wwPDB EM Validation Summary Report

Oct 26, 2026 – 03:09 PM EDT

PDB ID	:	9OCS / pdb_00009ocs
EMDB ID	:	EMD-70330
Title	:	High-resolution cryo-EM structure of the CIII2CIV1 respiratory supercomplex from Bacillus subtilis (composite)
Authors	:	Zheng, W.; Gu, M.; Zong, Y.; Zhu, J.; Zhang, K.
Deposited on	:	2025-04-25
Resolution	:	2.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

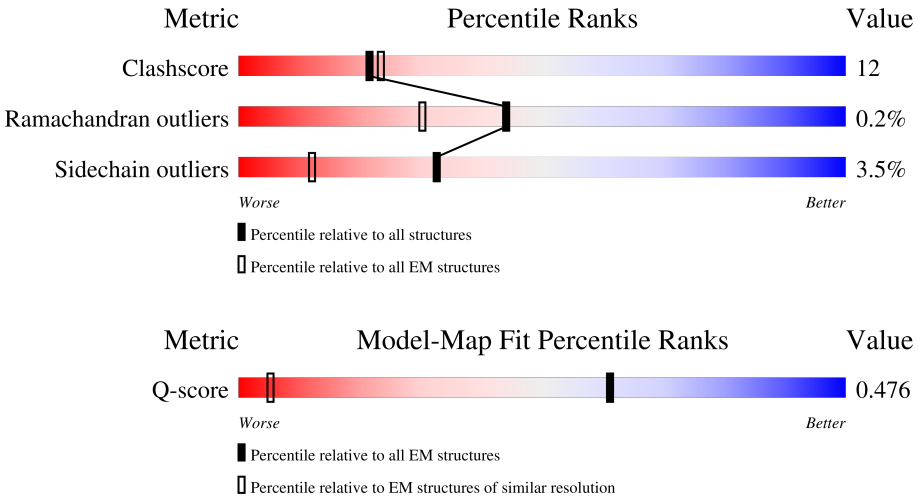
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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)	:	2.51

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.00 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	1659 (1.50 - 2.50)

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 <=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	167	74% 67% 29% • •
1	a	167	68% 63% 30% • 5%
2	B	224	7% 66% 33% •
2	b	224	5% 67% 31% •

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Mol	Chain	Length	Quality of chain
3	C	255	53% 69% 29%
3	c	255	48% 71% 28%
4	D	57	40% 84% 14%
4	d	57	16% 79% 19%
5	E	81	11% 72% 23% 5%
5	e	81	72% 23% 5%
6	F	23	61% 100%
6	f	23	100%
7	G	29	59% 76% 24%
7	g	29	7% 93% 7%
8	H	44	41% 86% 9% 5%
8	h	44	18% 84% 16%
9	I	120	99% 74% 23%
9	i	120	35% 75% 23%
10	J	120	77% 86% 13%
11	K	110	21% 78% 22%
12	L	207	70% 29%
13	M	622	68% 27%
14	N	356	12% 65% 27% 6%

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
15	FES	A	201	-	-	X	-
16	HEC	B	301	X	-	-	-
16	HEC	C	302	X	-	-	-
16	HEC	J	201	X	-	-	-
16	HEC	N	401	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
16	HEC	b	301	X	-	-	-
16	HEC	c	302	X	-	-	-
22	HAS	M	701	X	-	-	-
22	HAS	M	702	X	-	-	-
26	CUA	N	402	-	-	X	-

2 Entry composition (i)

There are 26 unique types of molecules in this entry. The entry contains 27762 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 Menaquinol:cytochrome c reductase iron-sulfur subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	163	Total	C	N	O	S	0	0
			1290	825	216	239	10		
1	a	158	Total	C	N	O	S	0	0
			1255	804	208	234	9		

- Molecule 2 is a protein called Menaquinol:cytochrome c reductase cytochrome b subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	224	Total	C	N	O	S	0	0
			1804	1207	292	293	12		
2	b	224	Total	C	N	O	S	0	0
			1804	1207	292	293	12		

- Molecule 3 is a protein called Menaquinol:cytochrome c reductase cytochrome c subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	255	Total	C	N	O	S	0	0
			1986	1293	325	357	11		
3	c	255	Total	C	N	O	S	0	0
			1985	1292	325	357	11		

- Molecule 4 is a protein called YqgW.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	56	Total	C	N	O	S	0	0
			433	297	68	66	2		
4	d	56	Total	C	N	O	S	0	0
			433	297	68	66	2		

- Molecule 5 is a protein called YqgY.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	77	Total	C	N	O	S	0	0
			645	447	91	101	6		
5	e	77	Total	C	N	O	S	0	0
			645	447	91	101	6		

- Molecule 6 is a protein called QcrF.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	23	Total	C	N	O	0	0
			114	69	23	22		
6	f	23	Total	C	N	O	0	0
			114	69	23	22		

- Molecule 7 is a protein called QcrG.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	29	Total	C	N	O	S	0	0
			221	147	32	39	3		
7	g	29	Total	C	N	O	S	0	0
			221	147	32	39	3		

- Molecule 8 is a protein called YqzM.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	44	Total	C	N	O	S	0	0
			342	223	55	62	2		
8	h	44	Total	C	N	O	S	0	0
			342	223	55	62	2		

- Molecule 9 is a protein called YlbA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	119	Total	C	N	O	S	0	0
			941	603	153	181	4		
9	i	119	Total	C	N	O	S	0	0
			941	603	153	181	4		

- Molecule 10 is a protein called Cytochrome c-550.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	120	Total	C	N	O	S	0	0
			895	567	147	176	5		

- Molecule 11 is a protein called Cytochrome c oxidase subunit 4B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	110	Total	C	N	O	S	0	0
			894	604	141	144	5		

- Molecule 12 is a protein called Cytochrome c oxidase subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	207	Total	C	N	O	S	0	0
			1647	1104	251	282	10		

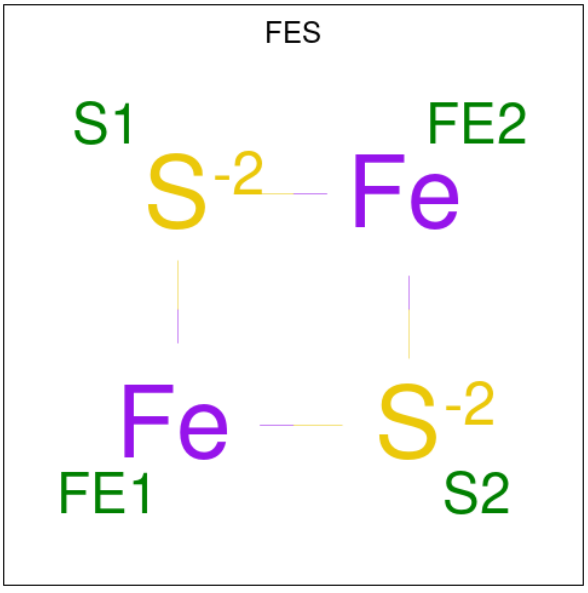
- Molecule 13 is a protein called Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	603	Total	C	N	O	S	0	0
			4748	3206	745	771	26		

- Molecule 14 is a protein called Cytochrome c oxidase subunit 2.

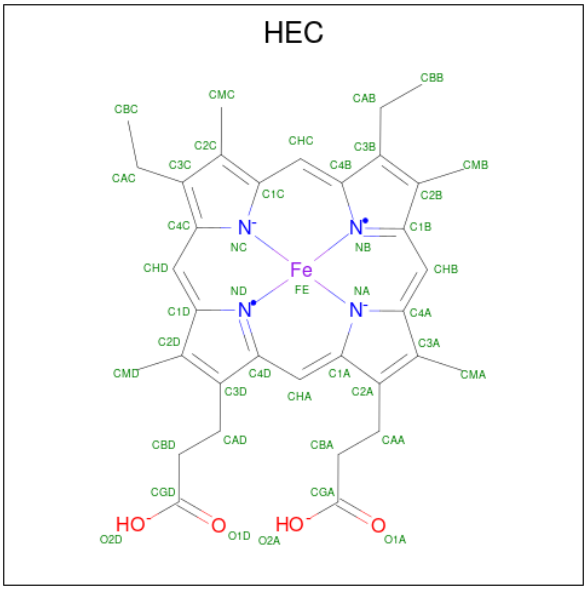
Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	335	Total	C	N	O	S	0	0
			2649	1704	437	496	12		

- Molecule 15 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



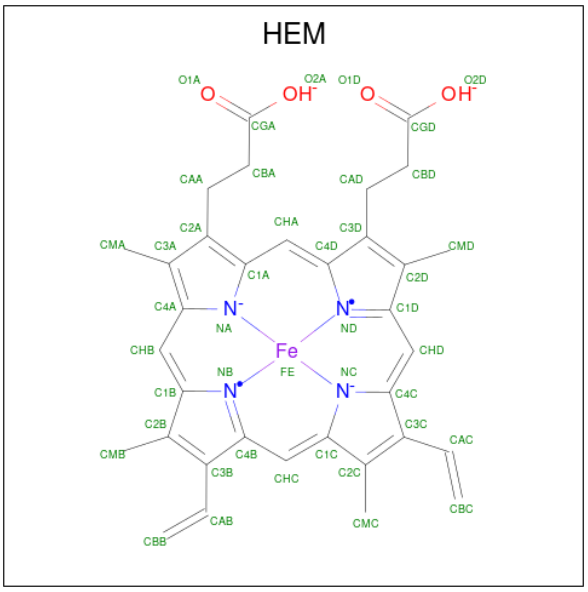
Mol	Chain	Residues	Atoms	AltConf
15	A	1	Total Fe S 4 2 2	0
15	a	1	Total Fe S 4 2 2	0

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



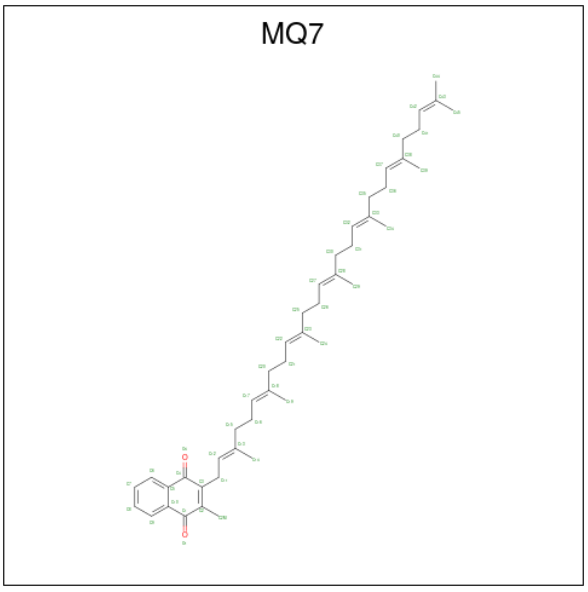
Mol	Chain	Residues	Atoms	AltConf
16	B	1	Total C Fe N O 43 34 1 4 4	0
16	C	1	Total C Fe N O 43 34 1 4 4	0
16	J	1	Total C Fe N O 43 34 1 4 4	0
16	N	1	Total C Fe N O 43 34 1 4 4	0
16	b	1	Total C Fe N O 43 34 1 4 4	0
16	c	1	Total C Fe N O 43 34 1 4 4	0

- Molecule 17 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



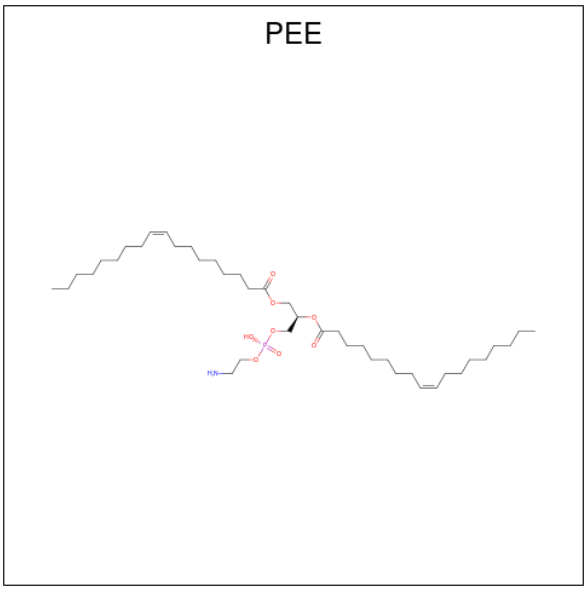
Mol	Chain	Residues	Atoms					AltConf
17	B	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
17	B	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
17	b	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
17	b	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 18 is MENAQUINONE-7 (CCD ID: MQ7) (formula: $C_{46}H_{64}O_2$).



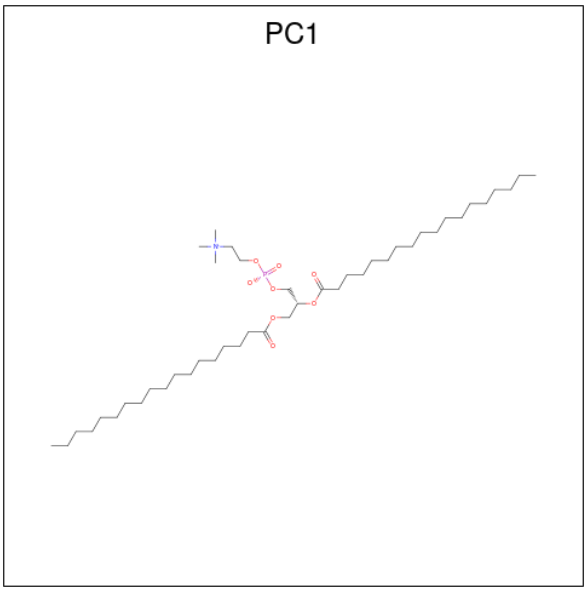
Mol	Chain	Residues	Atoms			AltConf
18	B	1	Total	C	O	0
			48	46	2	
18	C	1	Total	C	O	0
			48	46	2	
18	b	1	Total	C	O	0
			48	46	2	
18	c	1	Total	C	O	0
			48	46	2	

- Molecule 19 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: $C_{41}H_{78}NO_8P$).



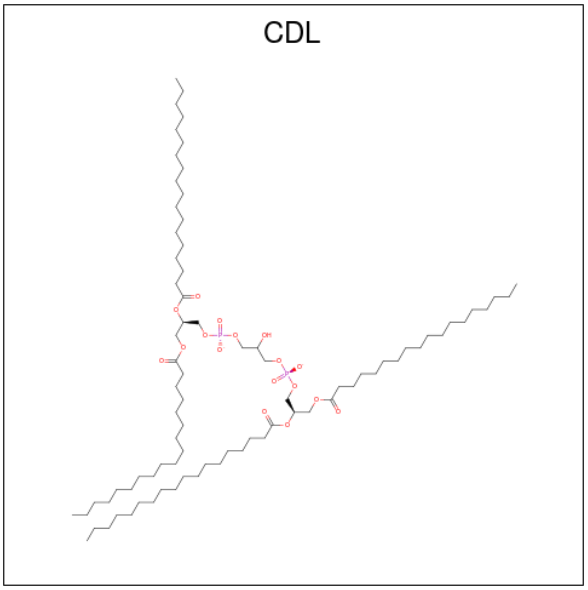
Mol	Chain	Residues	Atoms					AltConf
19	C	1	Total	C	N	O	P	0
			42	32	1	8	1	
19	J	1	Total	C	N	O	P	0
			40	30	1	8	1	
19	L	1	Total	C	N	O	P	0
			51	41	1	8	1	
19	c	1	Total	C	N	O	P	0
			42	32	1	8	1	

- Molecule 20 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
20	C	1	Total	C	N	O	P	0
			48	38	1	8	1	
20	c	1	Total	C	N	O	P	0
			43	33	1	8	1	

- Molecule 21 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



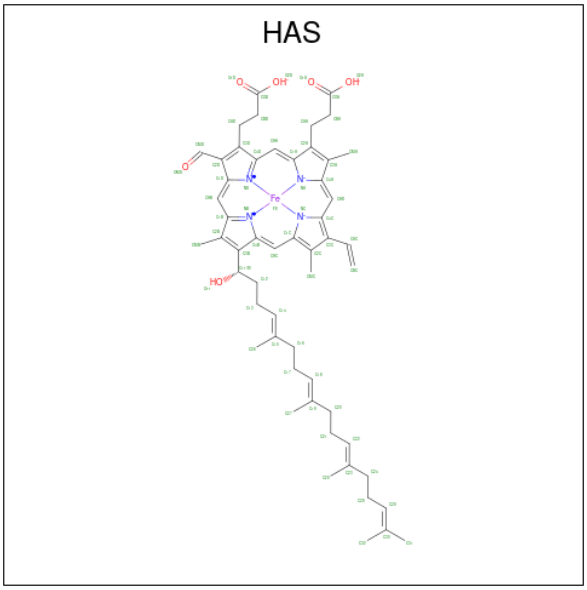
Mol	Chain	Residues	Atoms				AltConf
21	J	1	Total	C	O	P	0
			100	81	17	2	
21	K	1	Total	C	O	P	0
			100	81	17	2	

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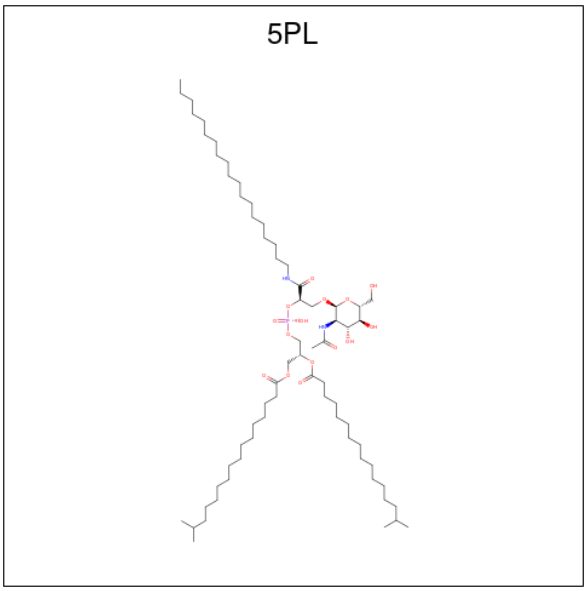
Mol	Chain	Residues	Atoms				AltConf
21	L	1	Total	C	O	P	0
			98	79	17	2	

- Molecule 22 is HEME-AS (CCD ID: HAS) (formula: $C_{54}H_{64}FeN_4O_6$).



Mol	Chain	Residues	Atoms					AltConf
22	M	1	Total	C	Fe	N	O	0
			65	54	1	4	6	
22	M	1	Total	C	Fe	N	O	0
			65	54	1	4	6	

- Molecule 23 is (1R,4S,6R)-6-({[2-(ACETYLAMINO)-2-DEOXY-ALPHA-D-GLUCOPYRANOSYL]OXY}METHYL)-4-HYDROXY-1-{[(15-METHYLHEXADECANOYL)OXY]METHYL}-4-OXIDO-7-OXO-3,5-DIOXA-8-AZA-4-PHOSPHAHEPTACOS-1-YL 15-METHYLHEXADECANOATE (CCD ID: 5PL) (formula: $C_{67}H_{129}N_2O_{15}P$).



Mol	Chain	Residues	Atoms					AltConf
23	M	1	Total	C	N	O	P	0
			85	67	2	15	1	

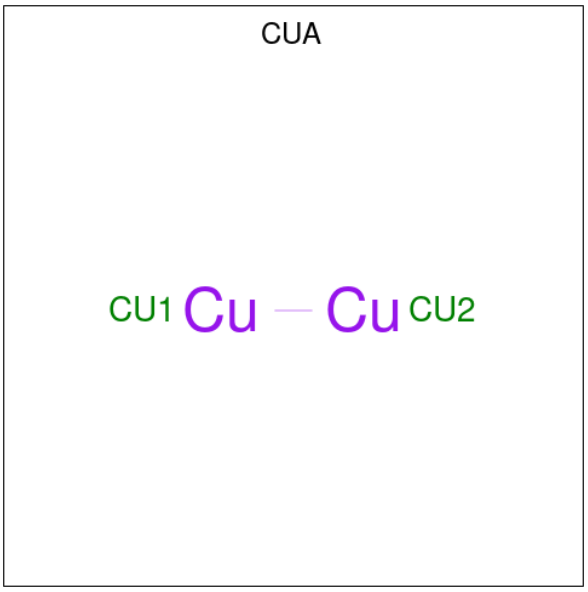
- Molecule 24 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		AltConf
24	M	1	Total	Cu	0
			1	1	

- Molecule 25 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
25	M	1	Total	Mg	0
			1	1	

- Molecule 26 is DINUCLEAR COPPER ION (CCD ID: CUA) (formula: Cu_2).



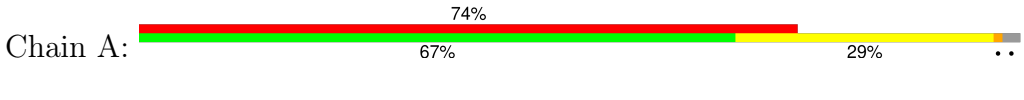
Mol	Chain	Residues	Atoms		AltConf
			Total	Cu	
26	N	1	2	2	0

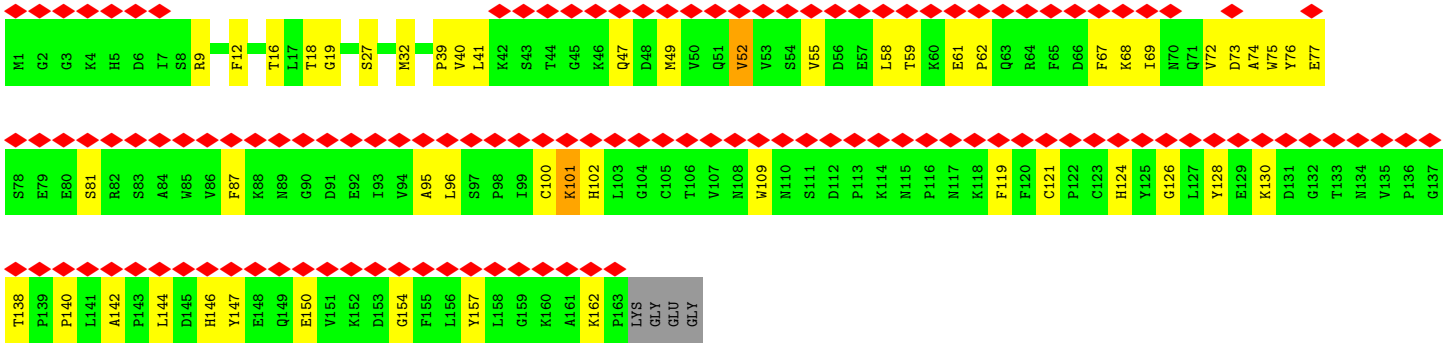
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Menaquinol:cytochrome c reductase iron-sulfur subunit

Chain A:

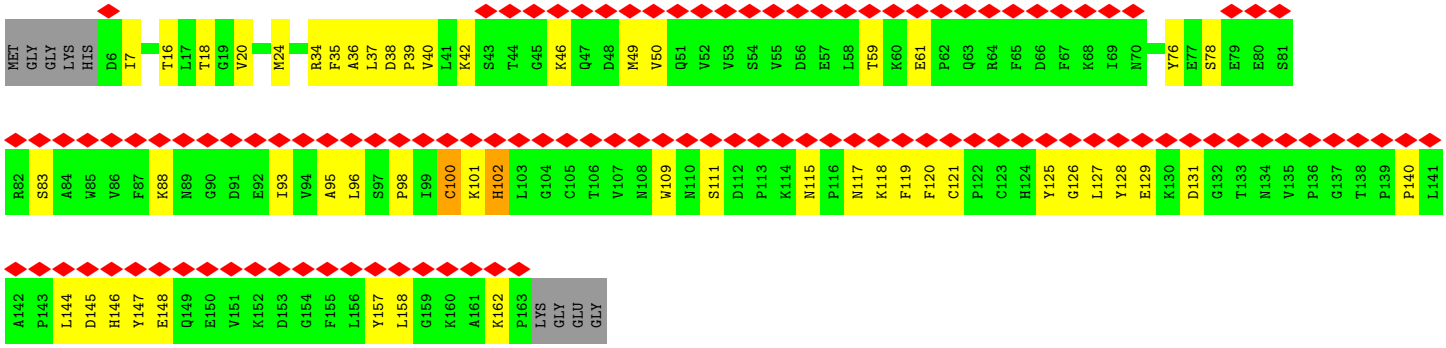




• Molecule 1: Menaquinol:cytochrome c reductase iron-sulfur subunit

Chain a:

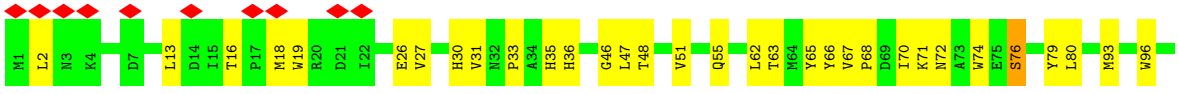


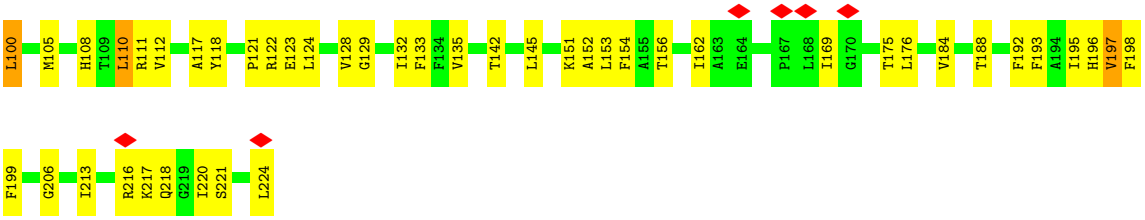


• Molecule 2: Menaquinol:cytochrome c reductase cytochrome b subunit

Chain B:

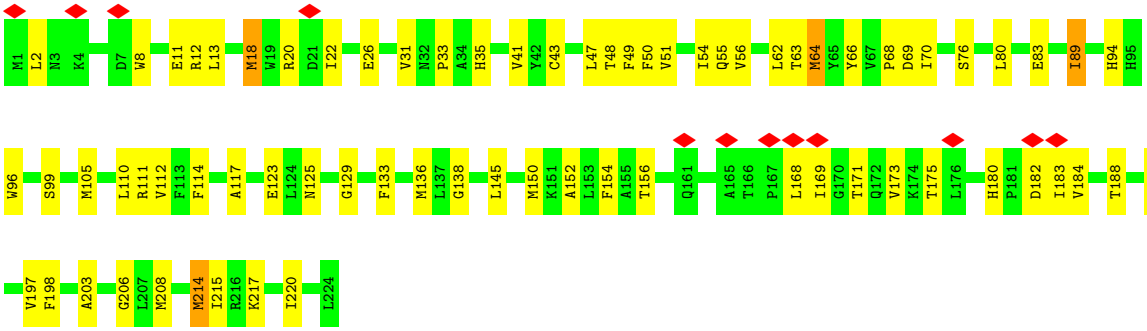






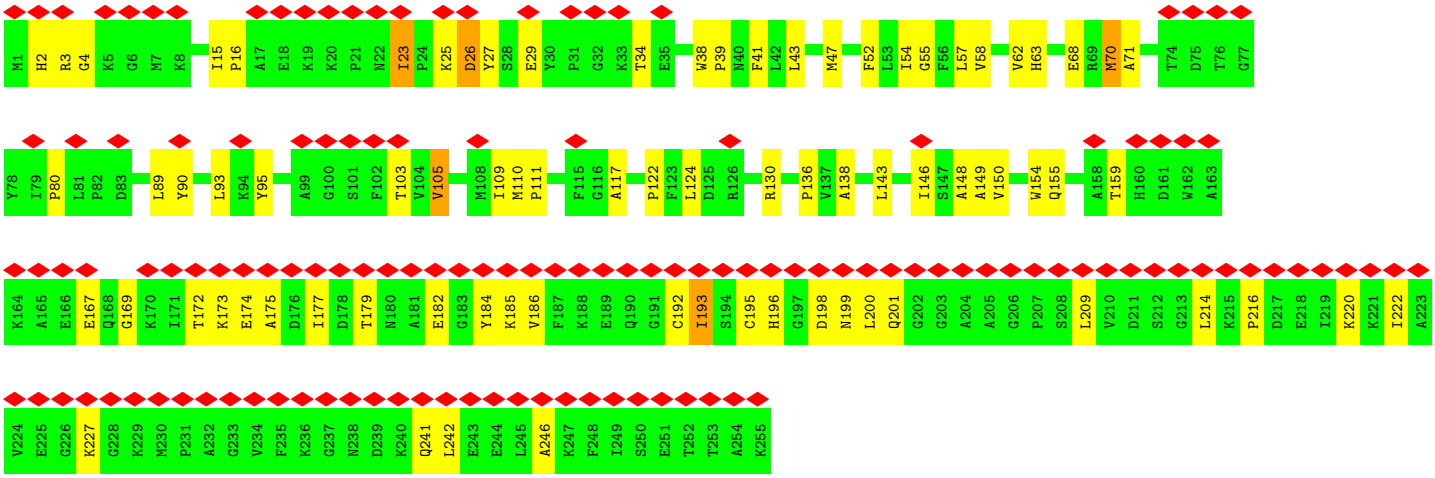
• Molecule 2: Menaquinol:cytochrome c reductase cytochrome b subunit





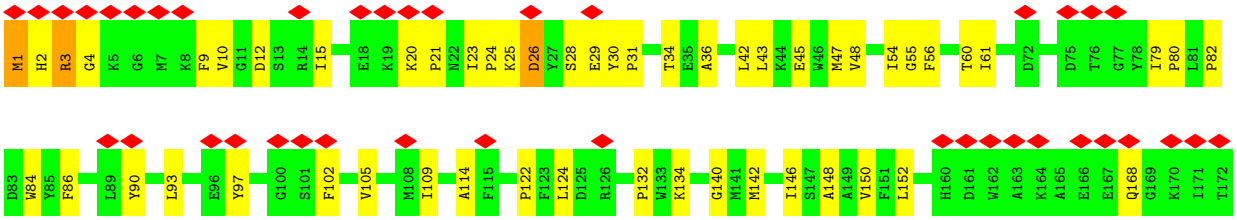
• Molecule 3: Menaquinol:cytochrome c reductase cytochrome c subunit

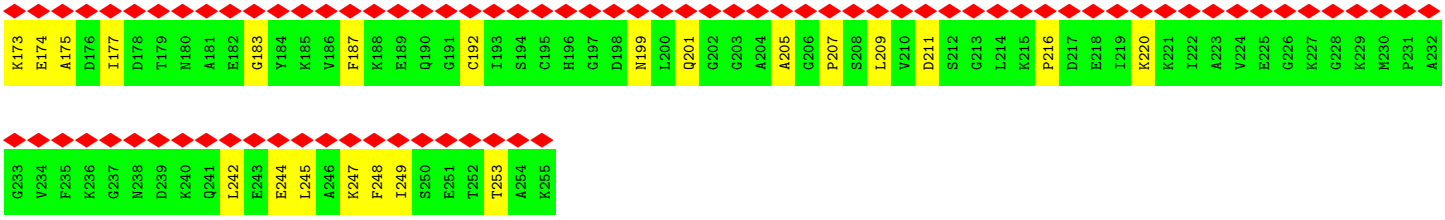




• Molecule 3: Menaquinol:cytochrome c reductase cytochrome c subunit



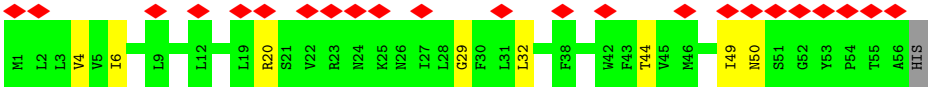




• Molecule 4: YqgW

Chain D:

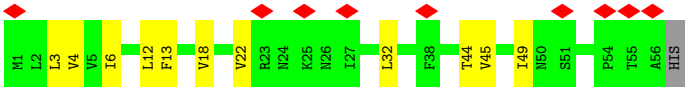




• Molecule 4: YqgW

Chain d:

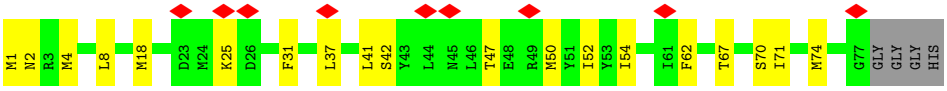




• Molecule 5: YqgY

Chain E:

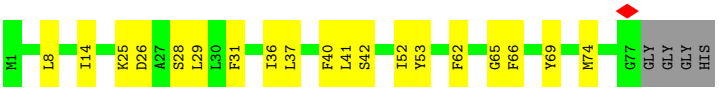




• Molecule 5: YqgY

Chain e:

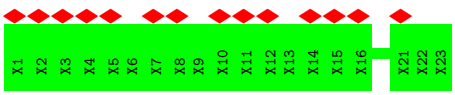




• Molecule 6: QcrF

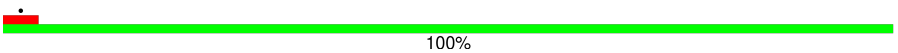
Chain F:





• Molecule 6: QcrF

Chain f:

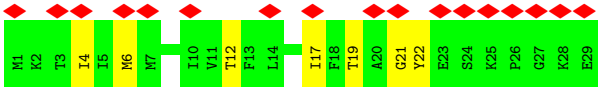




• Molecule 7: QcrG

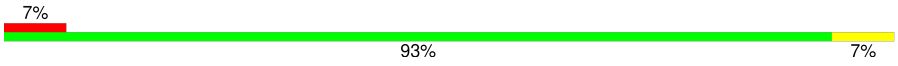
Chain G:

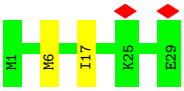




• Molecule 7: QcrG

Chain g:

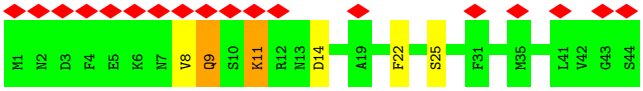




• Molecule 8: YqzM

Chain H:

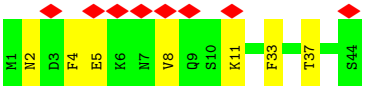




• Molecule 8: YqzM

Chain h:

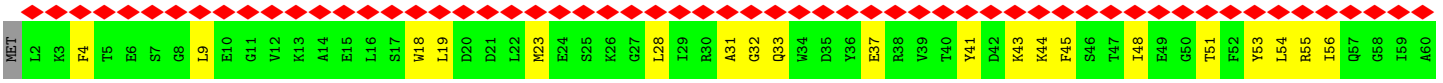


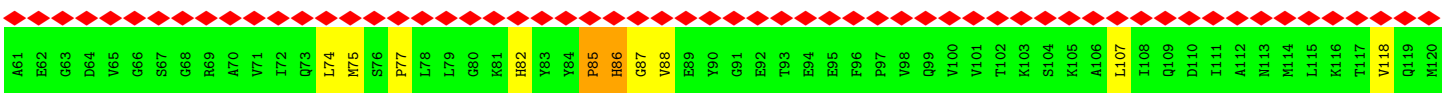


• Molecule 9: YlbA

Chain I:



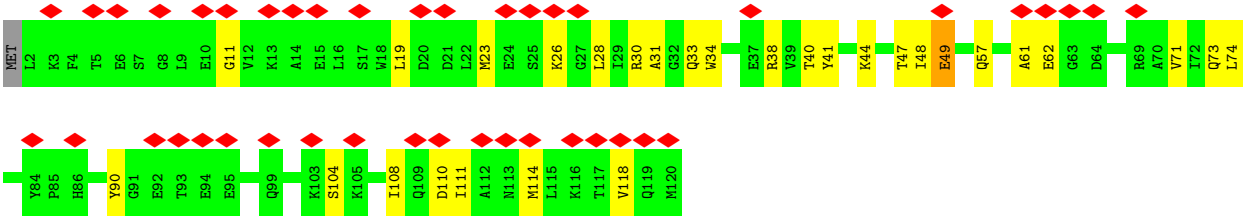




• Molecule 9: YlbA

Chain i:

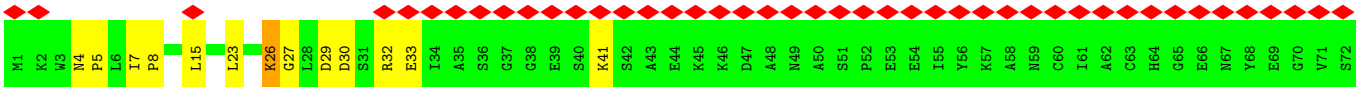


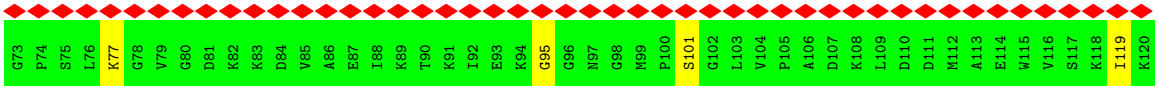


• Molecule 10: Cytochrome c-550

Chain J:







• Molecule 11: Cytochrome c oxidase subunit 4B

Chain K:

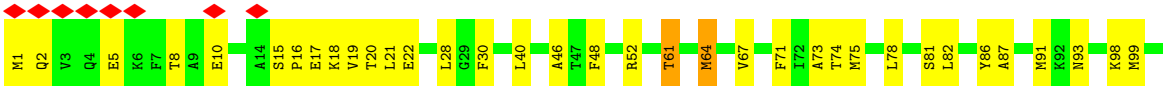




• Molecule 12: Cytochrome c oxidase subunit 3

Chain L:



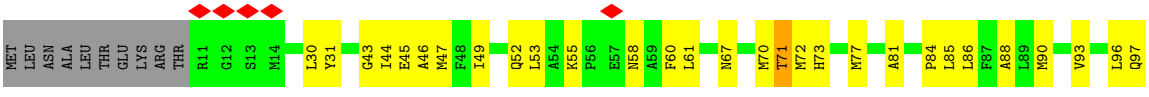


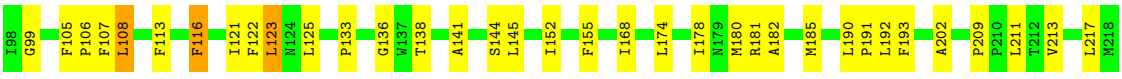


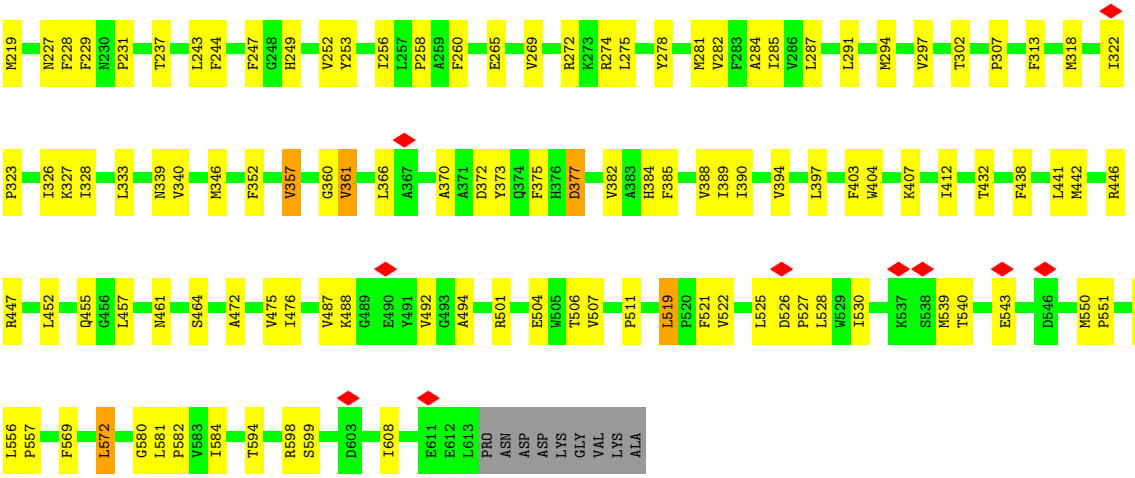
• Molecule 13: Cytochrome c oxidase subunit 1

Chain M:





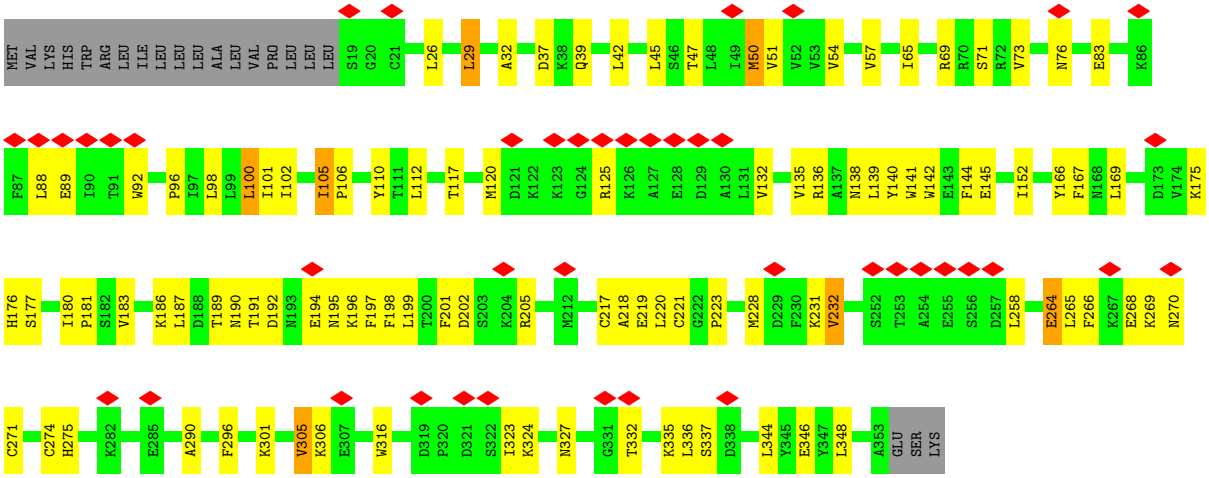




• Molecule 14: Cytochrome c oxidase subunit 2

Chain N:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	70713	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.825	Depositor
Minimum map value	-0.430	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	297.0, 297.0, 297.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FES, 5PL, PC1, CUA, HAS, MQ7, CU, HEM, MG, HEC, CDL, PEE

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	0.17	0/1326	0.39	0/1796
1	a	0.16	0/1290	0.37	0/1750
2	B	0.20	0/1863	0.37	0/2533
2	b	0.20	0/1863	0.34	0/2533
3	C	0.15	0/2040	0.34	0/2759
3	c	0.20	0/2039	0.43	2/2757 (0.1%)
4	D	0.13	0/444	0.27	0/605
4	d	0.13	0/444	0.26	0/605
5	E	0.13	0/667	0.22	0/900
5	e	0.17	0/667	0.27	0/900
7	G	0.12	0/224	0.35	0/299
7	g	0.14	0/224	0.26	0/299
8	H	0.17	0/349	0.40	0/468
8	h	0.15	0/349	0.27	0/468
9	I	0.14	0/959	0.42	1/1291 (0.1%)
9	i	0.13	0/959	0.29	0/1291
10	J	0.18	0/910	0.48	2/1221 (0.2%)
11	K	0.16	0/920	0.31	0/1243
12	L	0.18	0/1698	0.29	0/2304
13	M	0.19	0/4912	0.35	0/6695
14	N	0.24	0/2706	0.42	0/3660
All	All	0.18	0/26853	0.36	5/36377 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	J	26	LYS	CB-CG-CD	8.85	131.65	111.30
3	c	1	MET	CB-CA-C	6.91	123.22	110.10
10	J	26	LYS	CG-CD-CE	-6.83	95.59	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	c	1	MET	CB-CG-SD	6.54	132.32	112.70
9	I	86	HIS	N-CA-C	5.88	117.84	107.61

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1290	0	1254	38	0
1	a	1255	0	1216	39	0
2	B	1804	0	1813	73	0
2	b	1804	0	1813	60	0
3	C	1986	0	1999	64	0
3	c	1985	0	1993	83	0
4	D	433	0	463	6	0
4	d	433	0	463	5	0
5	E	645	0	642	12	0
5	e	645	0	642	16	0
6	F	114	0	25	0	0
6	f	114	0	26	0	0
7	G	221	0	241	3	0
7	g	221	0	241	2	0
8	H	342	0	334	7	0
8	h	342	0	334	7	0
9	I	941	0	938	30	0
9	i	941	0	938	18	0
10	J	895	0	909	15	0
11	K	894	0	923	26	0
12	L	1647	0	1645	51	0
13	M	4748	0	4773	124	0
14	N	2649	0	2680	77	0
15	A	4	0	0	2	0
15	a	4	0	0	1	0
16	B	43	0	30	6	0
16	C	43	0	32	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	J	43	0	32	0	0
16	N	43	0	32	3	0
16	b	43	0	31	6	0
16	c	43	0	30	3	0
17	B	86	0	60	11	0
17	b	86	0	60	3	0
18	B	48	0	64	6	0
18	C	48	0	64	4	0
18	b	48	0	64	1	0
18	c	48	0	64	8	0
19	C	42	0	54	4	0
19	J	40	0	53	0	0
19	L	51	0	78	5	0
19	c	42	0	52	2	0
20	C	48	0	73	3	0
20	c	43	0	60	2	0
21	J	100	0	154	13	0
21	K	100	0	156	3	0
21	L	98	0	149	8	0
22	M	130	0	124	14	0
23	M	85	0	128	10	0
24	M	1	0	0	0	0
25	M	1	0	0	0	0
26	N	2	0	0	3	0
All	All	27762	0	27949	651	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 12.

The worst 5 of 651 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)
14:N:221:CYS:SG	26:N:402:CUA:CU1	1.21	1.27
14:N:217:CYS:SG	26:N:402:CUA:CU2	1.34	1.17
18:B:304:MQ7:H7	3:c:1:MET:N	1.73	1.02
18:B:304:MQ7:H7	3:c:1:MET:H1	1.21	0.97
2:B:31:VAL:HG11	16:B:301:HEC:HAB	1.50	0.93

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	161/167 (96%)	147 (91%)	14 (9%)	0	100 100
1	a	156/167 (93%)	142 (91%)	14 (9%)	0	100 100
2	B	222/224 (99%)	209 (94%)	12 (5%)	1 (0%)	24 21
2	b	222/224 (99%)	219 (99%)	2 (1%)	1 (0%)	24 21
3	C	253/255 (99%)	238 (94%)	14 (6%)	1 (0%)	30 27
3	c	253/255 (99%)	241 (95%)	10 (4%)	2 (1%)	16 11
4	D	54/57 (95%)	52 (96%)	2 (4%)	0	100 100
4	d	54/57 (95%)	53 (98%)	1 (2%)	0	100 100
5	E	75/81 (93%)	75 (100%)	0	0	100 100
5	e	75/81 (93%)	74 (99%)	1 (1%)	0	100 100
7	G	27/29 (93%)	20 (74%)	6 (22%)	1 (4%)	2 1
7	g	27/29 (93%)	27 (100%)	0	0	100 100
8	H	42/44 (96%)	39 (93%)	3 (7%)	0	100 100
8	h	42/44 (96%)	39 (93%)	3 (7%)	0	100 100
9	I	117/120 (98%)	113 (97%)	3 (3%)	1 (1%)	14 9
9	i	117/120 (98%)	115 (98%)	2 (2%)	0	100 100
10	J	118/120 (98%)	110 (93%)	8 (7%)	0	100 100
11	K	108/110 (98%)	104 (96%)	4 (4%)	0	100 100
12	L	205/207 (99%)	202 (98%)	3 (2%)	0	100 100
13	M	601/622 (97%)	582 (97%)	18 (3%)	1 (0%)	43 42
14	N	333/356 (94%)	314 (94%)	19 (6%)	0	100 100
All	All	3262/3369 (97%)	3115 (96%)	139 (4%)	8 (0%)	44 42

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	3	ARG
2	B	16	THR
3	c	3	ARG
3	c	26	ASP
7	G	22	TYR

5.3.2 Protein sidechains (i)

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	142/144 (99%)	139 (98%)	3 (2%)	47 52
1	a	139/144 (96%)	134 (96%)	5 (4%)	31 31
2	B	188/188 (100%)	183 (97%)	5 (3%)	39 42
2	b	188/188 (100%)	179 (95%)	9 (5%)	23 21
3	C	205/205 (100%)	194 (95%)	11 (5%)	20 17
3	c	205/205 (100%)	204 (100%)	1 (0%)	81 87
4	D	45/46 (98%)	45 (100%)	0	100 100
4	d	45/46 (98%)	41 (91%)	4 (9%)	9 6
5	E	66/67 (98%)	63 (96%)	3 (4%)	24 23
5	e	66/67 (98%)	64 (97%)	2 (3%)	36 38
7	G	25/25 (100%)	23 (92%)	2 (8%)	11 8
7	g	25/25 (100%)	25 (100%)	0	100 100
8	H	37/37 (100%)	35 (95%)	2 (5%)	20 17
8	h	37/37 (100%)	36 (97%)	1 (3%)	39 42
9	I	100/101 (99%)	98 (98%)	2 (2%)	48 54
9	i	100/101 (99%)	96 (96%)	4 (4%)	28 27
10	J	96/96 (100%)	94 (98%)	2 (2%)	47 52
11	K	94/94 (100%)	91 (97%)	3 (3%)	34 35
12	L	173/173 (100%)	168 (97%)	5 (3%)	37 40
13	M	490/506 (97%)	474 (97%)	16 (3%)	33 34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
14	N	291/311 (94%)	274 (94%)	17 (6%)	18 15
All	All	2757/2806 (98%)	2660 (96%)	97 (4%)	32 32

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	N	50	MET
1	a	18	THR
14	N	100	LEU
14	N	198	PHE
1	a	121	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
14	N	270	ASN
2	b	180	HIS
14	N	327	ASN
2	b	35	HIS
3	c	199	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 31 ligands modelled in this entry, 2 are monoatomic - leaving 29 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	PEE	J	203	-	39,39,50	0.33	0	42,44,55	0.43	0
18	MQ7	b	304	-	49,49,49	0.39	0	61,63,63	0.67	1 (1%)
17	HEM	b	303	2	50,50,50	1.59	9 (18%)	67,82,82	1.58	12 (17%)
19	PEE	c	303	-	41,41,50	0.33	0	44,46,55	0.40	0
21	CDL	K	201	-	99,99,99	0.28	0	105,111,111	0.38	0
16	HEC	C	302	-	50,50,50	3.09	31 (62%)	68,82,82	2.26	28 (41%)
22	HAS	M	702	13	72,72,72	2.39	26 (36%)	87,109,109	2.43	32 (36%)
16	HEC	J	201	-	50,50,50	3.10	30 (60%)	68,82,82	2.25	28 (41%)
18	MQ7	C	301	-	49,49,49	0.42	0	61,63,63	0.68	2 (3%)
15	FES	a	201	1	0,4,4	-	-	-		
18	MQ7	B	304	-	49,49,49	0.38	0	61,63,63	0.55	1 (1%)
22	HAS	M	701	13	72,72,72	2.41	27 (37%)	87,109,109	2.30	32 (36%)
17	HEM	B	302	2	50,50,50	1.59	9 (18%)	67,82,82	1.68	13 (19%)
17	HEM	b	302	2	50,50,50	1.58	9 (18%)	67,82,82	1.66	14 (20%)
20	PC1	C	304	-	47,47,53	0.30	0	53,55,61	0.33	0
19	PEE	C	303	-	41,41,50	0.33	0	44,46,55	0.43	0
21	CDL	L	302	-	97,97,99	0.28	0	103,109,111	0.44	0
21	CDL	J	202	-	99,99,99	0.30	0	105,111,111	0.52	1 (0%)
20	PC1	c	304	-	42,42,53	0.55	0	48,50,61	0.51	1 (2%)
16	HEC	c	302	3	50,50,50	3.82	31 (62%)	68,82,82	9.13	31 (45%)
15	FES	A	201	1	0,4,4	-	-	-		
19	PEE	L	301	-	50,50,50	0.31	0	53,55,55	0.41	0
16	HEC	b	301	2	50,50,50	2.83	25 (50%)	68,82,82	2.49	27 (39%)
23	5PL	M	703	-	84,85,85	0.25	0	95,101,101	0.53	1 (1%)
16	HEC	N	401	14	50,50,50	2.90	27 (54%)	68,82,82	2.38	28 (41%)
18	MQ7	c	301	-	49,49,49	0.39	0	61,63,63	0.49	1 (1%)
17	HEM	B	303	2	50,50,50	1.60	10 (20%)	67,82,82	1.55	11 (16%)
16	HEC	B	301	2	50,50,50	2.95	28 (56%)	68,82,82	2.43	22 (32%)
26	CUA	N	402	-	0,1,1	-	-	-		

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	PEE	J	203	-	-	7/43/43/54	-
18	MQ7	b	304	-	-	8/41/61/61	0/2/2/2
17	HEM	b	303	2	-	6/14/54/54	-
19	PEE	c	303	-	-	8/45/45/54	-
21	CDL	K	201	-	-	15/110/110/110	-
16	HEC	C	302	-	1/1/3/7	5/14/54/54	-
22	HAS	M	702	13	1/1/8/18	15/42/82/82	-
16	HEC	J	201	-	1/1/3/7	10/14/54/54	-
18	MQ7	C	301	-	-	10/41/61/61	0/2/2/2
18	MQ7	B	304	-	-	11/41/61/61	0/2/2/2
15	FES	a	201	1	-	-	0/1/1/1
22	HAS	M	701	13	1/1/8/18	14/42/82/82	-
17	HEM	B	302	2	-	7/14/54/54	-
17	HEM	b	302	2	-	9/14/54/54	-
20	PC1	C	304	-	-	11/51/51/57	-
19	PEE	C	303	-	-	5/45/45/54	-
21	CDL	L	302	-	-	25/108/108/110	-
21	CDL	J	202	-	-	18/110/110/110	-
20	PC1	c	304	-	-	14/46/46/57	-
16	HEC	c	302	3	1/1/3/7	10/14/54/54	-
15	FES	A	201	1	-	-	0/1/1/1
19	PEE	L	301	-	-	7/54/54/54	-
16	HEC	b	301	2	1/1/3/7	5/14/54/54	-
23	5PL	M	703	-	-	17/87/107/107	0/1/1/1
16	HEC	N	401	14	1/1/3/7	7/14/54/54	-
18	MQ7	c	301	-	-	9/41/61/61	0/2/2/2
17	HEM	B	303	2	-	8/14/54/54	-
16	HEC	B	301	2	1/1/3/7	11/14/54/54	-

The worst 5 of 262 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	c	302	HEC	CAC-C3C	10.00	1.76	1.51
16	c	302	HEC	CMC-C2C	9.43	1.70	1.50
22	M	701	HAS	C3B-C2B	5.75	1.47	1.34
16	J	201	HEC	C3B-C2B	5.72	1.49	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	C	302	HEC	C3B-C2B	5.70	1.49	1.36

The worst 5 of 286 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
16	c	302	HEC	CAC-C3C-C2C	-52.59	43.69	126.89
16	c	302	HEC	CMC-C2C-C3C	-46.69	26.59	125.62
16	c	302	HEC	CAC-C3C-C4C	13.73	143.79	124.91
16	c	302	HEC	CBC-CAC-C3C	12.33	145.86	112.42
22	M	702	HAS	C2D-C3D-C4D	-8.03	100.62	106.43

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
16	B	301	HEC	NA
16	C	302	HEC	NA
16	J	201	HEC	NA
16	N	401	HEC	NA
16	b	301	HEC	NA

5 of 272 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	B	302	HEM	C2C-C3C-CAC-CBC
17	b	302	HEM	C2C-C3C-CAC-CBC
17	b	302	HEM	C4C-C3C-CAC-CBC
18	C	301	MQ7	C12-C11-C3-C2
18	C	301	MQ7	C12-C11-C3-C4

There are no ring outliers.

27 monomers are involved in 124 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	b	304	MQ7	1	0
17	b	303	HEM	2	0
19	c	303	PEE	2	0
21	K	201	CDL	3	0
16	C	302	HEC	3	0
22	M	702	HAS	8	0
18	C	301	MQ7	4	0
15	a	201	FES	1	0

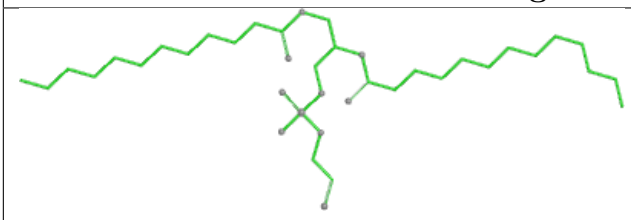
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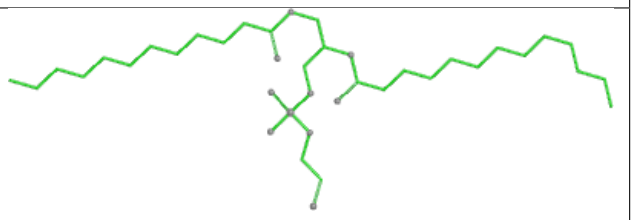
Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	B	304	MQ7	6	0
22	M	701	HAS	6	0
17	B	302	HEM	3	0
17	b	302	HEM	1	0
20	C	304	PC1	3	0
19	C	303	PEE	4	0
21	L	302	CDL	8	0
21	J	202	CDL	13	0
20	c	304	PC1	2	0
16	c	302	HEC	3	0
15	A	201	FES	2	0
19	L	301	PEE	5	0
16	b	301	HEC	6	0
23	M	703	5PL	10	0
16	N	401	HEC	3	0
18	c	301	MQ7	8	0
17	B	303	HEM	8	0
16	B	301	HEC	6	0
26	N	402	CUA	3	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 then 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.

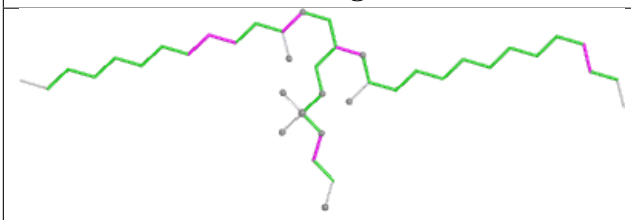
Ligand PEE J 203



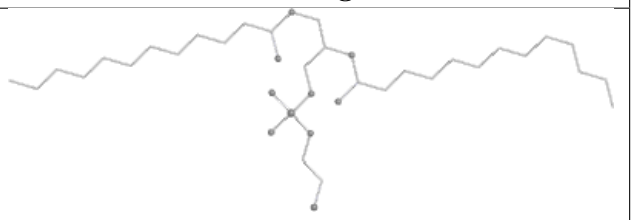
Bond lengths



Bond angles

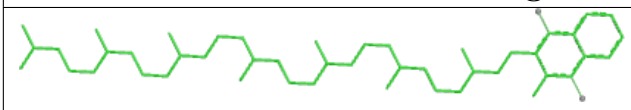


Torsions

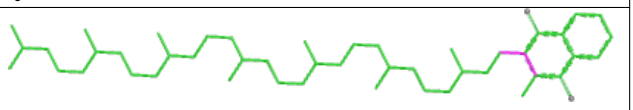


Rings

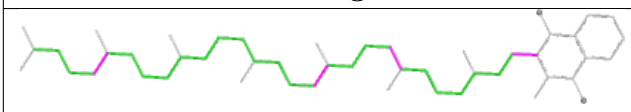
Ligand MQ7 b 304



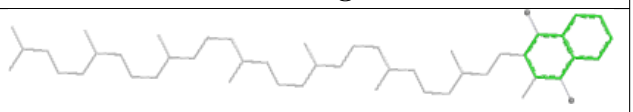
Bond lengths



Bond angles

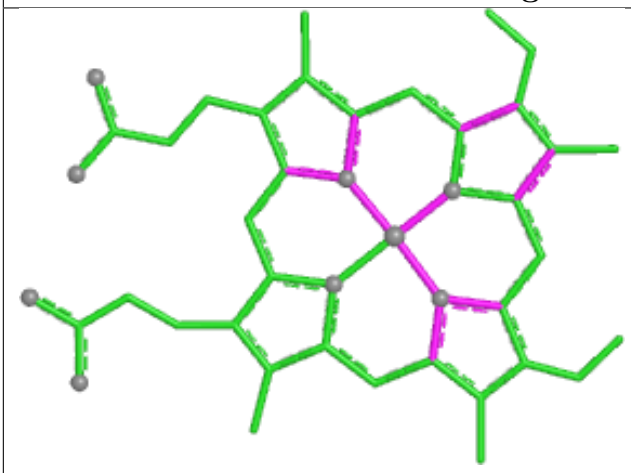


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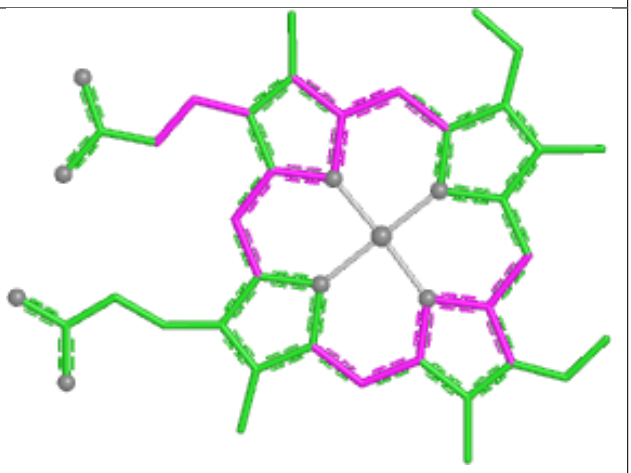


Rings

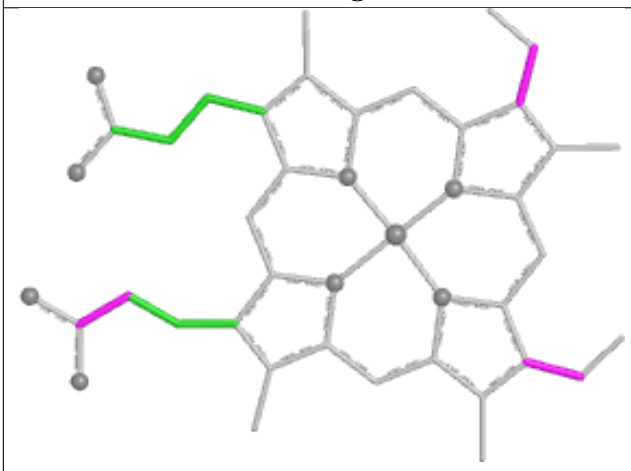
Ligand HEM b 303



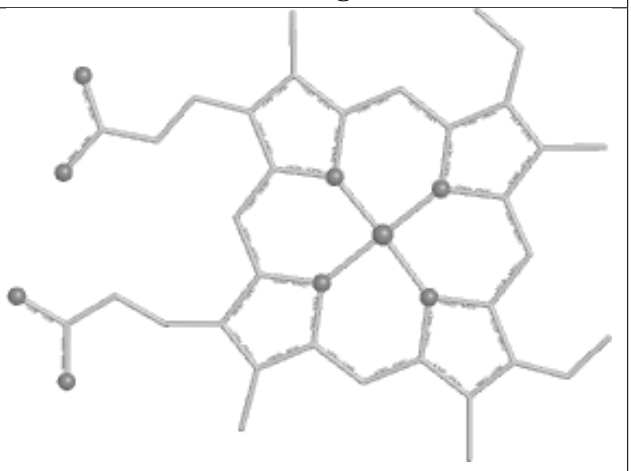
Bond lengths



Bond angles

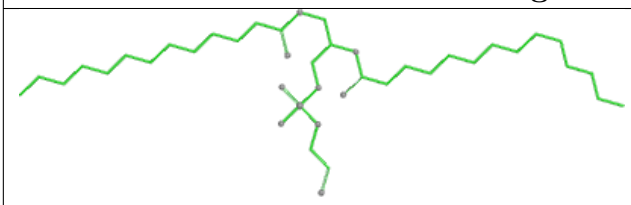


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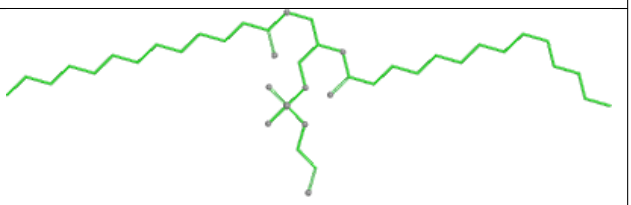


Rings

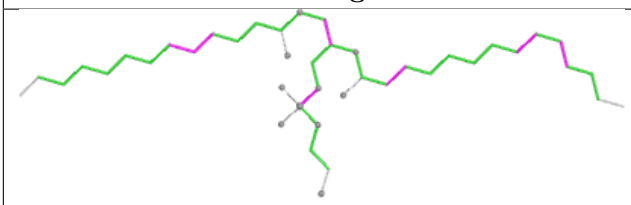
Ligand PEE c 303



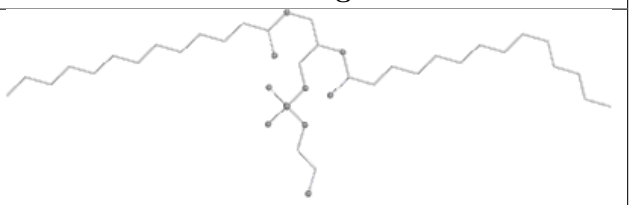
Bond lengths



Bond angles

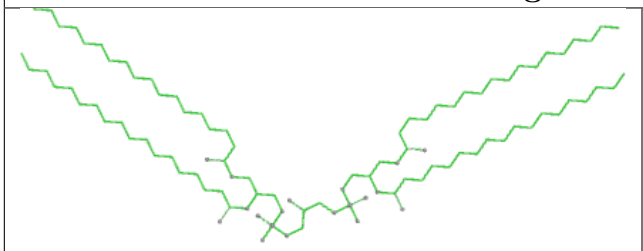


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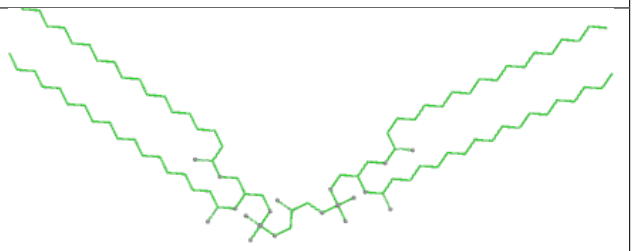


Rings

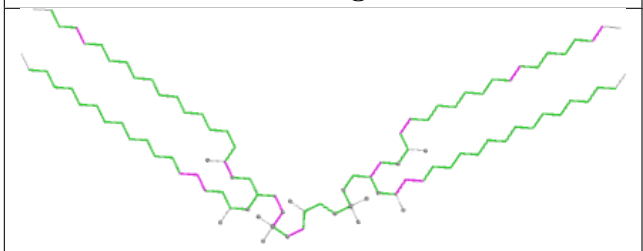
Ligand CDL K 201



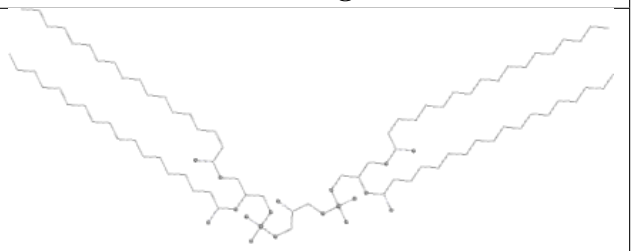
Bond lengths



Bond angles

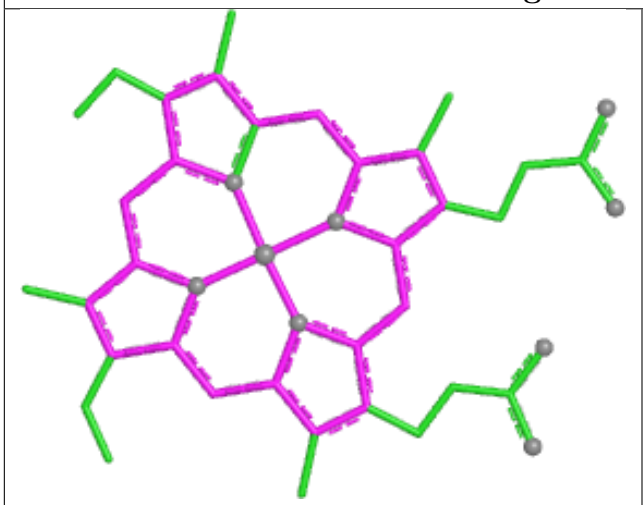


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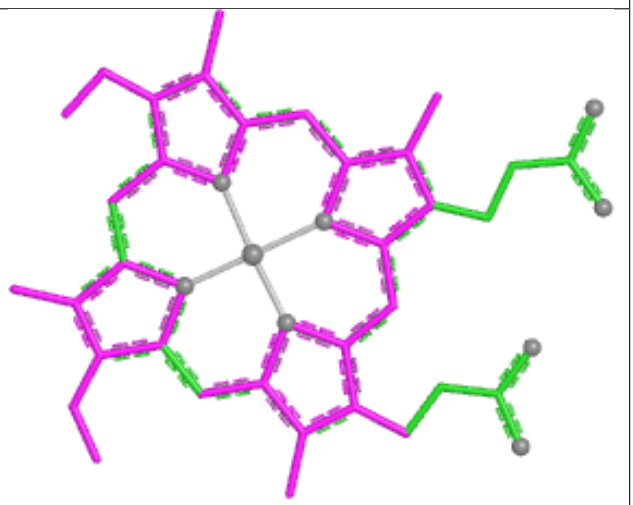


Rings

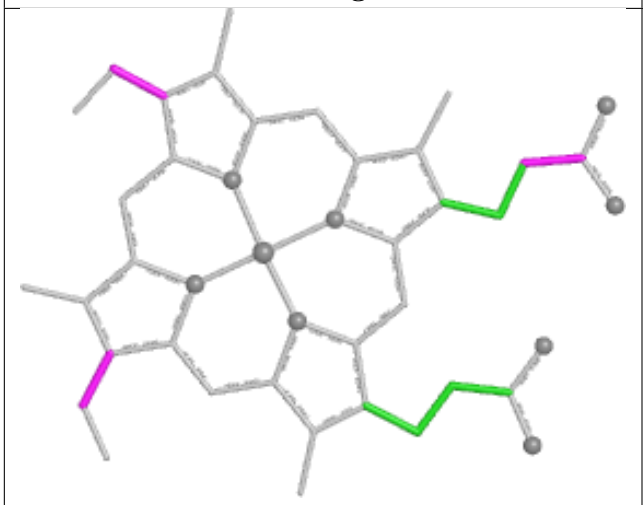
Ligand HEC C 302



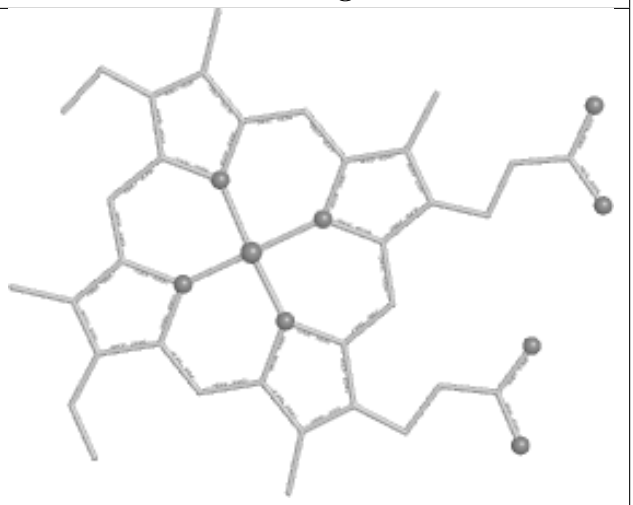
Bond lengths



Bond angles

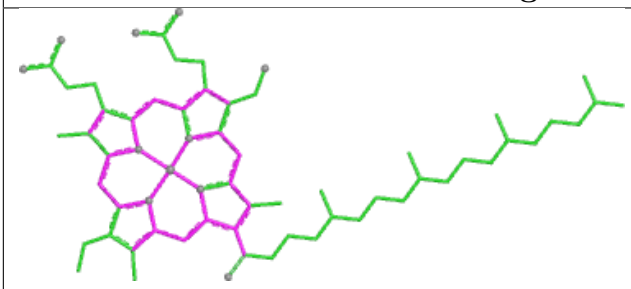


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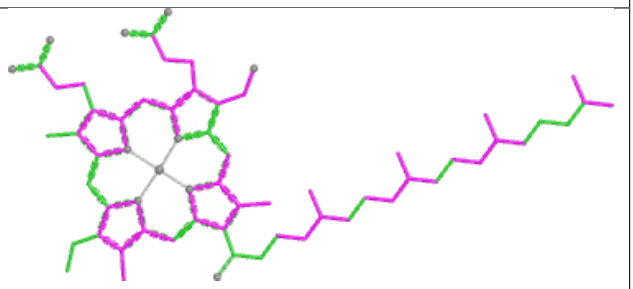


Rings

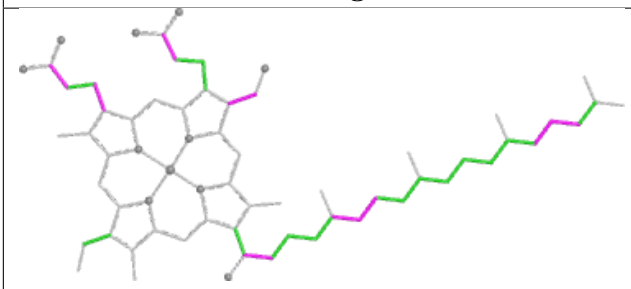
Ligand HAS M 702



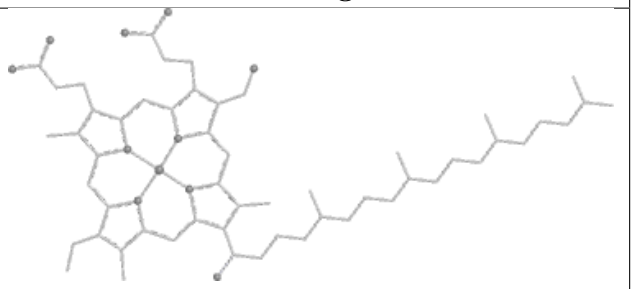
Bond lengths



Bond angles

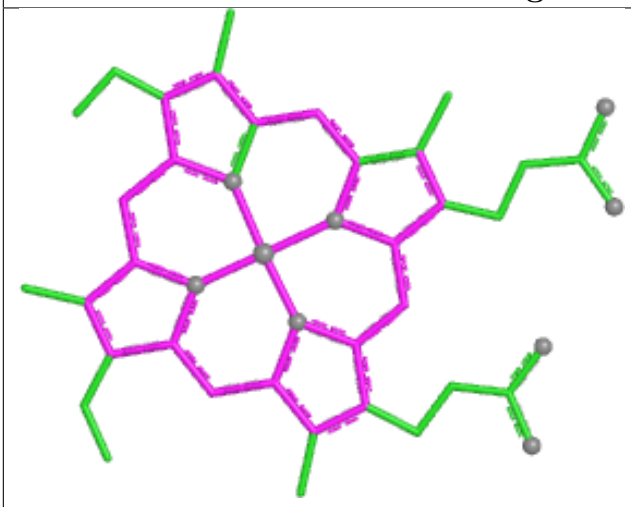


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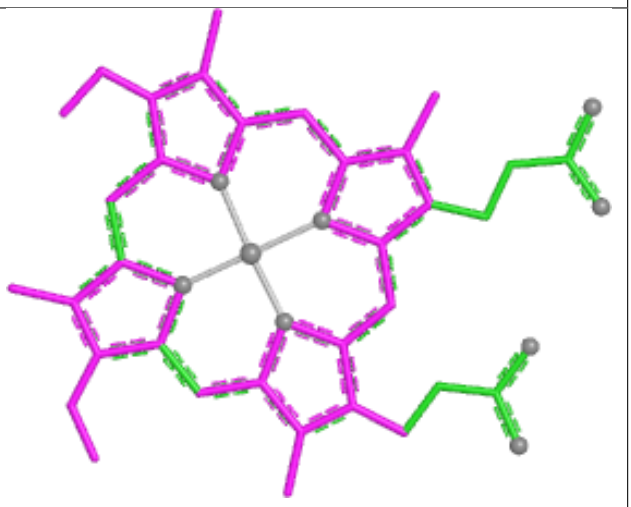


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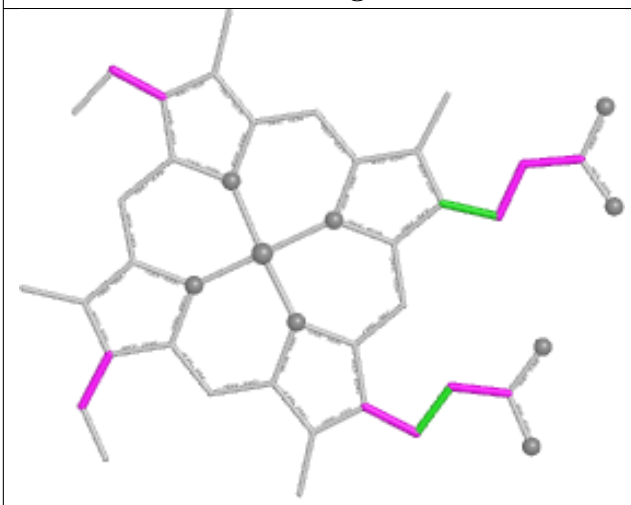
Ligand HEC J 201



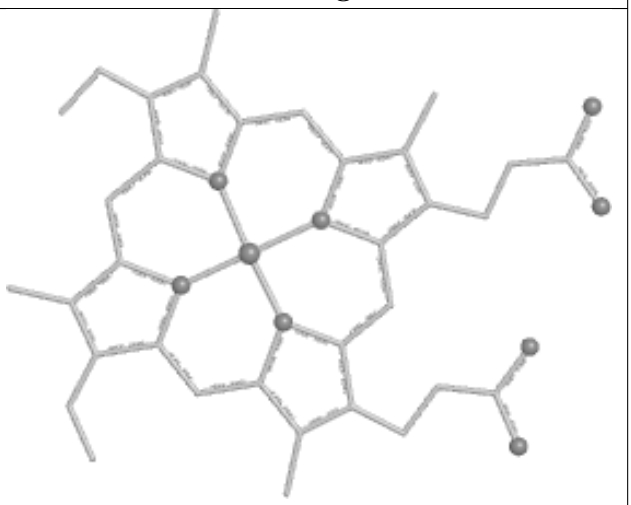
Bond lengths



Bond angles



Torsions



Rings

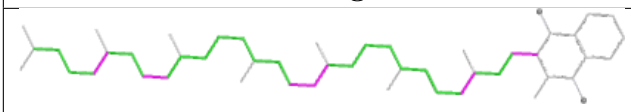
Ligand MQ7 C 301



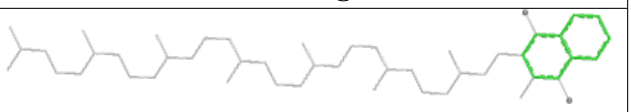
Bond lengths



Bond angles



Torsions



Rings

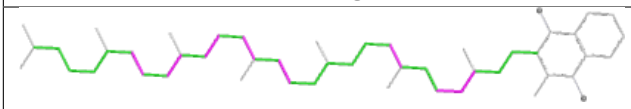
Ligand MQ7 B 304



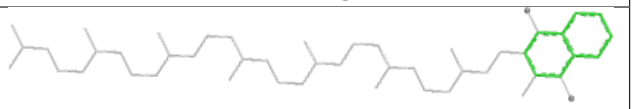
Bond lengths



Bond angles

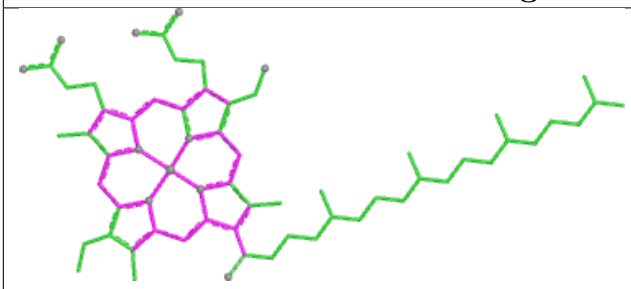


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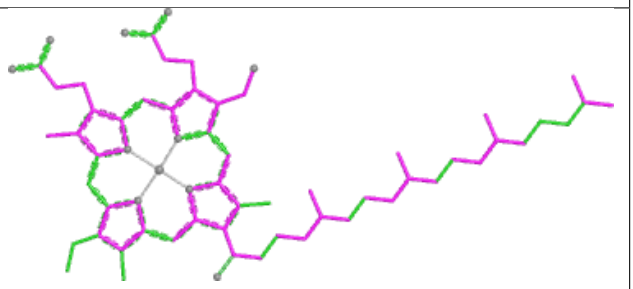


Rings

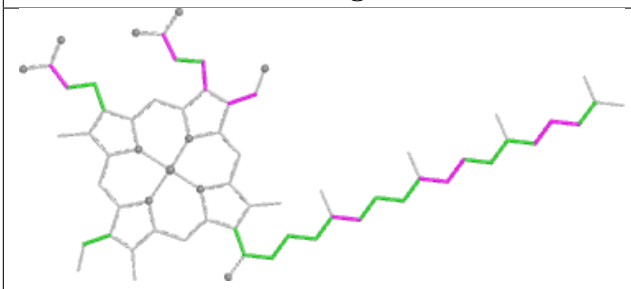
Ligand HAS M 701



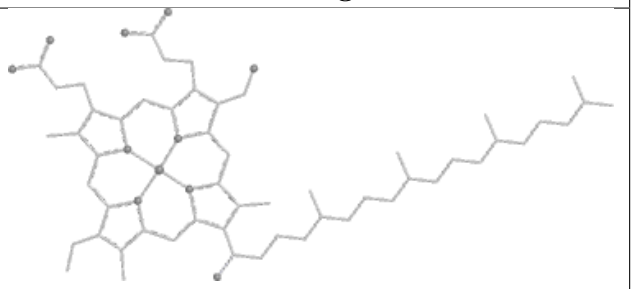
Bond lengths



Bond angles

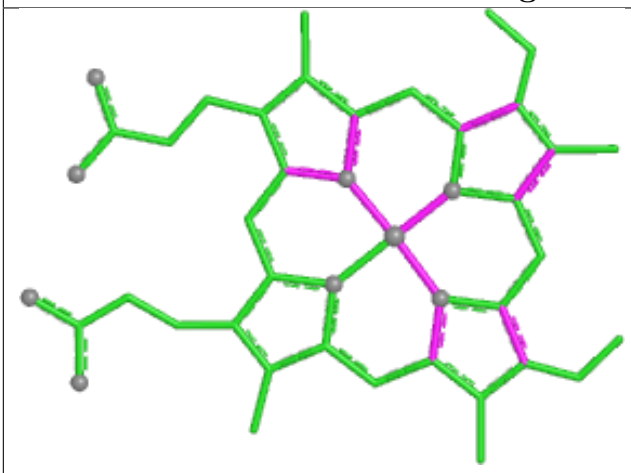


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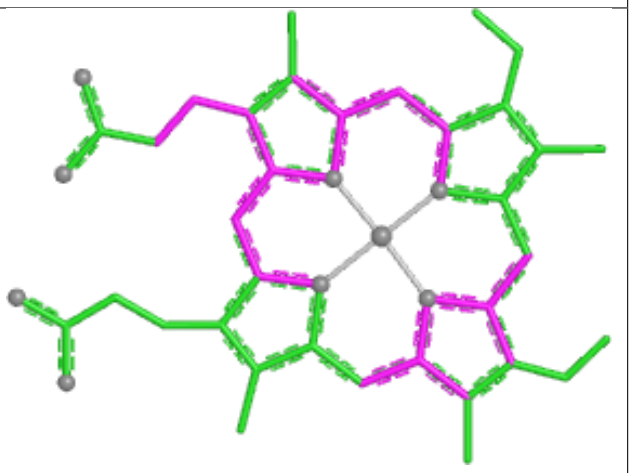


Rings

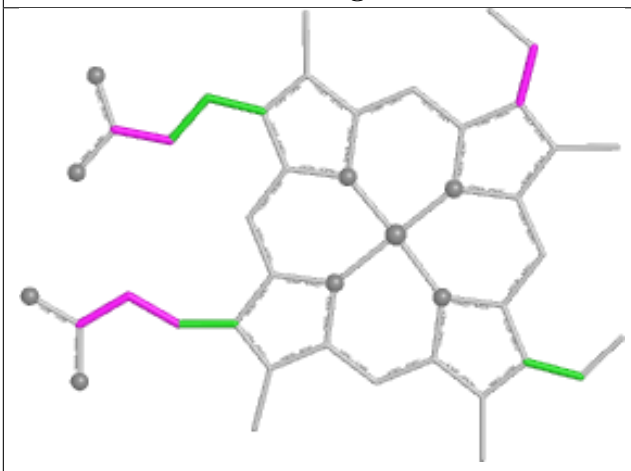
Ligand HEM B 302



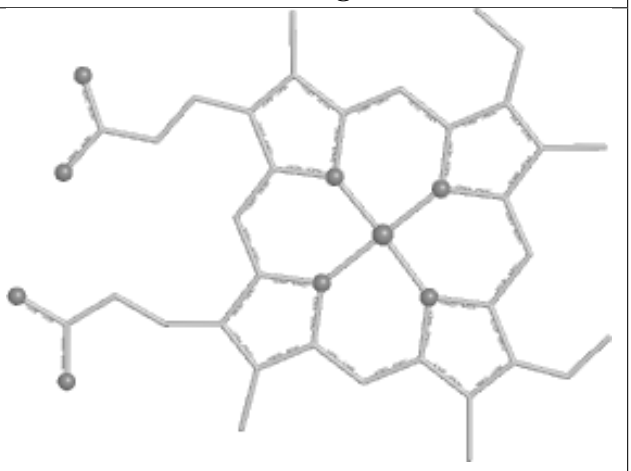
Bond lengths



Bond angles

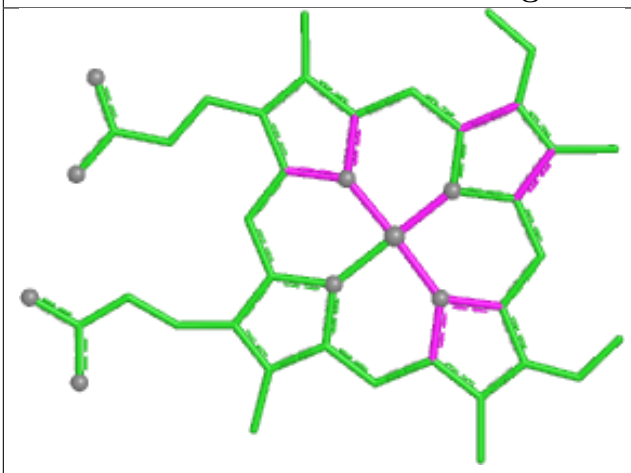


Torsions

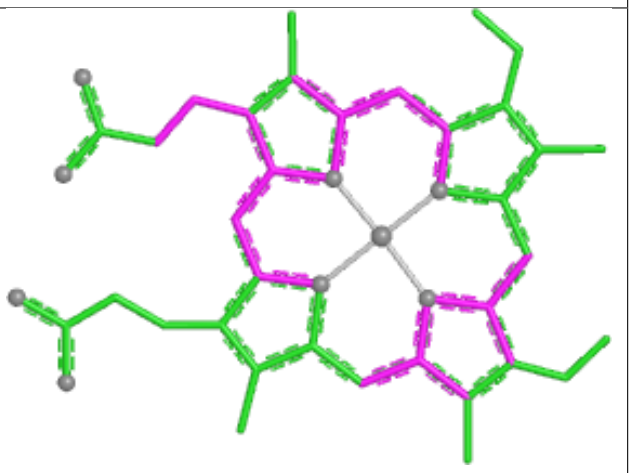


Rings

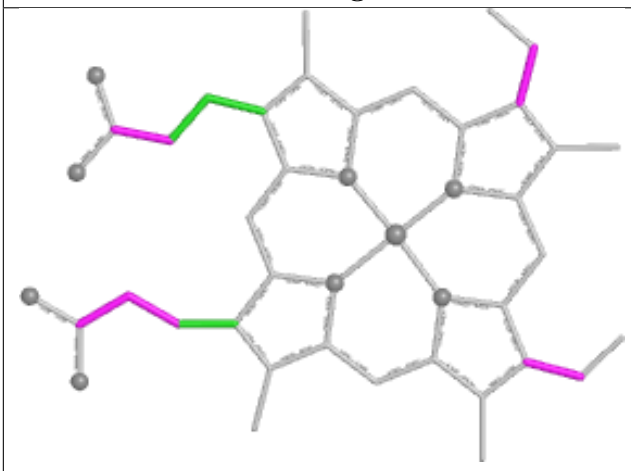
Ligand HEM b 302



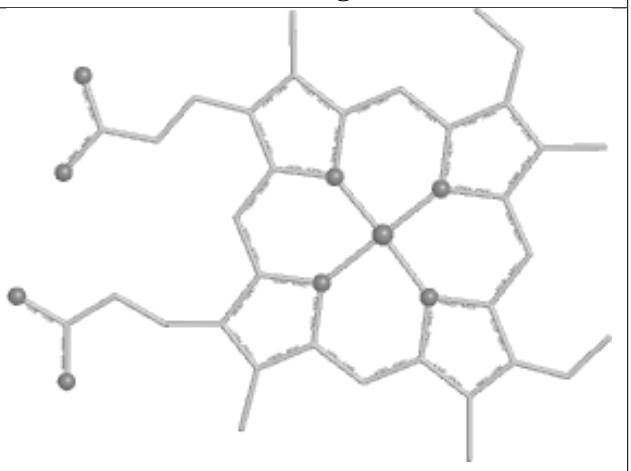
Bond lengths



Bond angles

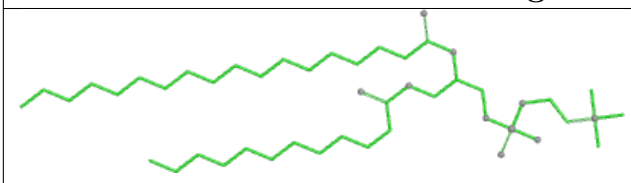


Torsions

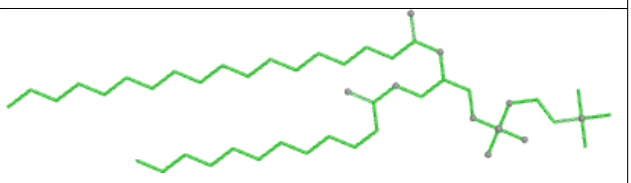


Rings

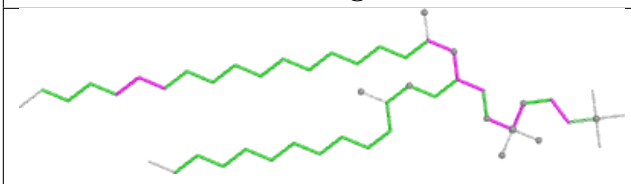
Ligand PC1 C 304



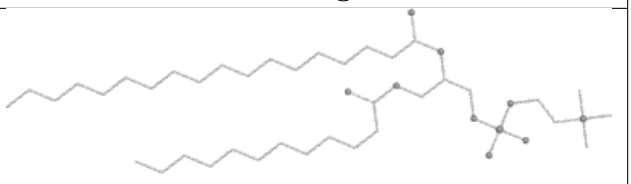
Bond lengths



Bond angles

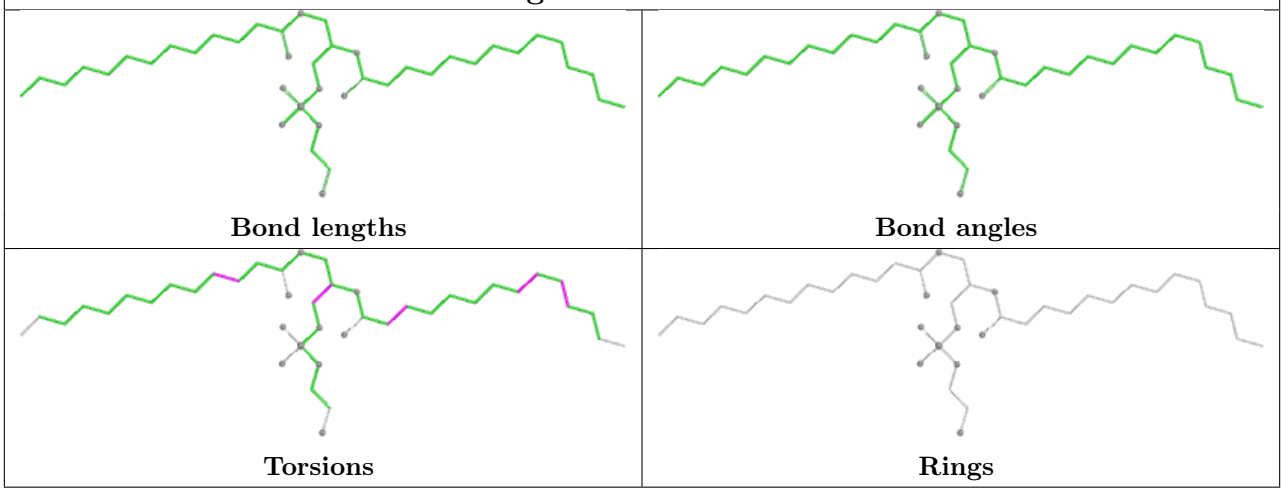


Torsions

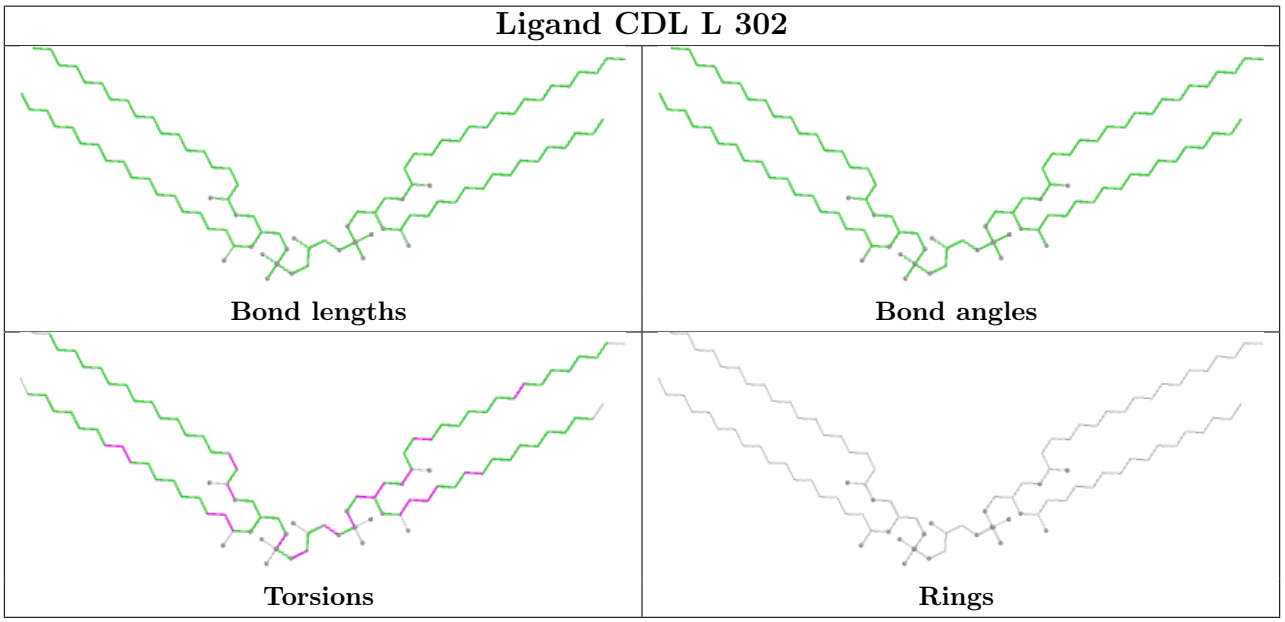


Rings

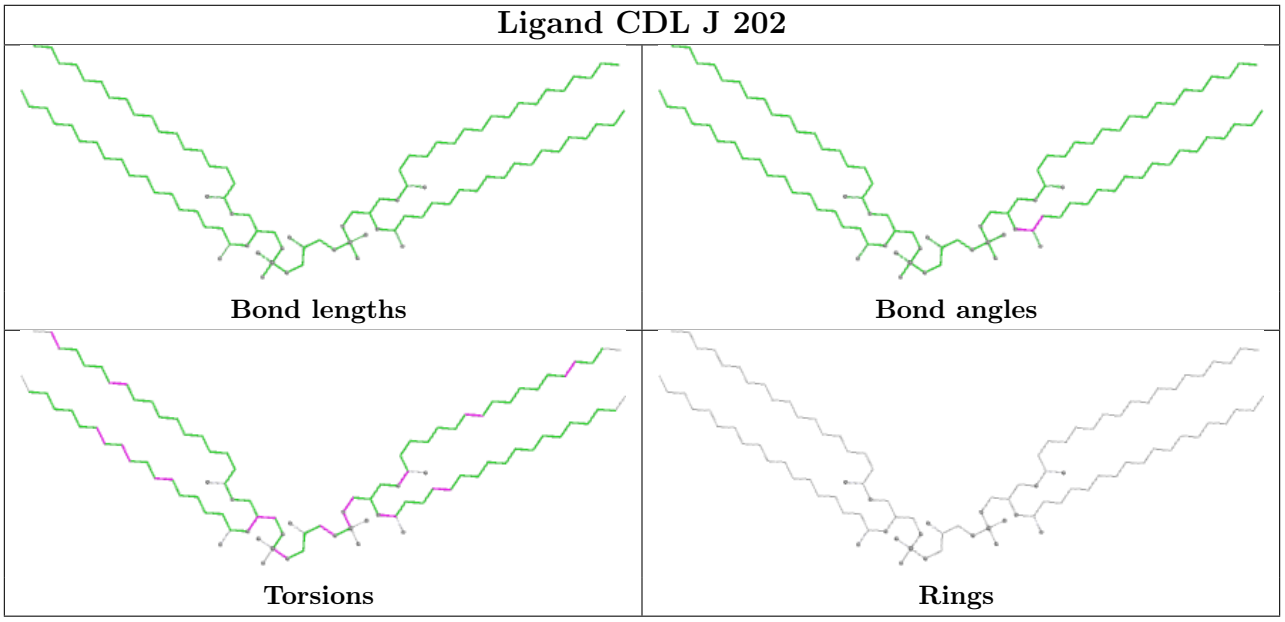
Ligand PEE C 303



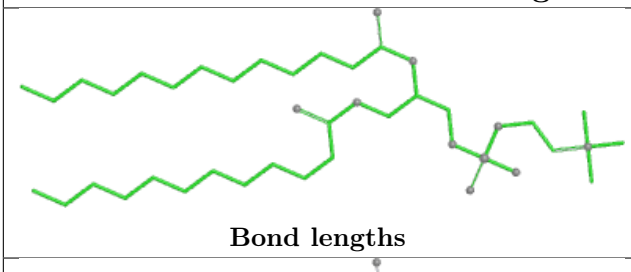
Ligand CDL L 302



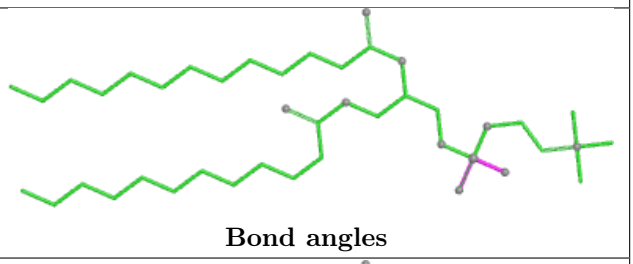
Ligand CDL J 202



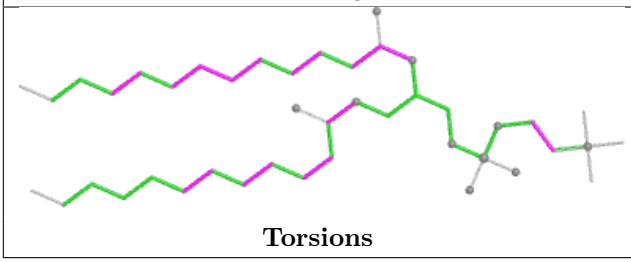
Ligand PC1 c 304



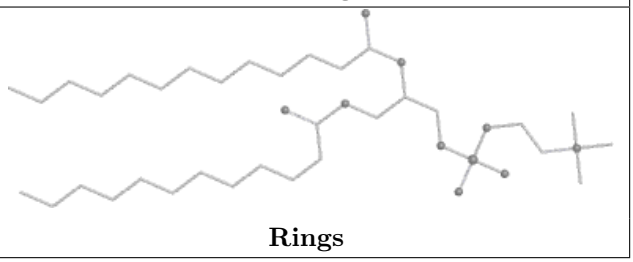
Bond lengths



Bond angles

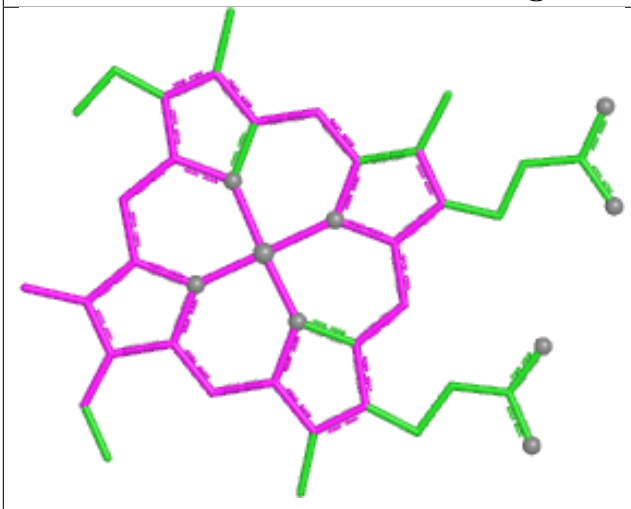


Torsions

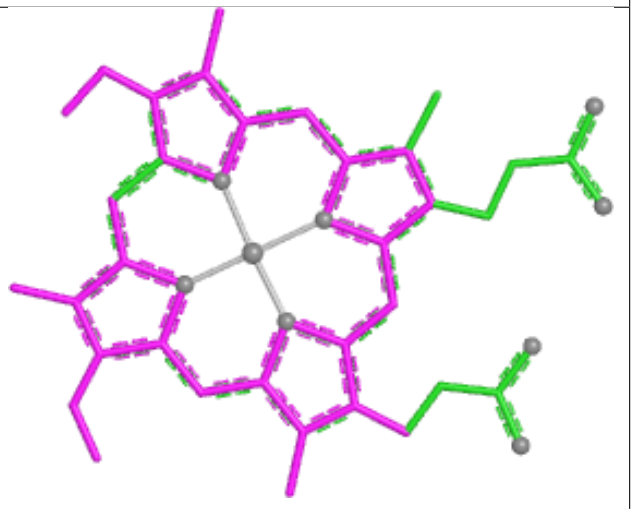


Rings

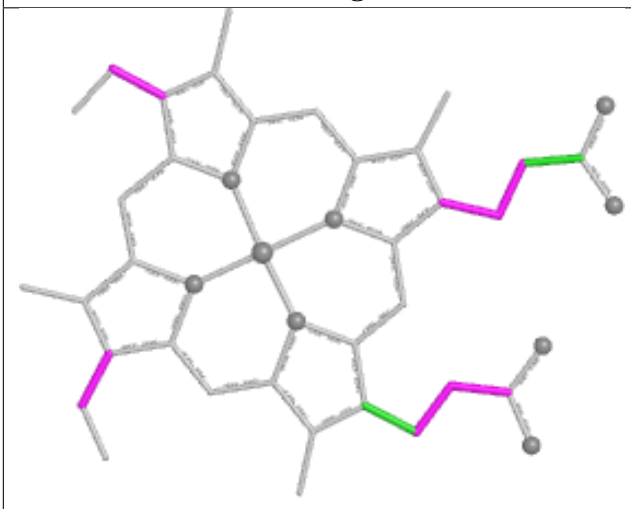
Ligand HEC c 302



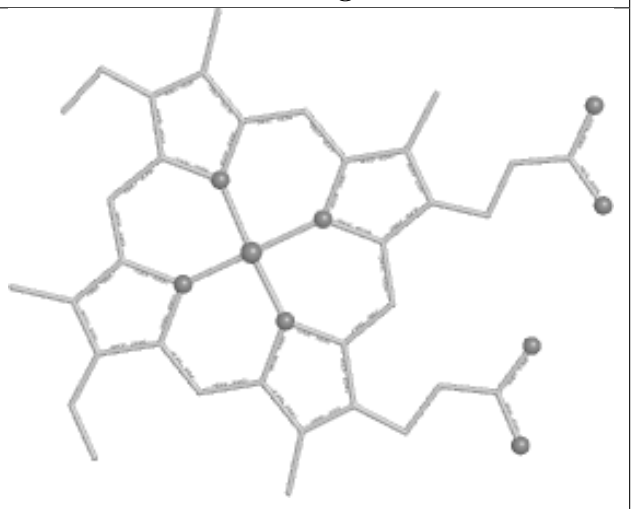
Bond lengths



Bond angles

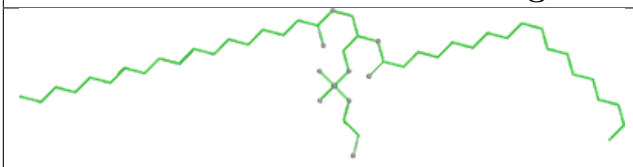


Torsions

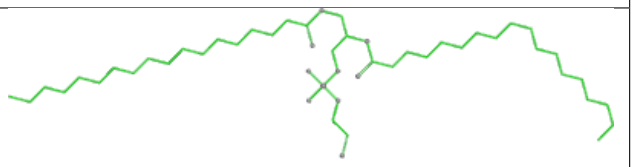


Rings

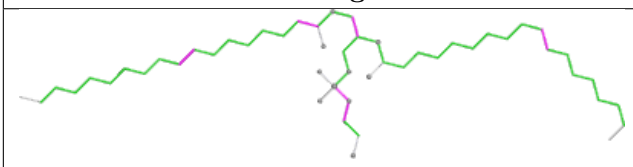
Ligand PEE L 301



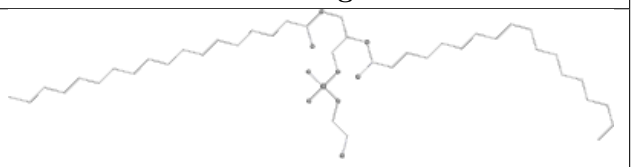
Bond lengths



Bond angles

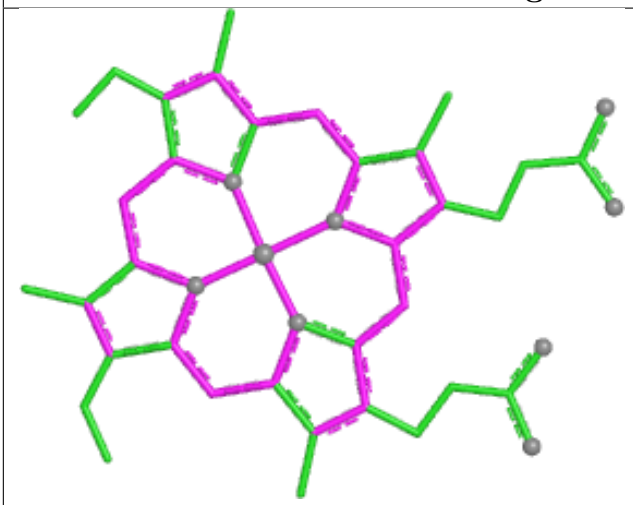


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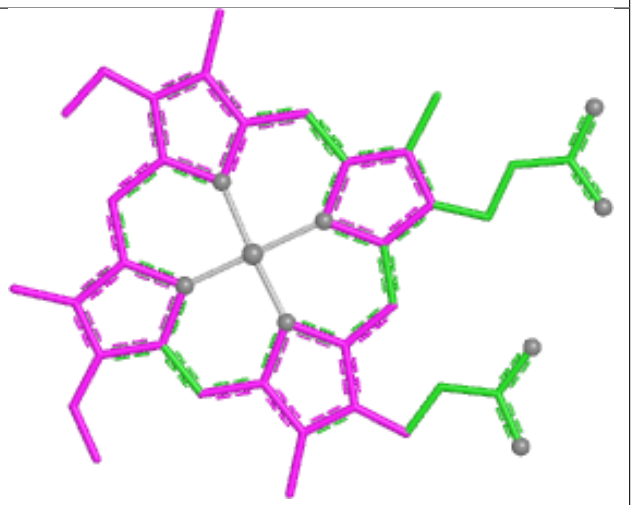


Rings

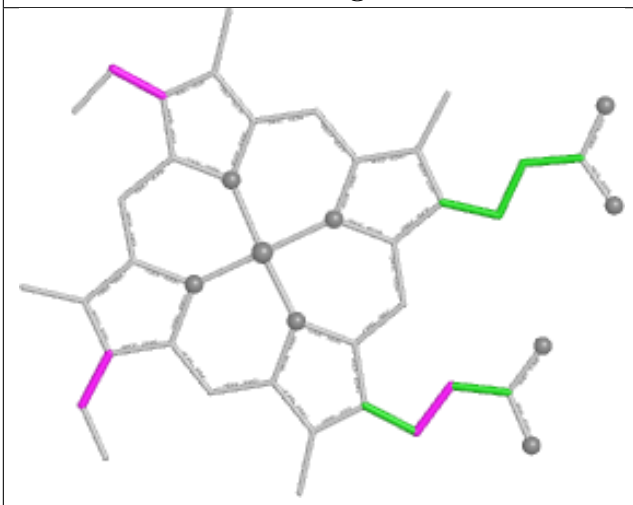
Ligand HEC b 301



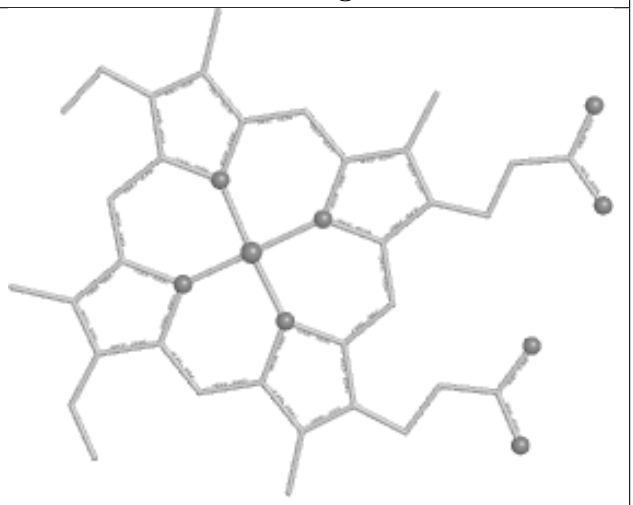
Bond lengths



Bond angles

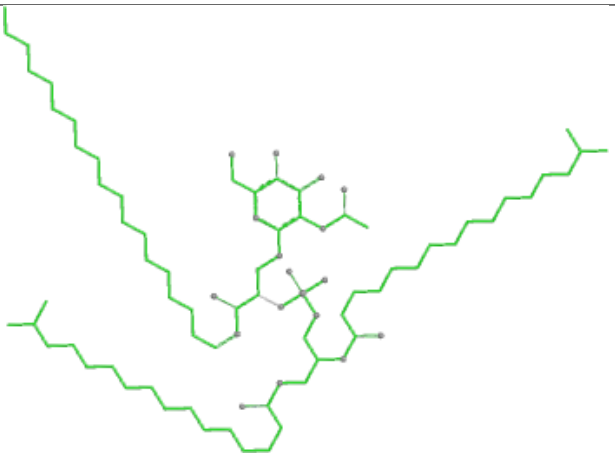


Torsions

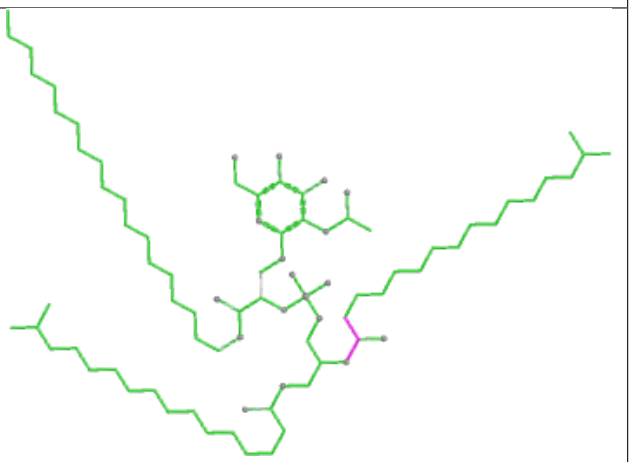


Rings

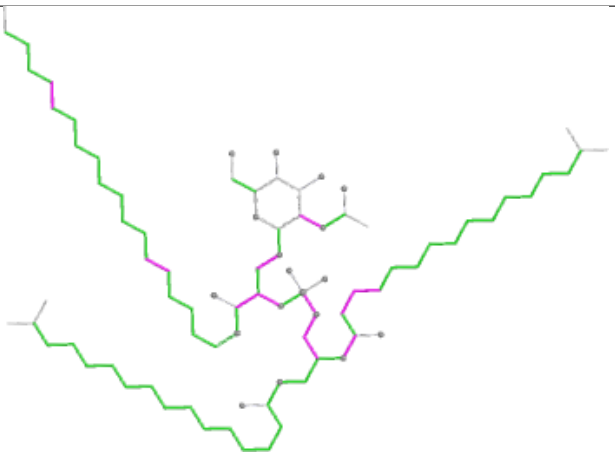
Ligand 5PL M 703



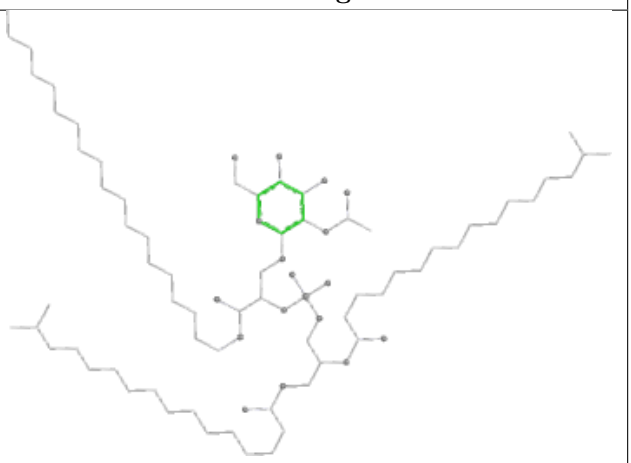
Bond lengths



Bond angles

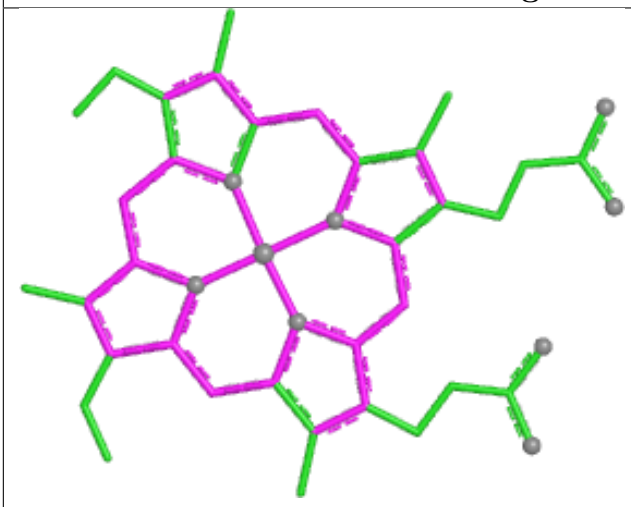


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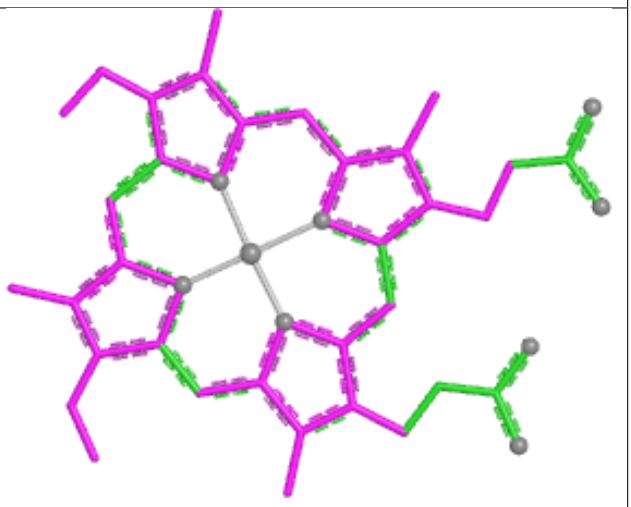


Rings

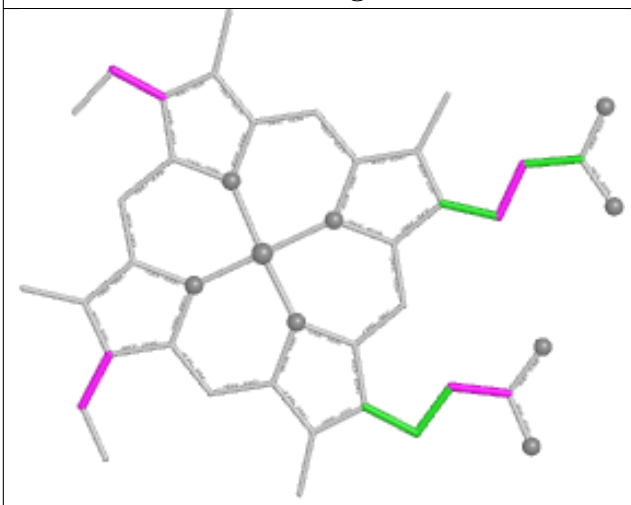
Ligand HEC N 401



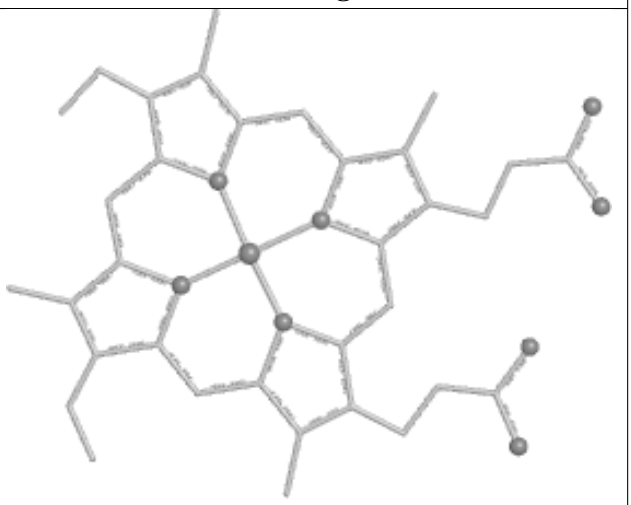
Bond lengths



Bond angles



Torsions



Rings

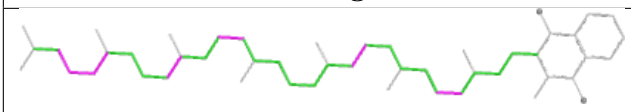
Ligand MQ7 c 301



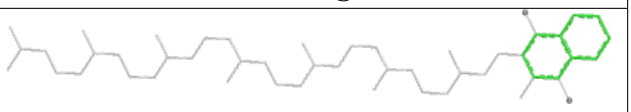
Bond lengths



Bond angles

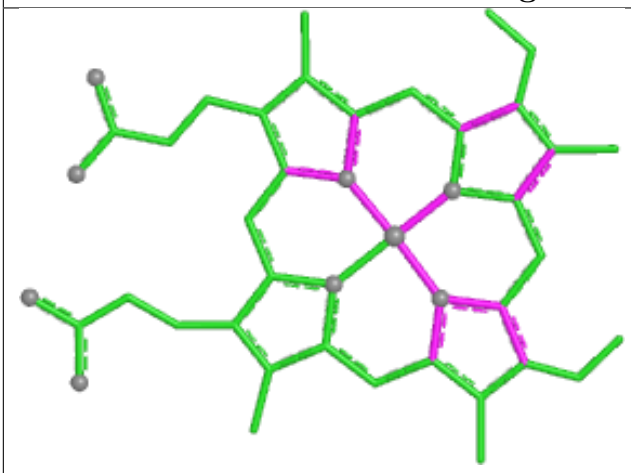


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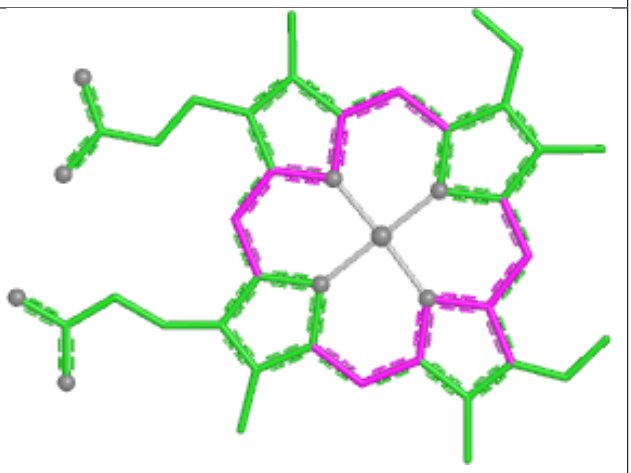


Rings

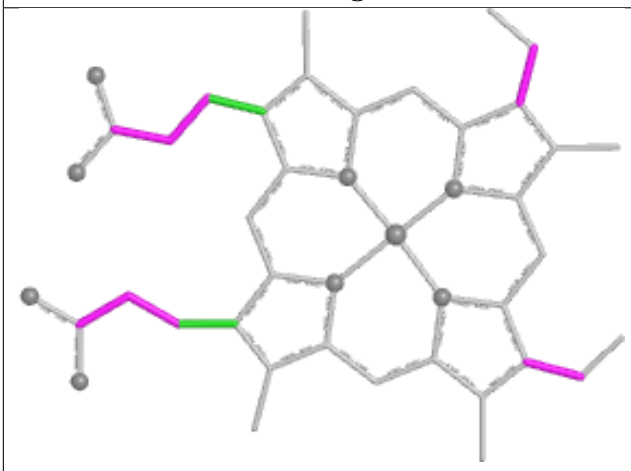
Ligand HEM B 303



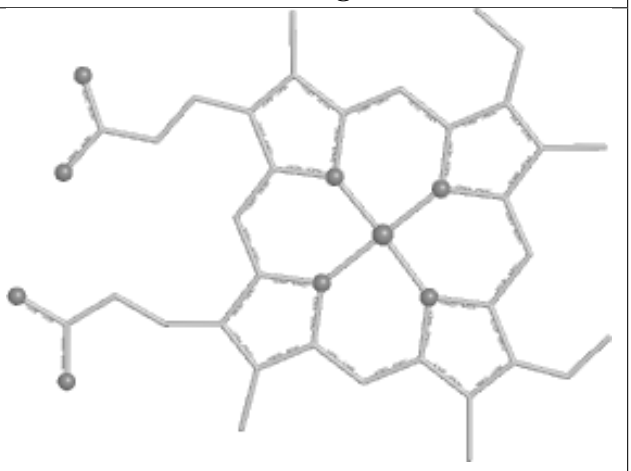
Bond lengths



Bond angles

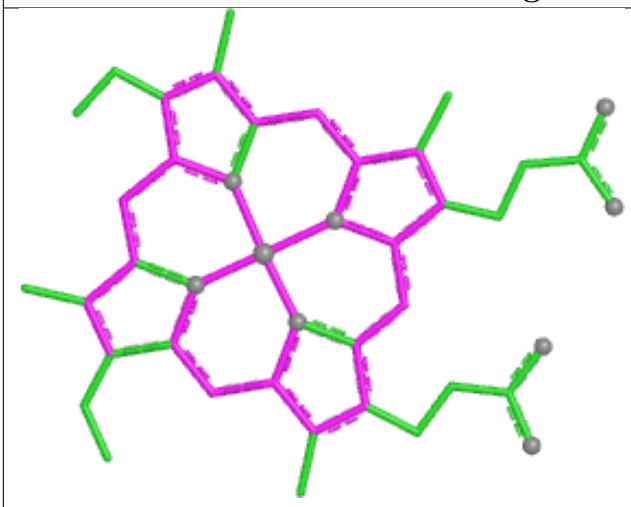


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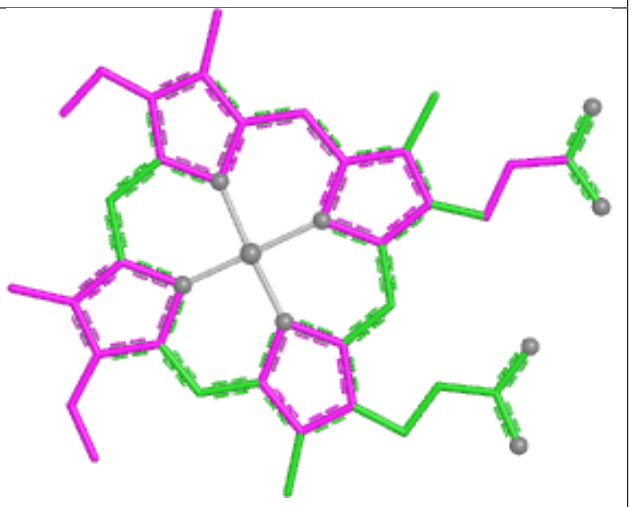


Rings

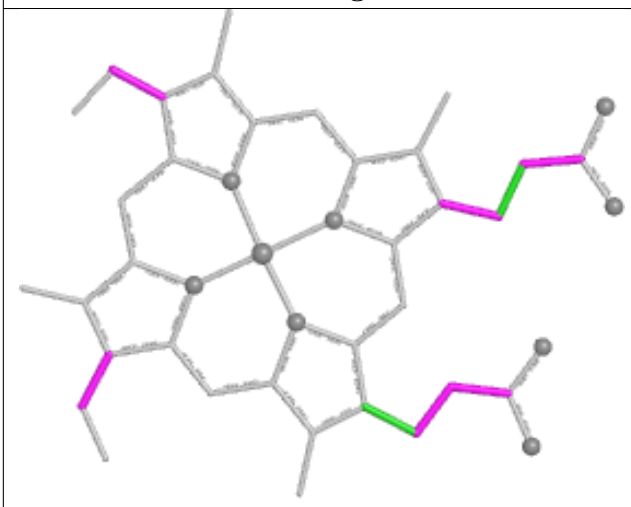
Ligand HEC B 301



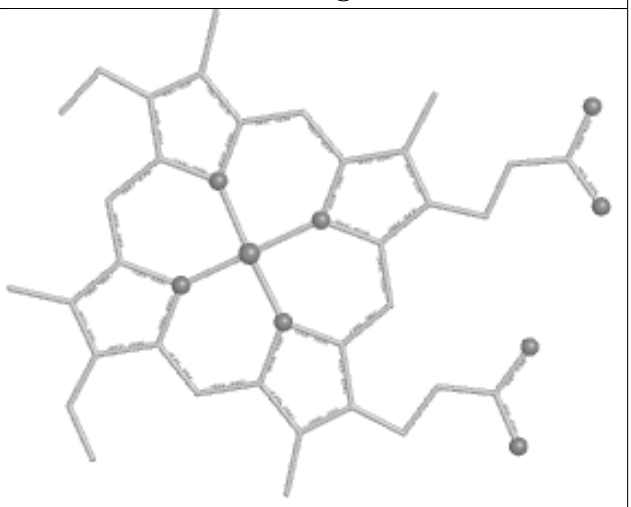
Bond lengths



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.

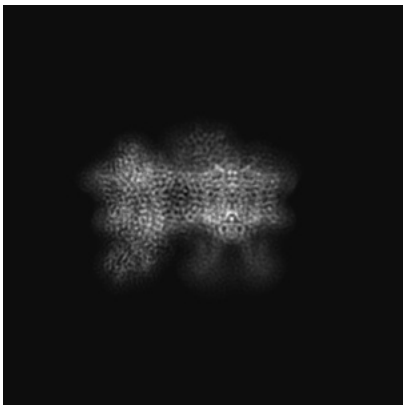
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-70330. These allow visual inspection of the internal detail of the map and identification of artifacts.

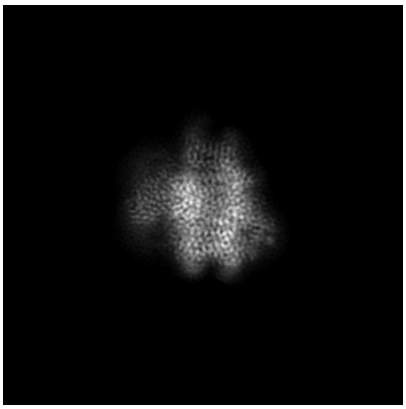
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

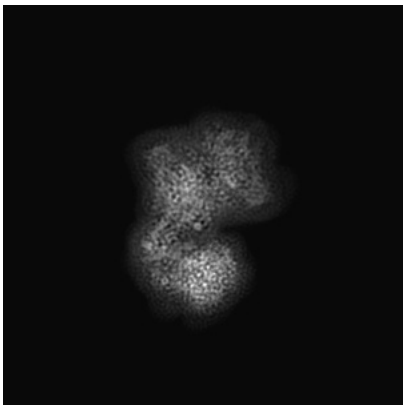
6.1.1 Primary map



X

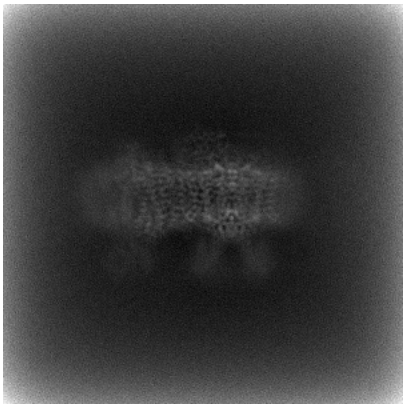


Y

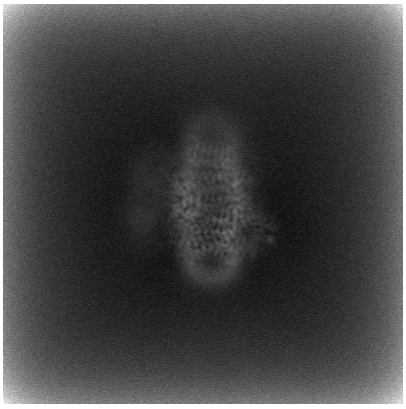


Z

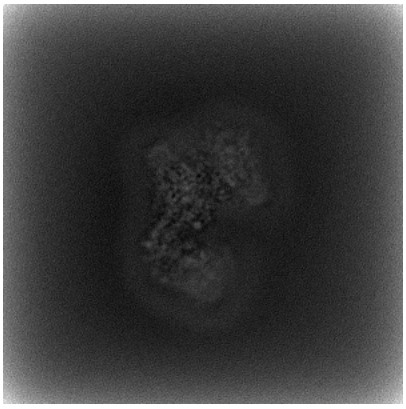
6.1.2 Raw map



X



Y



Z

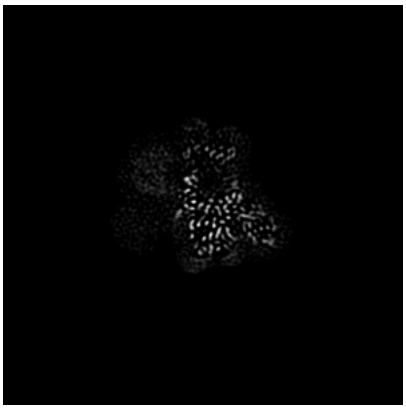
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

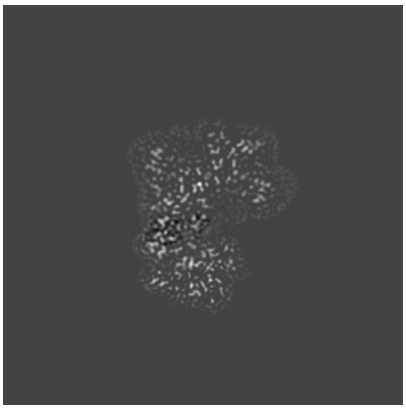
6.2.1 Primary map



X Index: 180

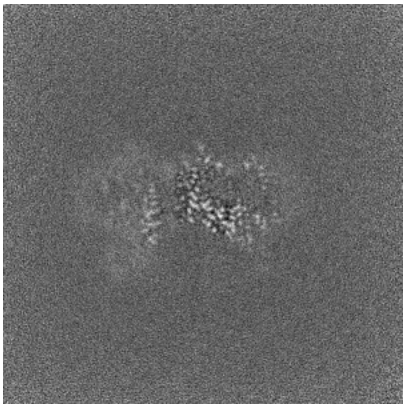


Y Index: 180

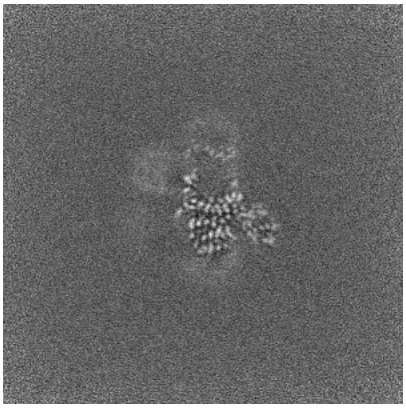


Z Index: 180

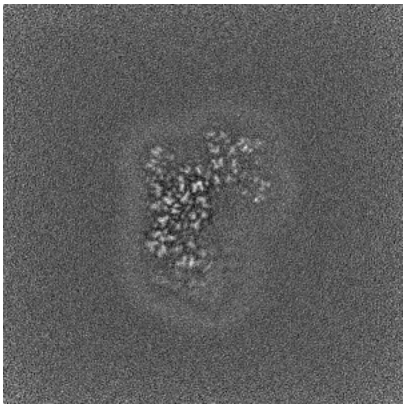
6.2.2 Raw map



X Index: 180



Y Index: 180

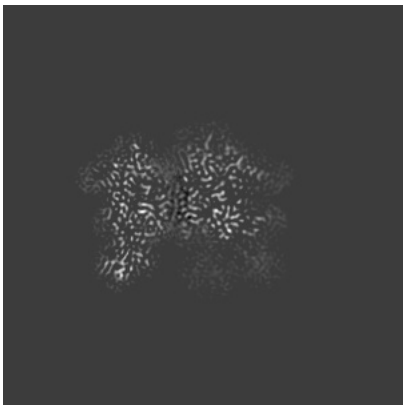


Z Index: 180

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: 169

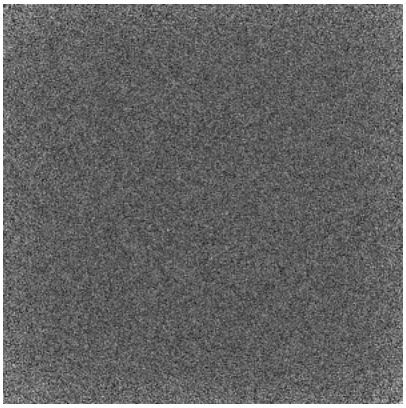


Y Index: 127

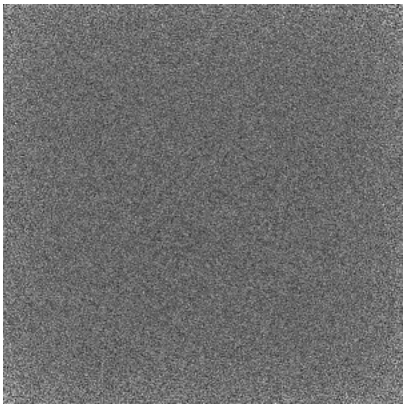


Z Index: 170

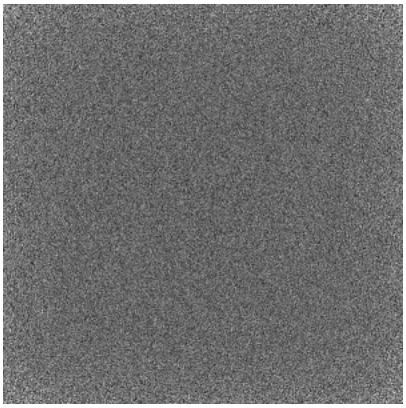
6.3.2 Raw map



X Index: 0



Y Index: 0

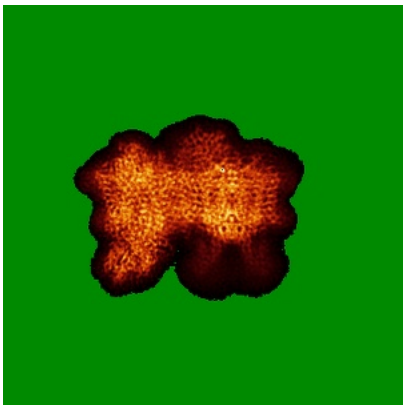


Z Index: 0

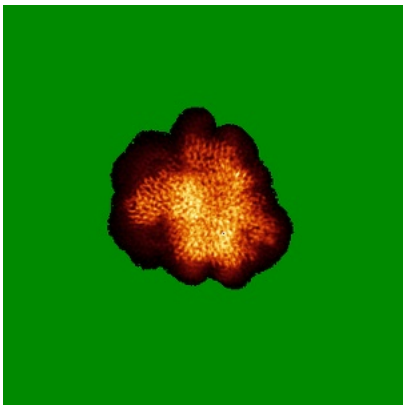
The images above show the largest variance slices of the map in three orthogonal directions.

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

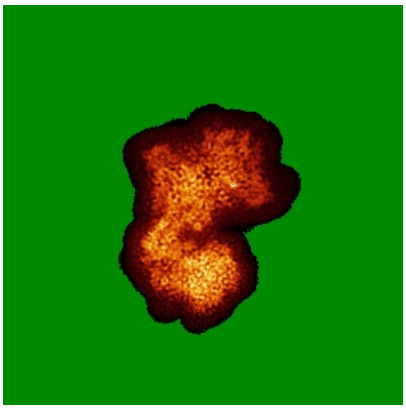
6.4.1 Primary map



X

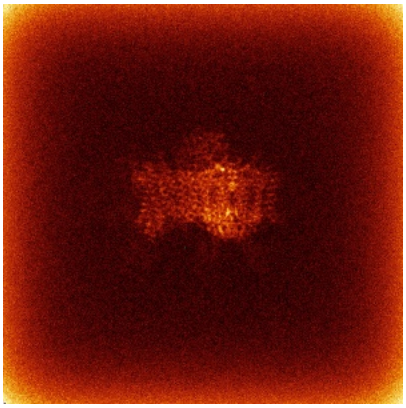


Y

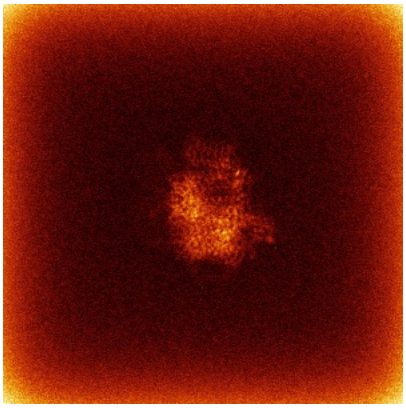


Z

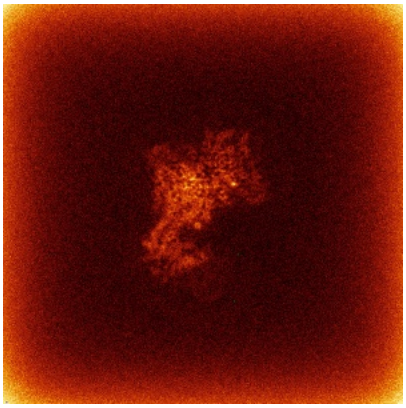
6.4.2 Raw map



X



Y

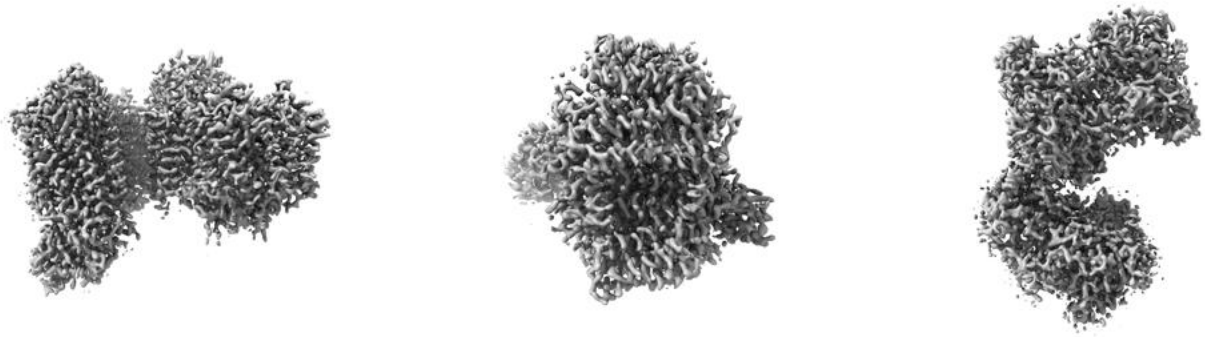


Z

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)

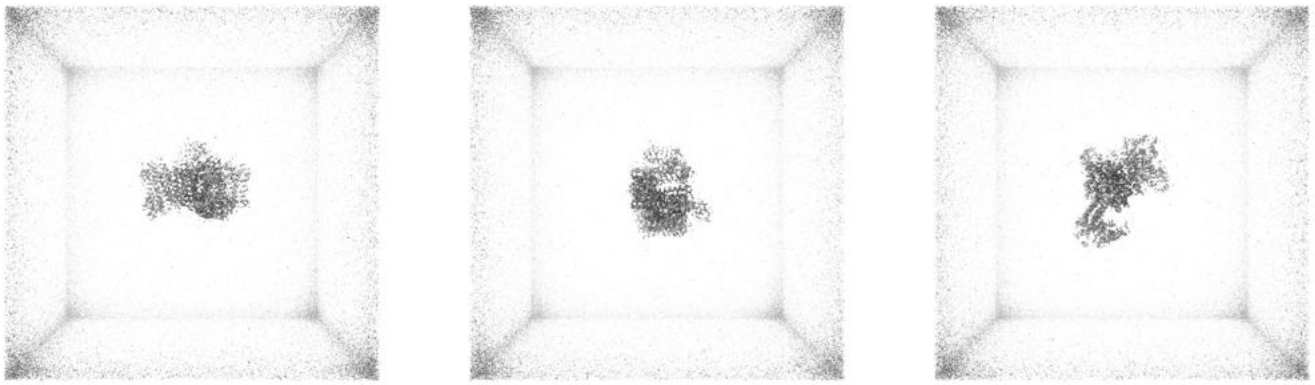
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

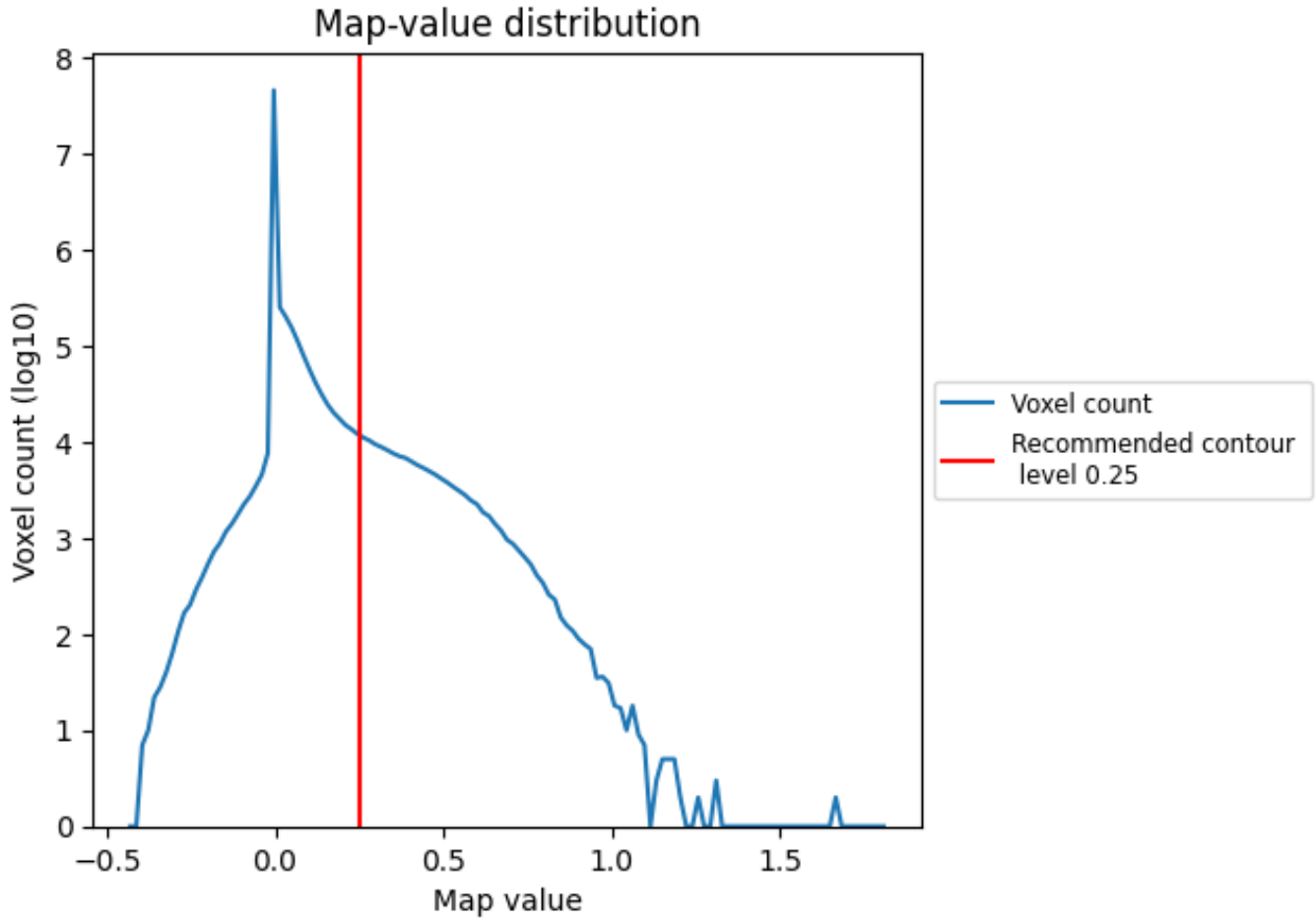
6.6 Mask visualisation (i)

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

7 Map analysis

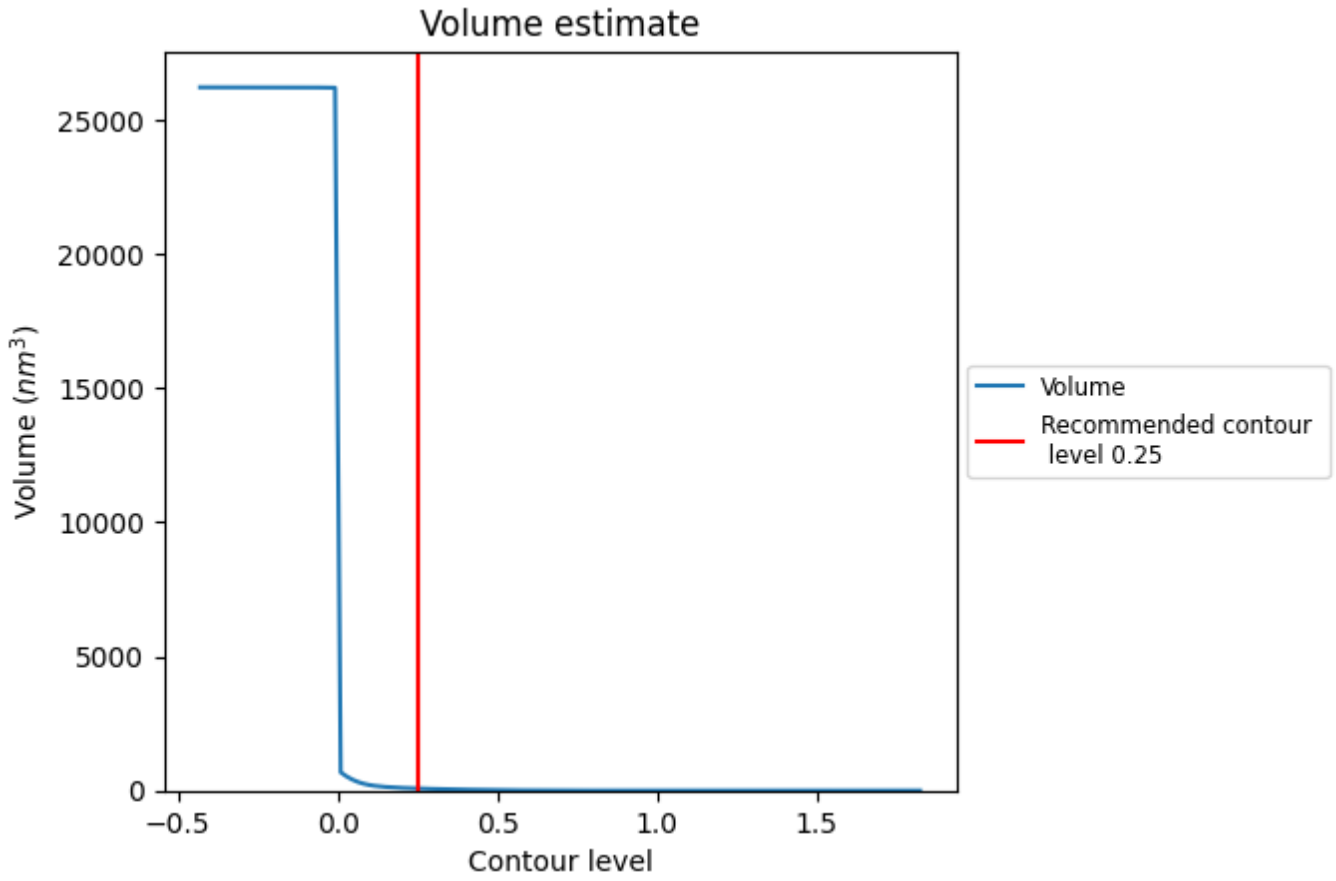
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

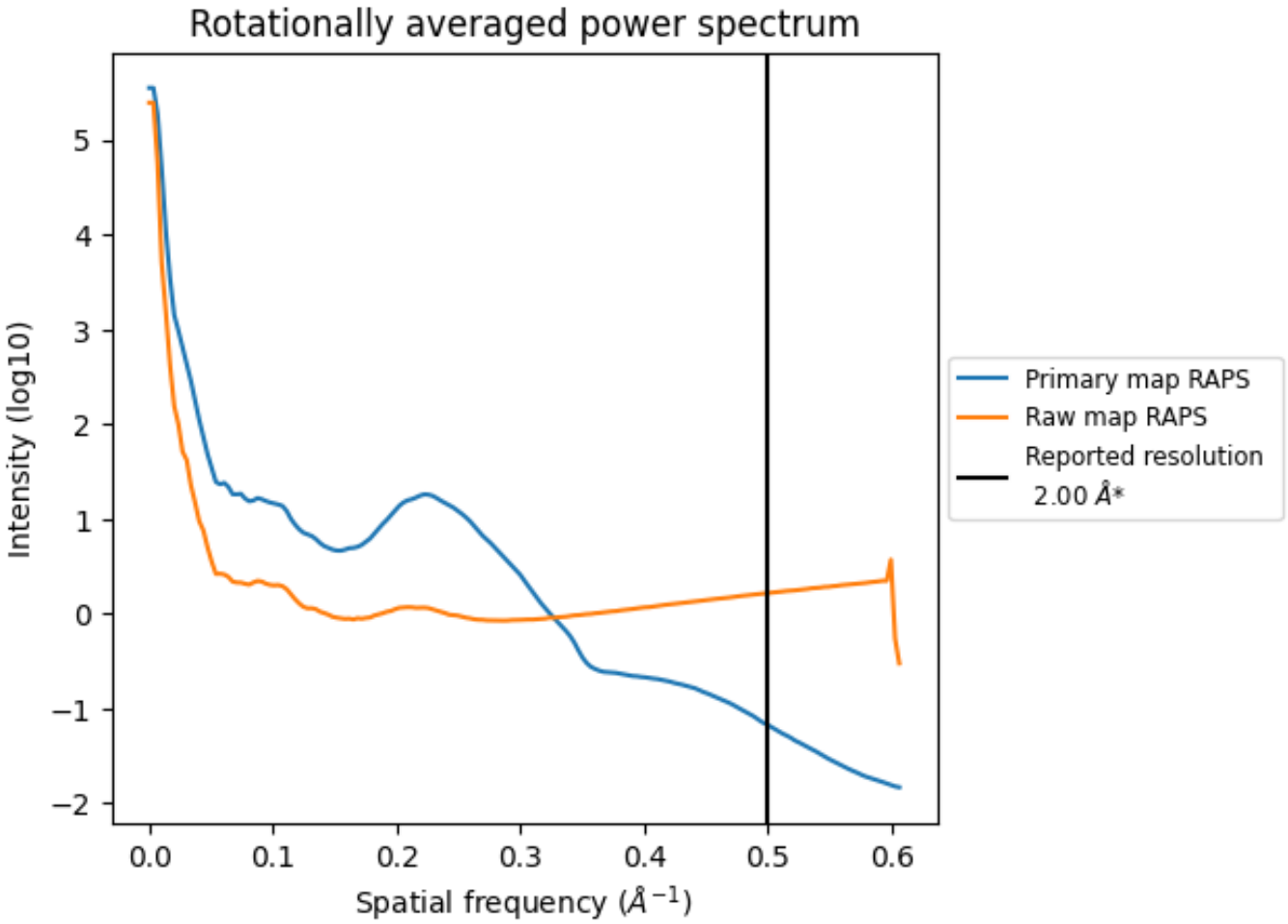
7.2 Volume estimate (i)



The volume at the recommended contour level is 78 nm^3; this corresponds to an approximate mass of 70 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 (i)

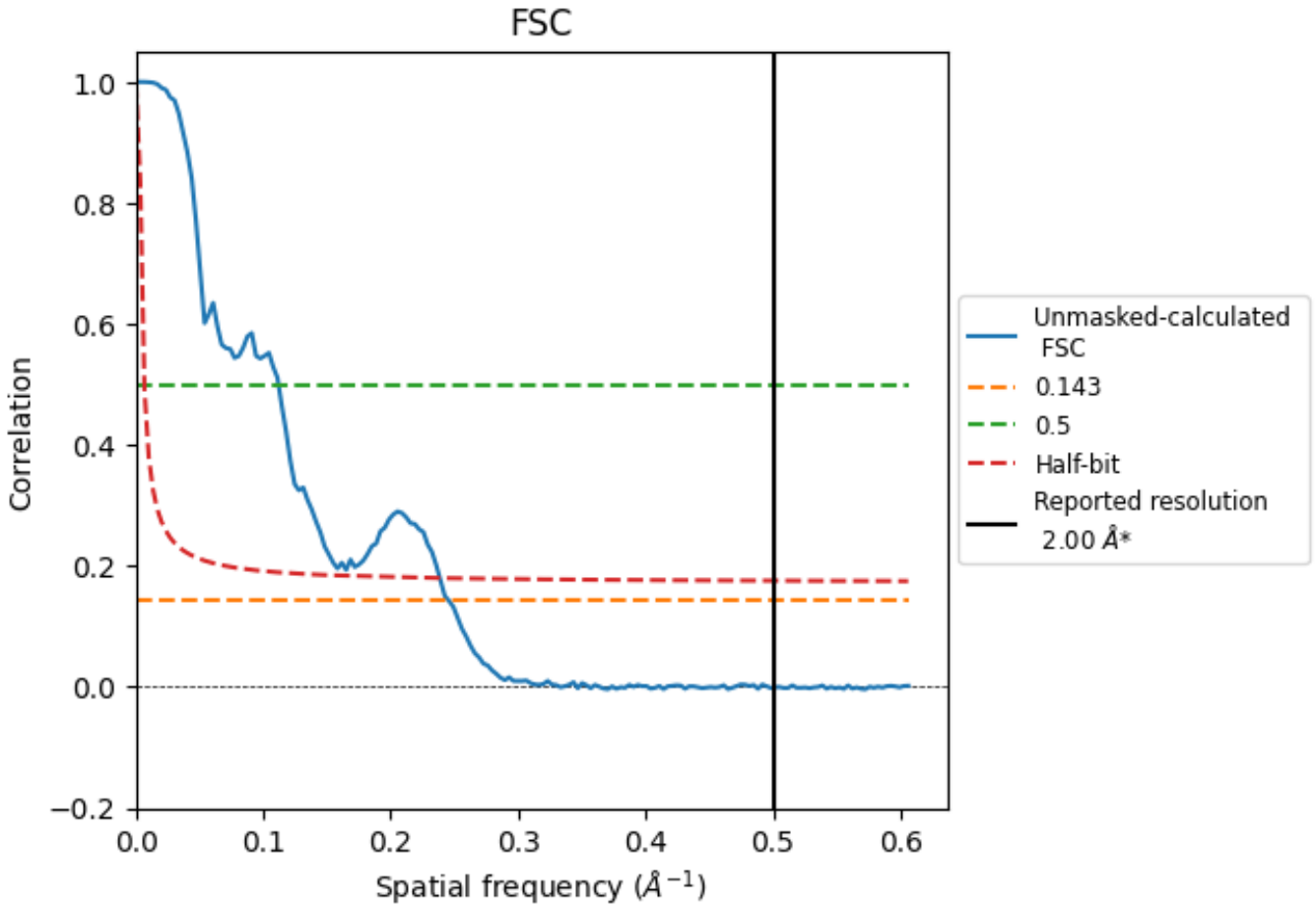


*Reported resolution corresponds to spatial frequency of 0.500 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.500 Å^{-1}

8.2 Resolution estimates (i)

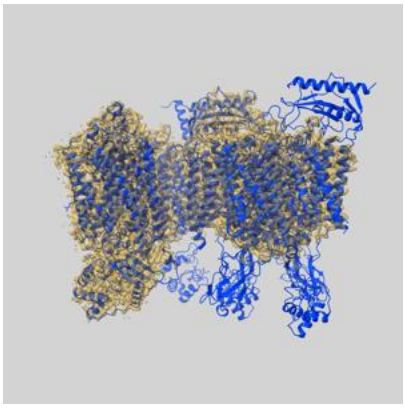
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.07	8.94	4.19

*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 4.07 differs from the reported value 2.0 by more than 10 %

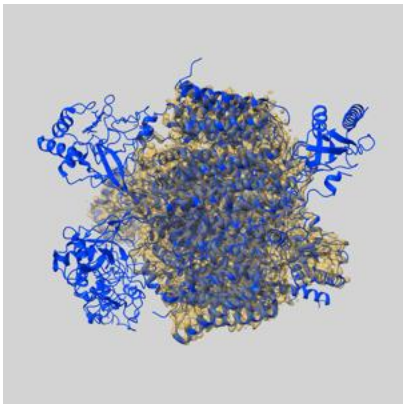
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-70330 and PDB model 9OCS. Per-residue inclusion information can be found in section 3 on page 15.

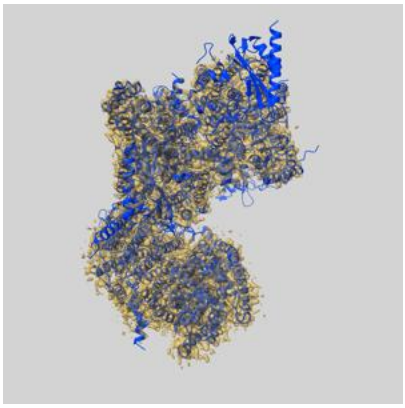
9.1 Map-model overlay



X



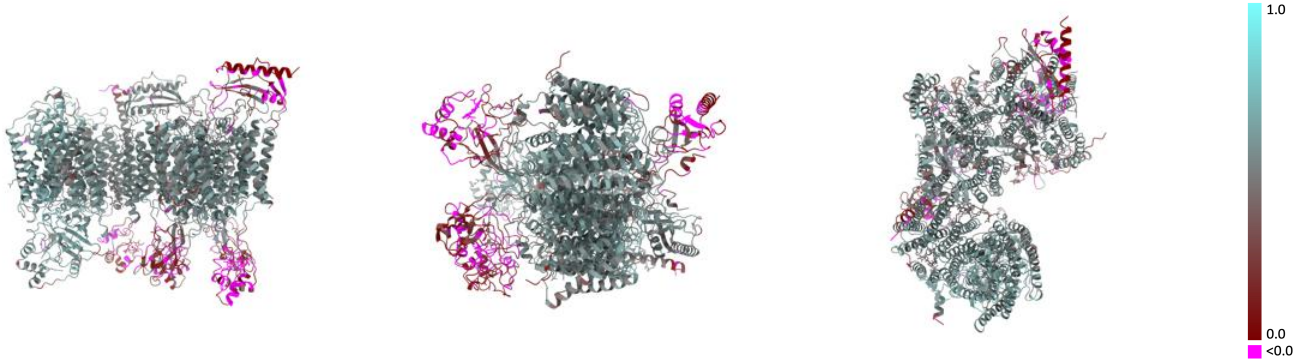
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.25 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.

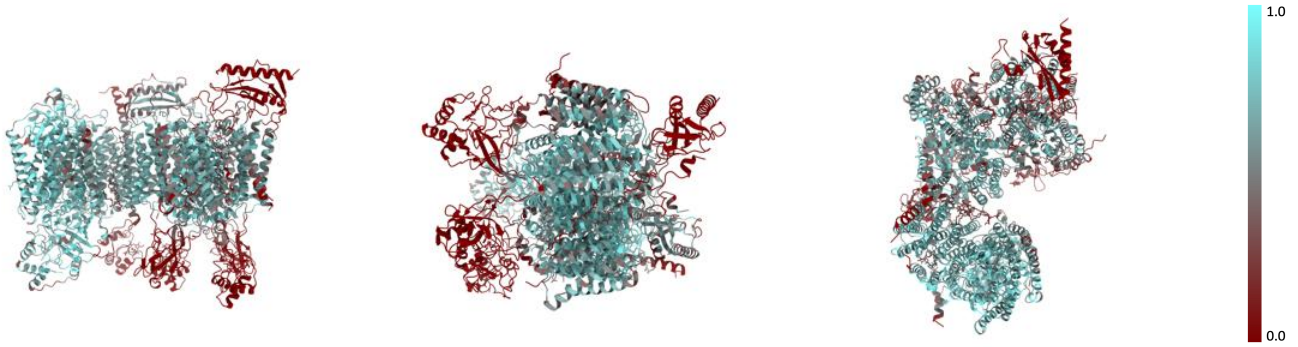
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

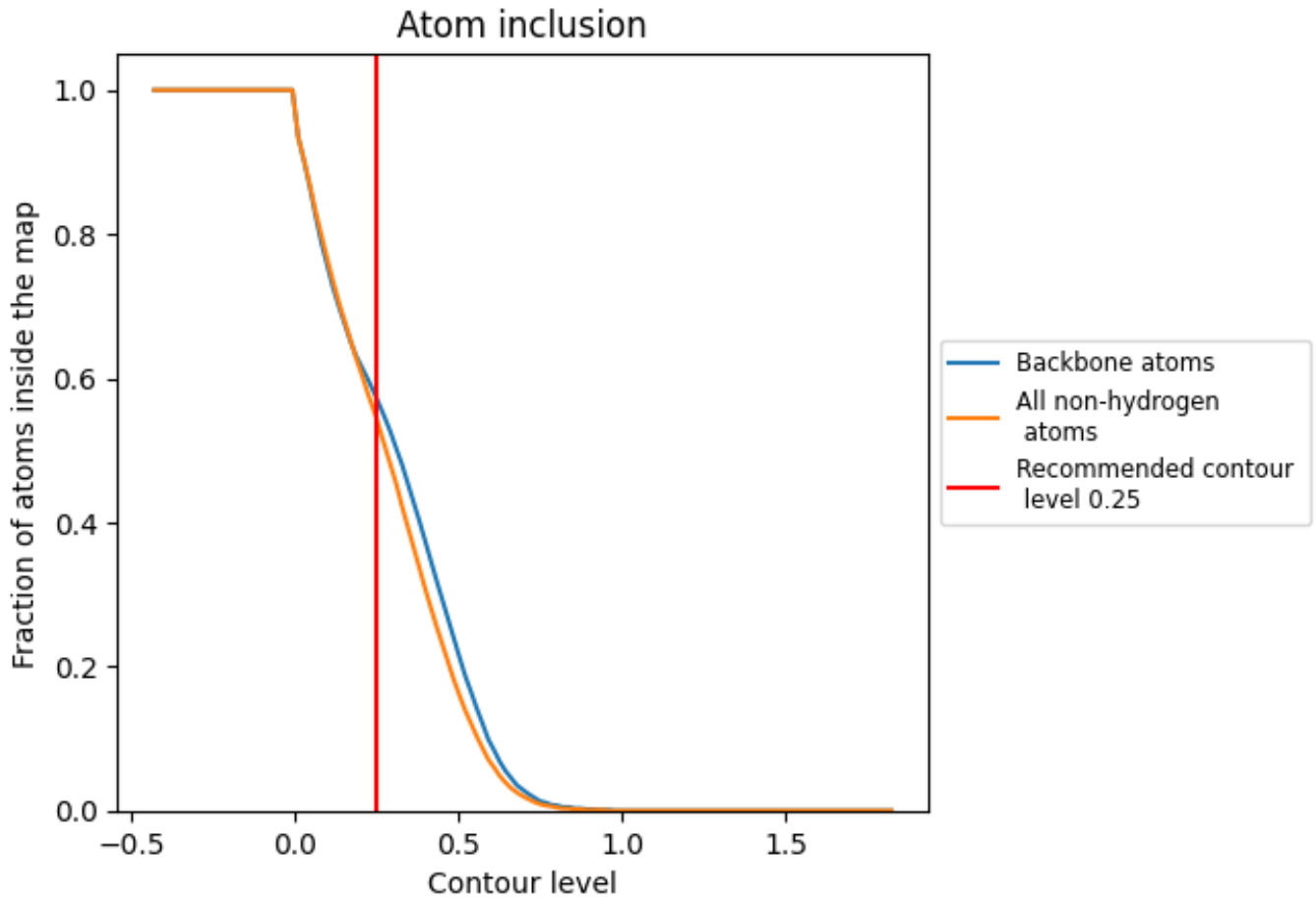
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.25).

9.4 Atom inclusion (i)



At the recommended contour level, 57% of all backbone atoms, 54% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5440	0.4760
A	0.1750	0.2860
B	0.6830	0.5590
C	0.3470	0.3710
D	0.4180	0.4790
E	0.6470	0.5590
F	0.3680	0.5290
G	0.3450	0.4690
H	0.3970	0.4270
I	0.0000	0.1250
J	0.1820	0.1890
K	0.6100	0.5110
L	0.7160	0.5550
M	0.7630	0.5950
N	0.6760	0.5630
a	0.2060	0.3290
b	0.7250	0.5610
c	0.3960	0.3750
d	0.5630	0.5110
e	0.8100	0.5770
f	0.7720	0.5440
g	0.6640	0.5330
h	0.6320	0.5100
i	0.4800	0.5120

