



## wwPDB EM Validation Summary Report ⓘ

Jun 23, 2025 – 01:09 PM EDT

PDB ID : 9C7H / pdb\_00009c7h  
EMDB ID : EMD-45282  
Title : Cryo-EM structure of respiratory supercomplex III  
Authors : Zhang, Z.; Maharjan, R.; Tringides, M.  
Deposited on : 2024-06-10  
Resolution : 2.78 Å(reported)

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<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>.

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

EMDB validation analysis : 0.0.1.dev118  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

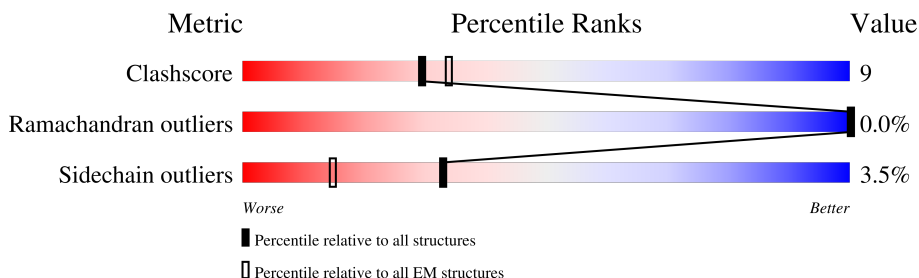
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.78 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	91	
1	Ab	91	
2	1	64	
2	Ac	64	
3	2	299	
3	4	299	
3	Ae	299	
3	Af	299	

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Mol	Chain	Length	Quality of chain
4	3	56	
4	Ad	56	
5	5	480	
5	u	480	
6	6	453	
6	v	453	
7	7	379	
7	w	379	
8	8	326	
8	x	326	
9	9	111	
9	y	111	
10	Aa	82	
10	z	82	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	FES	2	301	-	-	X	-
11	FES	4	301	-	-	X	-

## 2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 32776 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 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	68	Total	C	N	O	S	0	0
			561	341	101	114	5		
1	Ab	68	Total	C	N	O	S	0	0
			561	341	101	114	5		

- Molecule 2 is a protein called Ubiquinol-cytochrome c reductase complex 7.2 kDa protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	60	Total	C	N	O	0	0
			493	322	87	84		
2	Ac	60	Total	C	N	O	0	0
			493	322	87	84		

- Molecule 3 is a protein called Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	195	Total	C	N	O	S	0	0
			1513	953	264	289	7		
3	4	196	Total	C	N	O	S	0	0
			1515	954	265	289	7		
3	Af	39	Total	C	N	O	S	0	0
			275	172	53	47	3		
3	Ae	39	Total	C	N	O	S	0	0
			271	169	52	47	3		

- Molecule 4 is a protein called Cytochrome b-c1 complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	51	Total	C	N	O	S	0	0
			417	279	74	63	1		
4	Ad	51	Total	C	N	O	S	0	0
			417	279	74	63	1		

- Molecule 5 is a protein called Cytochrome b-c1 complex subunit 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	435	Total	C	N	O	S	0	0
			3374	2105	594	656	19		
5	u	435	Total	C	N	O	S	0	0
			3373	2105	594	655	19		

- Molecule 6 is a protein called Cytochrome b-c1 complex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	418	Total	C	N	O	S	0	0
			3140	1966	556	610	8		
6	v	418	Total	C	N	O	S	0	0
			3140	1966	556	610	8		

- Molecule 7 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	379	Total	C	N	O	S	0	0
			3025	2031	471	502	21		
7	w	379	Total	C	N	O	S	0	0
			3025	2031	471	502	21		

- Molecule 8 is a protein called Cytochrome c1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	239	Total	C	N	O	S	0	0
			1903	1215	328	345	15		
8	x	238	Total	C	N	O	S	0	0
			1896	1211	326	343	16		

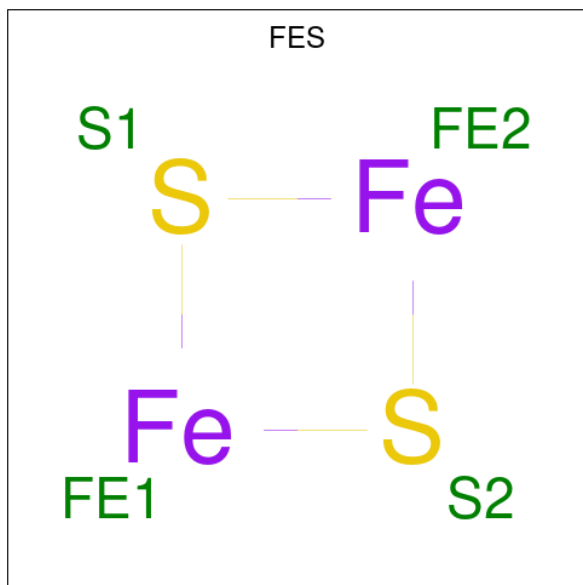
- Molecule 9 is a protein called Cytochrome b-c1 complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	101	Total	C	N	O	S	0	0
			893	572	157	162	2		
9	y	101	Total	C	N	O	S	0	0
			893	572	157	162	2		

- Molecule 10 is a protein called Cytochrome b-c1 complex subunit 8.

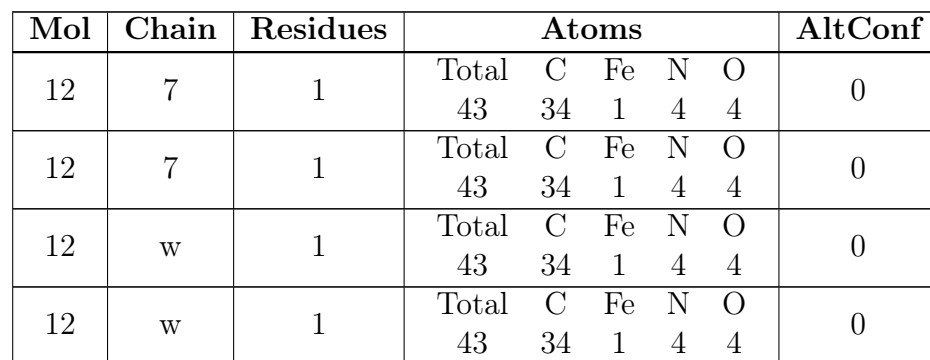
Mol	Chain	Residues	Atoms					AltConf	Trace
10	z	79	Total	C	N	O	S	0	0
			666	434	122	108	2		
10	Aa	79	Total	C	N	O	S	0	0
			666	434	122	108	2		

- Molecule 11 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula:  $\text{Fe}_2\text{S}_2$ ).



Mol	Chain	Residues	Atoms			AltConf
11	2	1	Total	Fe	S	0
			4	2	2	
11	4	1	Total	Fe	S	0
			4	2	2	

- Molecule 12 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula:  $\text{C}_{34}\text{H}_{32}\text{FeN}_4\text{O}_4$ ).



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- The chemical structure of HEC (Hydroxyethylchlorin) is shown. It features a central iron atom (Fe) coordinated by four nitrogen atoms (N) in a porphyrin-like ring. The structure includes various side chains and a central hydroxyl group (OH). The atoms are labeled with green text, and the central iron atom is labeled with a purple 'Fe'. The side chains are labeled with green text: CAA, CBA, CAD, CBD, CMA, C3A, C4A, C4B, C1B, C2B, C3B, CAB, CBB, C3C, C4C, C2C, CMC, C3D, C2D, CMD, C1D, C4D, C3A, C4A, C4B, C1B, C2B, C3B, CAB, CBB, C3C, C4C, C2C, CMC, C3D, C2D, CMD, C1D, C4D.

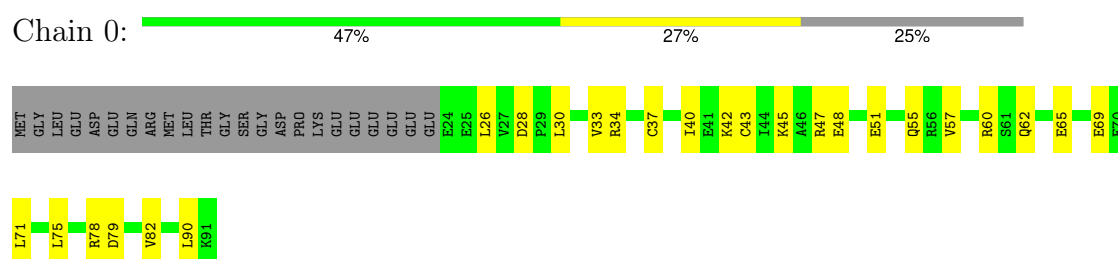
Mol	Chain	Residues	Atoms					AltConf
13	8	1	Total 43	C 34	Fe 1	N 4	O 4	0
13	x	1	Total 43	C 34	Fe 1	N 4	O 4	0



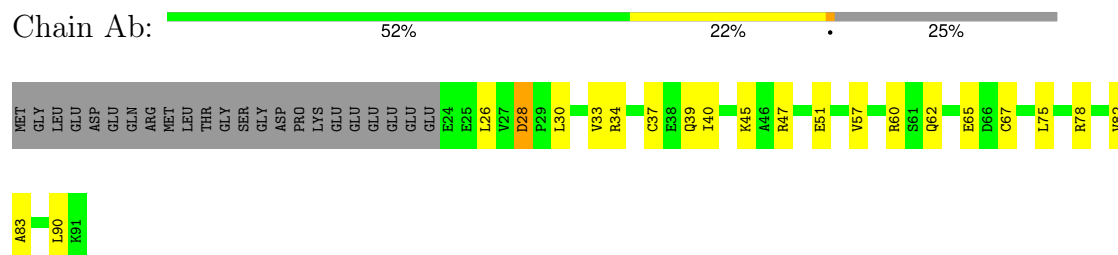
### 3 Residue-property plots [i](#)

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.

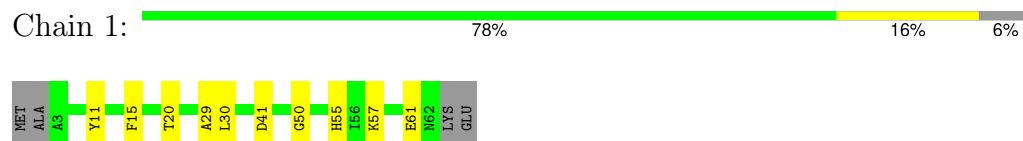
- Molecule 1: Cytochrome b-c1 complex subunit 6, mitochondrial



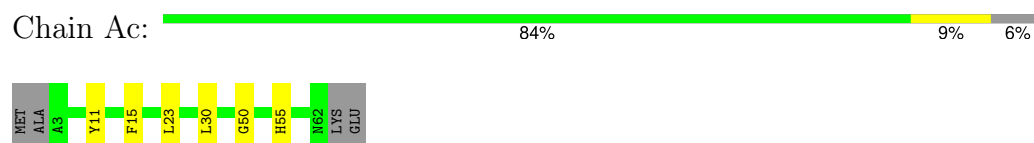
- Molecule 1: Cytochrome b-c1 complex subunit 6, mitochondrial



- Molecule 2: Ubiquinol-cytochrome c reductase complex 7.2 kDa protein

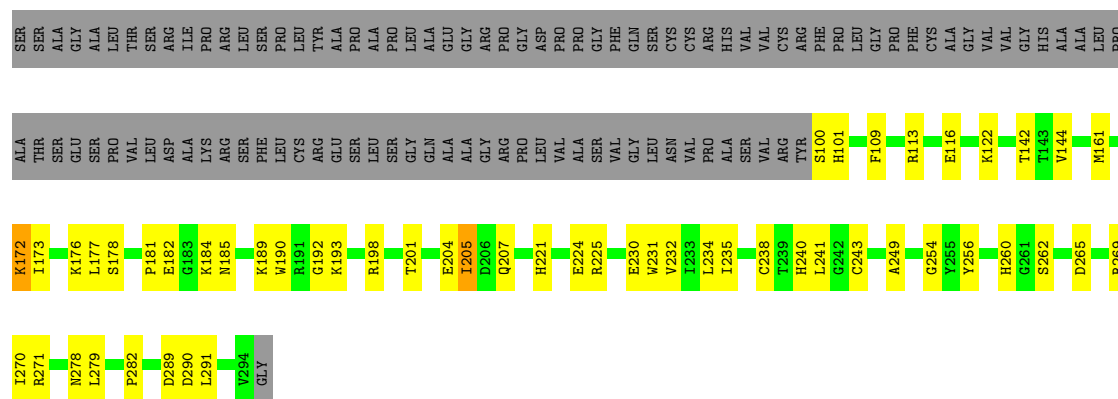


- Molecule 2: Ubiquinol-cytochrome c reductase complex 7.2 kDa protein



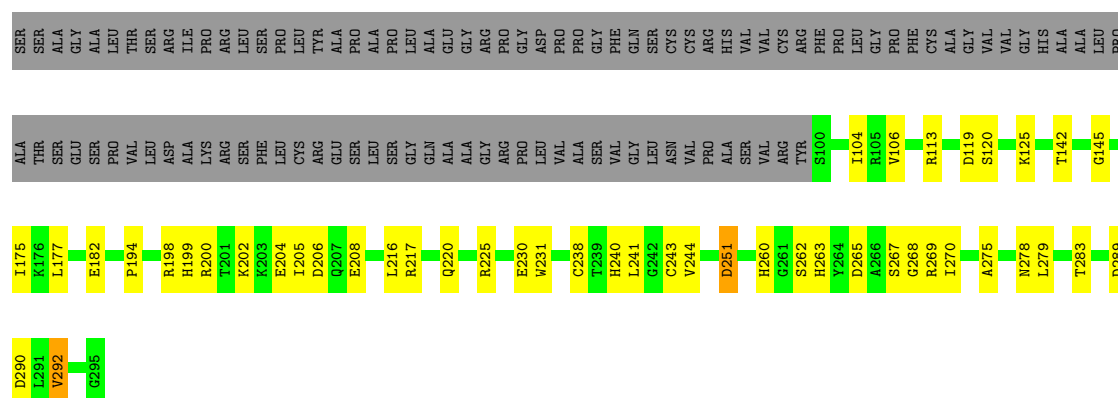
- Molecule 3: Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1





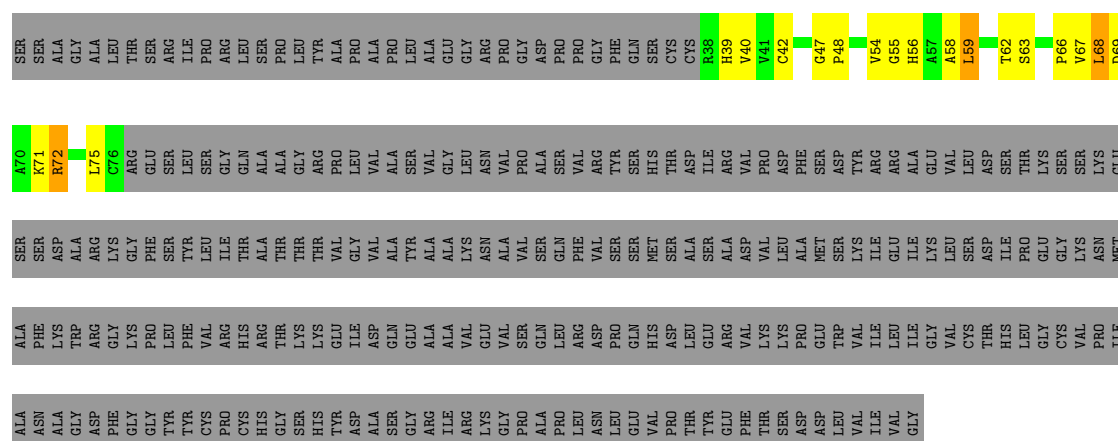
- Molecule 3: Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1

Chain 4: 50% 15% 34%



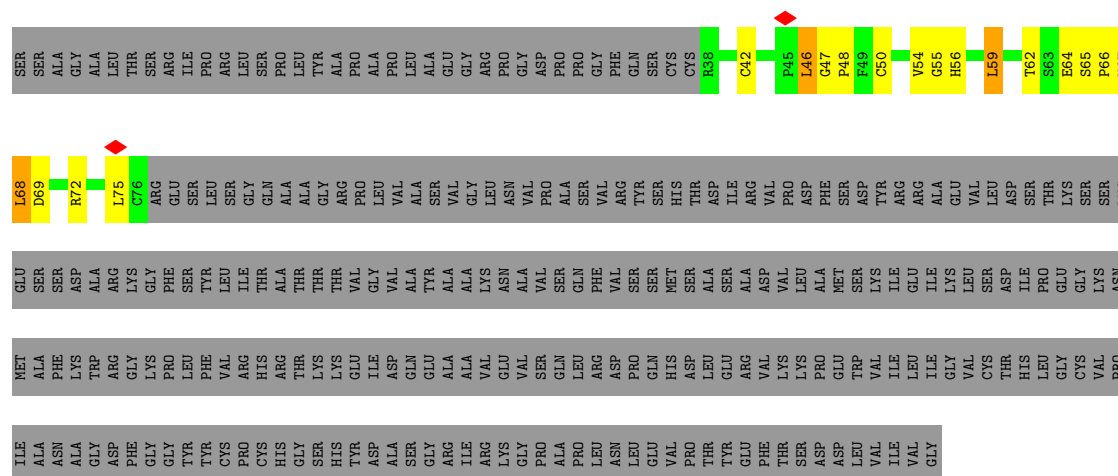
- Molecule 3: Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1

Chain Af: 7% 5% 87%



- Molecule 3: Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1

Chain Ae: 7% 5% 87%



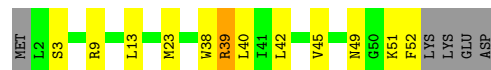
- Molecule 4: Cytochrome b-c1 complex subunit 10

Chain 3: 75% 16% 9%



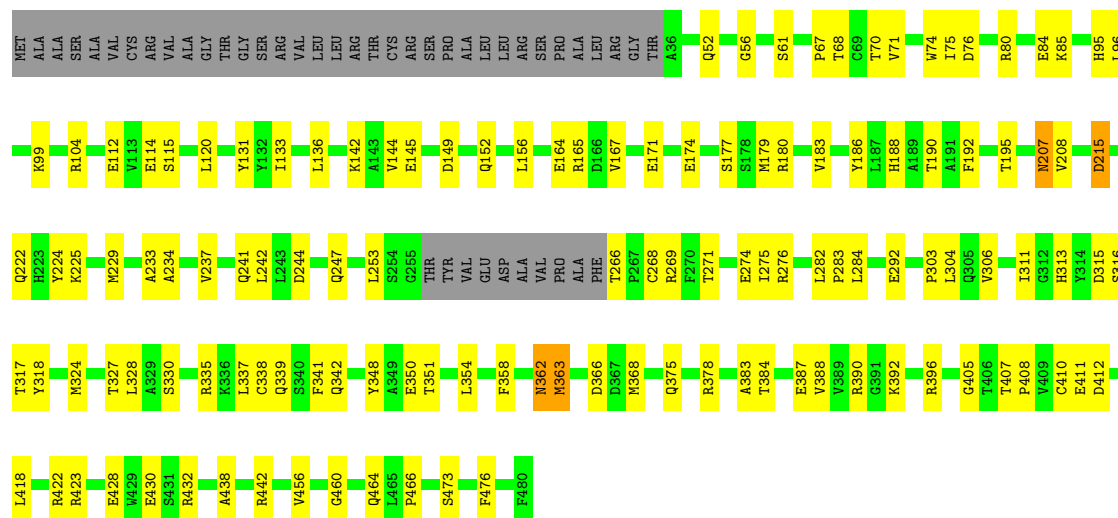
- Molecule 4: Cytochrome b-c1 complex subunit 10

Chain Ad: 70% 20% 9%



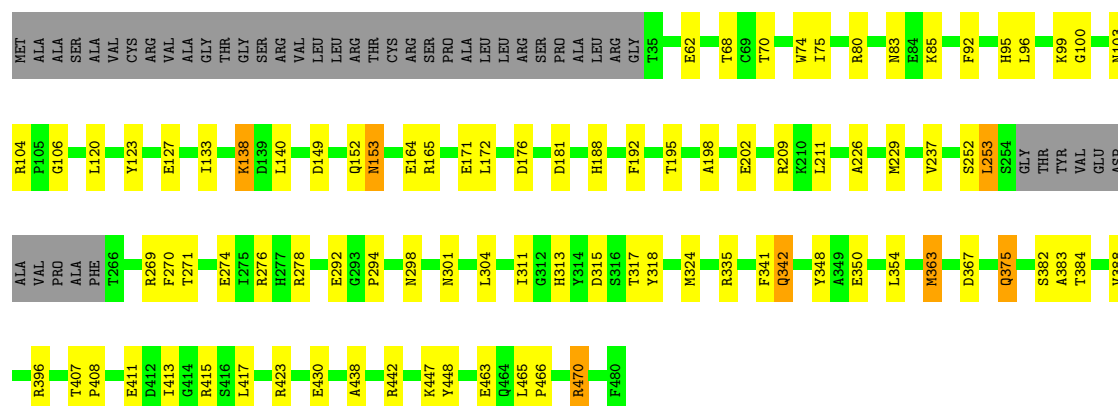
- Molecule 5: Cytochrome b-c1 complex subunit 1, mitochondrial

Chain 5: 64% 26% 9%



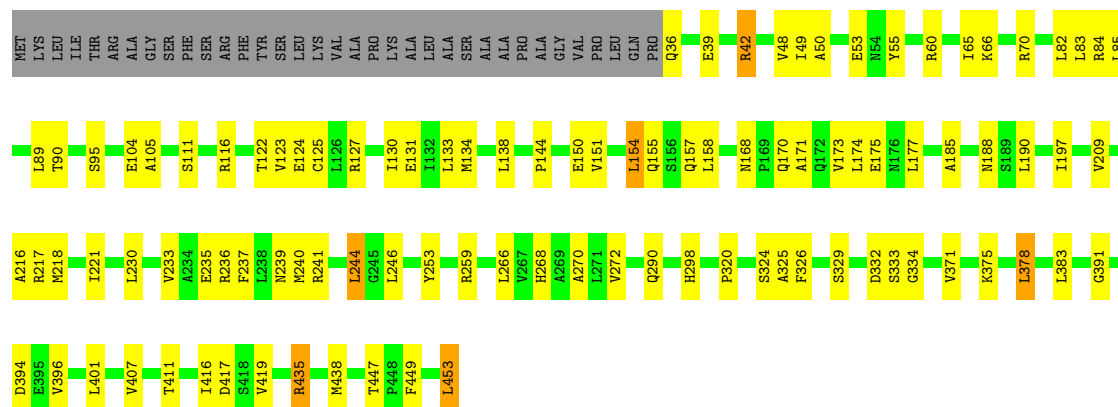
- Molecule 5: Cytochrome b-c1 complex subunit 1, mitochondrial

Chain u:  72% 17% 9%



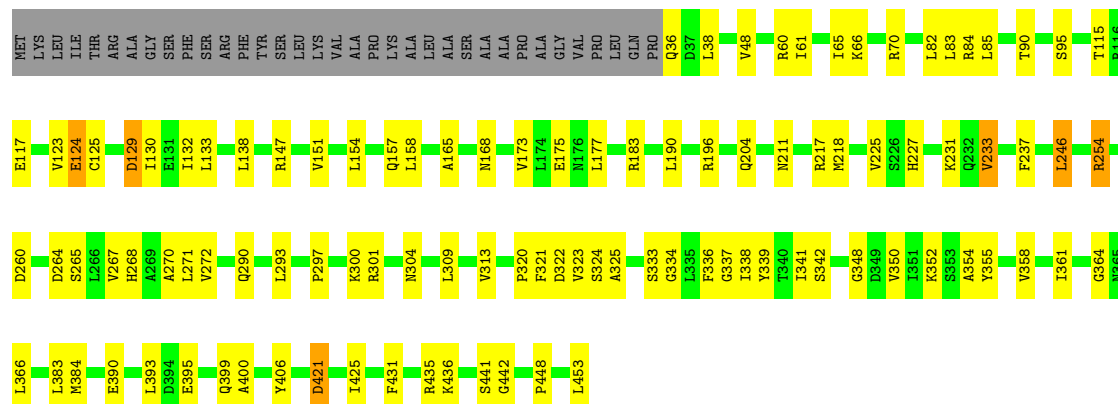
- Molecule 6: Cytochrome b-c1 complex subunit 2, mitochondrial

Chain 6:  70% 21% 8%




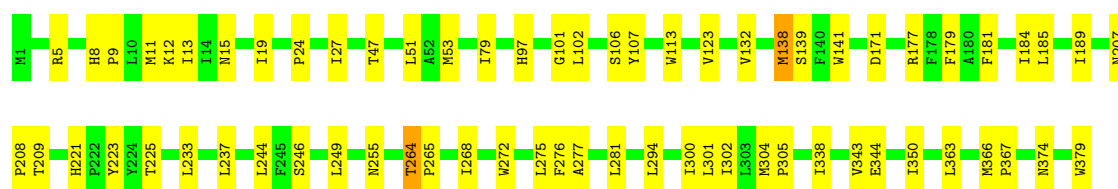
- Molecule 6: Cytochrome b-c1 complex subunit 2, mitochondrial

Chain v:  69% 22% 8%




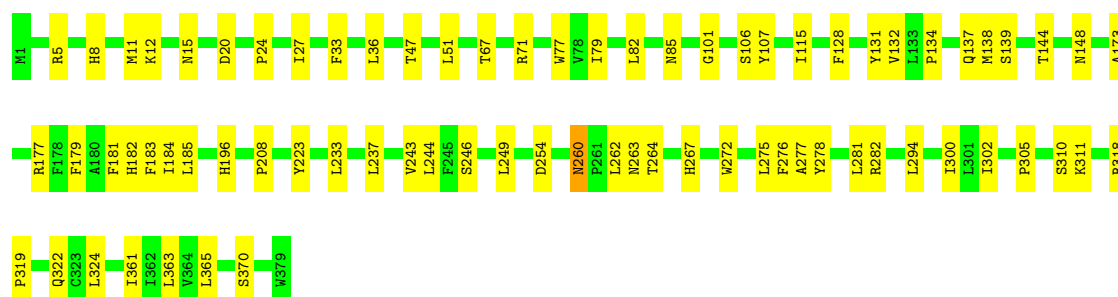
- Molecule 7: Cytochrome b

Chain 7:  82% 17%



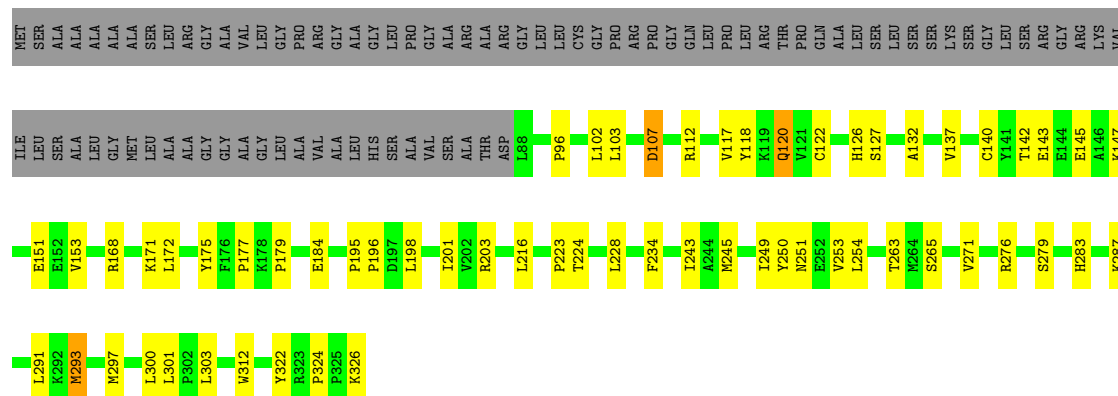
• Molecule 7: Cytochrome b

Chain w:  80% 20%



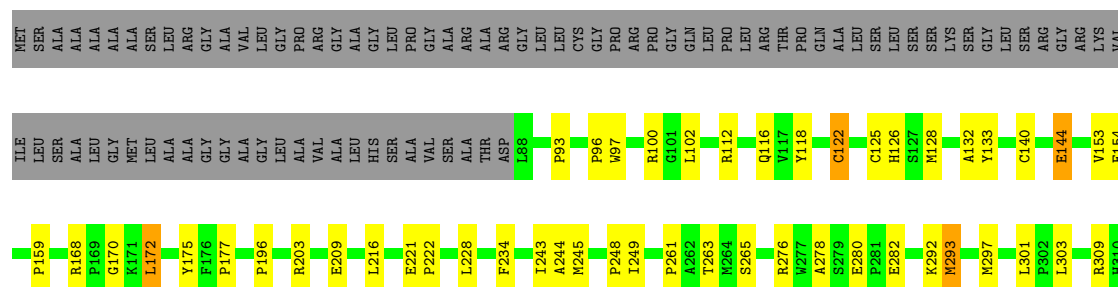
• Molecule 8: Cytochrome c1

Chain 8:  55% 18% 27%



• Molecule 8: Cytochrome c1

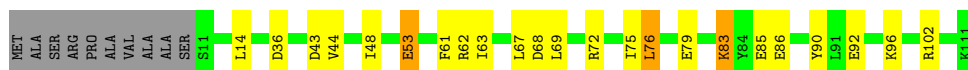
Chain x:  56% 15% 27%





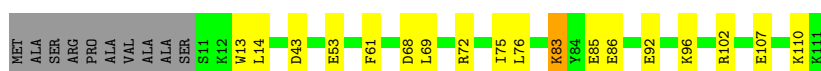
- Molecule 9: Cytochrome b-c1 complex subunit 7

Chain 9: 70% 18% 9%



- Molecule 9: Cytochrome b-c1 complex subunit 7

Chain y: 75% 15% 9%



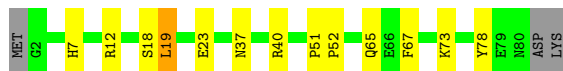
- Molecule 10: Cytochrome b-c1 complex subunit 8

Chain z: 77% 18% 2%



- Molecule 10: Cytochrome b-c1 complex subunit 8

Chain Aa: 80% 15% 2%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	43845	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.408	Depositor
Minimum map value	-0.717	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	547.84, 547.84, 547.84	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEC, HEM, FES

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	0	0.19	0/567	0.32	0/759
1	Ab	0.12	0/567	0.27	0/759
2	1	0.14	0/506	0.25	0/683
2	Ac	0.12	0/506	0.21	0/683
3	2	0.13	0/1546	0.27	0/2093
3	4	0.11	0/1548	0.25	0/2094
3	Ae	0.21	0/277	0.55	0/379
3	Af	0.20	0/281	0.52	0/383
4	3	0.14	0/433	0.32	0/593
4	Ad	0.14	0/433	0.30	0/593
5	5	0.14	0/3442	0.27	0/4667
5	u	0.14	0/3441	0.27	0/4667
6	6	0.13	0/3192	0.28	0/4322
6	v	0.15	0/3192	0.29	0/4322
7	7	0.16	0/3123	0.29	0/4269
7	w	0.17	0/3123	0.32	0/4269
8	8	0.15	0/1961	0.27	0/2660
8	x	0.14	0/1954	0.26	0/2652
9	9	0.13	0/913	0.25	0/1223
9	y	0.13	0/913	0.25	0/1223
10	Aa	0.14	0/688	0.24	0/931
10	z	0.16	0/688	0.29	0/931
All	All	0.15	0/33294	0.28	0/45155

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.



## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	561	0	540	21	0
1	Ab	561	0	540	16	0
2	1	493	0	491	6	0
2	Ac	493	0	491	3	0
3	2	1513	0	1495	36	0
3	4	1515	0	1496	38	0
3	Ae	271	0	265	22	0
3	Af	275	0	276	19	0
4	3	417	0	414	5	0
4	Ad	417	0	414	8	0
5	5	3374	0	3272	82	0
5	u	3373	0	3272	57	0
6	6	3140	0	3121	67	0
6	v	3140	0	3121	64	0
7	7	3025	0	3090	45	0
7	w	3025	0	3090	53	0
8	8	1903	0	1850	46	0
8	x	1896	0	1845	40	0
9	9	893	0	888	14	0
9	y	893	0	888	10	0
10	Aa	666	0	663	9	0
10	z	666	0	663	12	0
11	2	4	0	0	2	0
11	4	4	0	0	3	0
12	7	86	0	60	7	0
12	w	86	0	60	8	0
13	8	43	0	31	4	0
13	x	43	0	32	5	0
All	All	32776	0	32368	585	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 9.

The worst 5 of 585 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Af:47:GLY:HA2	3:Af:67:VAL:HG12	1.58	0.84
6:v:320:PRO:HB3	3:Af:75:LEU:HB3	1.61	0.82
1:Ab:75:LEU:HD23	1:Ab:78:ARG:HH12	1.45	0.80
7:w:67:THR:O	7:w:71:ARG:HB2	1.83	0.78
3:Ae:47:GLY:HA3	3:Ae:66:PRO:HA	1.65	0.78

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	66/91 (72%)	63 (96%)	3 (4%)	0	100	100
1	Ab	66/91 (72%)	64 (97%)	2 (3%)	0	100	100
2	1	58/64 (91%)	57 (98%)	1 (2%)	0	100	100
2	Ac	58/64 (91%)	57 (98%)	1 (2%)	0	100	100
3	2	193/299 (64%)	187 (97%)	6 (3%)	0	100	100
3	4	194/299 (65%)	191 (98%)	3 (2%)	0	100	100
3	Ae	37/299 (12%)	30 (81%)	7 (19%)	0	100	100
3	Af	37/299 (12%)	30 (81%)	7 (19%)	0	100	100
4	3	49/56 (88%)	47 (96%)	2 (4%)	0	100	100
4	Ad	49/56 (88%)	48 (98%)	1 (2%)	0	100	100
5	5	431/480 (90%)	418 (97%)	13 (3%)	0	100	100
5	u	431/480 (90%)	421 (98%)	10 (2%)	0	100	100
6	6	416/453 (92%)	409 (98%)	7 (2%)	0	100	100
6	v	416/453 (92%)	402 (97%)	13 (3%)	1 (0%)	44	71
7	7	377/379 (100%)	371 (98%)	6 (2%)	0	100	100
7	w	377/379 (100%)	371 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	8	237/326 (73%)	232 (98%)	5 (2%)	0	100	100
8	x	236/326 (72%)	231 (98%)	5 (2%)	0	100	100
9	9	99/111 (89%)	97 (98%)	2 (2%)	0	100	100
9	y	99/111 (89%)	98 (99%)	1 (1%)	0	100	100
10	Aa	77/82 (94%)	77 (100%)	0	0	100	100
10	z	77/82 (94%)	77 (100%)	0	0	100	100
All	All	4080/5280 (77%)	3978 (98%)	101 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	v	322	ASP

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	65/85 (76%)	62 (95%)	3 (5%)	23	52
1	Ab	65/85 (76%)	60 (92%)	5 (8%)	10	28
2	1	49/52 (94%)	48 (98%)	1 (2%)	50	78
2	Ac	49/52 (94%)	48 (98%)	1 (2%)	50	78
3	2	166/245 (68%)	162 (98%)	4 (2%)	44	74
3	4	165/245 (67%)	161 (98%)	4 (2%)	44	74
3	Ae	28/245 (11%)	25 (89%)	3 (11%)	5	15
3	Af	29/245 (12%)	25 (86%)	4 (14%)	3	8
4	3	40/46 (87%)	37 (92%)	3 (8%)	11	30
4	Ad	40/46 (87%)	38 (95%)	2 (5%)	20	48
5	5	363/397 (91%)	350 (96%)	13 (4%)	30	61
5	u	363/397 (91%)	348 (96%)	15 (4%)	26	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	6	329/355 (93%)	314 (95%)	15 (5%)	23	52
6	v	329/355 (93%)	314 (95%)	15 (5%)	23	52
7	7	332/332 (100%)	328 (99%)	4 (1%)	67	87
7	w	332/332 (100%)	329 (99%)	3 (1%)	75	91
8	8	203/259 (78%)	198 (98%)	5 (2%)	42	73
8	x	203/259 (78%)	196 (97%)	7 (3%)	32	63
9	9	93/99 (94%)	88 (95%)	5 (5%)	18	45
9	y	93/99 (94%)	89 (96%)	4 (4%)	25	54
10	Aa	70/73 (96%)	68 (97%)	2 (3%)	37	68
10	z	70/73 (96%)	68 (97%)	2 (3%)	37	68
All	All	3476/4376 (79%)	3356 (96%)	120 (4%)	33	62

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	u	95	HIS
10	Aa	19	LEU
5	u	470	ARG
3	Ae	68	LEU
4	Ad	13	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
7	7	255	ASN
10	Aa	65	GLN
5	u	323	HIS
3	Ae	39	HIS
2	Ac	55	HIS

### 5.3.3 RNA ⓘ

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	$\# Z  > 2$
11	FES	4	301	3	0,4,4	-	-	-		
13	HEC	8	401	8	32,50,50	2.12	3 (9%)	30,82,82	2.34	6 (20%)
12	HEM	w	401	7	42,50,50	1.46	5 (11%)	46,82,82	1.31	6 (13%)
12	HEM	w	402	-	42,50,50	1.46	5 (11%)	46,82,82	1.34	8 (17%)
11	FES	2	301	3	0,4,4	-	-	-		
12	HEM	7	401	7	42,50,50	1.46	5 (11%)	46,82,82	1.31	5 (10%)
12	HEM	7	402	-	42,50,50	1.45	5 (11%)	46,82,82	1.31	5 (10%)
13	HEC	x	401	8	32,50,50	2.11	3 (9%)	30,82,82	2.38	6 (20%)

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
11	FES	4	301	3	-	-	0/1/1/1
13	HEC	8	401	8	-	1/10/54/54	-
12	HEM	w	401	7	-	2/12/54/54	-
12	HEM	w	402	-	-	0/12/54/54	-
11	FES	2	301	3	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	HEM	7	401	7	-	1/12/54/54	-
12	HEM	7	402	-	-	0/12/54/54	-
13	HEC	x	401	8	-	2/10/54/54	-

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	8	401	HEC	C2B-C3B	-6.19	1.33	1.40
13	8	401	HEC	C3C-C2C	-6.06	1.33	1.40
13	x	401	HEC	C3C-C2C	-6.05	1.34	1.40
13	x	401	HEC	C2B-C3B	-5.98	1.34	1.40
13	x	401	HEC	C3D-C2D	5.40	1.53	1.37

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	x	401	HEC	CBB-CAB-C3B	-7.58	109.75	127.49
13	8	401	HEC	CBC-CAC-C3C	-7.39	110.19	127.49
13	x	401	HEC	CBC-CAC-C3C	-7.39	110.20	127.49
13	8	401	HEC	CBB-CAB-C3B	-7.36	110.27	127.49
13	8	401	HEC	CMC-C2C-C1C	-3.12	123.88	128.46

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	7	401	HEM	C3D-CAD-CBD-CGD
12	w	401	HEM	C3D-CAD-CBD-CGD
13	x	401	HEC	C3A-C2A-CAA-CBA
13	x	401	HEC	C1A-C2A-CAA-CBA
12	w	401	HEM	C1A-C2A-CAA-CBA

There are no ring outliers.

8 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	4	301	FES	3	0
13	8	401	HEC	4	0
12	w	401	HEM	5	0
12	w	402	HEM	3	0
11	2	301	FES	2	0

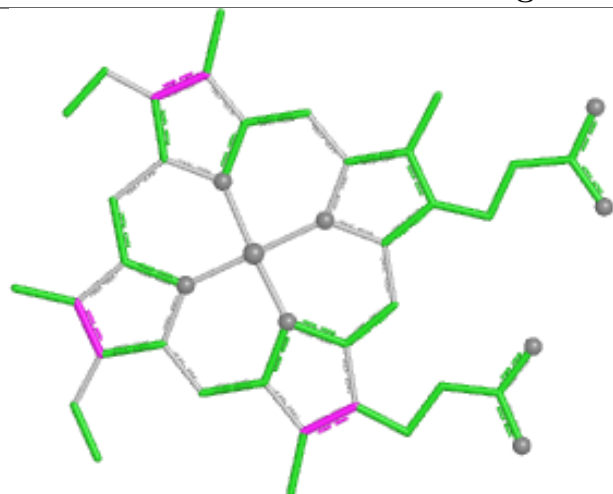
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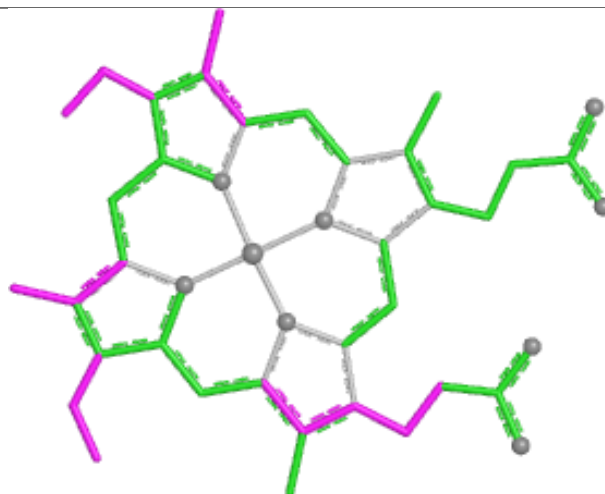
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	7	401	HEM	3	0
12	7	402	HEM	4	0
13	x	401	HEC	5	0

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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

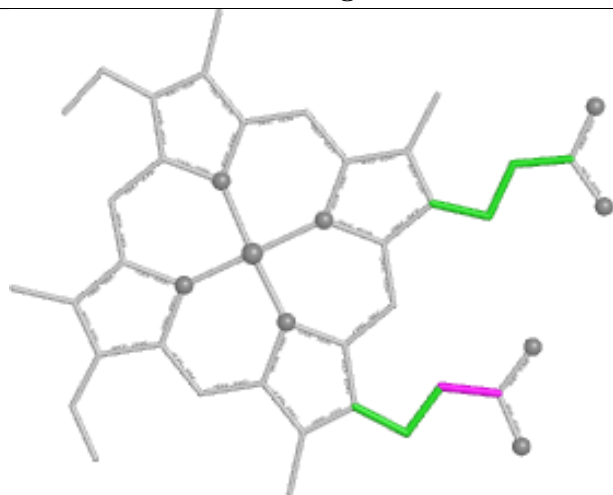
## Ligand HEC 8 401



Bond lengths



Bond angles

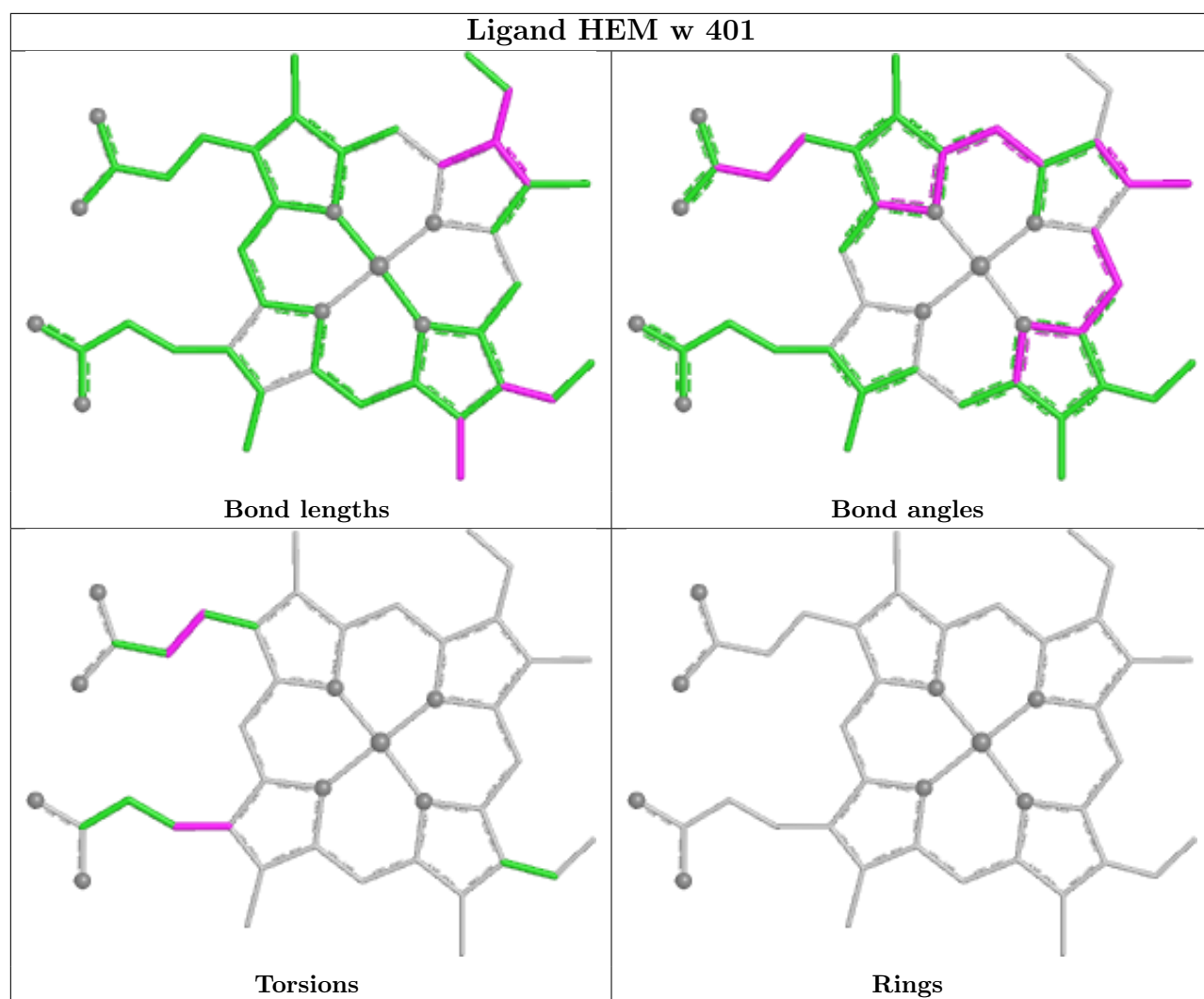


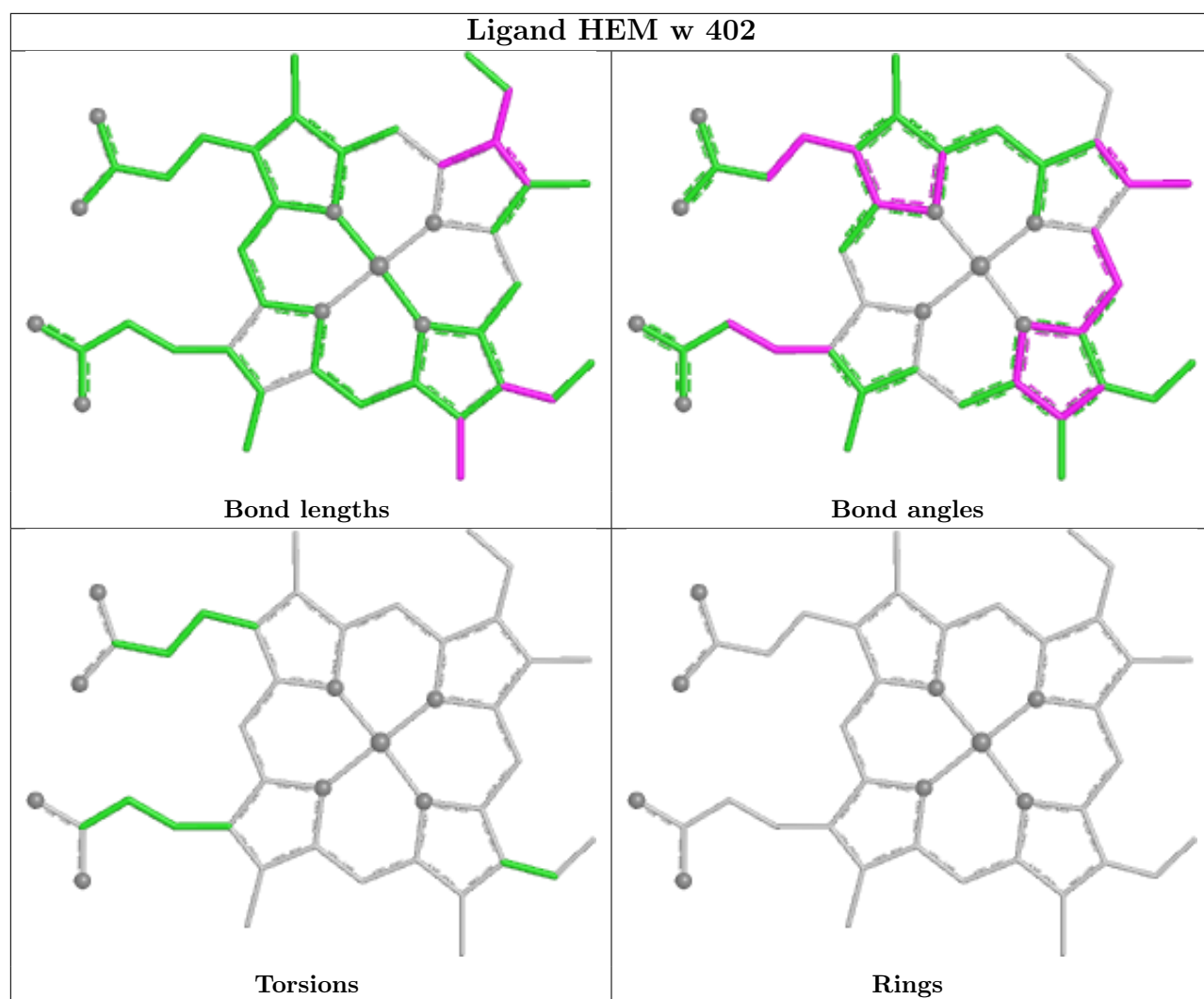
Torsions

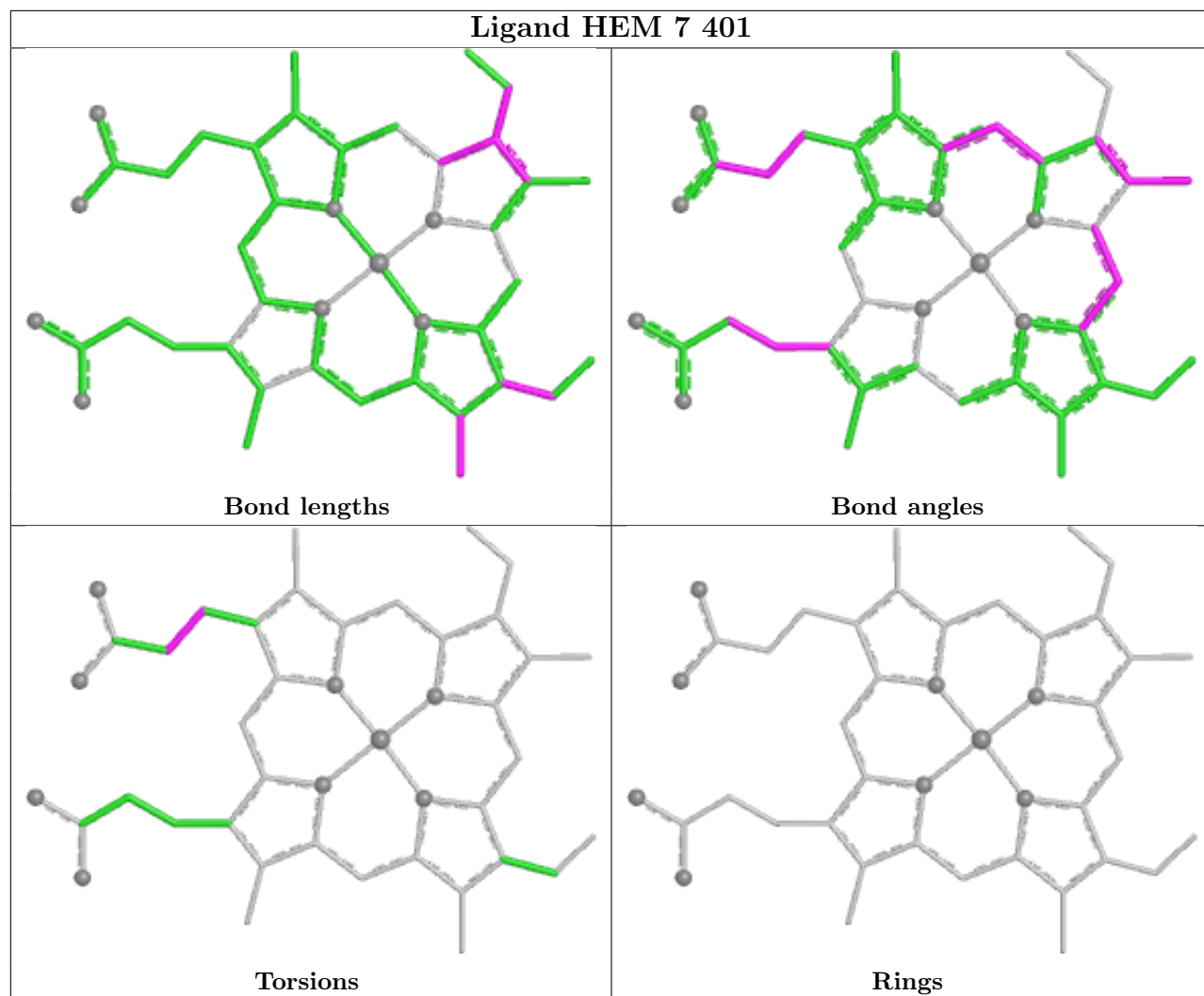


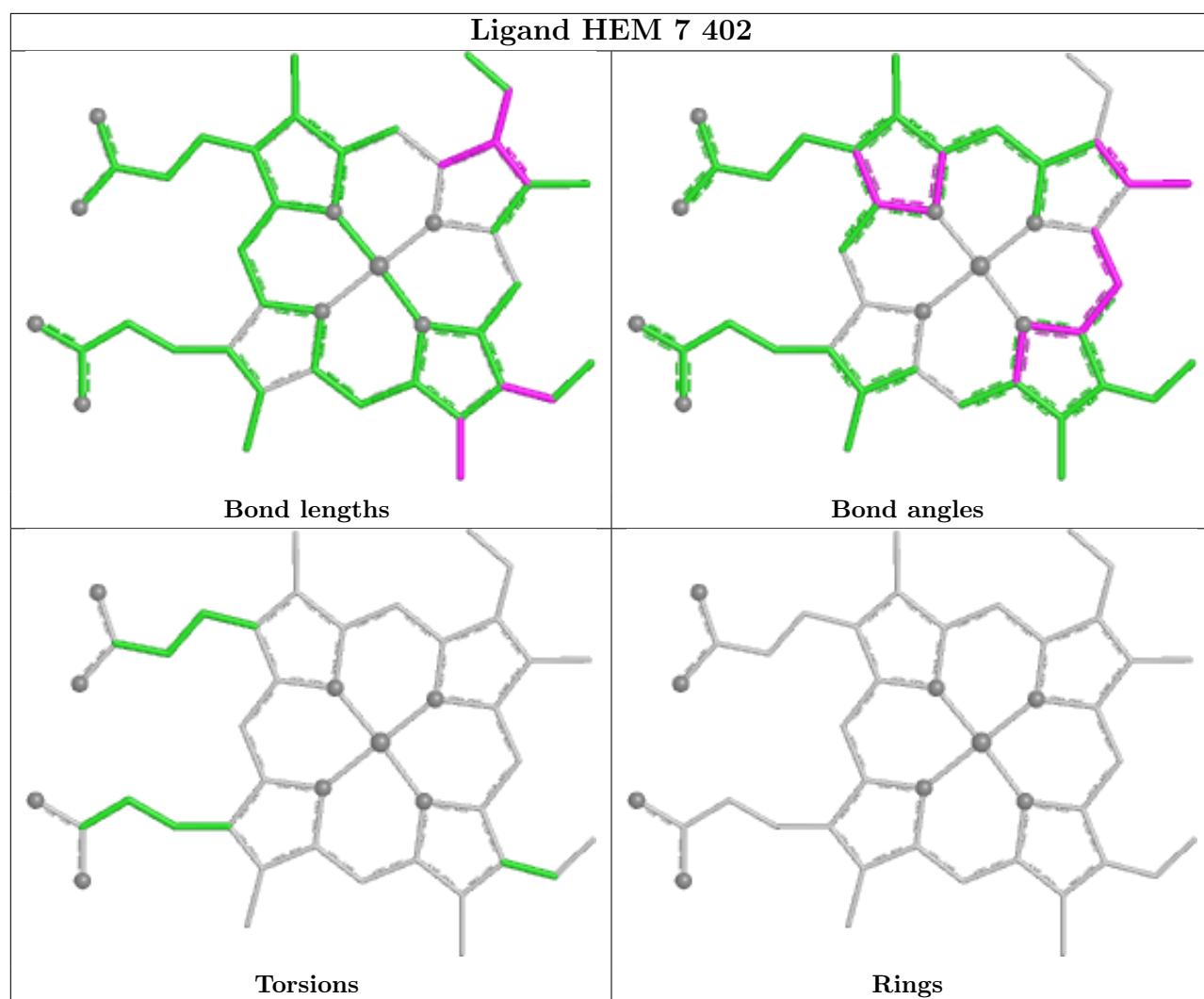
Rings

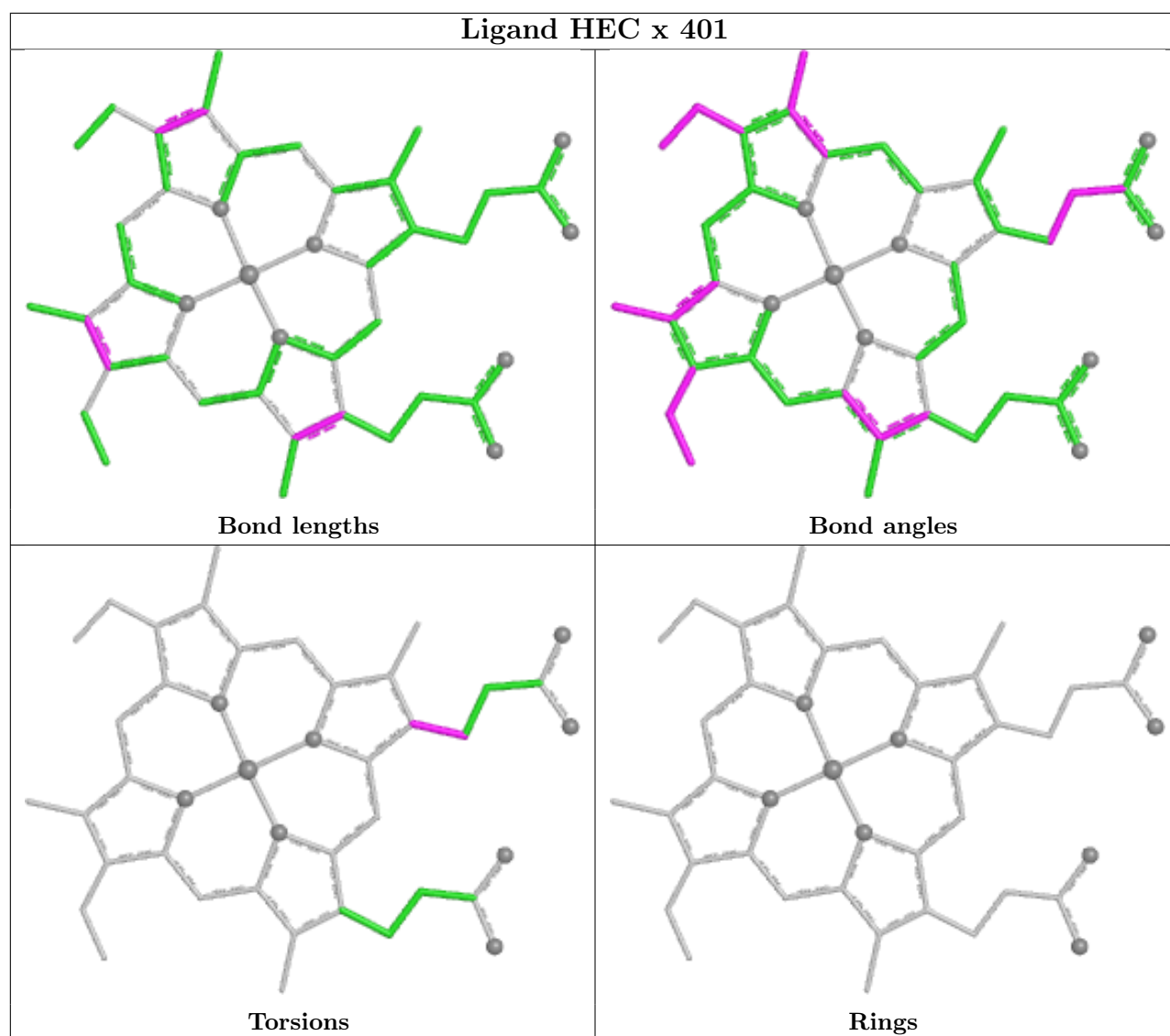












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

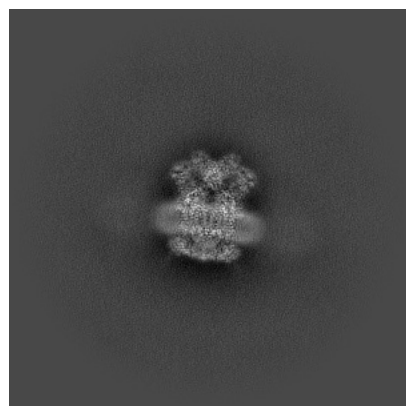
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45282. These allow visual inspection of the internal detail of the map and identification of artifacts.

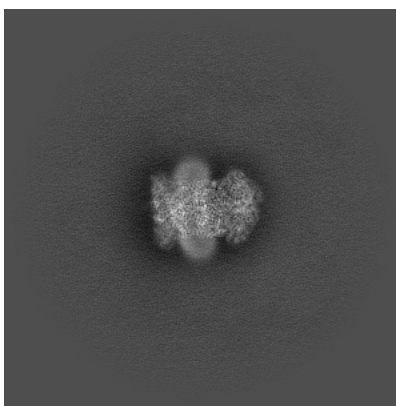
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

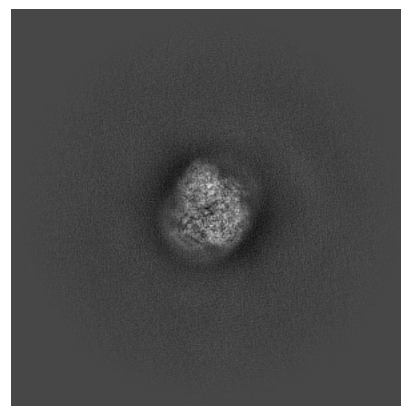
#### 6.1.1 Primary map



X

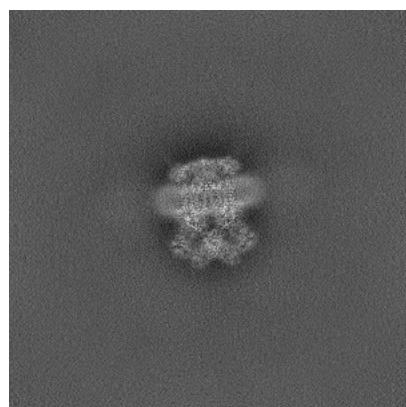


Y

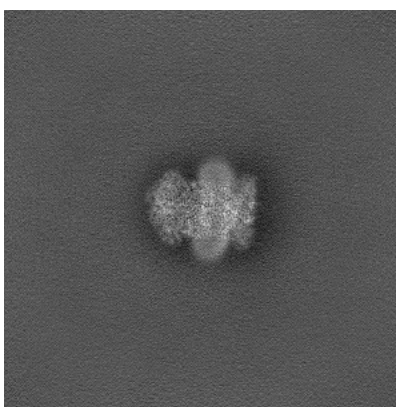


Z

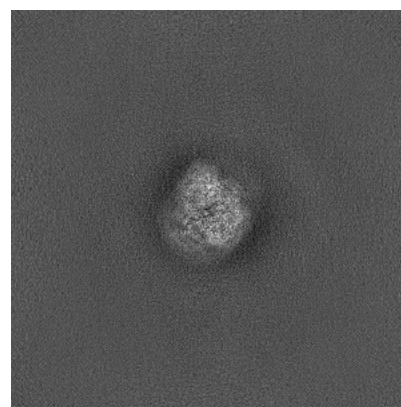
#### 6.1.2 Raw map



X



Y

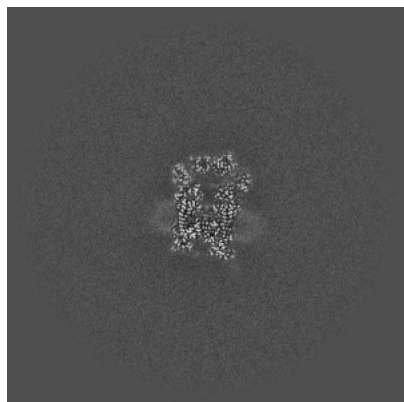


Z

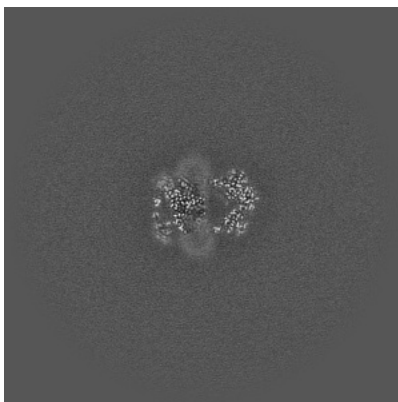
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

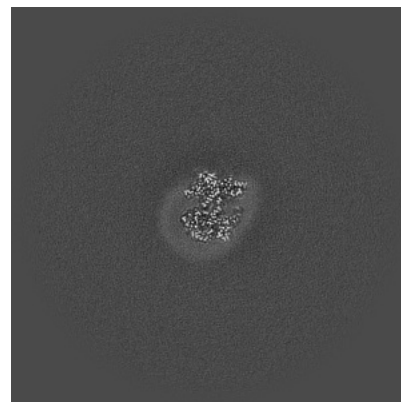
### 6.2.1 Primary map



X Index: 256

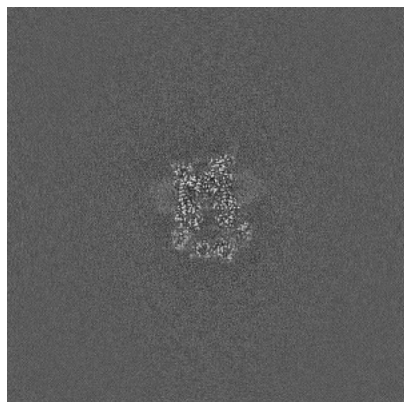


Y Index: 256

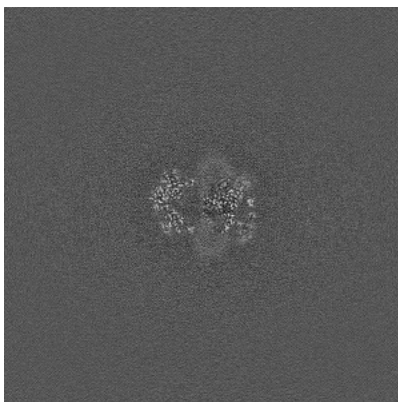


Z Index: 256

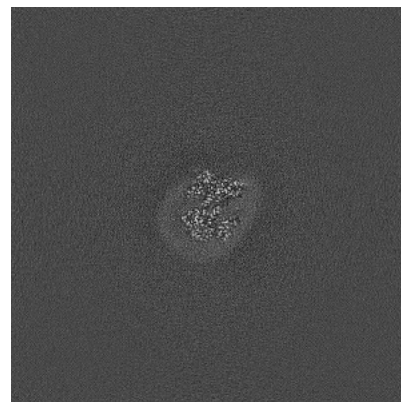
### 6.2.2 Raw map



X Index: 256



Y Index: 256



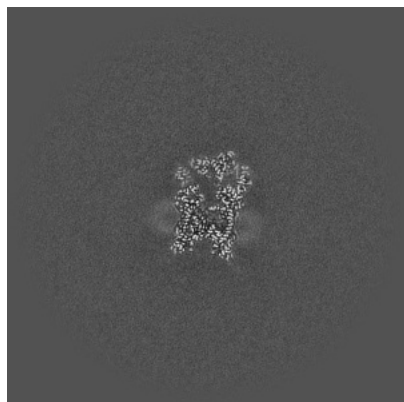
Z Index: 256

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

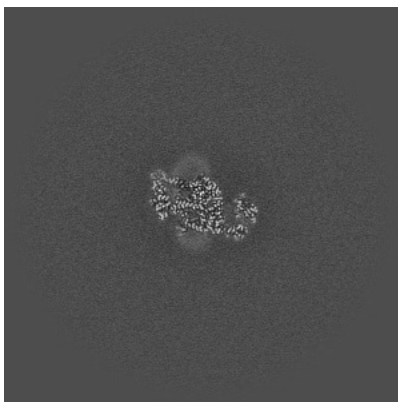


## 6.3 Largest variance slices [i](#)

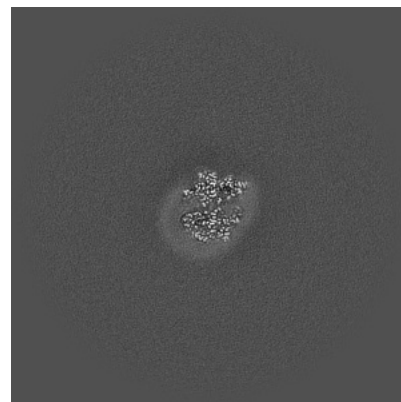
### 6.3.1 Primary map



X Index: 253

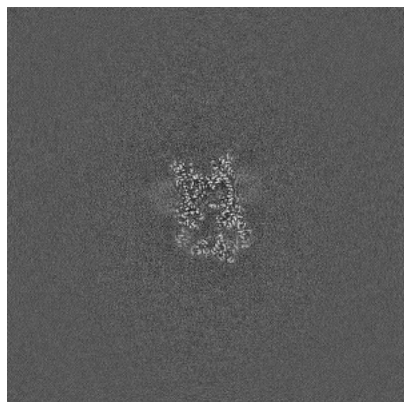


Y Index: 277

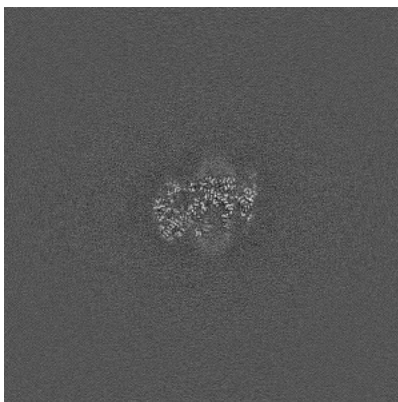


Z Index: 257

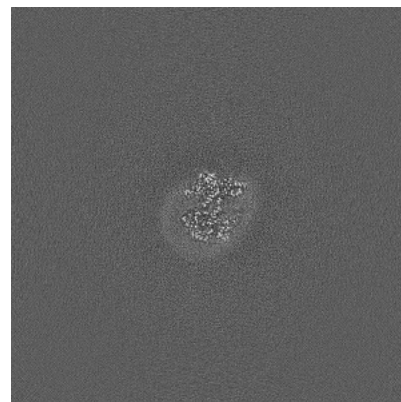
### 6.3.2 Raw map



X Index: 253



Y Index: 270



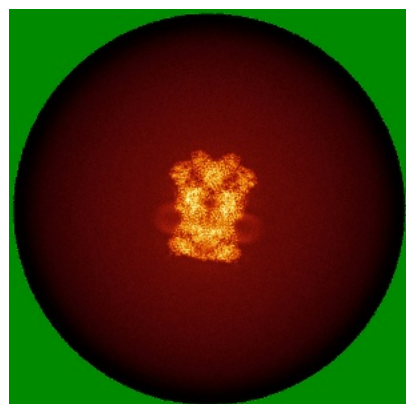
Z Index: 255

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

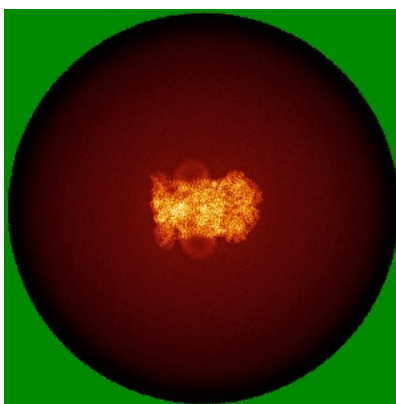


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

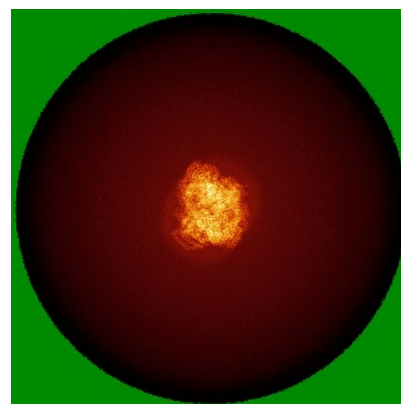
### 6.4.1 Primary map



X

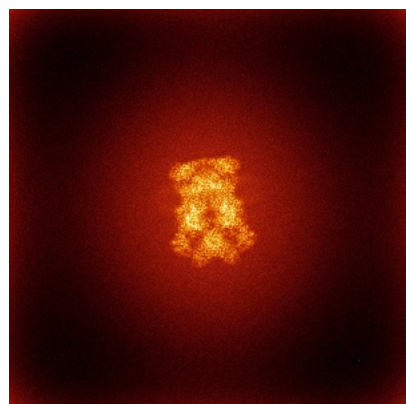


Y

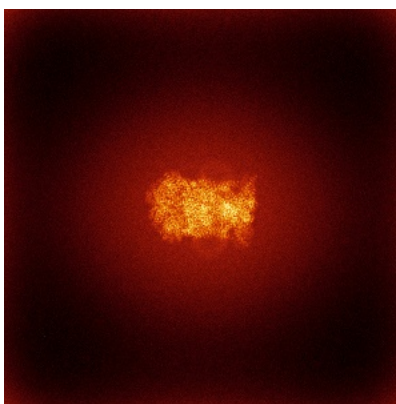


Z

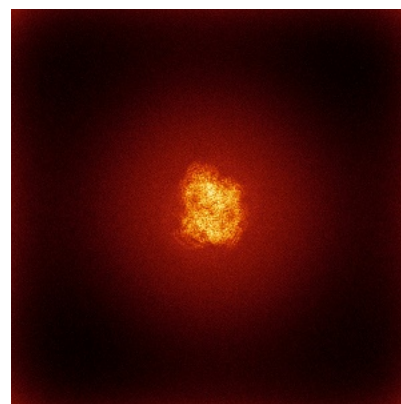
### 6.4.2 Raw map



X



Y

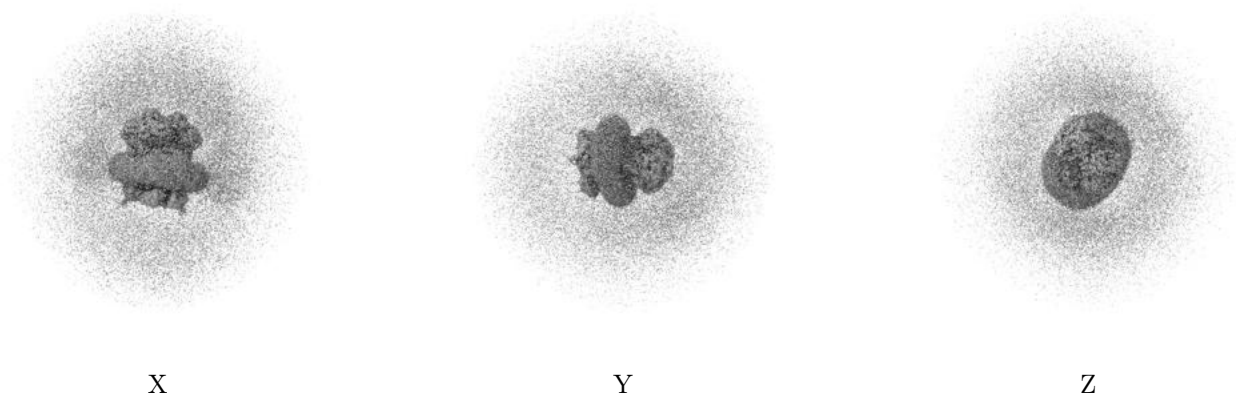


Z

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

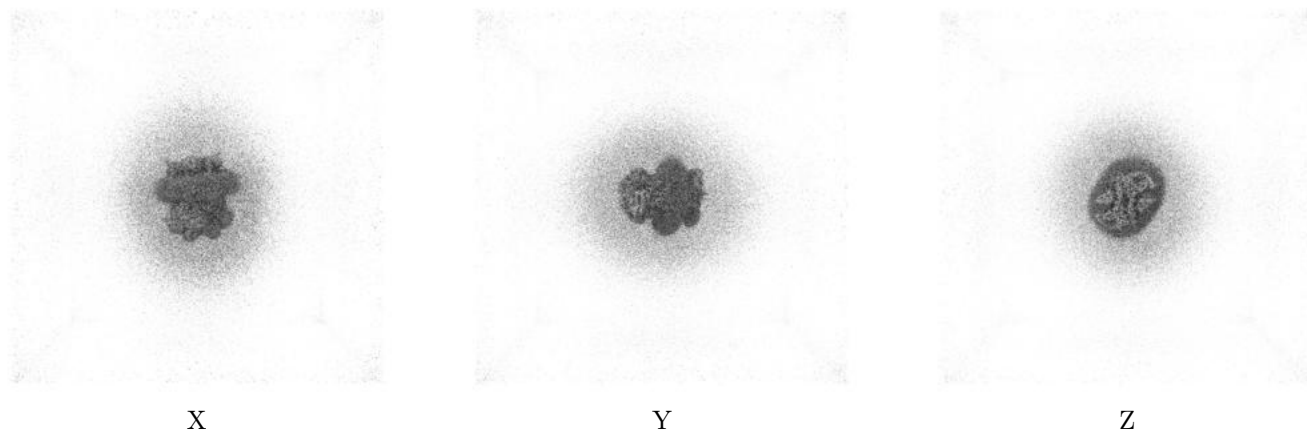
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

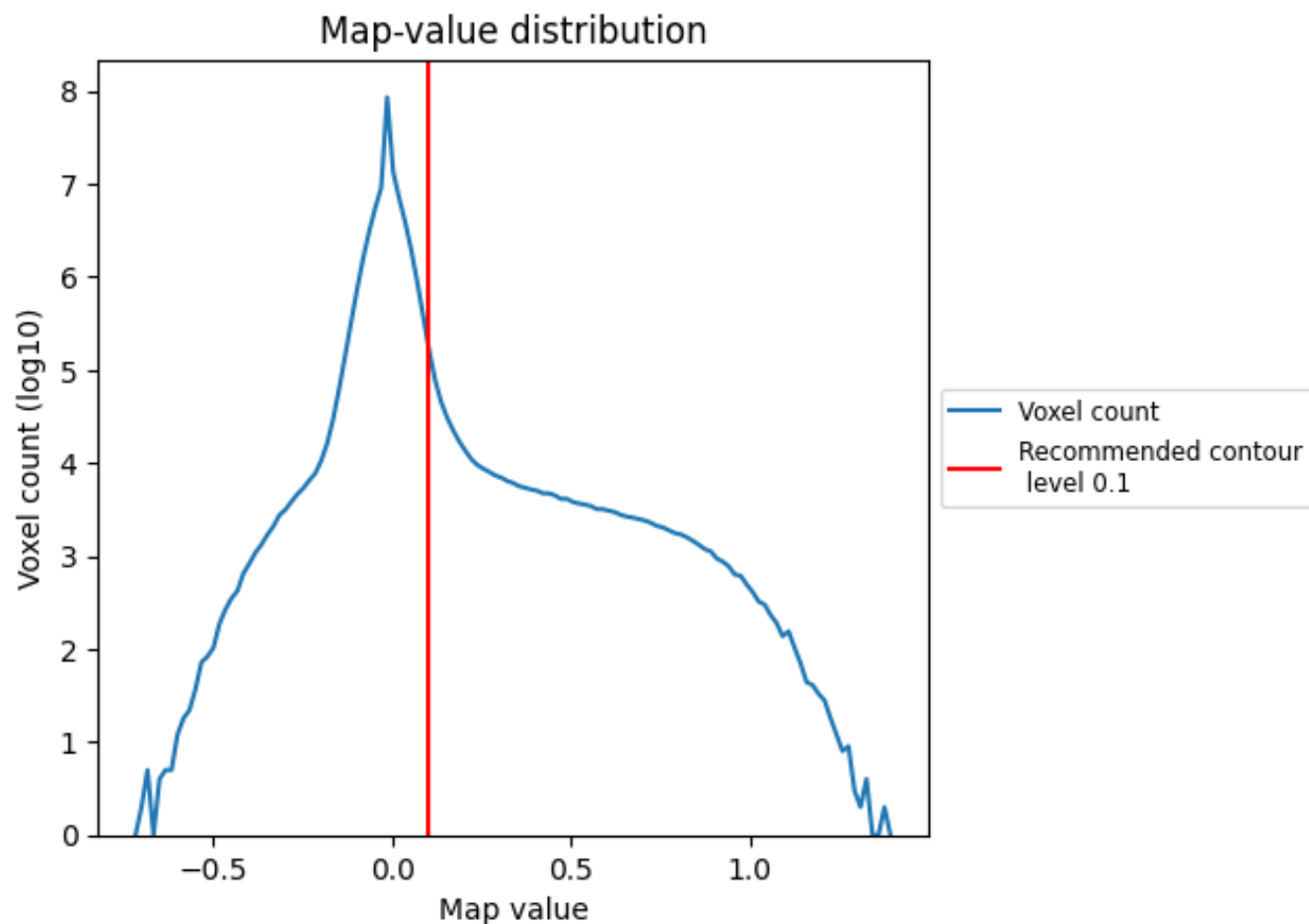
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

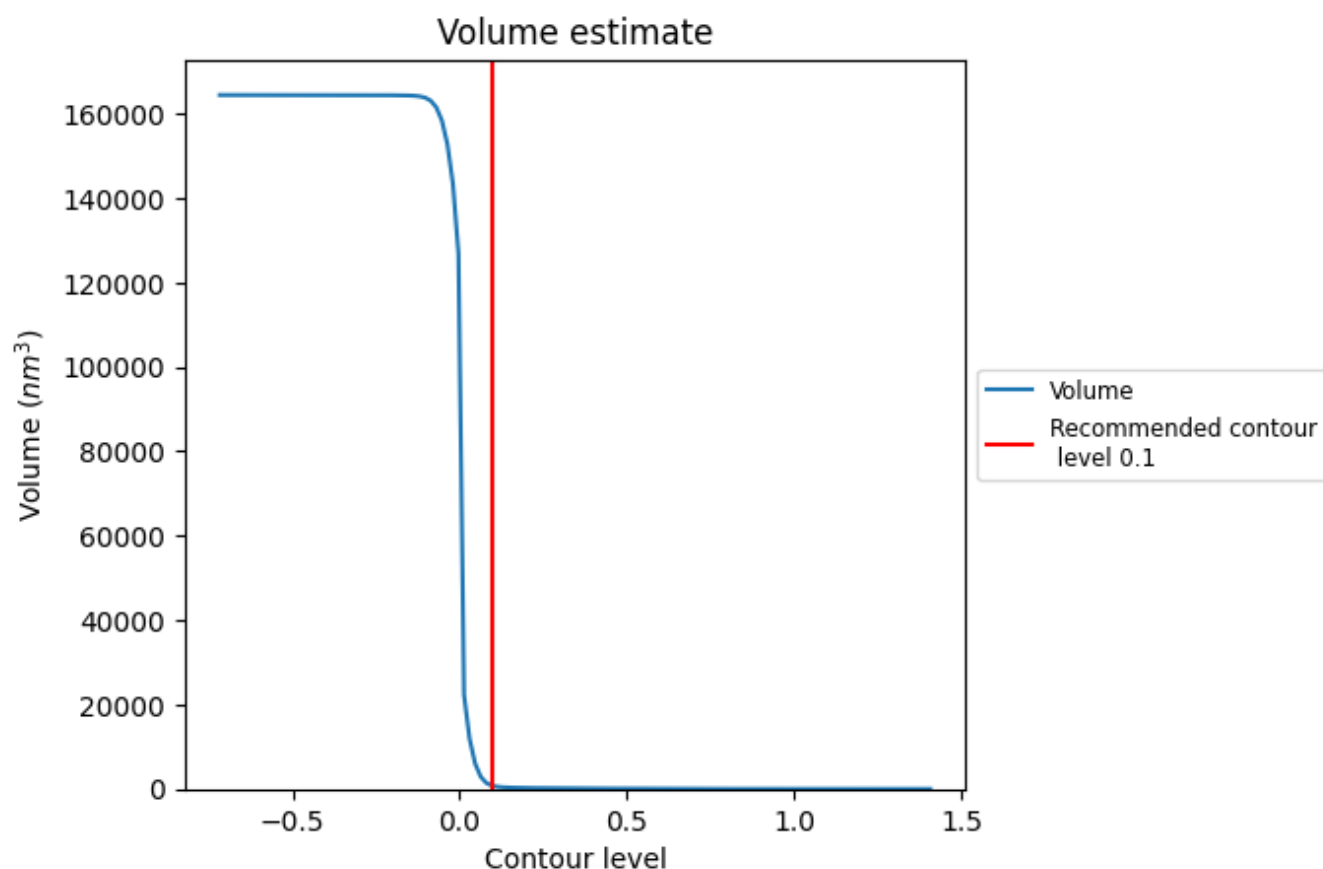
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

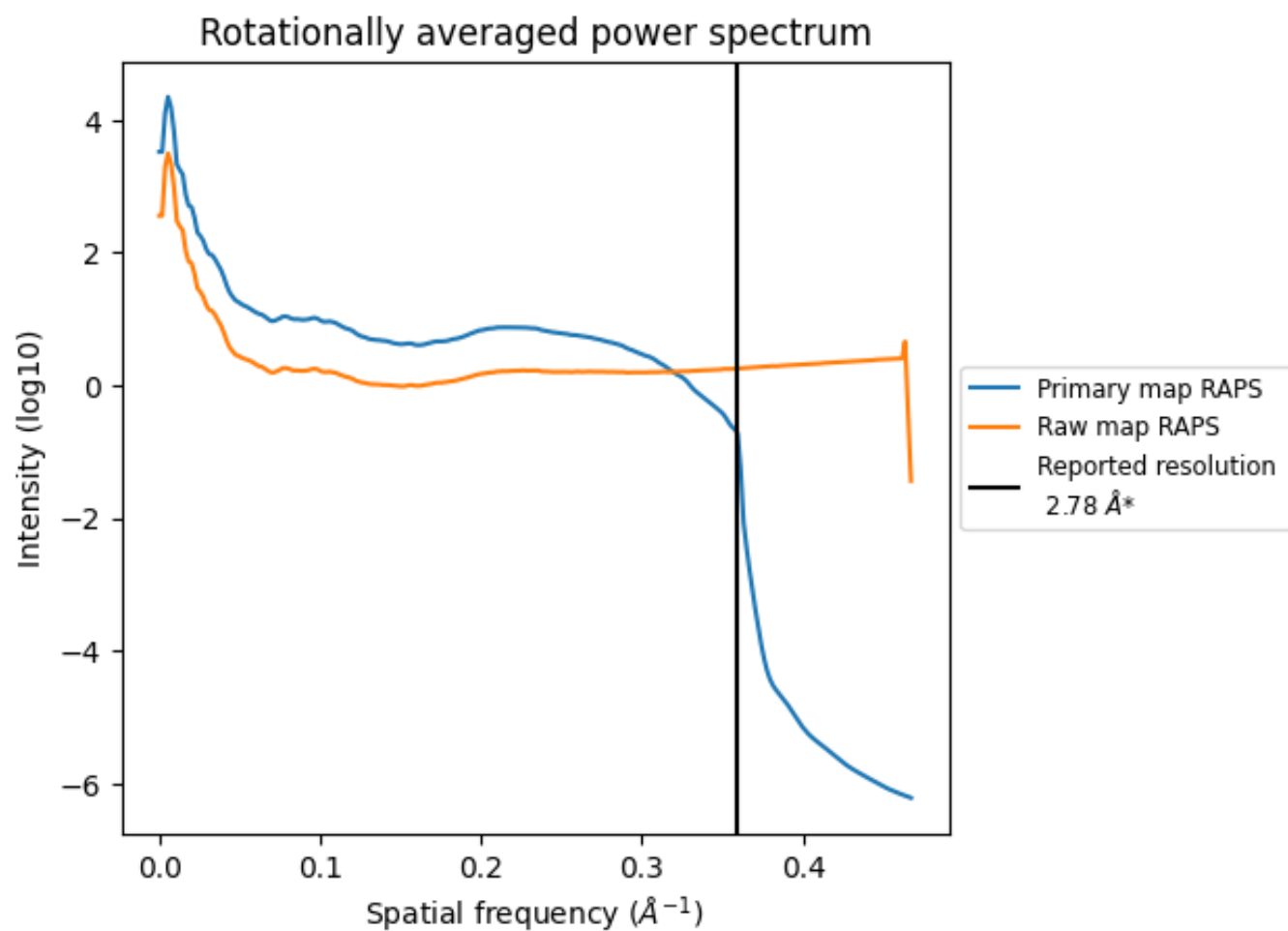
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 740  $\text{nm}^3$ ; this corresponds to an approximate mass of 668 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ

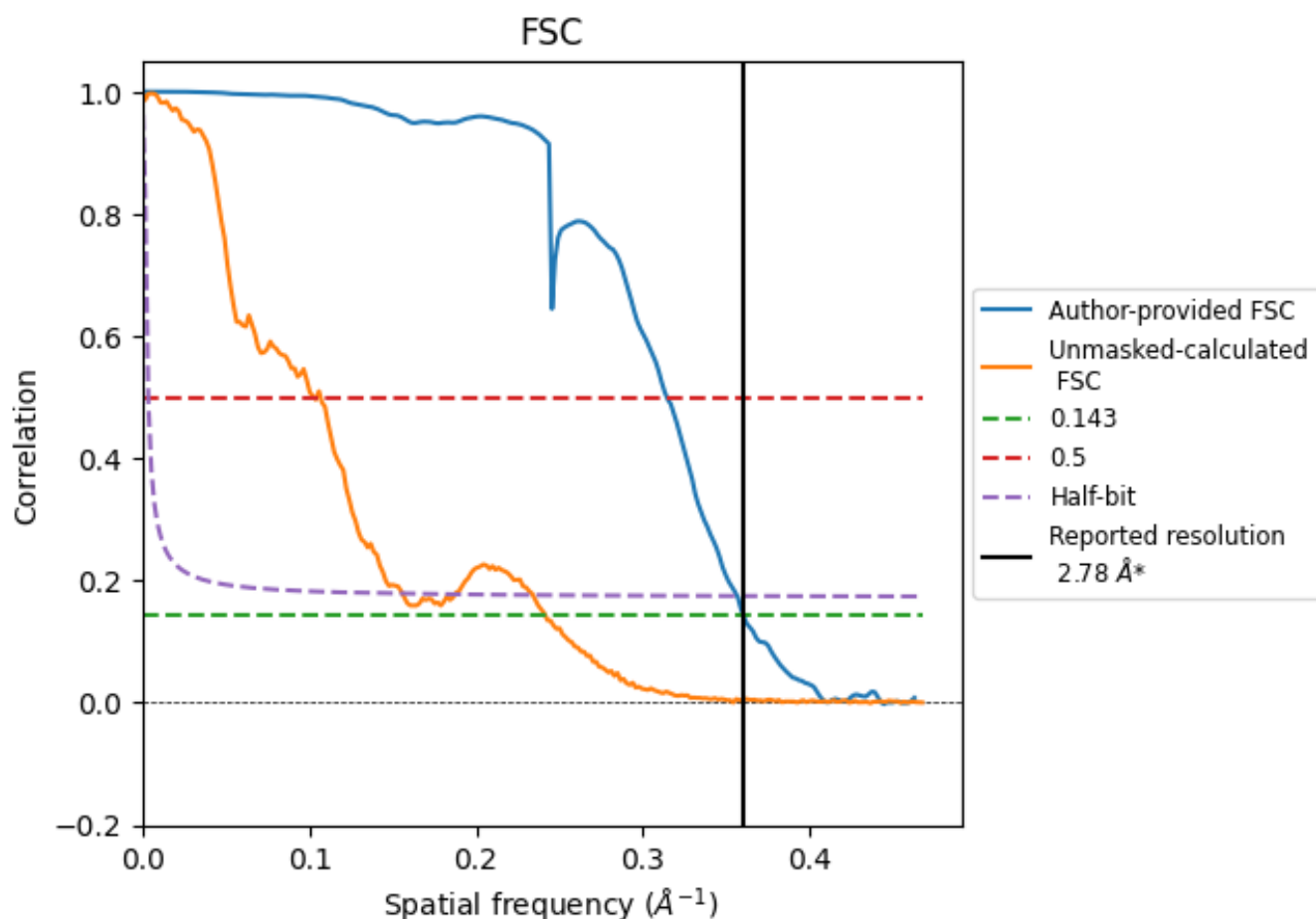


\*Reported resolution corresponds to spatial frequency of 0.360 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.360  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

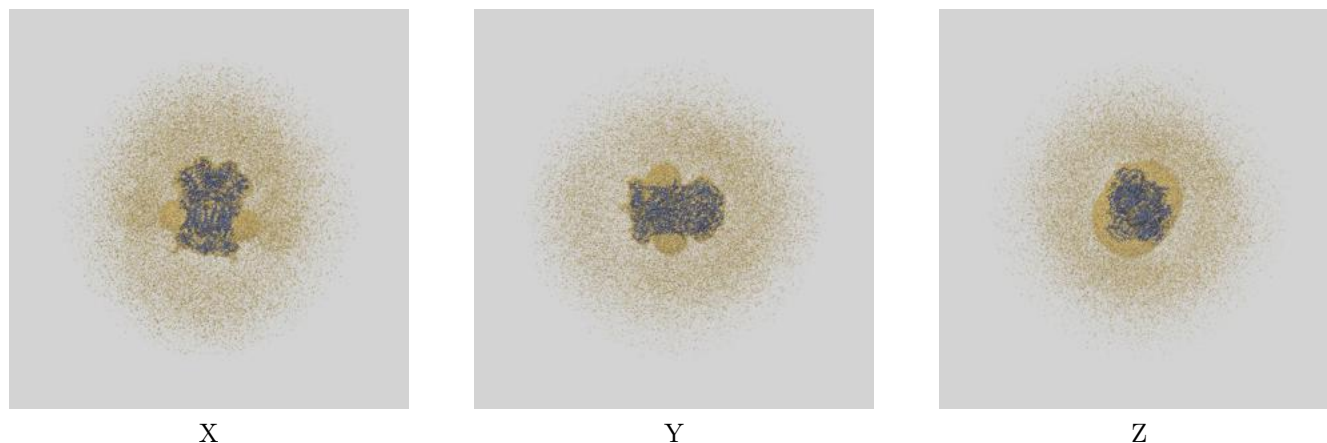
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.78	-	-
Author-provided FSC curve	2.78	3.18	2.81
Unmasked-calculated*	4.14	9.74	6.42

\*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 4.14 differs from the reported value 2.78 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45282 and PDB model 9C7H. Per-residue inclusion information can be found in section [3](#) on page [9](#).

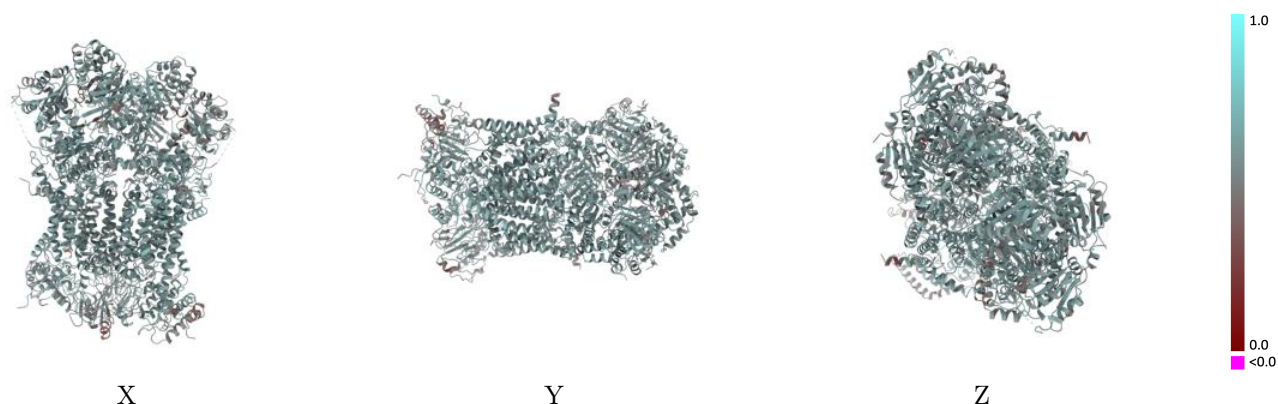
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

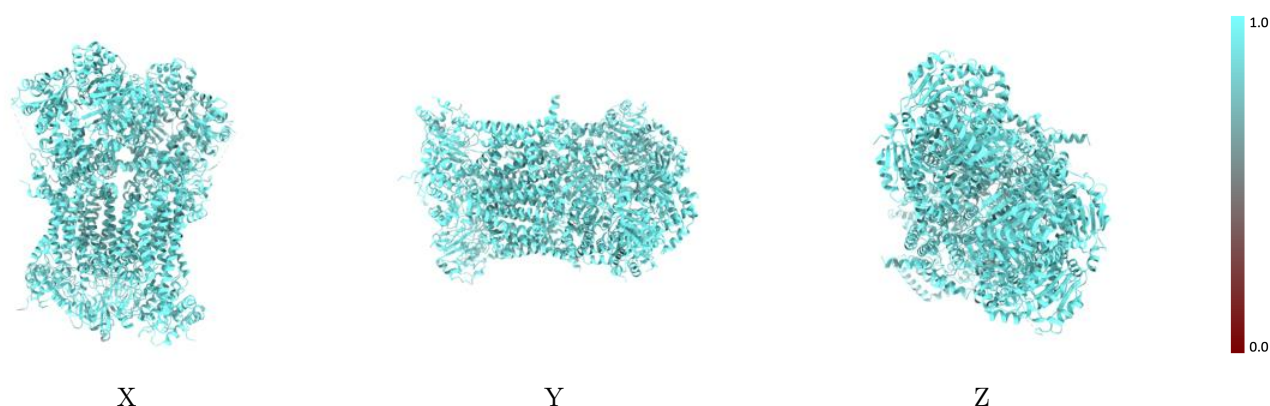


## 9.2 Q-score mapped to coordinate model [i](#)



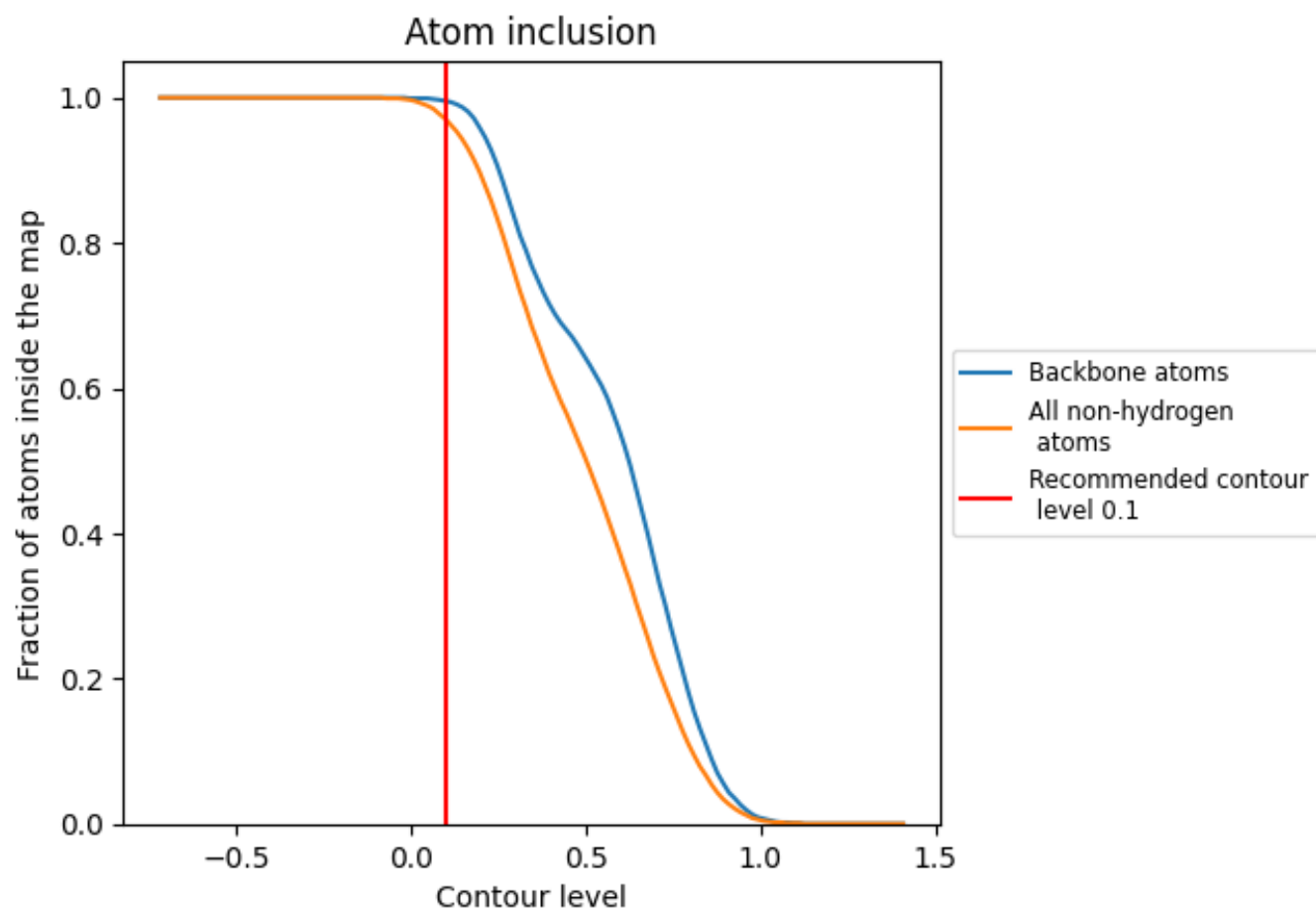
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).















































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.5620
0	 0.9270	 0.4850
1	 0.9850	 0.5790
2	 0.9480	 0.5240
3	 0.9880	 0.5590
4	 0.9480	 0.5220
5	 0.9750	 0.5700
6	 0.9760	 0.5660
7	 0.9840	 0.5850
8	 0.9760	 0.5750
9	 0.9580	 0.5680
Aa	 0.9780	 0.5630
Ab	 0.9230	 0.4900
Ac	 0.9730	 0.5590
Ad	 0.9750	 0.5560
Ae	 0.7960	 0.3980
Af	 0.8250	 0.4080
u	 0.9750	 0.5690
v	 0.9730	 0.5630
w	 0.9860	 0.5870
x	 0.9770	 0.5730
y	 0.9560	 0.5670
z	 0.9860	 0.5730

