wwPDB EM Validation Summary Report

Aug 23, 2026 – 06:09 am BST

PDB ID	:	8P65 / pdb_00008p65
EMDB ID	:	EMD-17461
Title	:	Cytochrome bc1 complex (Bos taurus)
Authors	:	Phillips, B.P.; Barra, I.M.C.C.; Meier, T.K.; Rimle, L.; von Ballmoos, C.
Deposited on	:	2023-05-25
Resolution	:	3.00 Å(reported)
Based on initial model	:	6FO2

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

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

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

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

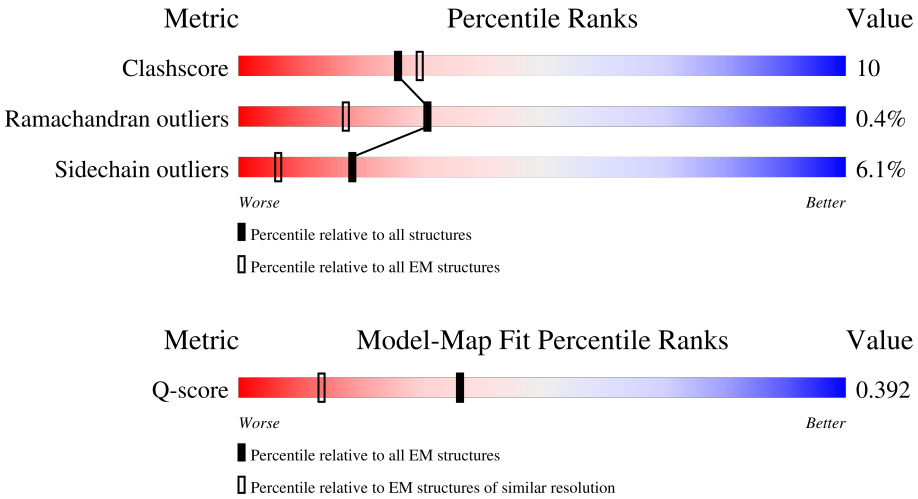
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	446	76% 23%
1	N	446	77% 22%
2	B	439	7% 75% 24%
2	O	439	6% 74% 23%

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Mol	Chain	Length	Quality of chain
3	C	379	76% 23%
3	P	379	78% 22%
4	D	241	74% 25%
4	Q	241	78% 20%
5	E	196	20% 70% 27%
5	R	196	18% 67% 30%
6	F	111	5% 71% 24% 5%
6	S	111	12% 69% 27%
7	G	82	6% 72% 27%
7	T	82	6% 77% 23%
8	H	78	14% 67% 24% 8%
8	U	78	15% 67% 26% 6%
9	I	54	31% 61% 33% 6%
9	V	54	37% 61% 39%
10	J	64	9% 62% 36%
10	W	64	11% 75% 23%
11	K	49	37% 63% 33%
11	X	49	43% 73% 22%

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
13	HEC	D	301	X	-	-	-
13	HEC	Q	301	X	-	-	-

2 Entry composition (i)

There are 14 unique types of molecules in this entry. The entry contains 33820 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 Cytochrome b-c1 complex subunit 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	446	Total	C	N	O	S	0	0
			3457	2161	609	667	20		
1	N	446	Total	C	N	O	S	0	0
			3457	2161	609	667	20		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	439	Total	C	N	O	S	0	0
			3280	2063	580	630	7		
2	O	439	Total	C	N	O	S	0	0
			3280	2063	580	630	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	305	GLU	GLN	conflict	UNP P23004
O	305	GLU	GLN	conflict	UNP P23004

- Molecule 3 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	379	Total	C	N	O	S	0	0
			3010	2018	472	501	19		
3	P	379	Total	C	N	O	S	0	0
			3010	2018	472	501	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	241	Total	C	N	O	S	0	0
			1918	1225	330	348	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	Q	241	Total	C	N	O	S	0	0
			1918	1225	330	348	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	196	Total	C	N	O	S	0	0
			1519	957	263	291	8		
5	R	196	Total	C	N	O	S	0	0
			1519	957	263	291	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	111	Total	C	N	O	S	0	0
			950	600	174	173	3		
6	S	111	Total	C	N	O	S	0	0
			950	600	174	173	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	57	ASP	ASN	conflict	UNP P00129
S	57	ASP	ASN	conflict	UNP P00129

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	82	Total	C	N	O	S	0	0
			689	446	129	112	2		
7	T	82	Total	C	N	O	S	0	0
			689	446	129	112	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	78	Total	C	N	O	S	0	0
			638	384	111	138	5		
8	U	78	Total	C	N	O	S	0	0
			638	384	111	138	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	54	Total	C	N	O	S	0	0
			383	239	71	71	2		
9	V	54	Total	C	N	O	S	0	0
			383	239	71	71	2		

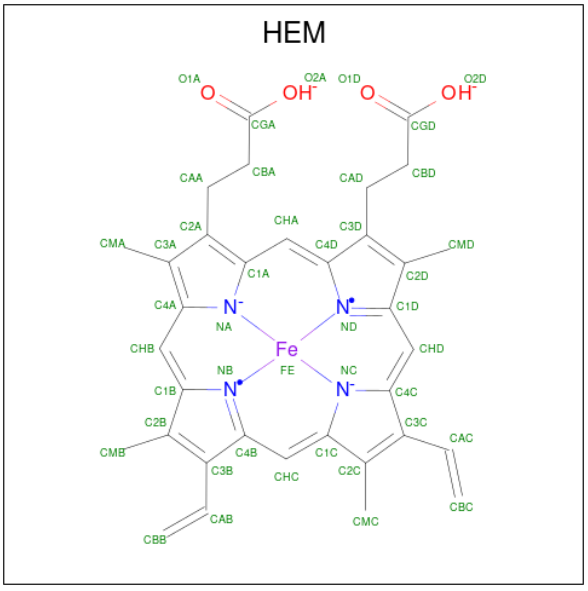
- Molecule 10 is a protein called Cytochrome b-c1 complex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	64	Total	C	N	O	S	0	0
			528	345	91	91	1		
10	W	64	Total	C	N	O	S	0	0
			528	345	91	91	1		

- Molecule 11 is a protein called Cytochrome b-c1 complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	49	Total	C	N	O	S	0	0
			405	270	72	62	1		
11	X	49	Total	C	N	O	S	0	0
			405	270	72	62	1		

- Molecule 12 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



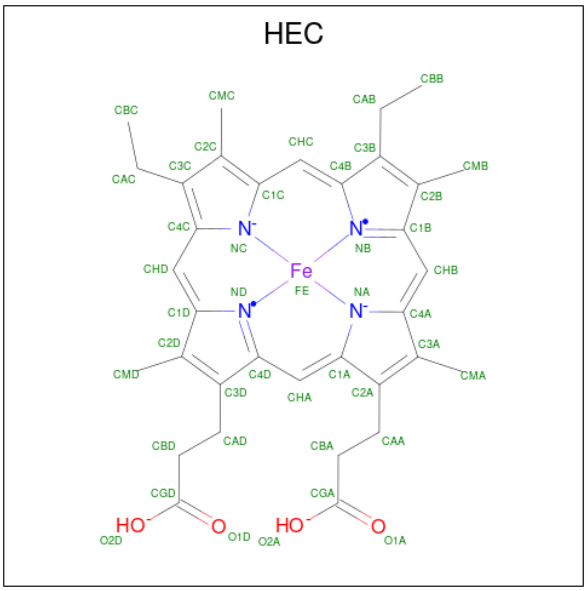
Mol	Chain	Residues	Atoms					AltConf
12	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

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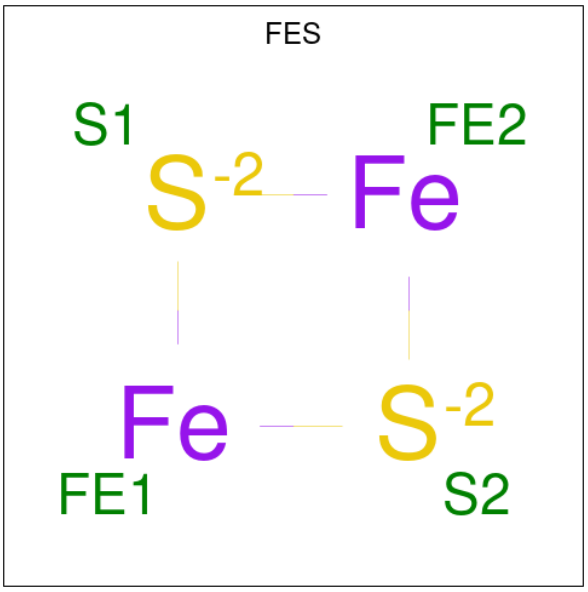
Mol	Chain	Residues	Atoms					AltConf
12	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
12	P	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
12	P	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 13 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{36}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 14 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
14	E	1	Total 4	Fe 2	S 2	0
14	R	1	Total 4	Fe 2	S 2	0

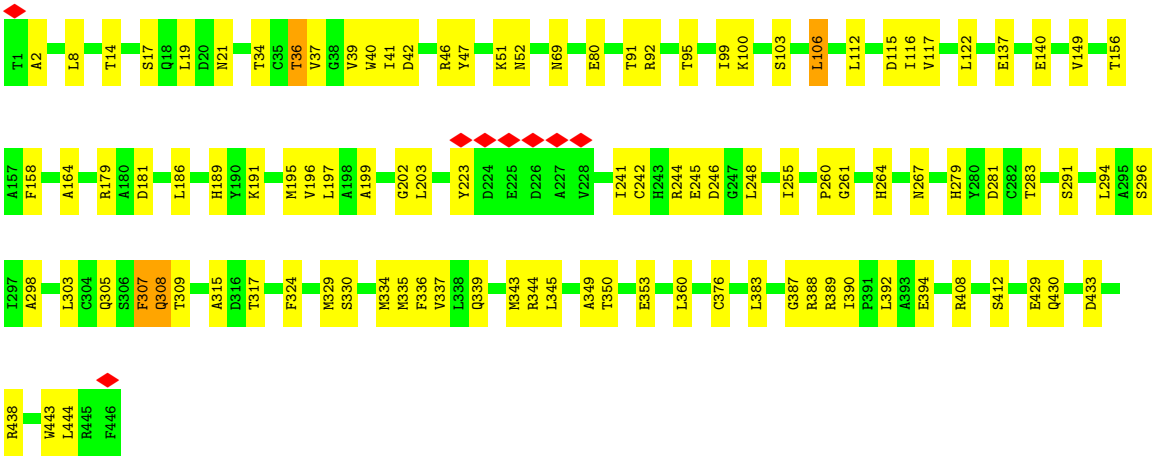
3 Residue-property plots (i)

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: Cytochrome b-c1 complex subunit 1, mitochondrial

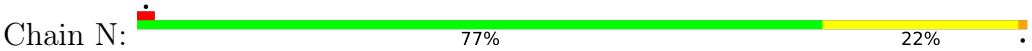
Chain A:

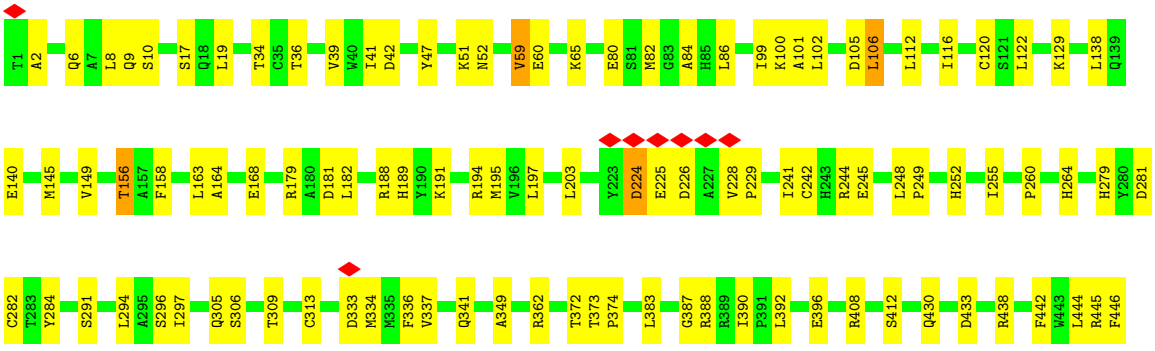




• Molecule 1: Cytochrome b-c1 complex subunit 1, mitochondrial

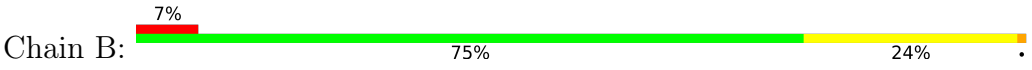
Chain N:

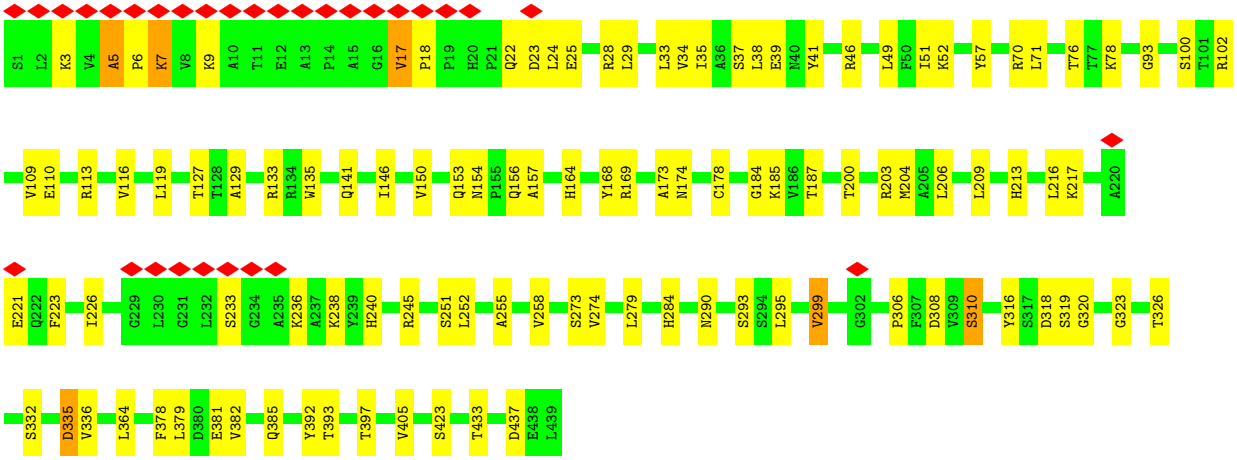




• Molecule 2: Cytochrome b-c1 complex subunit 2, mitochondrial

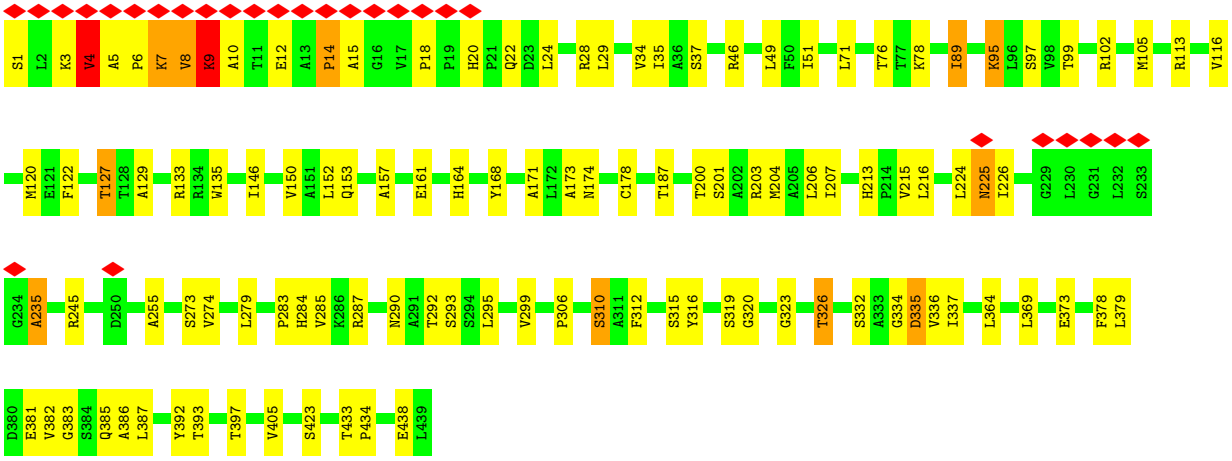
Chain B:



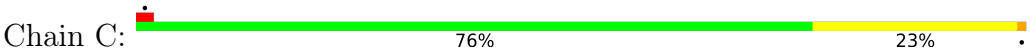


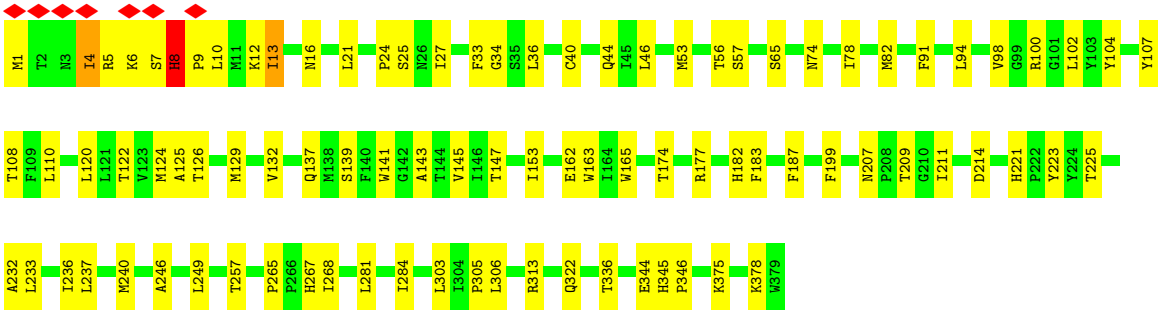
• Molecule 2: Cytochrome b-c1 complex subunit 2, mitochondrial



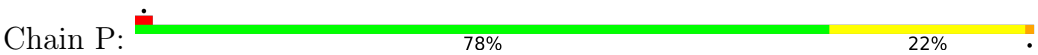


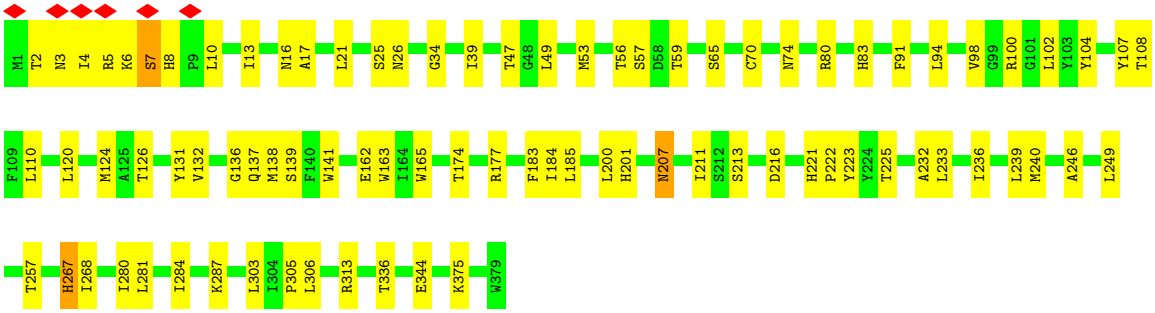
• Molecule 3: Cytochrome b





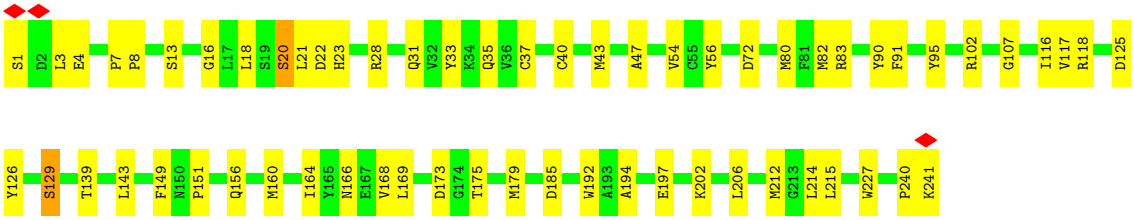
• Molecule 3: Cytochrome b



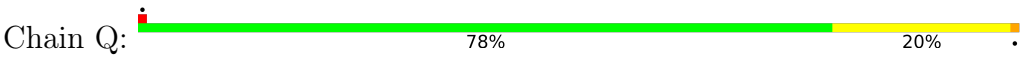


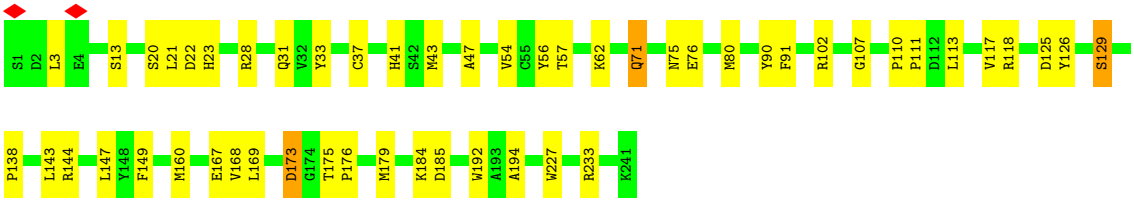
• Molecule 4: Cytochrome c1, heme protein, mitochondrial





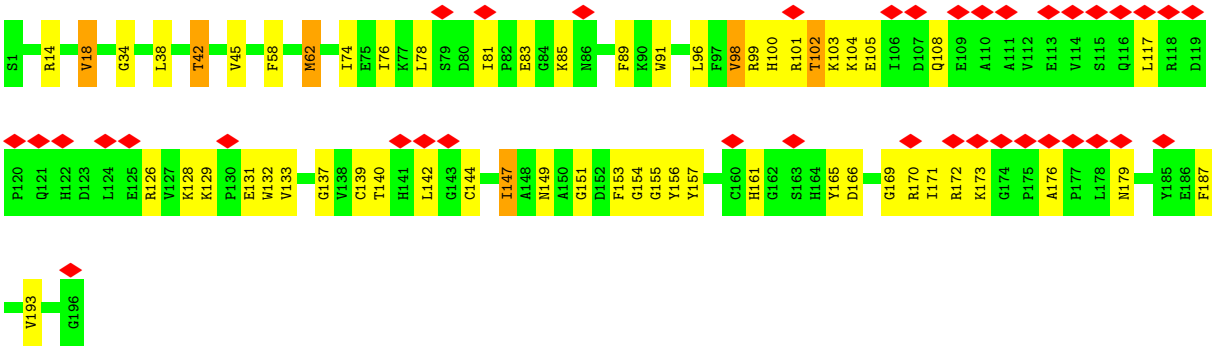
• Molecule 4: Cytochrome c1, heme protein, mitochondrial





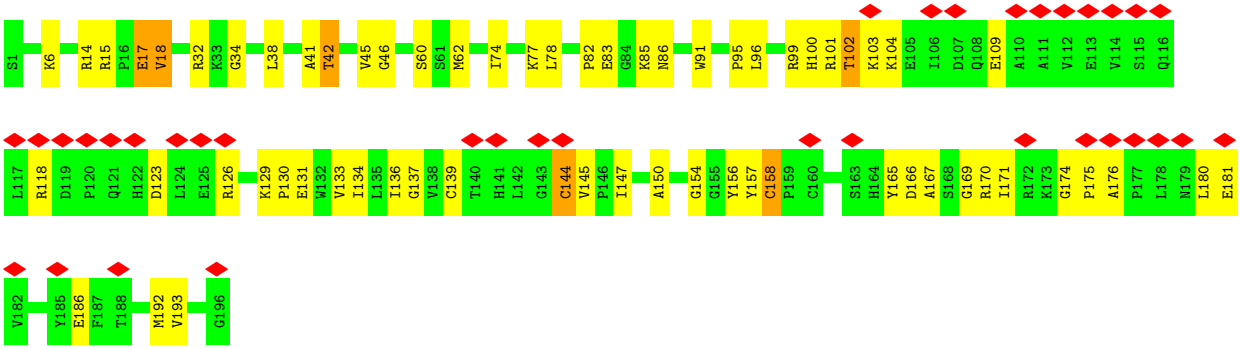
• Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial





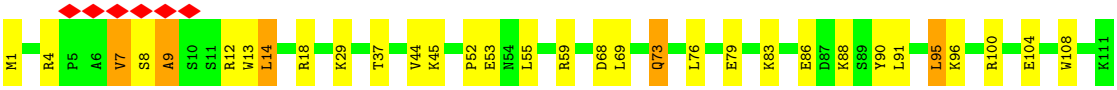
• Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial





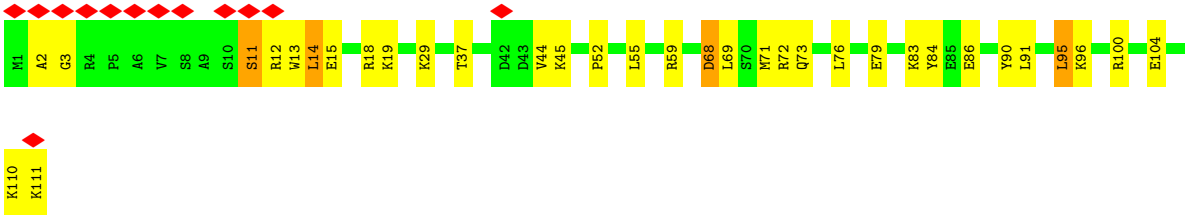
• Molecule 6: Cytochrome b-c1 complex subunit 7





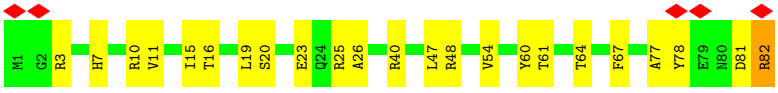
• Molecule 6: Cytochrome b-c1 complex subunit 7



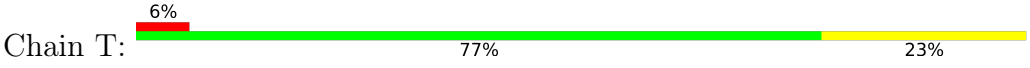


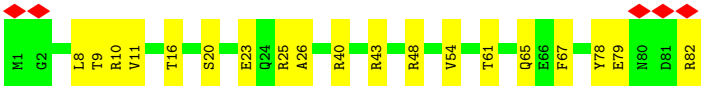
• Molecule 7: Cytochrome b-c1 complex subunit 8





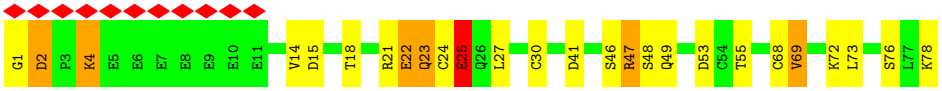
• Molecule 7: Cytochrome b-c1 complex subunit 8





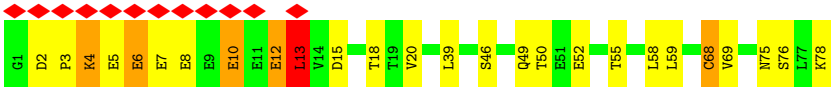
• Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial





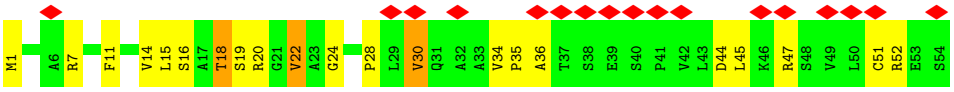
• Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial





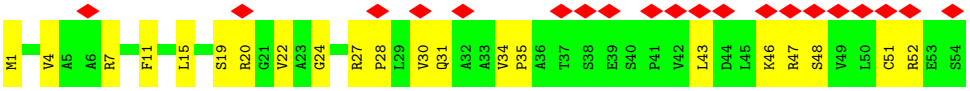
• Molecule 9: Cytochrome b-c1 complex subunit 9





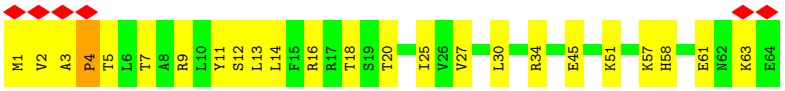
• Molecule 9: Cytochrome b-c1 complex subunit 9



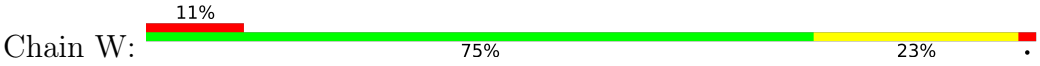


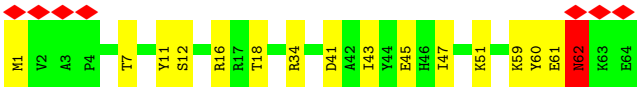
• Molecule 10: Cytochrome b-c1 complex subunit 9





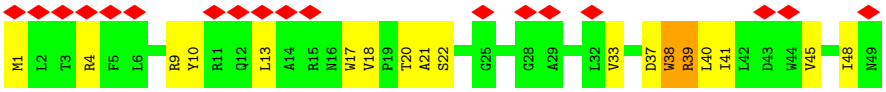
• Molecule 10: Cytochrome b-c1 complex subunit 9





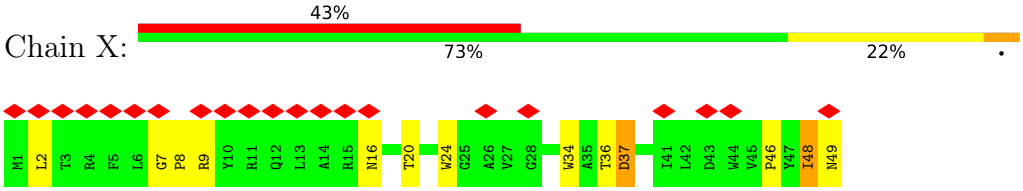
• Molecule 11: Cytochrome b-c1 complex subunit 10





• Molecule 11: Cytochrome b-c1 complex subunit 10

Chain X:


43%
73%
22%
M1
L2
T3
R4
F5
L6
G7
P8
R9
Y10
R11
Q12
L13
A14
R15
N16
T20
W24
G25
A26
V27
G28
W34
A35
T36
D37
T41
L42
D43
W44
V45
P46
Y47
I48
N49

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	140138	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CryoSPARC's own CTF correction	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2750	Depositor
Magnification	85000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	44.526	Depositor
Minimum map value	-22.986	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	6.5	Depositor
Map size (Å)	438.6, 438.6, 438.6	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.462, 1.462, 1.462	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, FES, 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	A	0.17	0/3530	0.37	0/4792
1	N	0.17	0/3530	0.37	0/4792
2	B	0.16	0/3342	0.36	0/4537
2	O	0.19	0/3342	0.42	0/4537
3	C	0.16	0/3107	0.35	0/4252
3	P	0.17	0/3107	0.35	0/4252
4	D	0.15	0/1977	0.37	0/2684
4	Q	0.14	0/1977	0.35	0/2684
5	E	0.16	0/1553	0.39	0/2100
5	R	0.15	0/1553	0.41	1/2100 (0.0%)
6	F	0.20	0/970	0.46	0/1301
6	S	0.17	0/970	0.46	0/1301
7	G	0.15	0/711	0.43	0/961
7	T	0.16	0/711	0.46	0/961
8	H	0.37	0/644	0.74	1/864 (0.1%)
8	U	0.42	0/644	0.75	0/864
9	I	0.18	0/388	0.57	0/528
9	V	0.16	0/388	0.53	0/528
10	J	0.16	0/541	0.40	0/729
10	W	0.17	0/541	0.38	0/729
11	K	0.34	0/420	0.59	1/578 (0.2%)
11	X	0.19	0/420	0.49	0/578
All	All	0.18	0/34366	0.41	3/46652 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	H	25	GLU	N-CA-C	-8.62	102.14	114.12
5	R	158	CYS	CB-CA-C	7.13	117.23	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	K	21	ALA	N-CA-C	-5.68	105.23	111.82

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	3457	0	3356	61	0
1	N	3457	0	3356	63	0
2	B	3280	0	3276	80	0
2	O	3280	0	3276	84	0
3	C	3010	0	3077	60	0
3	P	3010	0	3077	54	0
4	D	1918	0	1870	41	0
4	Q	1918	0	1870	41	0
5	E	1519	0	1503	42	0
5	R	1519	0	1504	46	0
6	F	950	0	949	19	0
6	S	950	0	949	25	0
7	G	689	0	688	17	0
7	T	689	0	688	14	0
8	H	638	0	602	20	0
8	U	638	0	602	25	0
9	I	383	0	410	23	0
9	V	383	0	410	25	0
10	J	528	0	533	18	0
10	W	528	0	533	11	0
11	K	405	0	409	12	0
11	X	405	0	409	12	0
12	C	86	0	60	14	0
12	P	86	0	60	14	0
13	D	43	0	32	2	0
13	Q	43	0	32	6	0
14	E	4	0	0	0	0
14	R	4	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	33820	0	33531	683	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 683 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)
5:R:158:CYS:HB3	14:R:201:FES:S1	2.04	0.98
4:Q:160:MET:SD	13:Q:301:HEC:ND	2.53	0.82
1:N:41:ILE:HG22	1:N:195:MET:HG2	1.62	0.81
1:A:41:ILE:HG22	1:A:195:MET:HG2	1.61	0.81
1:N:6:GLN:HG2	2:O:9:LYS:HB3	1.62	0.80

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	444/446 (100%)	426 (96%)	18 (4%)	0	100	100
1	N	444/446 (100%)	424 (96%)	19 (4%)	1 (0%)	43	76
2	B	437/439 (100%)	413 (94%)	22 (5%)	2 (0%)	24	60
2	O	437/439 (100%)	408 (93%)	23 (5%)	6 (1%)	9	36
3	C	377/379 (100%)	357 (95%)	19 (5%)	1 (0%)	36	70
3	P	377/379 (100%)	362 (96%)	15 (4%)	0	100	100
4	D	239/241 (99%)	236 (99%)	3 (1%)	0	100	100
4	Q	239/241 (99%)	237 (99%)	2 (1%)	0	100	100
5	E	194/196 (99%)	182 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
5	R	194/196 (99%)	182 (94%)	12 (6%)	0	100 100
6	F	109/111 (98%)	103 (94%)	5 (5%)	1 (1%)	14 48
6	S	109/111 (98%)	105 (96%)	3 (3%)	1 (1%)	14 48
7	G	80/82 (98%)	75 (94%)	5 (6%)	0	100 100
7	T	80/82 (98%)	75 (94%)	5 (6%)	0	100 100
8	H	76/78 (97%)	68 (90%)	7 (9%)	1 (1%)	9 38
8	U	76/78 (97%)	68 (90%)	7 (9%)	1 (1%)	9 38
9	I	52/54 (96%)	37 (71%)	15 (29%)	0	100 100
9	V	52/54 (96%)	39 (75%)	13 (25%)	0	100 100
10	J	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	7 34
10	W	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	7 34
11	K	47/49 (96%)	43 (92%)	4 (8%)	0	100 100
11	X	47/49 (96%)	41 (87%)	6 (13%)	0	100 100
All	All	4234/4278 (99%)	3996 (94%)	222 (5%)	16 (0%)	31 65

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	17	VAL
3	C	8	HIS
10	J	4	PRO
1	N	224	ASP
2	O	4	VAL

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	370/370 (100%)	349 (94%)	21 (6%)	18 52
1	N	370/370 (100%)	348 (94%)	22 (6%)	18 50
2	B	343/343 (100%)	331 (96%)	12 (4%)	32 65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	O	343/343 (100%)	321 (94%)	22 (6%)	16 48
3	C	327/327 (100%)	310 (95%)	17 (5%)	21 55
3	P	327/327 (100%)	304 (93%)	23 (7%)	14 44
4	D	206/206 (100%)	200 (97%)	6 (3%)	37 70
4	Q	206/206 (100%)	200 (97%)	6 (3%)	37 70
5	E	168/168 (100%)	157 (94%)	11 (6%)	15 47
5	R	168/168 (100%)	158 (94%)	10 (6%)	17 50
6	F	99/99 (100%)	90 (91%)	9 (9%)	9 33
6	S	99/99 (100%)	92 (93%)	7 (7%)	13 43
7	G	72/72 (100%)	66 (92%)	6 (8%)	10 37
7	T	72/72 (100%)	67 (93%)	5 (7%)	14 45
8	H	74/74 (100%)	64 (86%)	10 (14%)	4 18
8	U	74/74 (100%)	64 (86%)	10 (14%)	4 18
9	I	42/42 (100%)	39 (93%)	3 (7%)	13 43
9	V	42/42 (100%)	38 (90%)	4 (10%)	8 31
10	J	54/54 (100%)	51 (94%)	3 (6%)	19 52
10	W	54/54 (100%)	52 (96%)	2 (4%)	30 64
11	K	40/40 (100%)	33 (82%)	7 (18%)	2 10
11	X	40/40 (100%)	37 (92%)	3 (8%)	12 41
All	All	3590/3590 (100%)	3371 (94%)	219 (6%)	19 49

5 of 219 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	149	VAL
2	O	225	ASN
7	T	65	GLN
1	N	282	CYS
2	O	9	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
2	O	174	ASN

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Mol	Chain	Res	Type
3	P	137	GLN
2	O	313	ASN
2	O	400	GLN
4	Q	105	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)

8 ligands are modelled in this entry.

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	$\#\|Z\| > 2$
12	HEM	P	401	3	50,50,50	1.35	8 (16%)	66,82,82	1.24	8 (12%)
13	HEC	D	301	4	50,50,50	1.72	5 (10%)	68,82,82	1.38	8 (11%)
14	FES	R	201	5	0,4,4	-	-	-		
12	HEM	P	402	3	50,50,50	1.42	6 (12%)	66,82,82	1.29	7 (10%)
13	HEC	Q	301	4	50,50,50	1.72	5 (10%)	68,82,82	1.36	8 (11%)
14	FES	E	201	5	0,4,4	-	-	-		
12	HEM	C	402	3	50,50,50	1.41	6 (12%)	66,82,82	1.27	8 (12%)
12	HEM	C	401	3	50,50,50	1.35	7 (14%)	66,82,82	1.22	8 (12%)

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
12	HEM	P	401	3	-	3/14/54/54	-
13	HEC	D	301	4	1/1/3/7	0/14/54/54	-
14	FES	R	201	5	-	-	0/1/1/1
12	HEM	P	402	3	-	6/14/54/54	-
13	HEC	Q	301	4	1/1/3/7	1/14/54/54	-
14	FES	E	201	5	-	-	0/1/1/1
12	HEM	C	402	3	-	7/14/54/54	-
12	HEM	C	401	3	-	3/14/54/54	-

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	Q	301	HEC	C3D-C2D	8.05	1.53	1.36
13	D	301	HEC	C3D-C2D	8.01	1.53	1.36
13	Q	301	HEC	FE-ND	4.12	2.07	1.94
12	P	402	HEM	FE-ND	3.88	2.06	1.94
13	D	301	HEC	FE-ND	3.75	2.06	1.94

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	Q	301	HEC	C1D-ND-C4D	6.10	111.37	105.07
13	D	301	HEC	C1D-ND-C4D	6.08	111.35	105.07
12	P	401	HEM	C4A-NA-C1A	2.86	108.14	105.35
12	C	401	HEM	C4A-NA-C1A	2.84	108.13	105.35
13	D	301	HEC	CAA-CBA-CGA	-2.81	107.55	113.60

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
13	D	301	HEC	NA
13	Q	301	HEC	NA

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	C	402	HEM	C4D-C3D-CAD-CBD

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Mol	Chain	Res	Type	Atoms
12	P	402	HEM	C4D-C3D-CAD-CBD
12	P	402	HEM	C2A-CAA-CBA-CGA
12	P	402	HEM	C2D-C3D-CAD-CBD
12	C	402	HEM	C2D-C3D-CAD-CBD

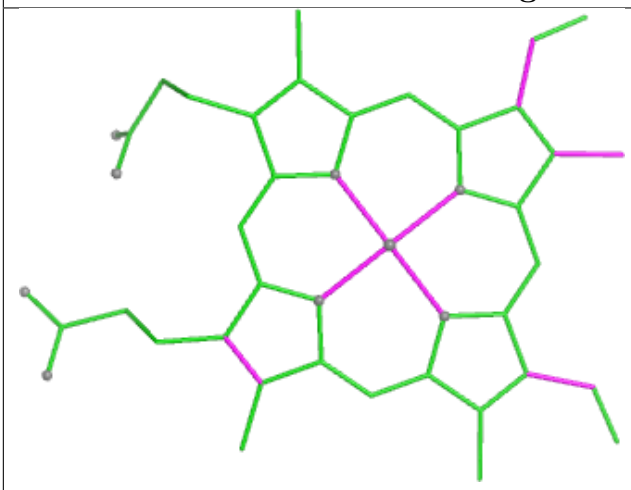
There are no ring outliers.

7 monomers are involved in 37 short contacts:

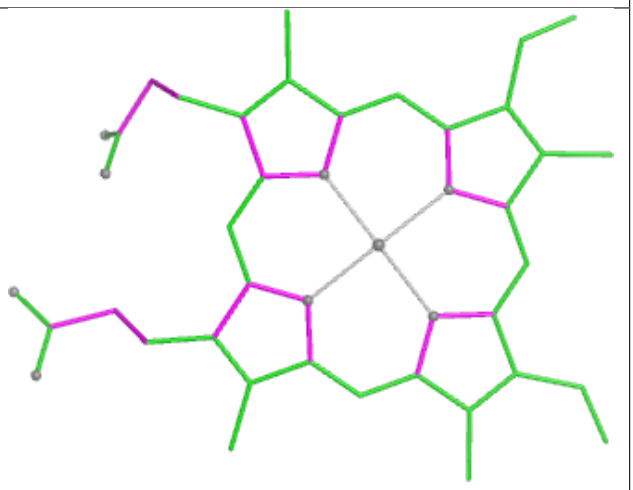
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	P	401	HEM	5	0
13	D	301	HEC	2	0
14	R	201	FES	1	0
12	P	402	HEM	9	0
13	Q	301	HEC	6	0
12	C	402	HEM	9	0
12	C	401	HEM	5	0

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.

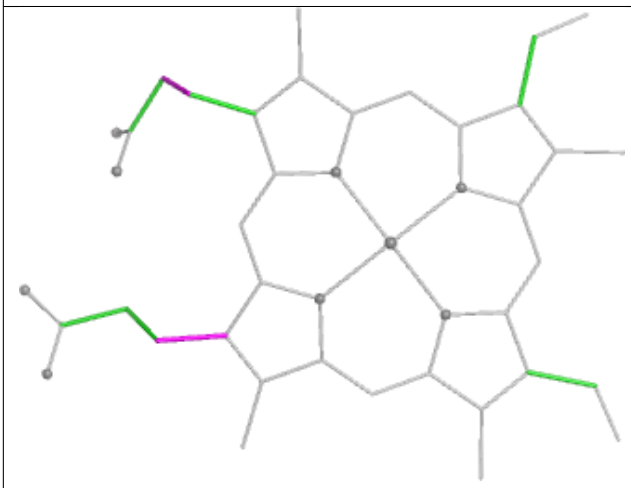
Ligand HEM P 401



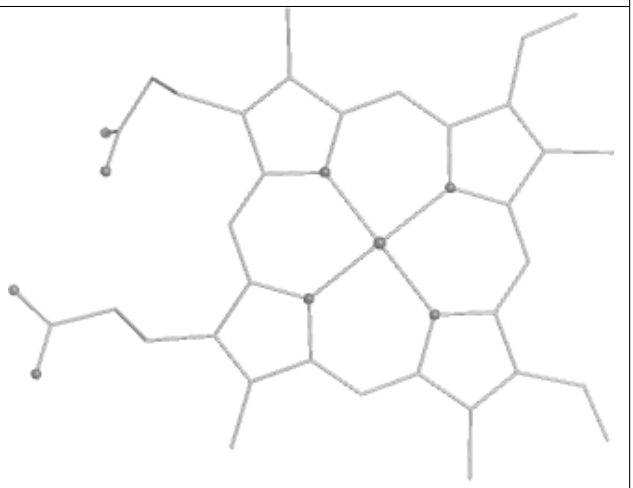
Bond lengths



Bond angles

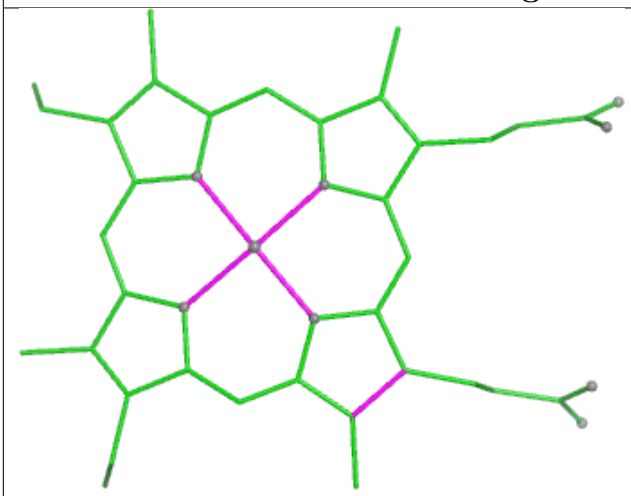


Torsions

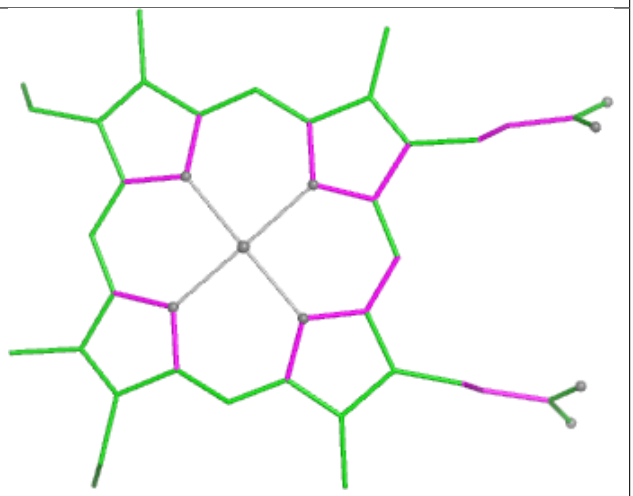


Rings

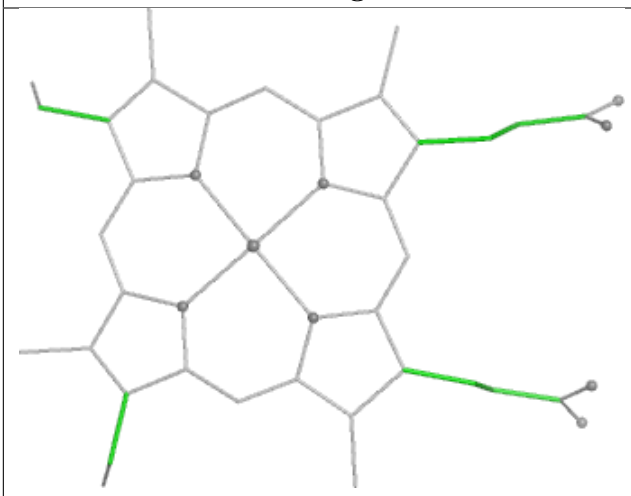
Ligand HEC D 301



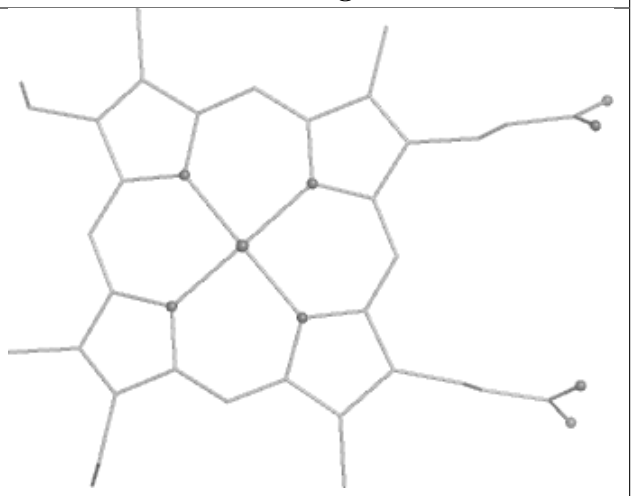
Bond lengths



Bond angles

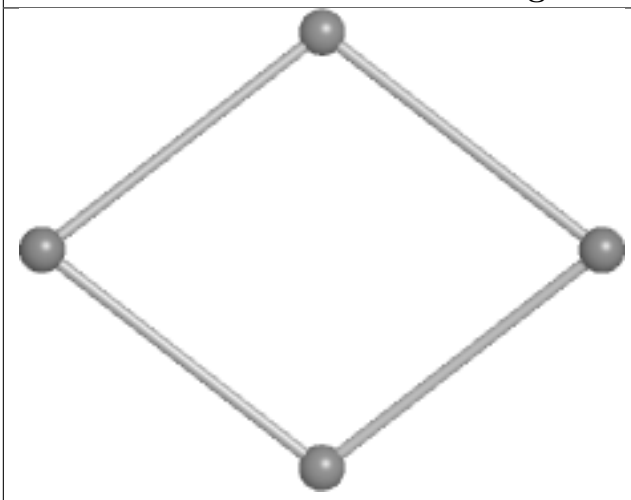


Torsions

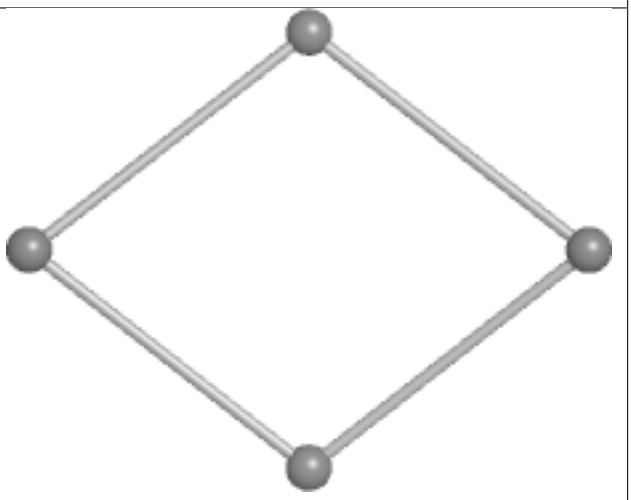


Rings

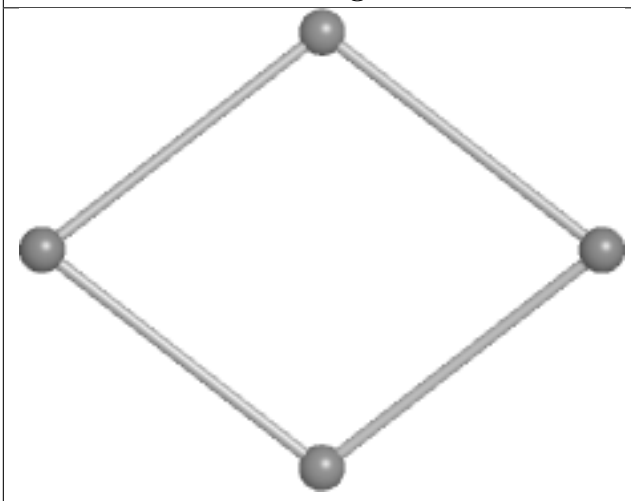
Ligand FES R 201



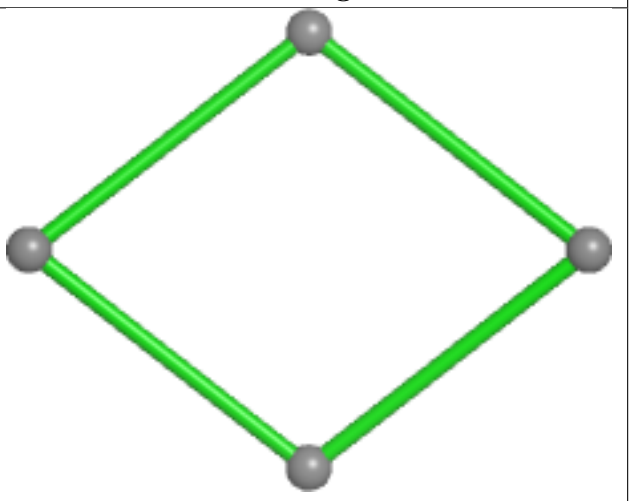
Bond lengths



Bond angles

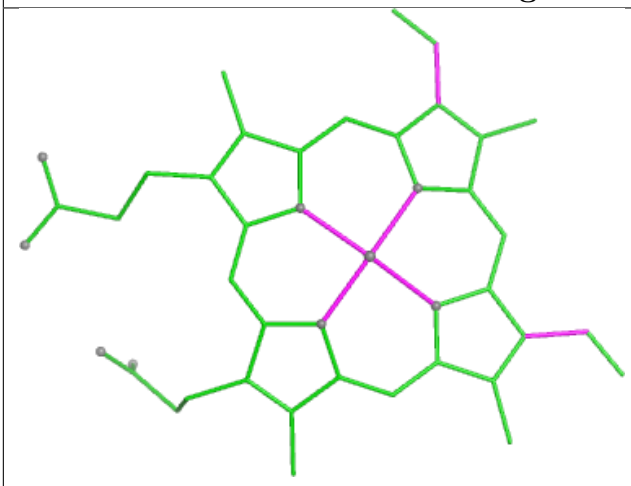


Torsions

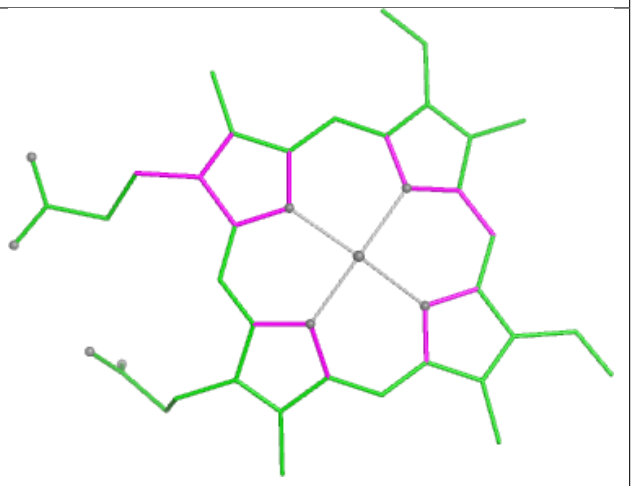


Rings

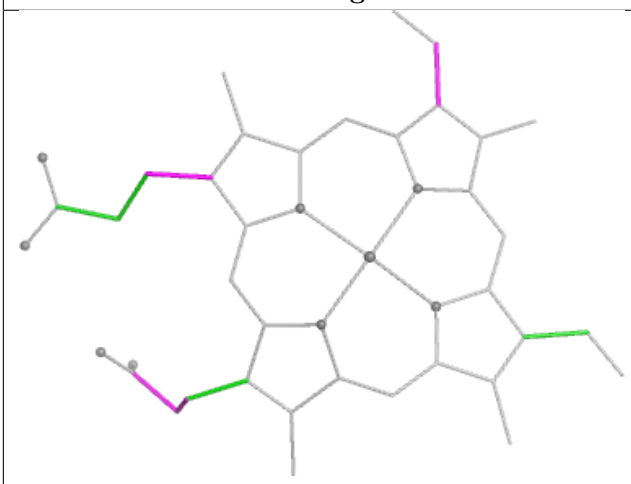
Ligand HEM P 402



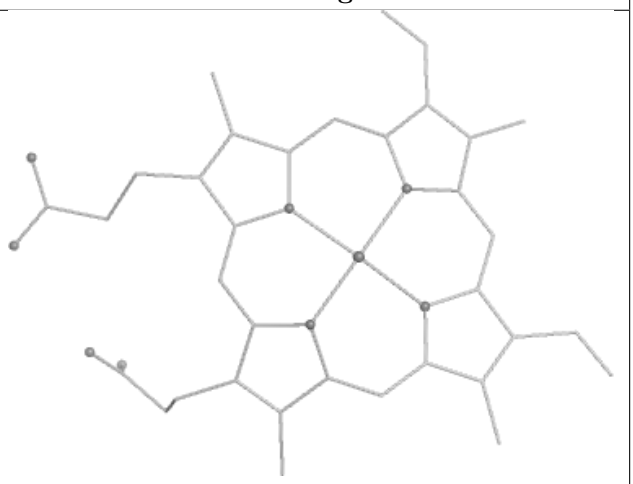
Bond lengths



Bond angles

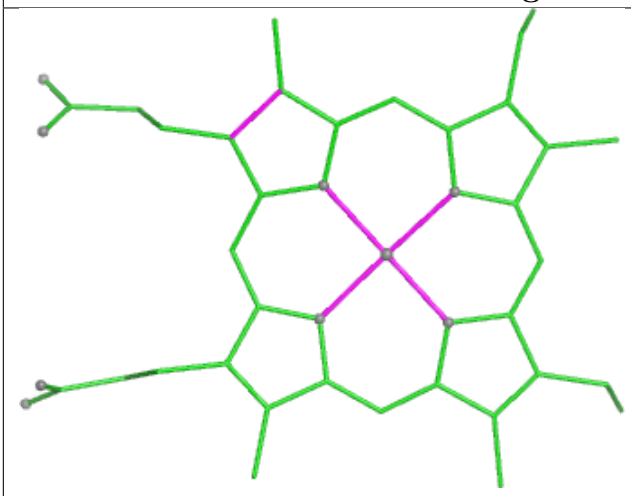


Torsions

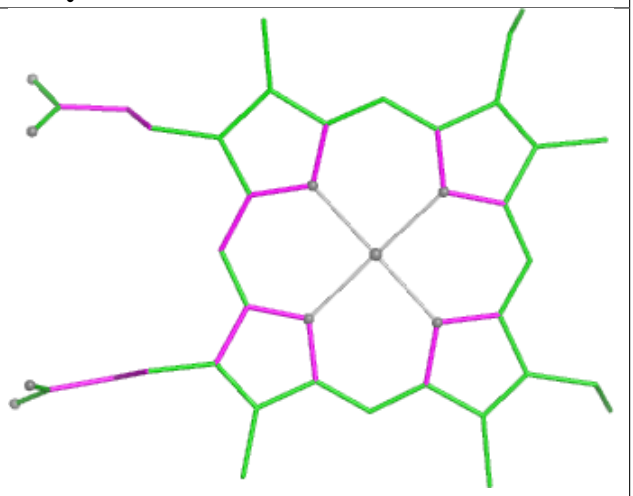


Rings

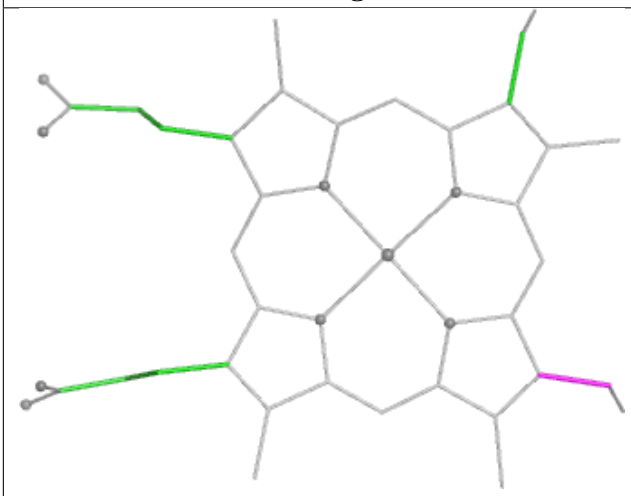
Ligand HEC Q 301



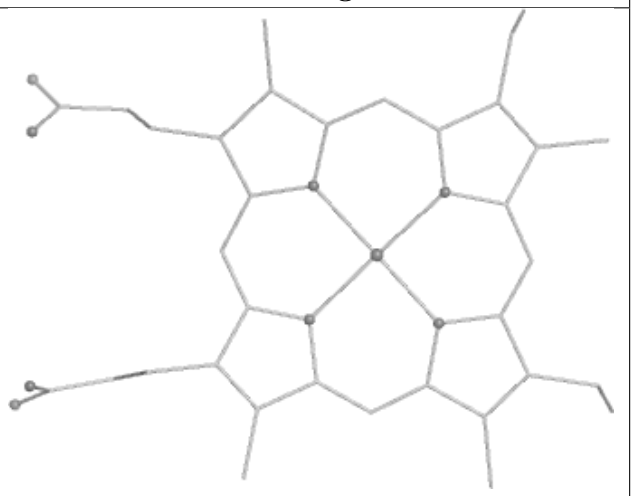
Bond lengths



Bond angles

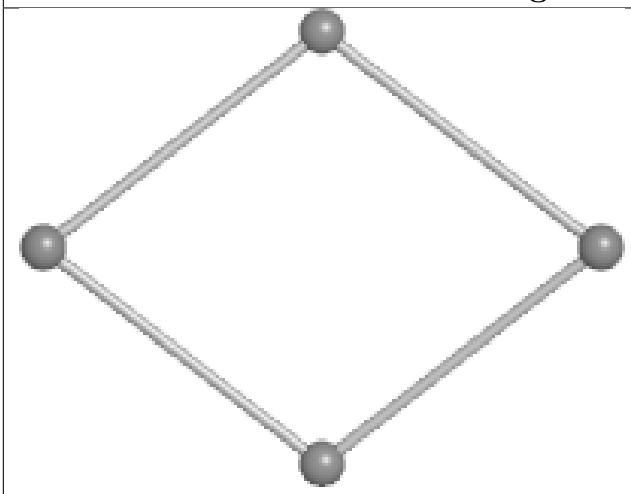


Torsions

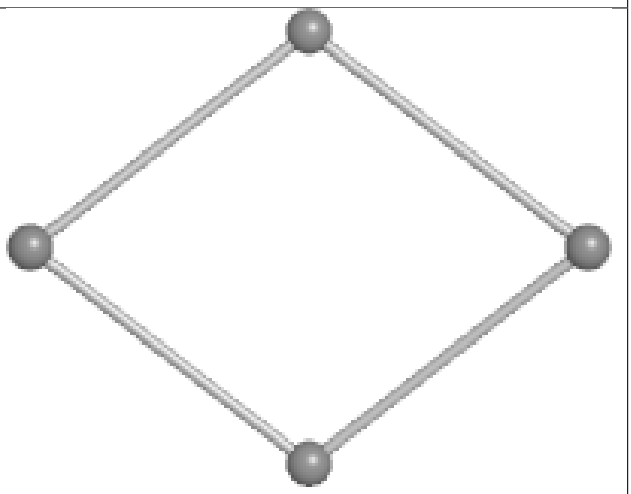


Rings

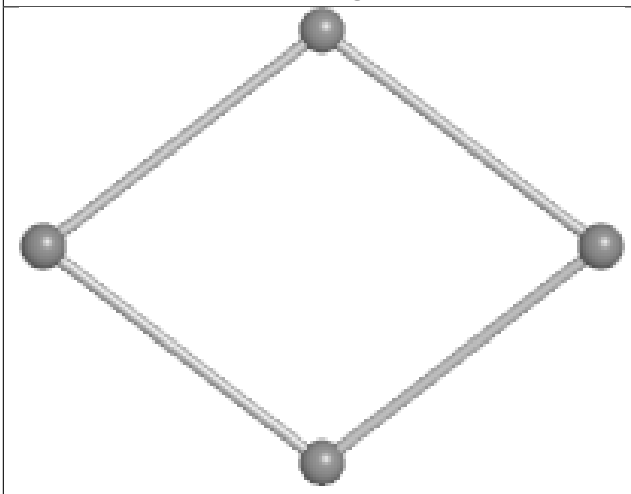
Ligand FES E 201



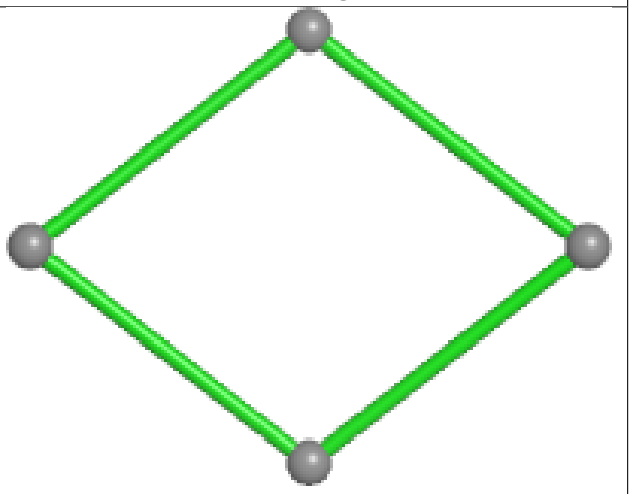
Bond lengths



Bond angles

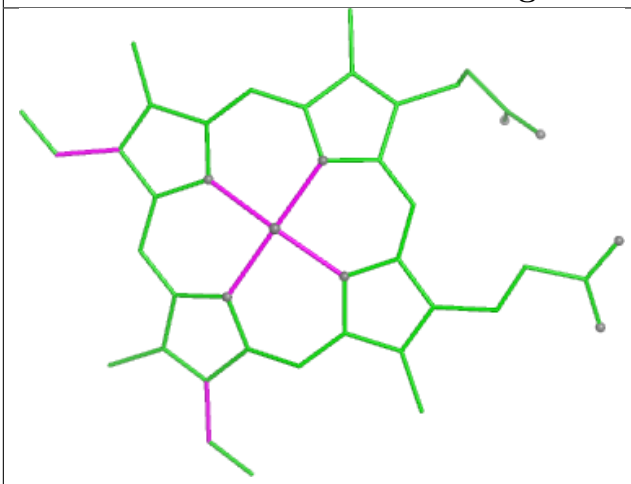


Torsions

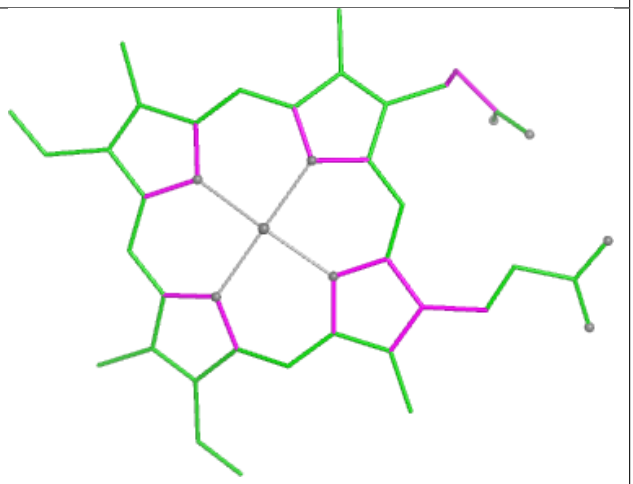


Rings

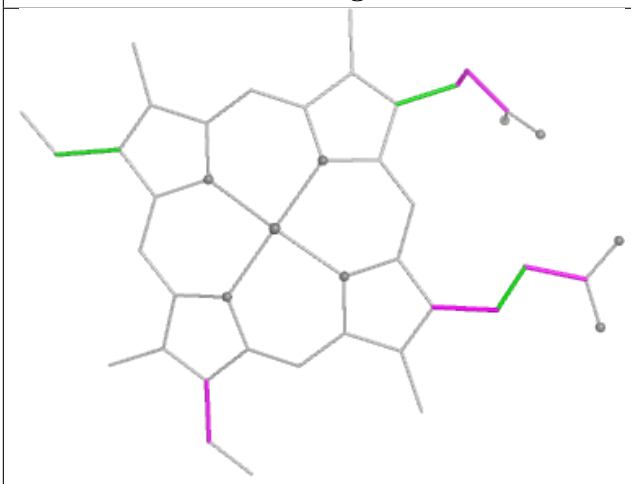
Ligand HEM C 402



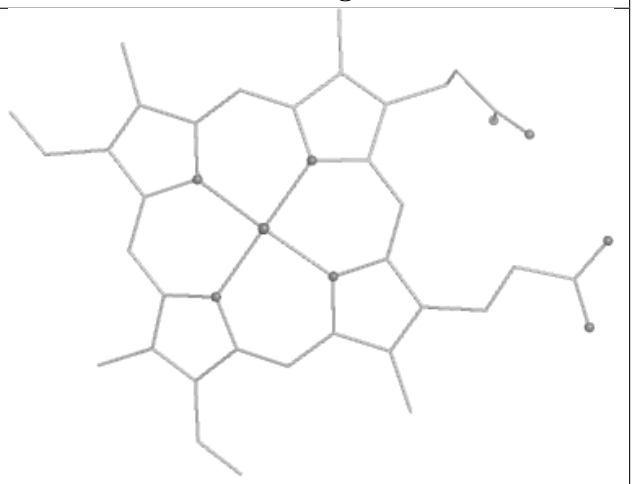
Bond lengths



Bond angles

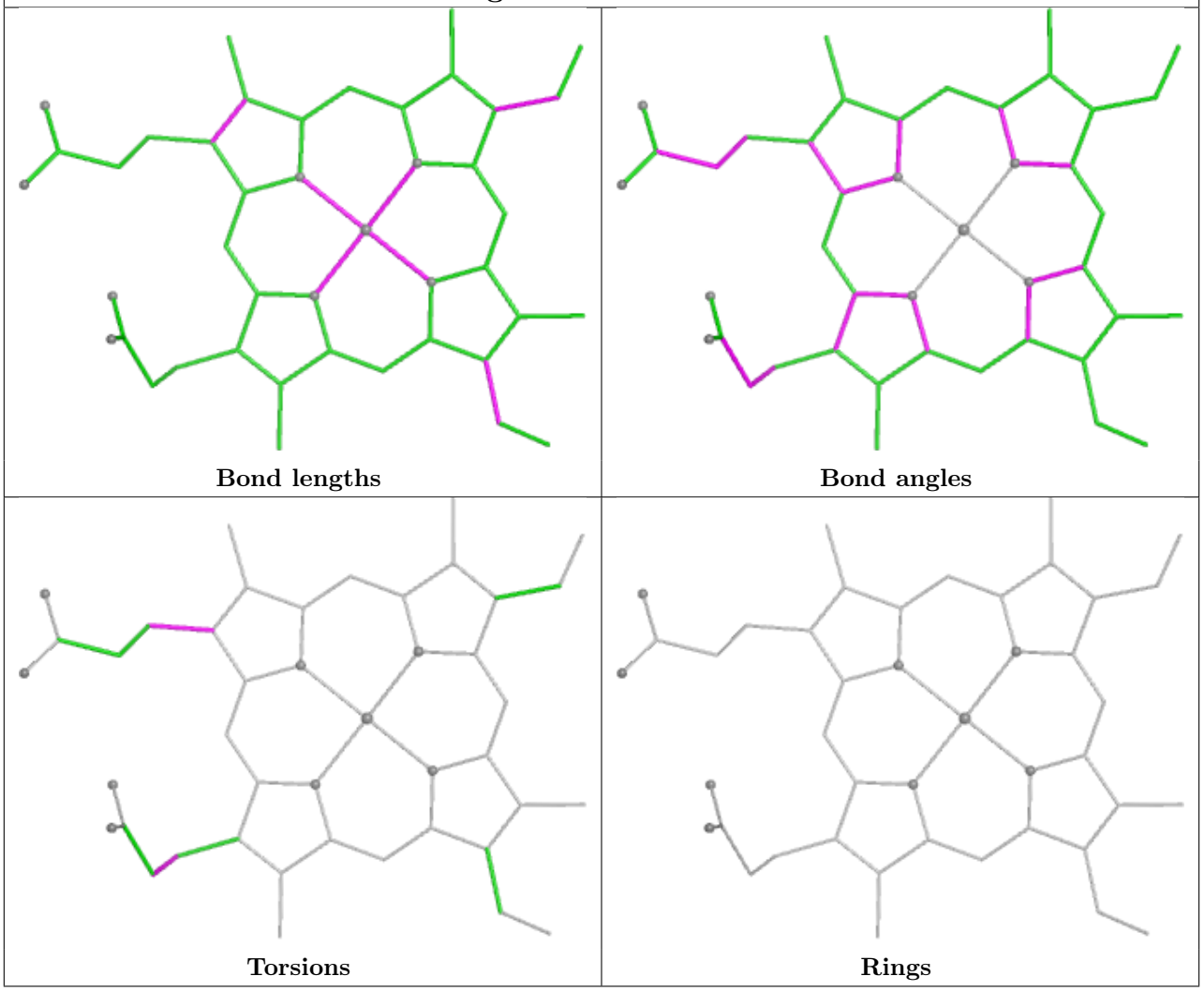


Torsions



Rings

Ligand HEM C 401



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.

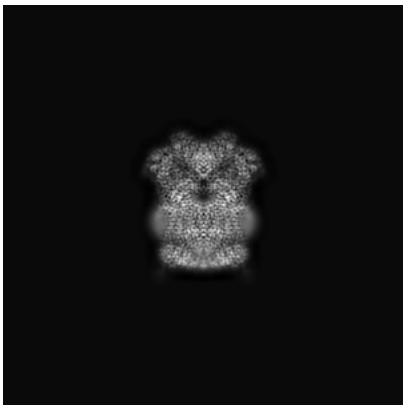
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-17461. These allow visual inspection of the internal detail of the map and identification of artifacts.

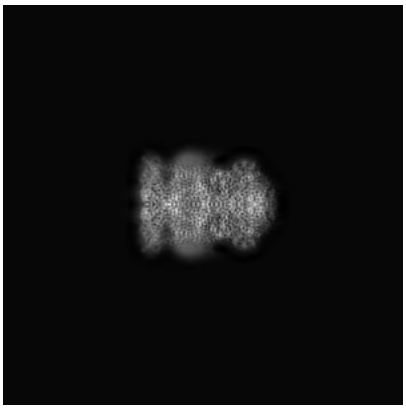
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

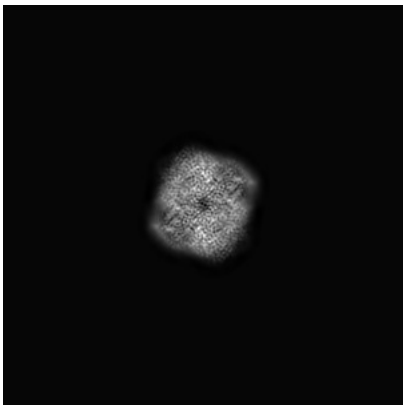
6.1.1 Primary map



X

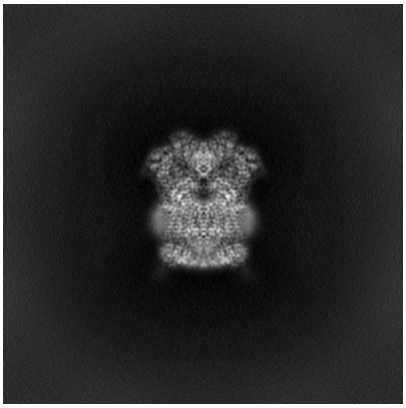


Y

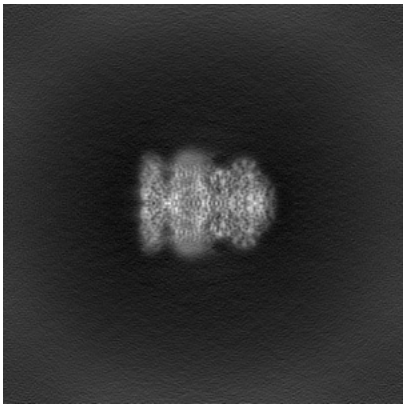


Z

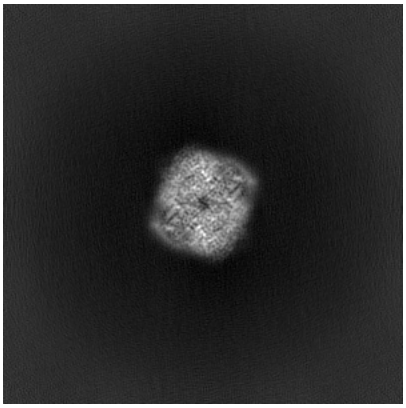
6.1.2 Raw map



X



Y

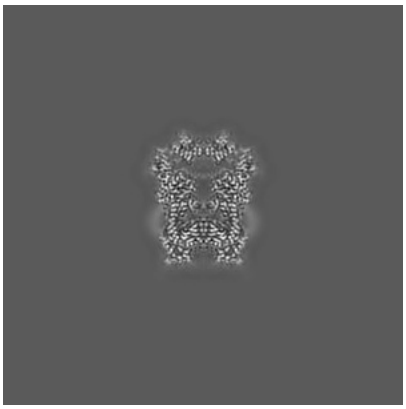


Z

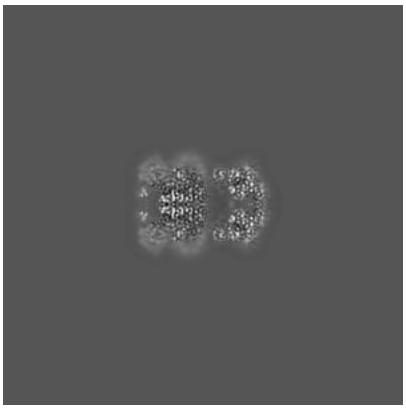
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

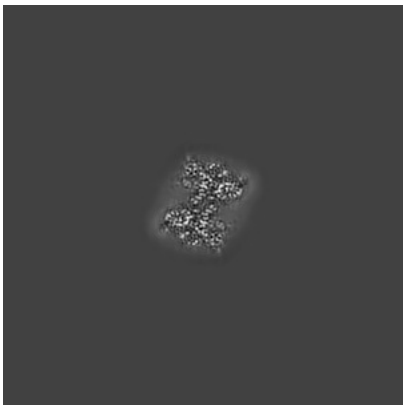
6.2.1 Primary map



X Index: 150

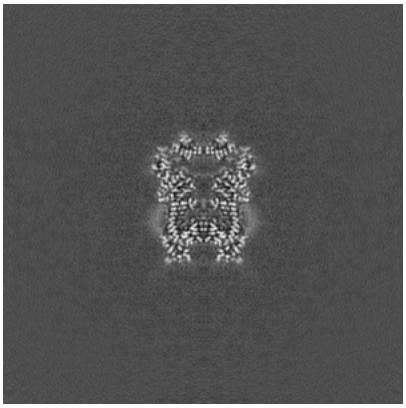


Y Index: 150

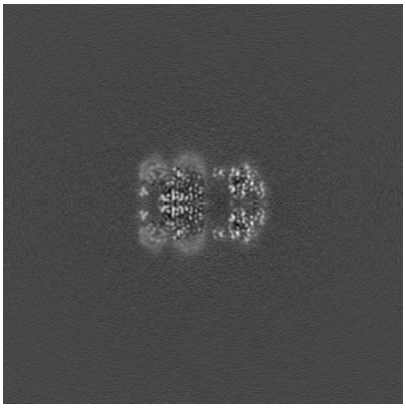


Z Index: 150

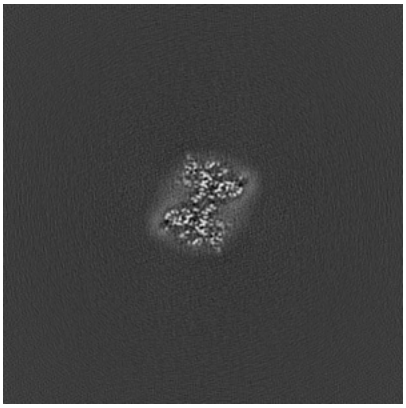
6.2.2 Raw map



X Index: 150



Y Index: 150

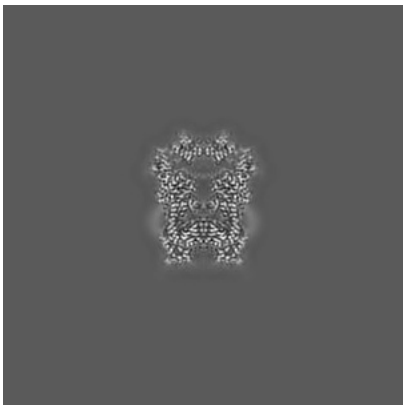


Z Index: 150

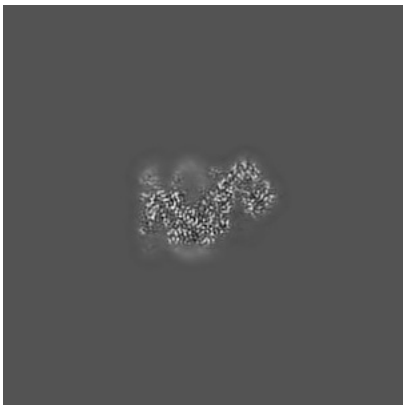
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

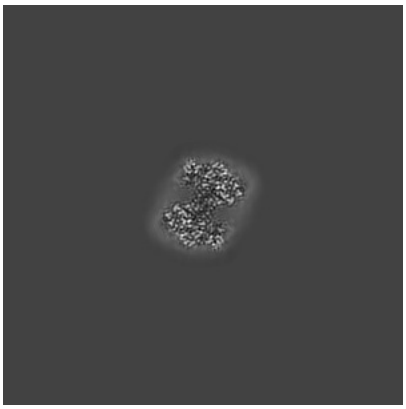
6.3.1 Primary map



X Index: 150

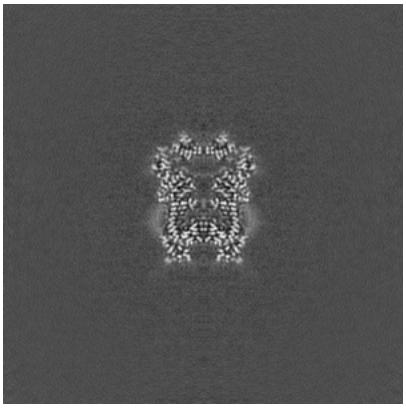


Y Index: 139

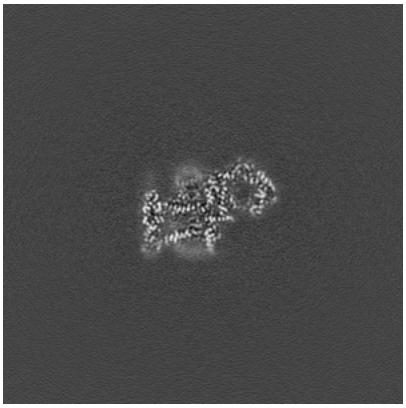


Z Index: 147

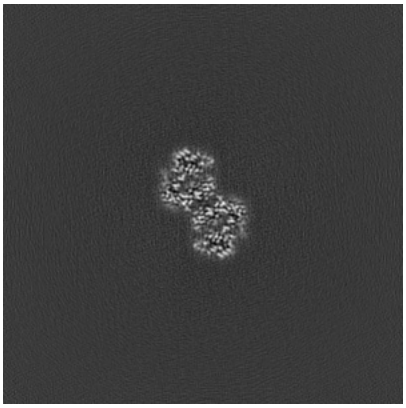
6.3.2 Raw map



X Index: 150



Y Index: 132

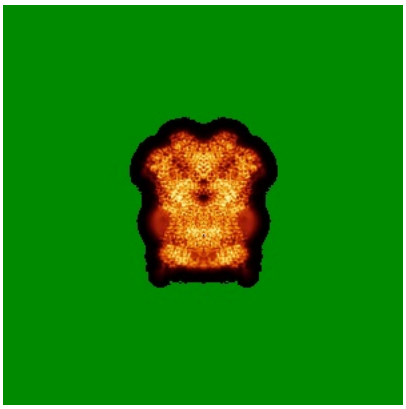


Z Index: 186

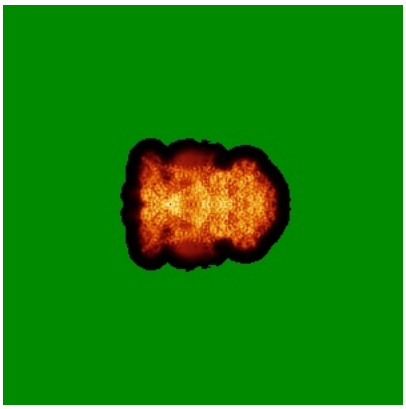
The images above show the largest variance slices of the map in three orthogonal directions.

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

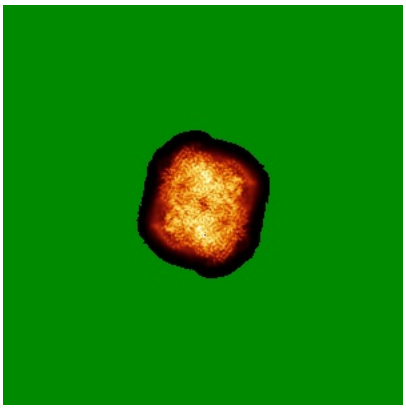
6.4.1 Primary map



X

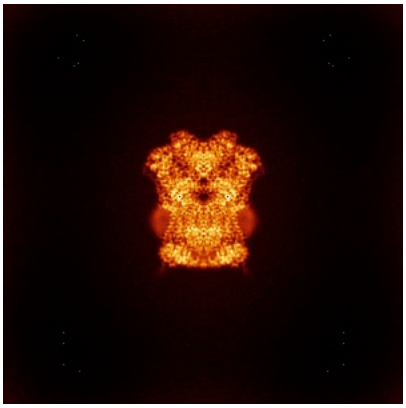


Y

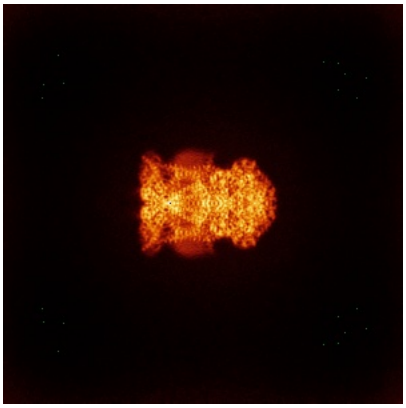


Z

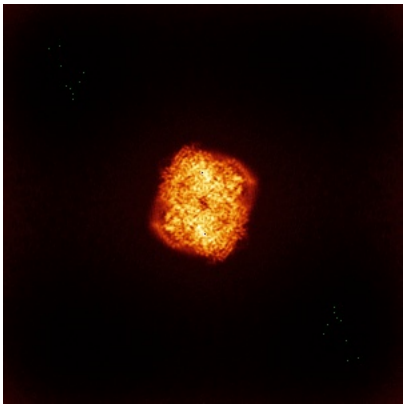
6.4.2 Raw map



X



Y

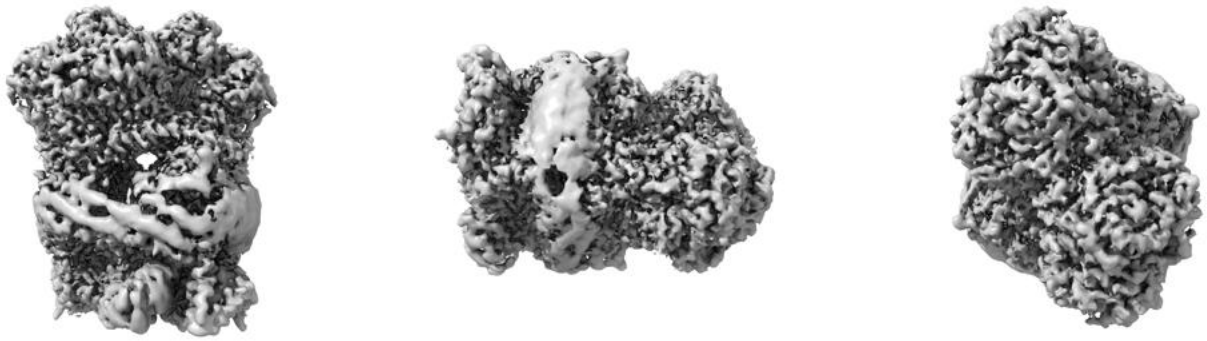


Z

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)

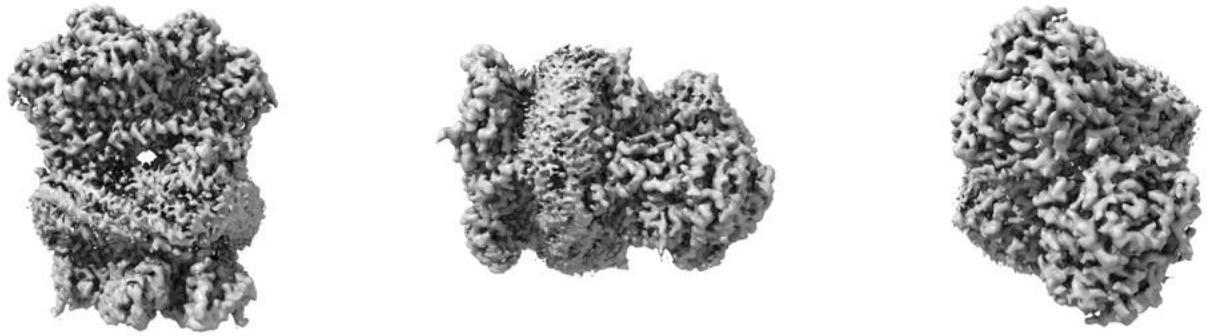
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 6.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

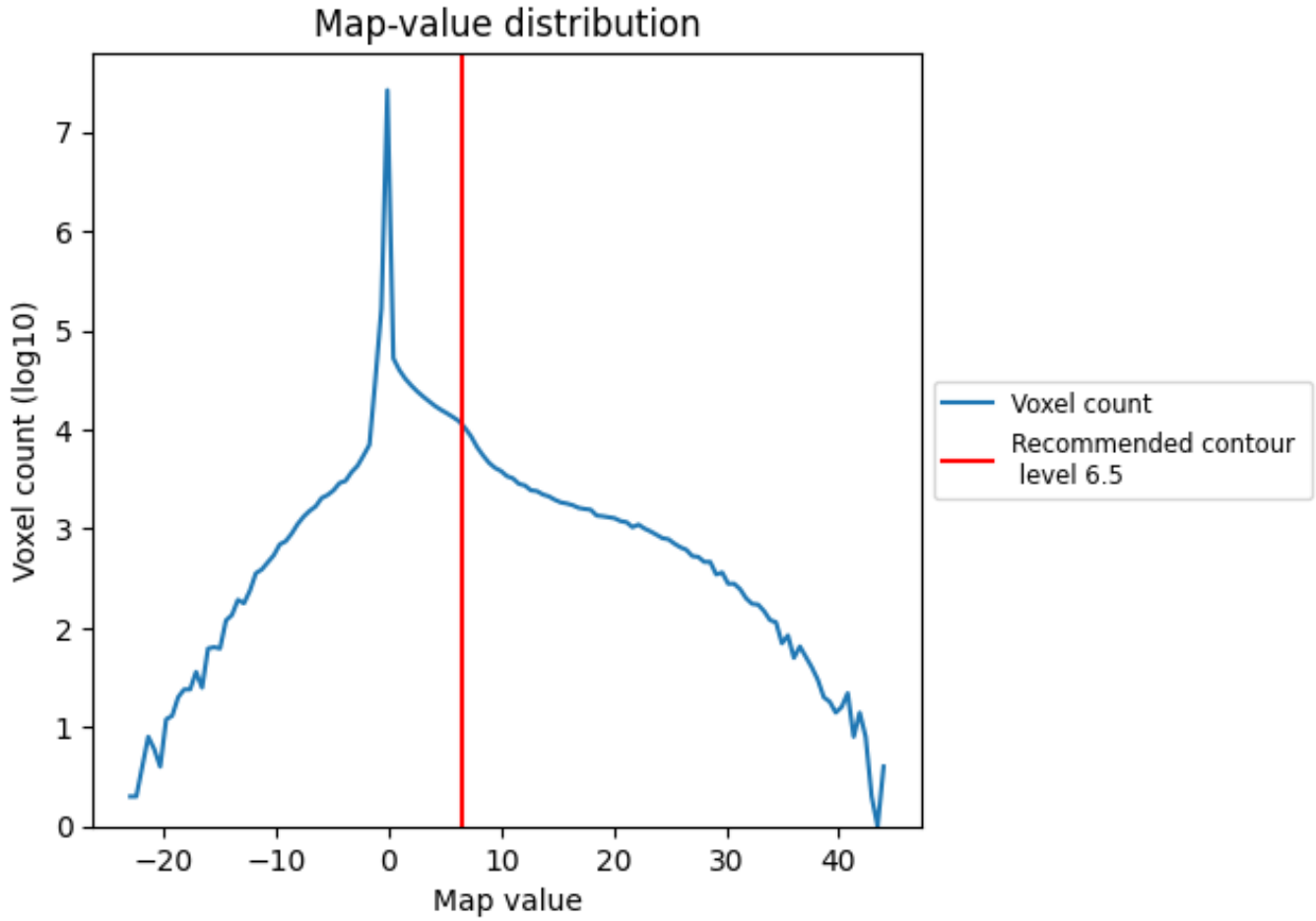
6.6 Mask visualisation (i)

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

7 Map analysis

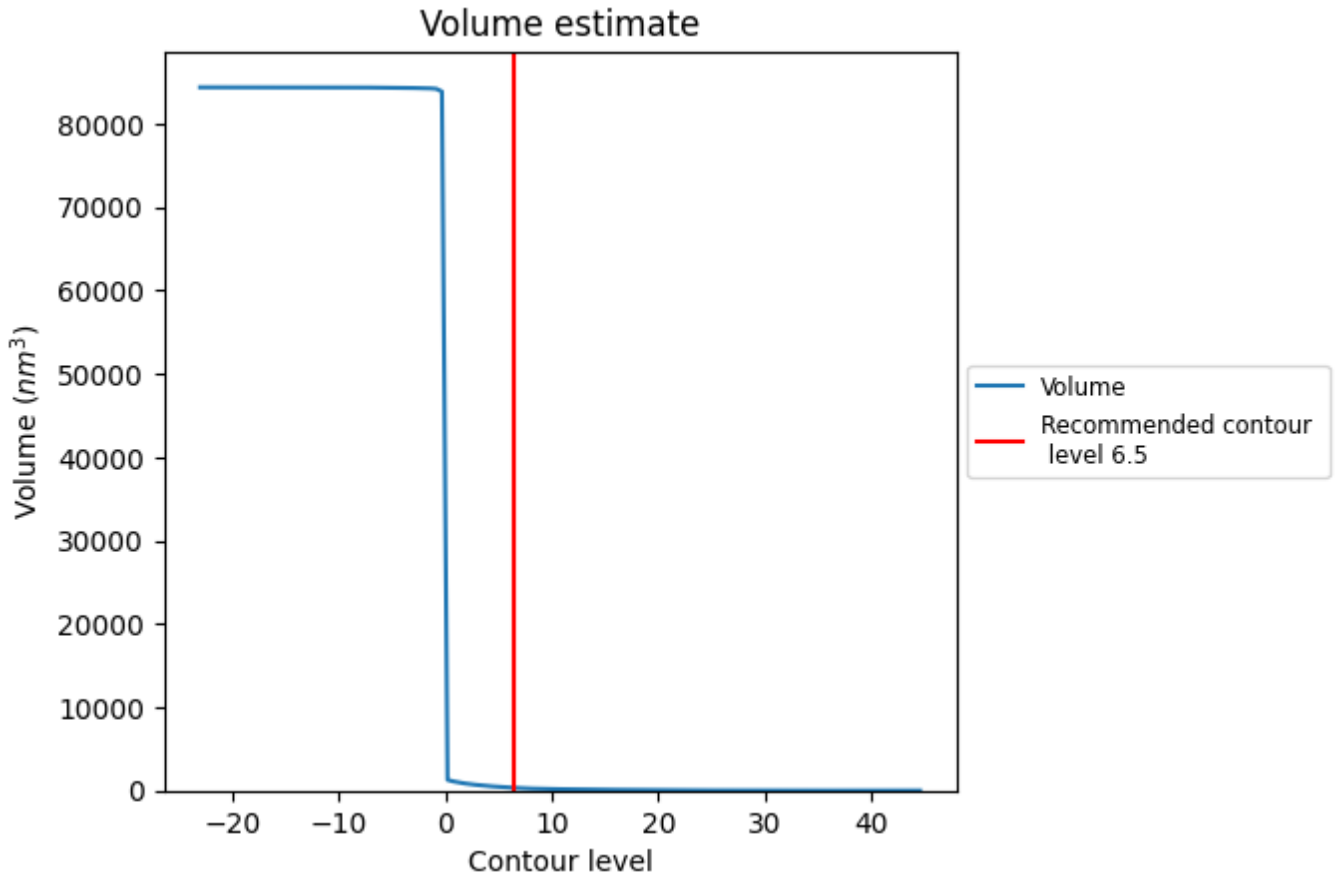
This section contains the results of statistical analysis of the map.

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.

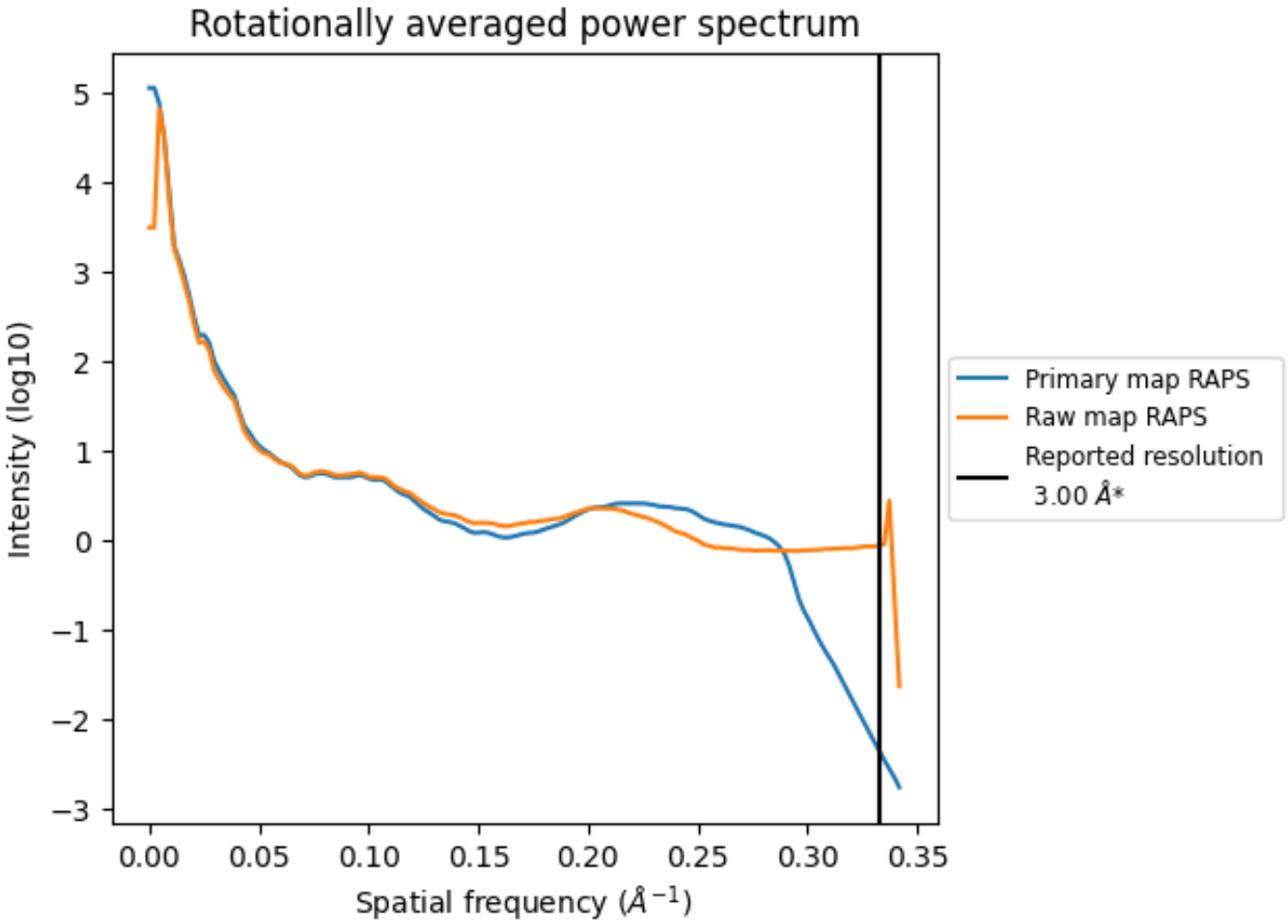
7.2 Volume estimate (i)



The volume at the recommended contour level is 326 nm^3; this corresponds to an approximate mass of 295 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)

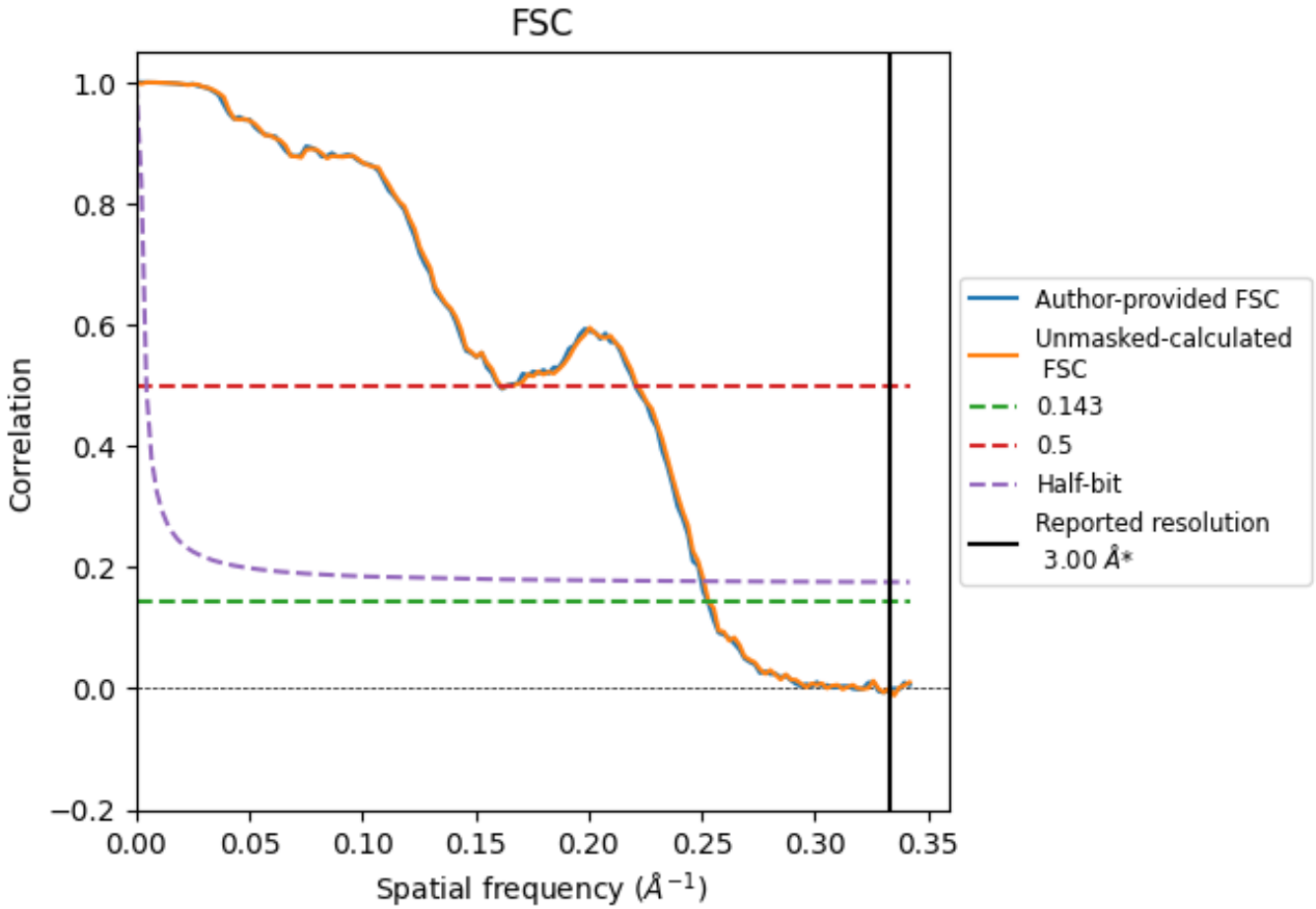


*Reported resolution corresponds to spatial frequency of 0.333 Å^{-1}

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 0.333 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.96	6.23	4.00
Unmasked-calculated*	3.95	6.21	3.98

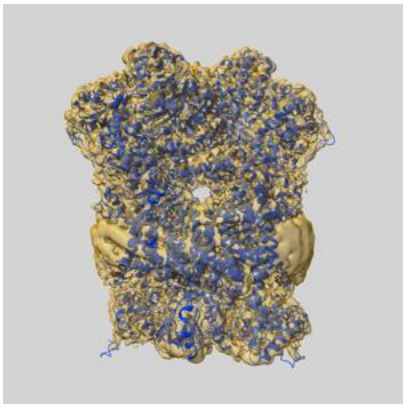
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.96 differs from the reported value 3.0 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.95 differs from the reported value 3.0 by more than 10 %

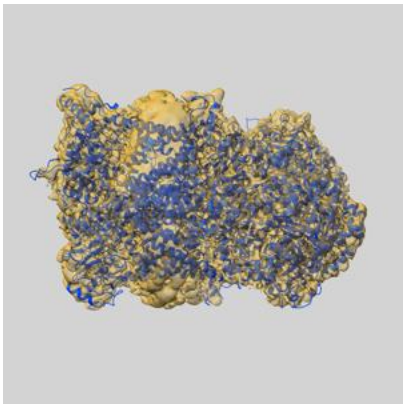
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-17461 and PDB model 8P65. Per-residue inclusion information can be found in section 3 on page 9.

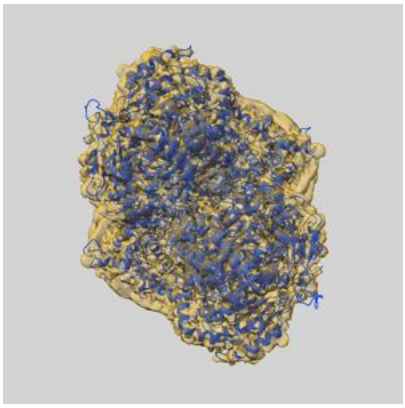
9.1 Map-model overlay



X



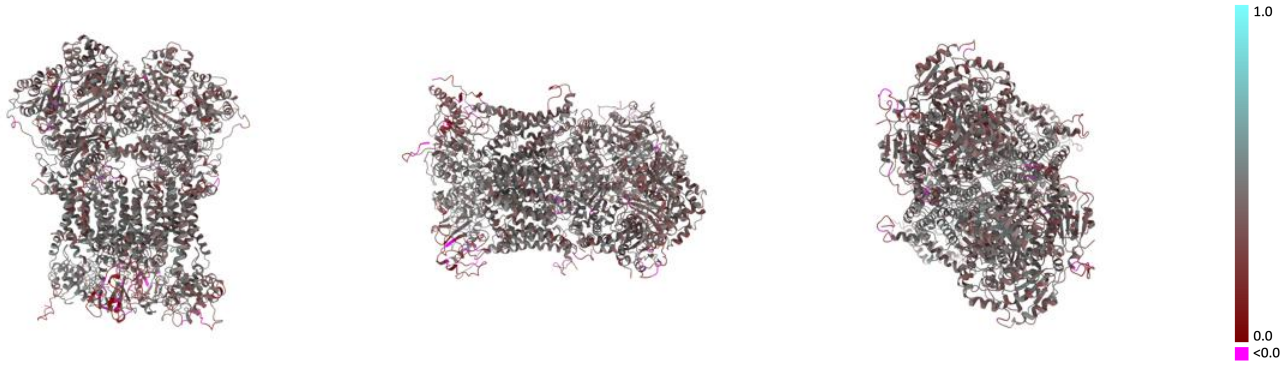
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 6.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

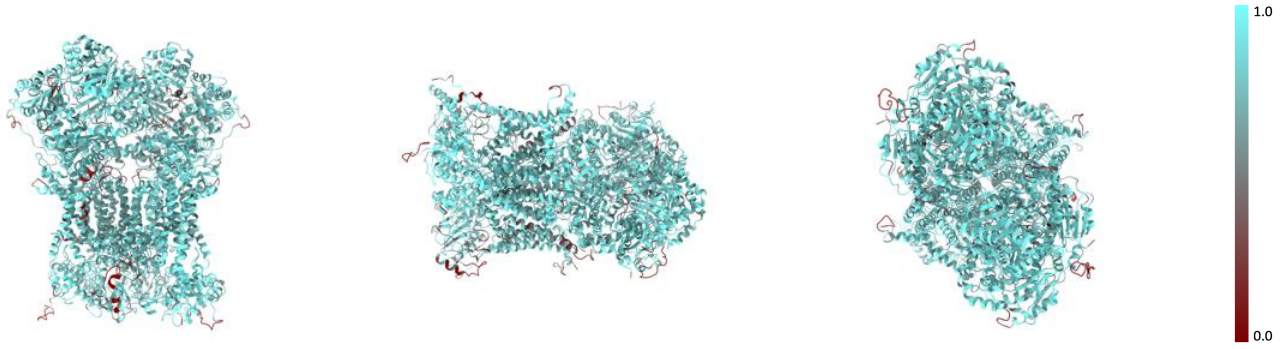
9.2 Q-score mapped to coordinate model (i)



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.

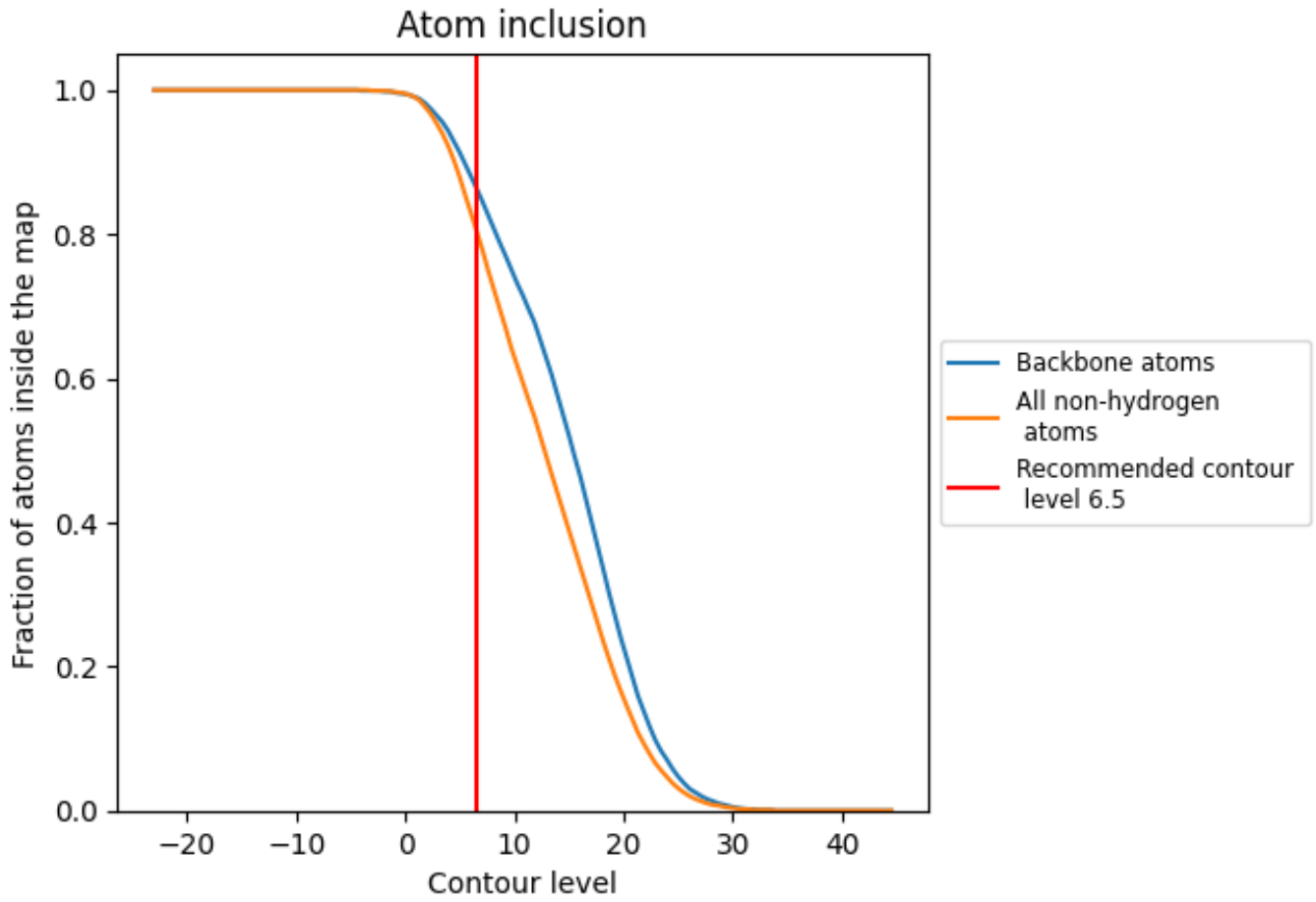
9.3 Atom inclusion mapped to coordinate model (i)



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 (6.5).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 81% 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 (6.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8070	0.3920
A	0.8410	0.3990
B	0.8120	0.3870
C	0.8460	0.4270
D	0.8860	0.4290
E	0.6830	0.2810
F	0.8220	0.3890
G	0.8520	0.4040
H	0.7090	0.3120
I	0.5520	0.2740
J	0.8240	0.3910
K	0.4590	0.2860
N	0.8560	0.4170
O	0.8140	0.3910
P	0.8530	0.4440
Q	0.8950	0.4510
R	0.6590	0.2700
S	0.8000	0.4010
T	0.8450	0.4170
U	0.7480	0.3700
V	0.5010	0.2840
W	0.8200	0.4200
X	0.4690	0.3040

