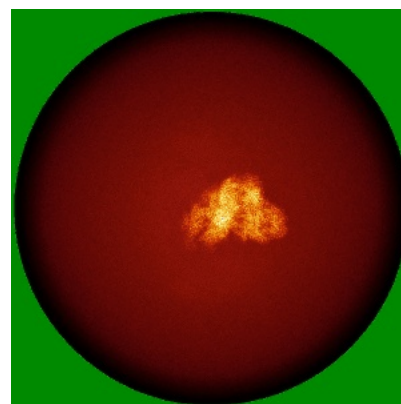
6.4.1 Primary map



X

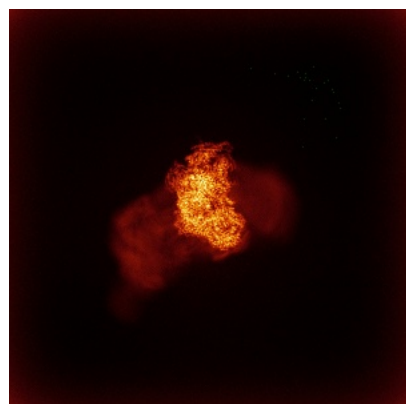


Y

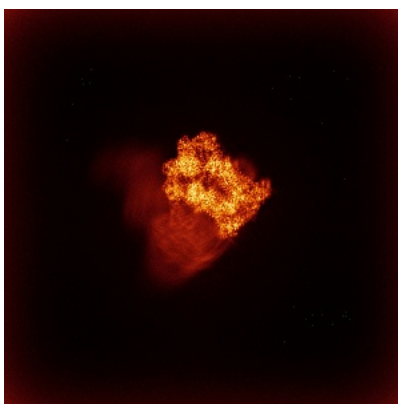


Z

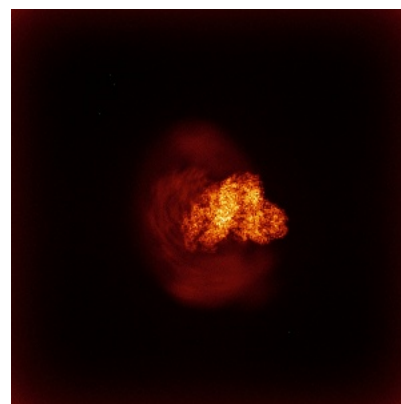
6.4.2 Raw map



X



Y

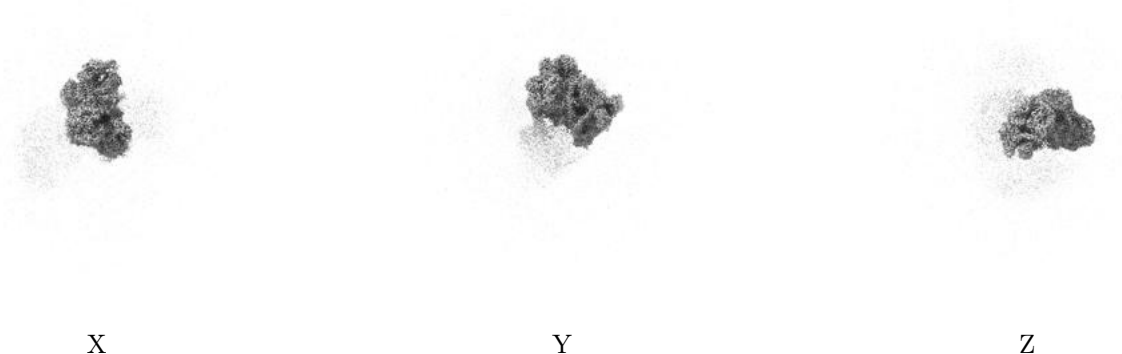


Z

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.

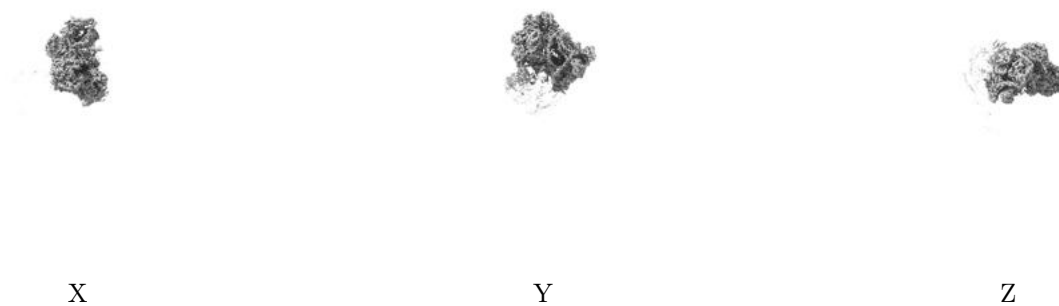
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.8. 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.

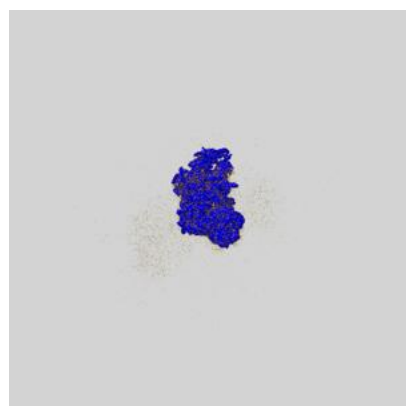
6.6 Mask visualisation [i](#)

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

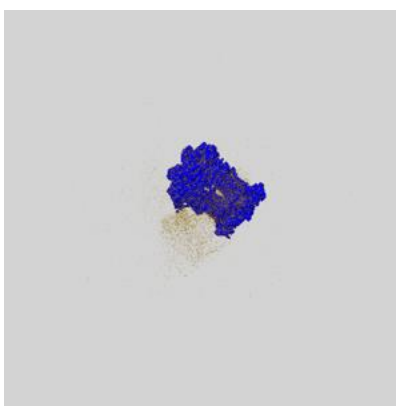
A mask typically either:

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

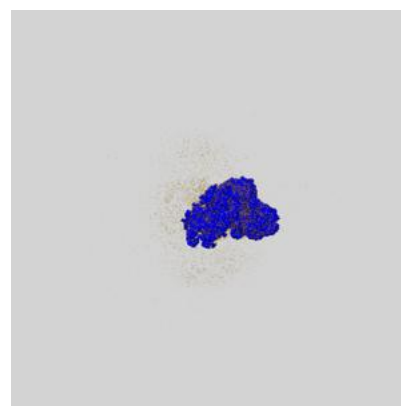
6.6.1 emd_51939_msk_1.map [i](#)



X



Y

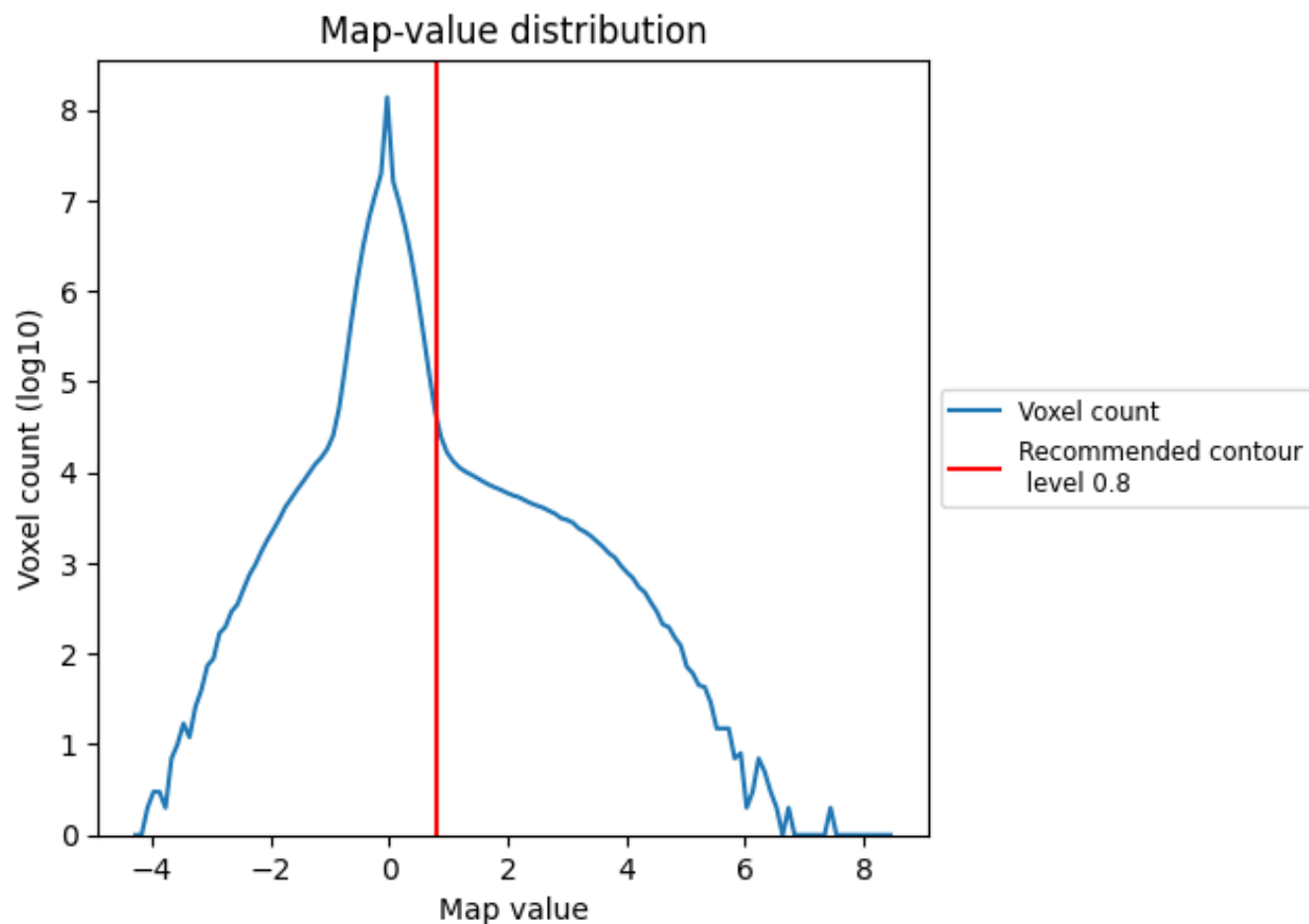


Z

7 Map analysis [i](#)

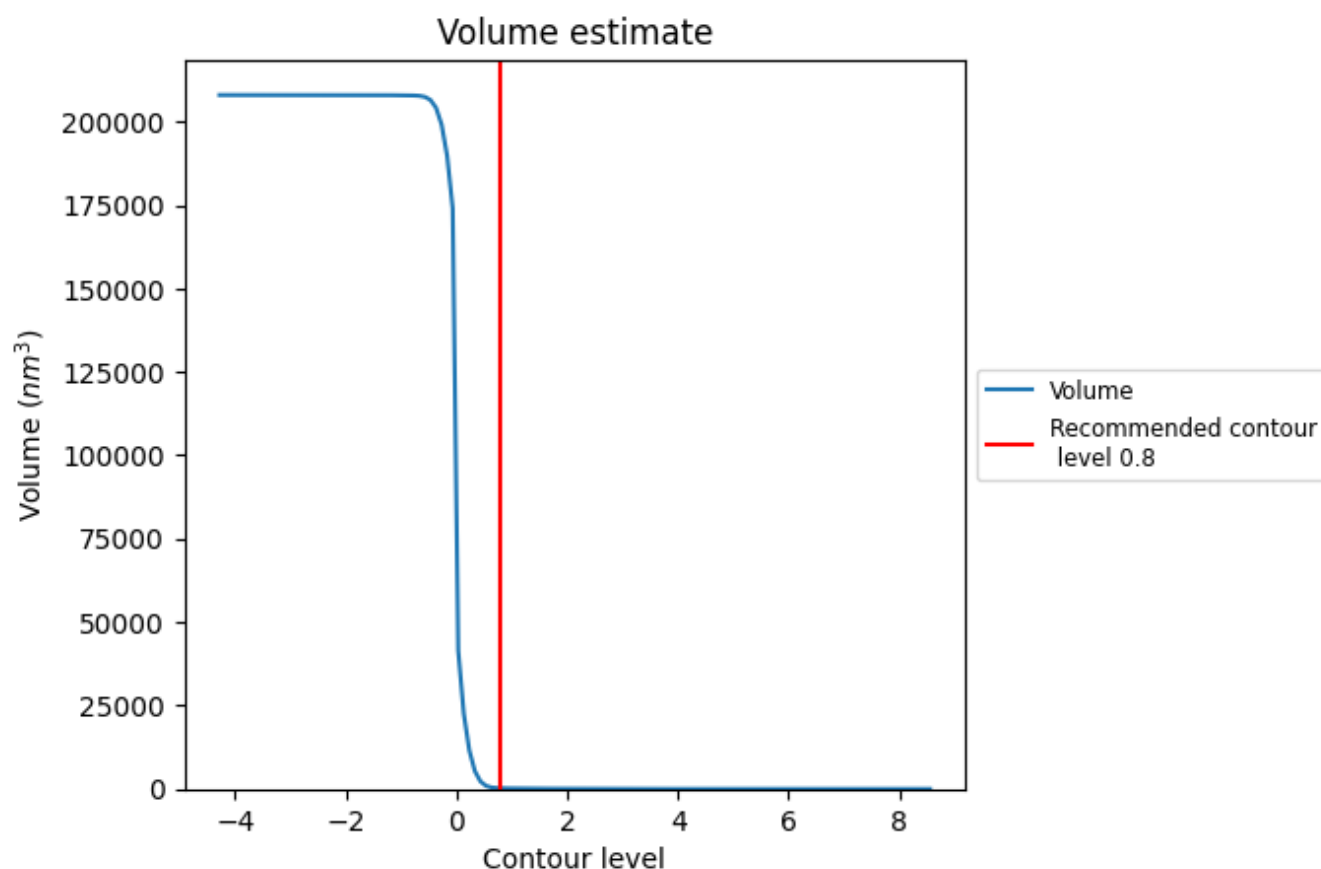
This section contains the results of statistical analysis of the map.

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.

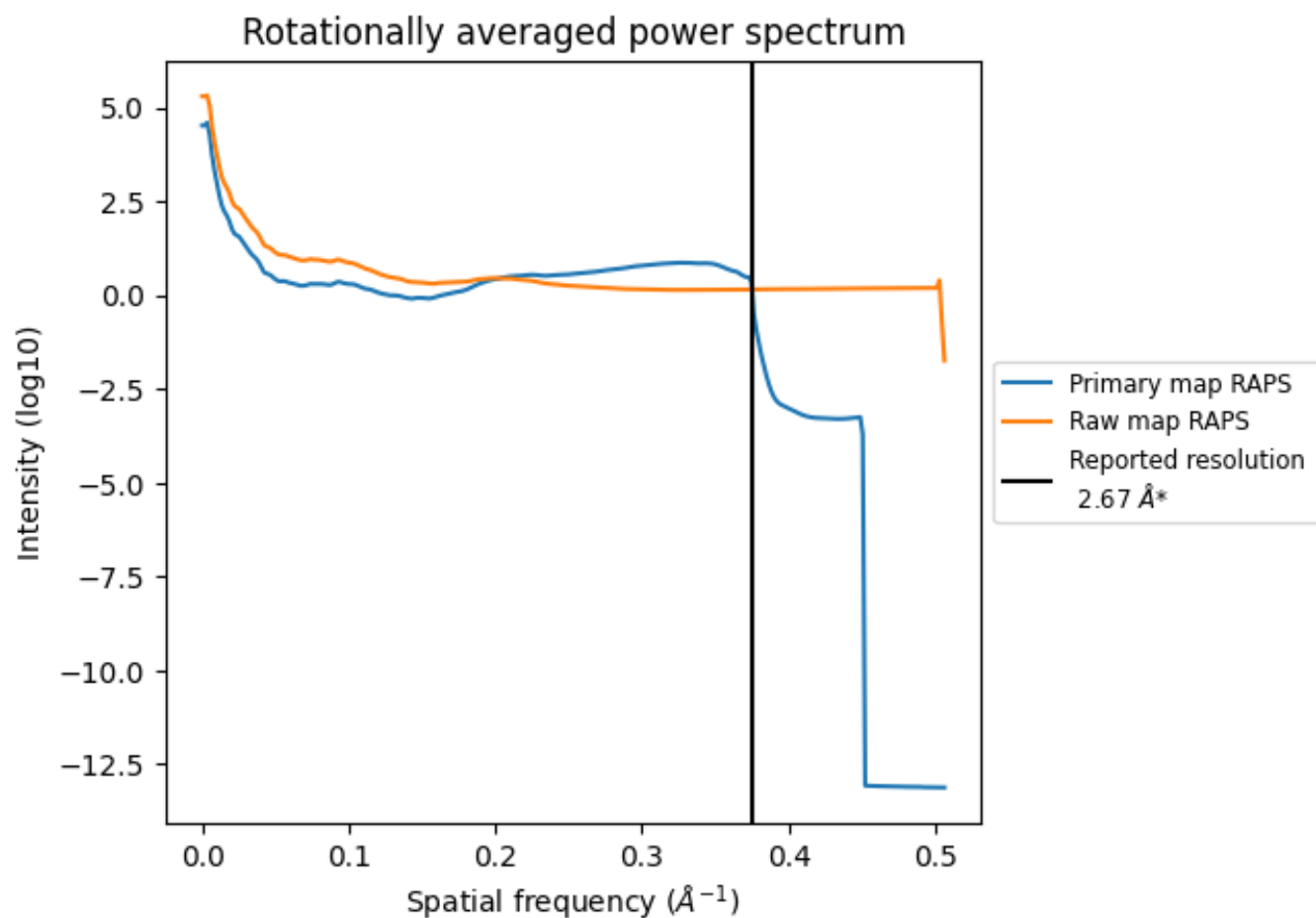
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 221 nm³; this corresponds to an approximate mass of 199 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 ⓘ

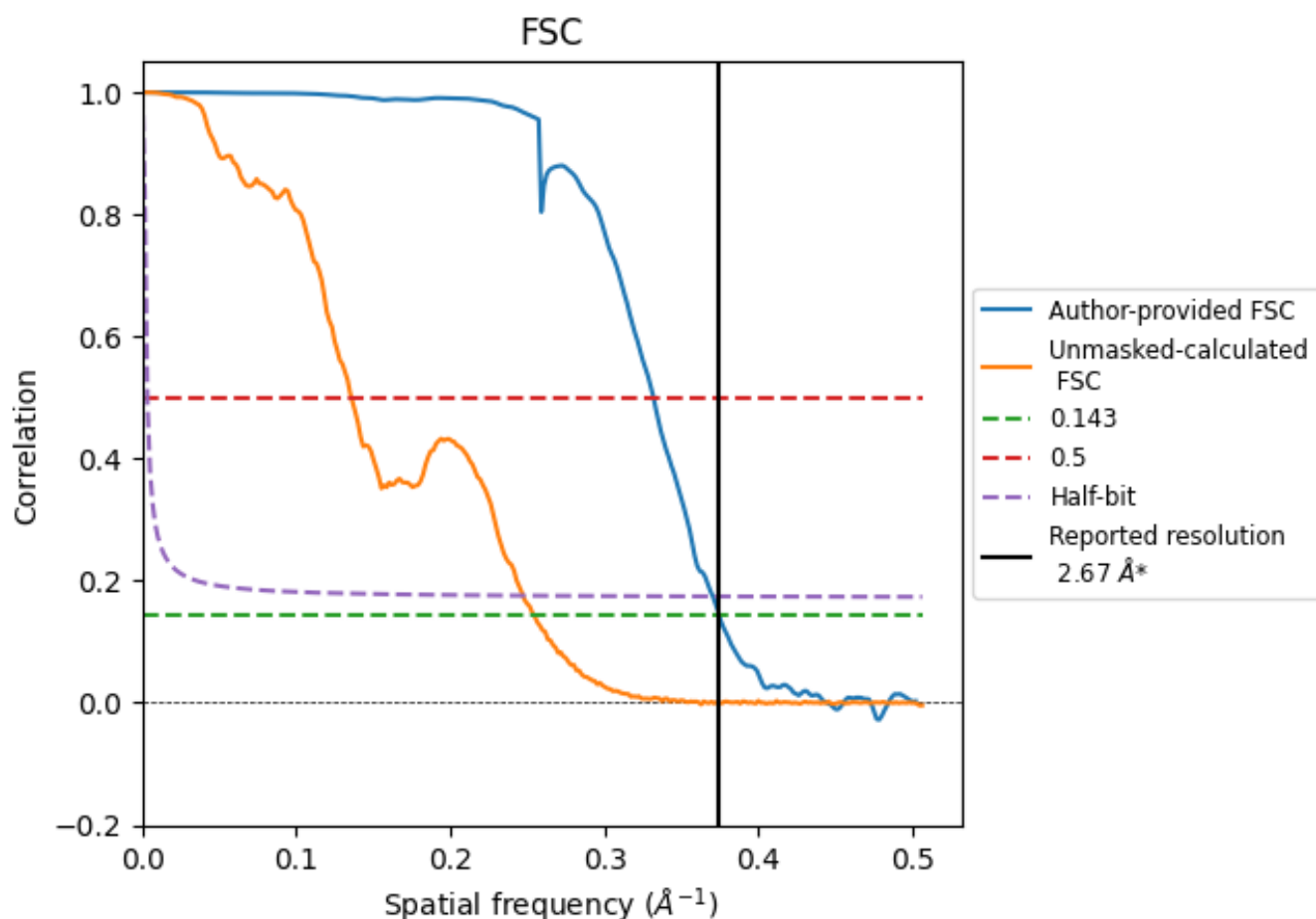


*Reported resolution corresponds to spatial frequency of 0.375 Å⁻¹

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 0.375 Å⁻¹

8.2 Resolution estimates [i](#)

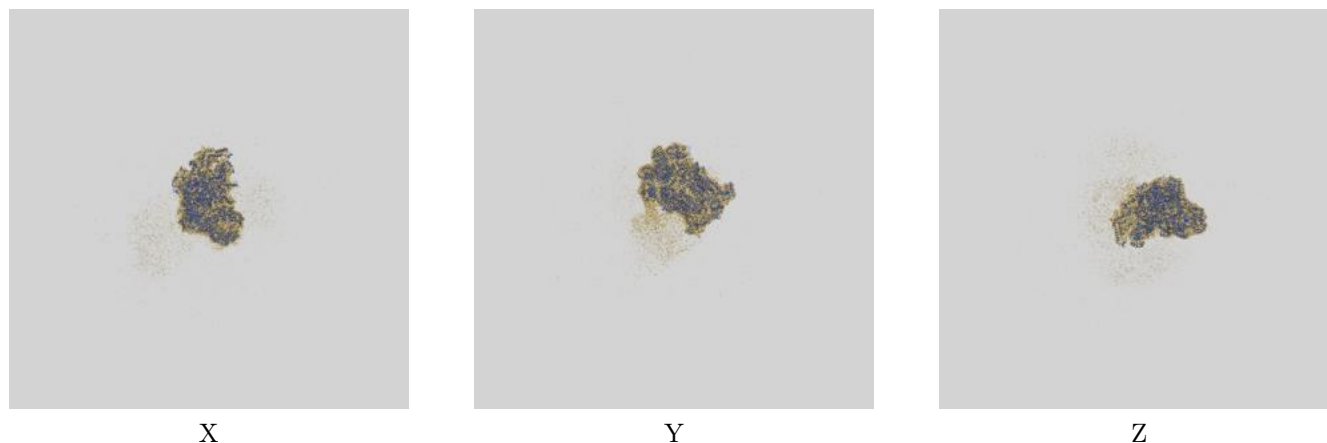
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.67	-	-
Author-provided FSC curve	2.67	3.01	2.70
Unmasked-calculated*	3.93	7.36	4.05

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.93 differs from the reported value 2.67 by more than 10 %

9 Map-model fit [i](#)

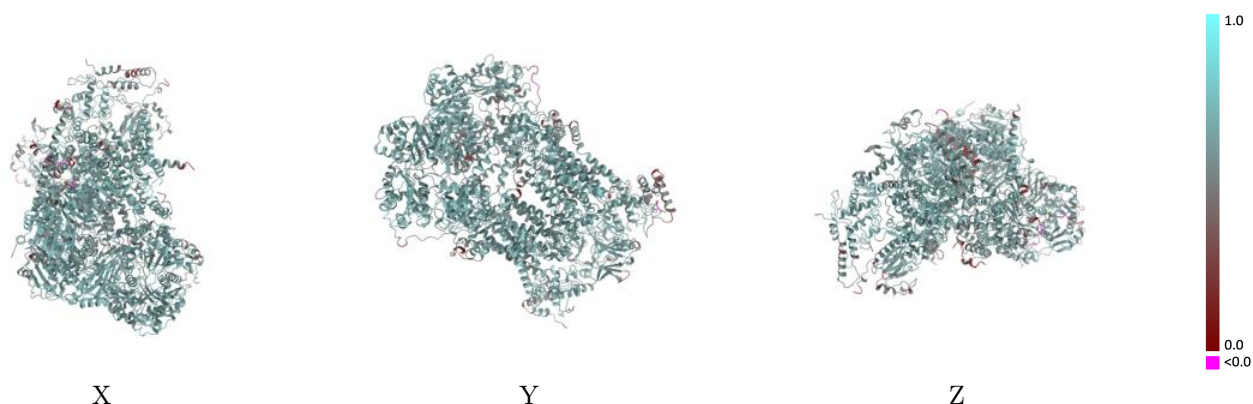
This section contains information regarding the fit between EMDB map EMD-51939 and PDB model 9H8T. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



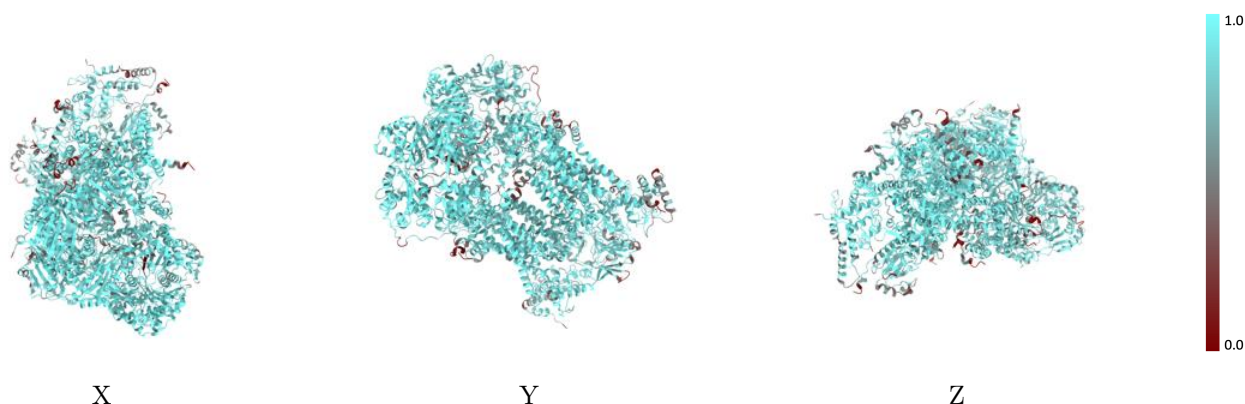
The images above show the 3D surface view of the map at the recommended contour level 0.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



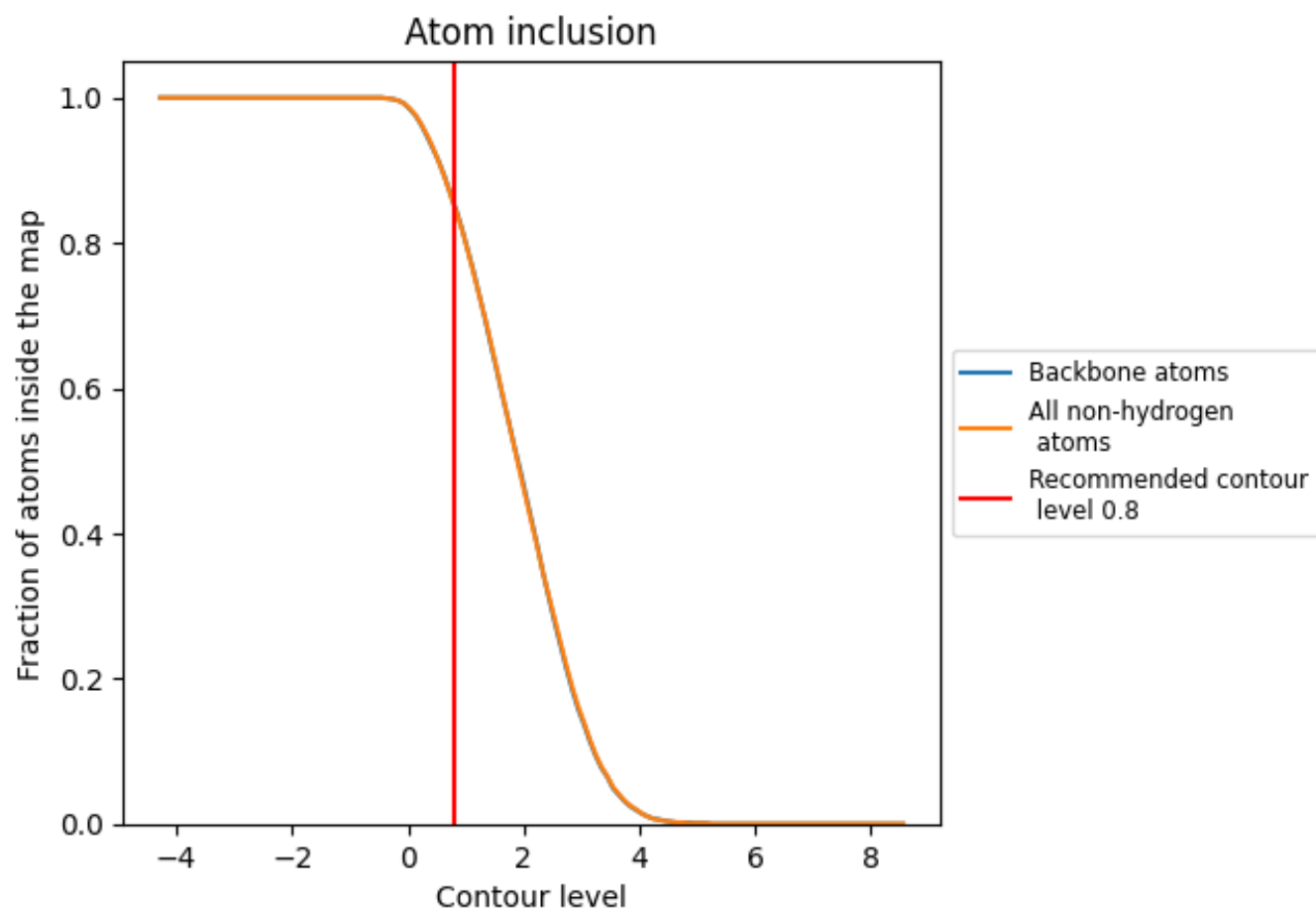
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.8).













































9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 85% 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 (0.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8520	 0.5980
A	 0.7960	 0.5850
C	 0.6640	 0.5140
D	 0.9010	 0.6190
E	 0.6030	 0.5080
F	 0.6250	 0.4590
G	 0.8930	 0.6200
H	 0.6940	 0.4730
J	 0.9260	 0.6380
K	 0.9110	 0.6260
L	 0.8530	 0.5950
T	 0.4000	 0.4550
a	 0.7250	 0.5370
c	 0.7760	 0.5550
d	 0.9120	 0.6120
e	 0.8080	 0.5870
f	 0.7360	 0.5340
g	 0.9020	 0.6270
h	 0.8500	 0.5990
j	 0.9140	 0.6240
k	 0.9060	 0.6170
l	 0.8850	 0.6110

