



## wwPDB EM Validation Summary Report ⓘ

Nov 16, 2024 – 01:42 PM EST

PDB ID : 9CE0  
EMDB ID : EMD-45489  
Title : DosP Apo Bent form  
Authors : Kumar, P.; Kober, D.L.  
Deposited on : 2024-06-25  
Resolution : 3.97 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
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)	:	2.39

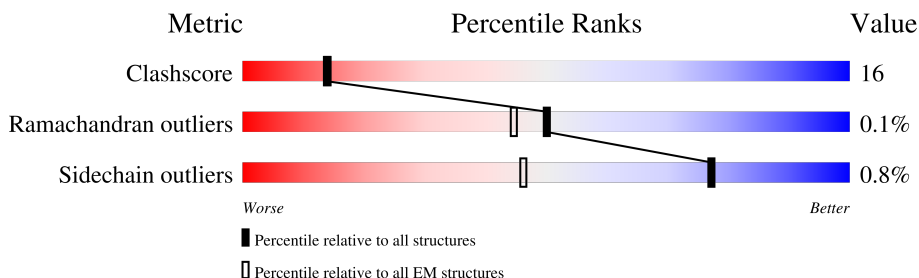
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.97 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	A	806	
1	B	806	

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
3	OXY	A	902	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12551 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.

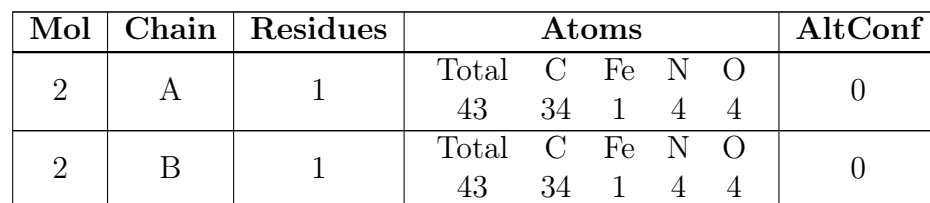
- Molecule 1 is a protein called Oxygen sensor protein DosP.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	787	Total	C	N	O	S	0	0
			6257	3961	1095	1168	33		
1	B	781	Total	C	N	O	S	0	0
			6204	3928	1085	1158	33		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP P76129
A	2	ARG	-	expression tag	UNP P76129
A	3	GLN	-	expression tag	UNP P76129
A	4	ASP	-	expression tag	UNP P76129
A	5	ALA	-	expression tag	UNP P76129
A	6	GLU	-	expression tag	UNP P76129
A	7	VAL	-	expression tag	UNP P76129
A	8	ILE	-	expression tag	UNP P76129
A	16	SER	ASN	conflict	UNP P76129
A	195	THR	ILE	conflict	UNP P76129
B	1	MET	-	expression tag	UNP P76129
B	2	ARG	-	expression tag	UNP P76129
B	3	GLN	-	expression tag	UNP P76129
B	4	ASP	-	expression tag	UNP P76129
B	5	ALA	-	expression tag	UNP P76129
B	6	GLU	-	expression tag	UNP P76129
B	7	VAL	-	expression tag	UNP P76129
B	8	ILE	-	expression tag	UNP P76129
B	16	SER	ASN	conflict	UNP P76129
B	195	THR	ILE	conflict	UNP P76129

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ) (labeled as "Ligand of Interest" by depositor).



- OXY
- O1 O = O O2

Mol	Chain	Residues	Atoms	AltConf
3	A	1	Total O 2 2	0



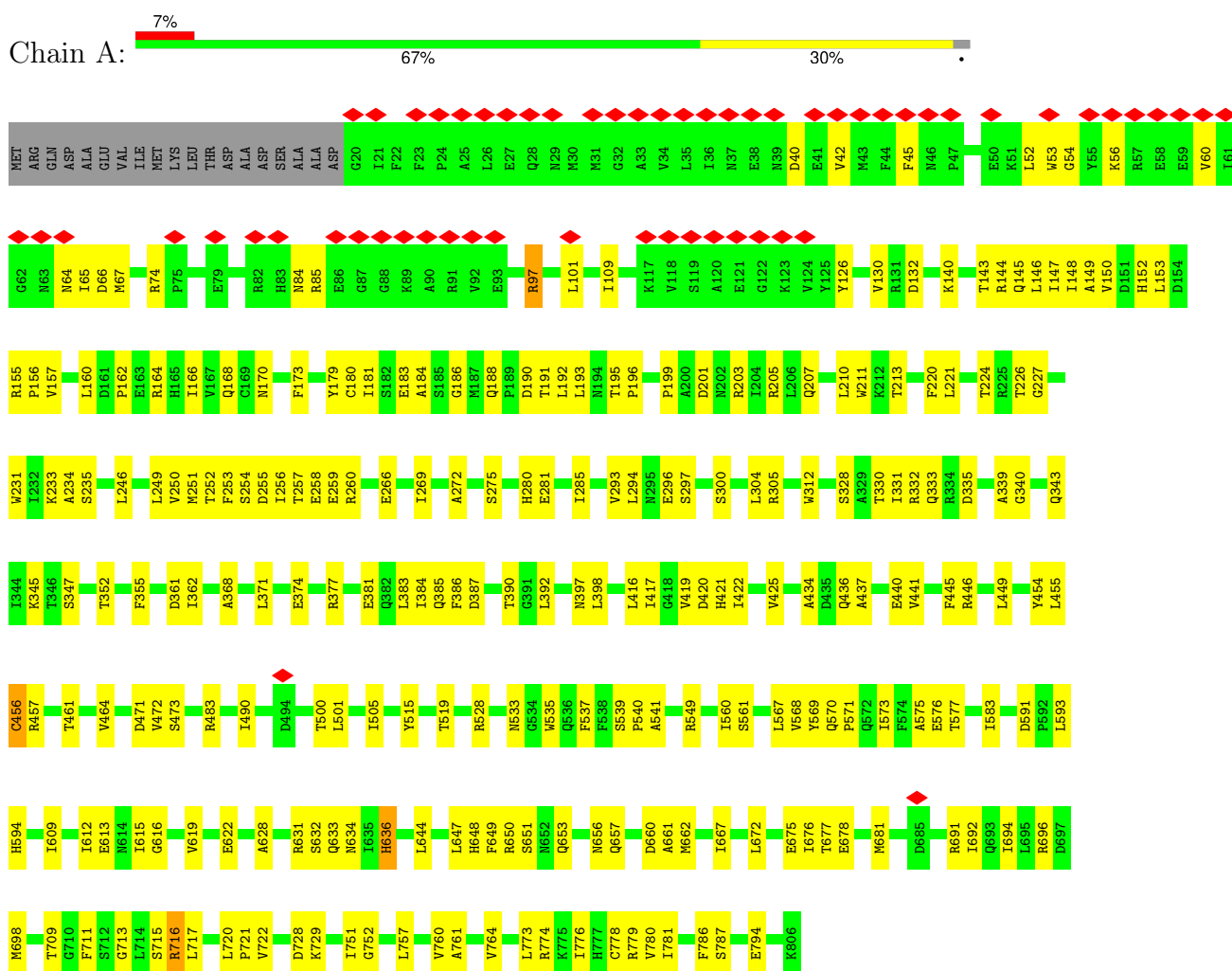
*Continued from previous page...*

Mol	Chain	Residues	Atoms		AltConf
3	B	1	Total	O	0
			2	2	

### 3 Residue-property plots

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

- Molecule 1: Oxygen sensor protein DosP



- Molecule 1: Oxygen sensor protein DosP



I727	R631	R513	S363	V159	P70	MET
D728	S632	D514	M366	L160	R71	ARG
K729	Q633	Y515	Q373	L249	D72	GLN
F731	R634	L516	Q373	R164	L73	ASP
V732	I635	T519	F253	Q168	R74	ALA
D733	H636	M524	T256	C169	I81	GLU
R734	I637	D525	I256	M170	R82	VAL
E738	H648	Y526	E259	R171	H83	ILE
K739	F649	I527	R260	T174	N84	LYS
R740	R650	R528	Q261	G178	R85	LEU
I741	S651	K529	R263	Y179	E86	THR
L744	H652	N530	Q264	C180	G87	ASP
L745	Q653	Q536	L265	I181	G88	ALA
L746	L654	F537	E266	S182	K89	ASP
E746	R655	R549	G267	E183	A90	ALA
A747	Q657	R549	N268	M187	R91	ALA
S750	V658	G553	I269	Q188	V92	ASP
I751	S659	N562	A272	P189	E93	
V760	M662	Q563	M273	D190	G94	
A761	D668	Q564	P277	T191	R97	
E762	Q671	L565	M282	L193	E98	
G763	M680	K566	I285	N194	L101	
V764	Q671	Q572	I286	T195	E102	
L773	M680	I573	N289	F198	I109	
R774	H684	T577	L304	R203	R112	
K775	D885	Y581	A437	I204	K117	
H777	I688	G882	L438	R205	V118	
C778	F689	I583	L439	L206	S119	
R779	K690	R588	V441	Q207	A120	
V780	R691	W589	C456	Q208	E121	
I781	I692	H590	R457	L209	N37	
Q782	I693	D591	T461	L210	E38	
F786	L695	P592	V464	W211	N39	
E793	R696	L593	S326	R215	D40	
E794	L702	V597	W327	D216	W43	
L803	D706	P598	I331	Q217	M46	
P804	D706	P599	P338	D218	M46	
K806	F707	F602	A339	E220	W53	
	G708	L605	Q343	L221	G54	
	T709	E611	G349	L222	Y55	
	S712	I612	S353	W231	K56	
	S715	E613	E357	I232	R57	
	R716	N614	R358	K233	E58	
	L717	W618	V359	A234	I47	
	V722	E622	A360	I236	I148	
	K726		D361	D241	A149	
			I362	H245	V150	
					D151	
					H152	
					L153	
					D154	
					R155	
					I156	
					P156	
					V157	
					L158	
					I159	

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	154173	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.985	Depositor
Minimum map value	-0.226	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.123	Depositor
Map size (Å)	413.30002, 413.30002, 413.30002	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6144532, 1.6144532, 1.6144532	Depositor



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.28	0/6385	0.48	0/8650
1	B	0.29	0/6330	0.49	0/8574
All	All	0.29	0/12715	0.49	0/17224

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 [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	6257	0	6236	206	0
1	B	6204	0	6184	198	0
2	A	43	0	30	5	0
2	B	43	0	30	6	0
3	A	2	0	0	2	0
3	B	2	0	0	0	0
All	All	12551	0	12480	389	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 16.

The worst 5 of 389 close contacts within the same asymmetric unit are listed below, sorted by

their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:LYS:O	1:A:143:THR:OG1	1.93	0.87
1:B:326:SER:OG	1:B:343:GLN:NE2	2.10	0.85
1:B:164:ARG:NE	1:B:210:LEU:O	2.09	0.84
1:B:536:GLN:OE1	1:B:537:PHE:N	2.10	0.84
1:A:422:ILE:HG21	1:A:461:THR:HG21	1.56	0.84

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	785/806 (97%)	730 (93%)	53 (7%)	2 (0%)	37	70
1	B	777/806 (96%)	732 (94%)	45 (6%)	0	100	100
All	All	1562/1612 (97%)	1462 (94%)	98 (6%)	2 (0%)	50	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53	TRP
1	A	636	HIS

### 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	683/698 (98%)	677 (99%)	6 (1%)	75	83
1	B	677/698 (97%)	672 (99%)	5 (1%)	81	86
All	All	1360/1396 (97%)	1349 (99%)	11 (1%)	77	84

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	384	ILE
1	B	549	ARG
1	B	740	ARG
1	B	685	ASP
1	A	549	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	139	GLN
1	B	343	GLN
1	B	693	GLN
1	B	653	GLN
1	A	670	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

4 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	$\# Z  > 2$
2	HEM	B	901	3,1	42,50,50	1.52	6 (14%)	46,82,82	1.33	6 (13%)
2	HEM	A	901	3	42,50,50	1.52	6 (14%)	46,82,82	1.25	4 (8%)
3	OXY	A	902	2	1,1,1	0.17	0	-		
3	OXY	B	902	2	1,1,1	0.17	0	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	B	901	3,1	-	1/12/54/54	-
2	HEM	A	901	3	-	5/12/54/54	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	HEM	C3C-C2C	-4.53	1.34	1.40
2	A	901	HEM	C3C-C2C	-4.53	1.34	1.40
2	B	901	HEM	C3C-CAC	3.38	1.55	1.47
2	A	901	HEM	C3C-CAC	3.36	1.55	1.47
2	A	901	HEM	C3C-C4C	3.08	1.45	1.41

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	HEM	C4B-CHC-C1C	2.71	126.13	122.56
2	A	901	HEM	C4D-ND-C1D	2.53	108.20	105.21
2	B	901	HEM	C4D-ND-C1D	2.49	108.15	105.21
2	B	901	HEM	C4C-CHD-C1D	2.40	125.73	122.56
2	B	901	HEM	C1B-NB-C4B	2.36	108.00	105.21

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

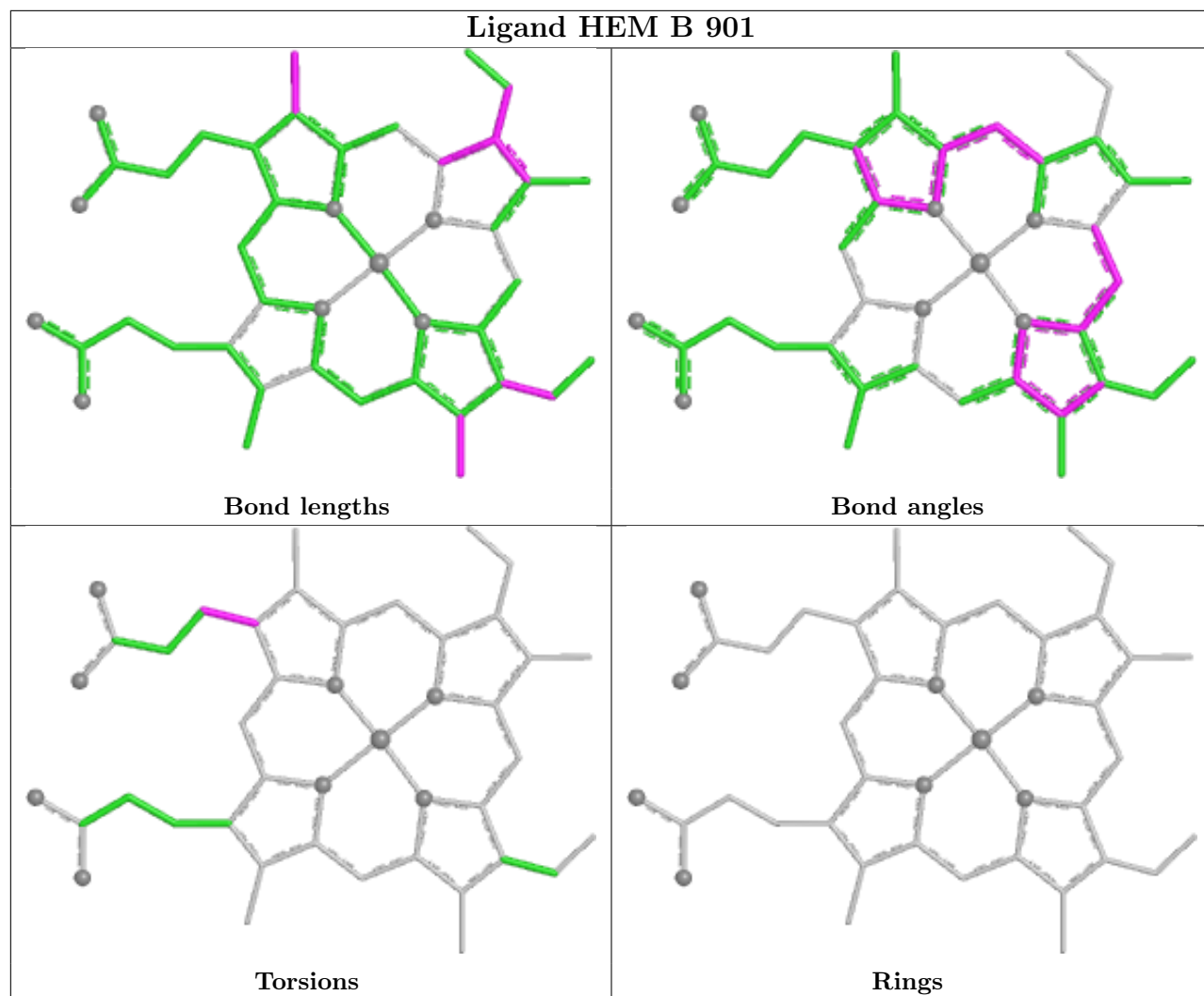
Mol	Chain	Res	Type	Atoms
2	A	901	HEM	C2A-CAA-CBA-CGA
2	A	901	HEM	C4D-C3D-CAD-CBD
2	A	901	HEM	C2D-C3D-CAD-CBD
2	A	901	HEM	CAA-CBA-CGA-O1A
2	A	901	HEM	CAA-CBA-CGA-O2A

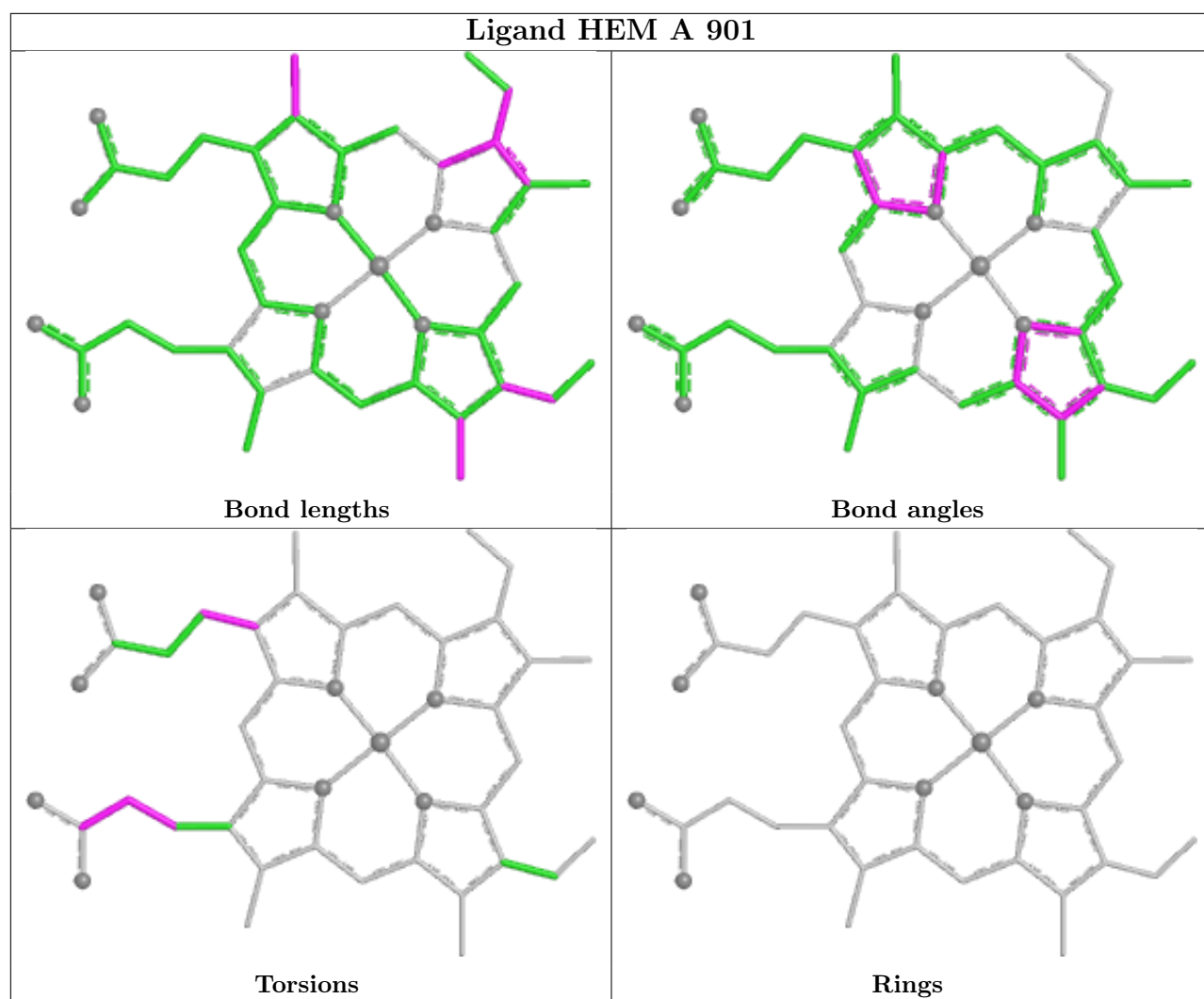
There are no ring outliers.

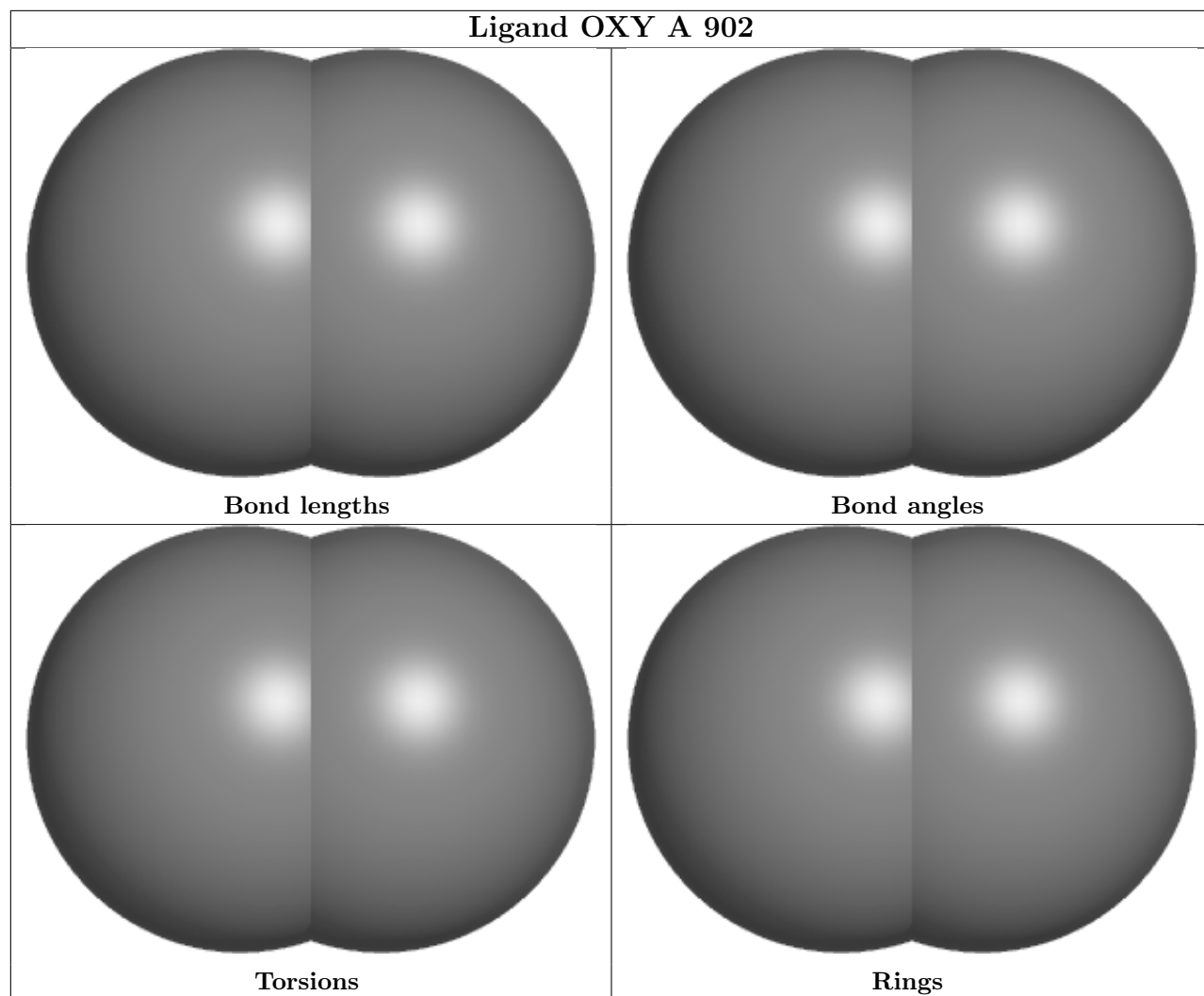
3 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	901	HEM	6	0
2	A	901	HEM	5	0
3	A	902	OXY	2	0

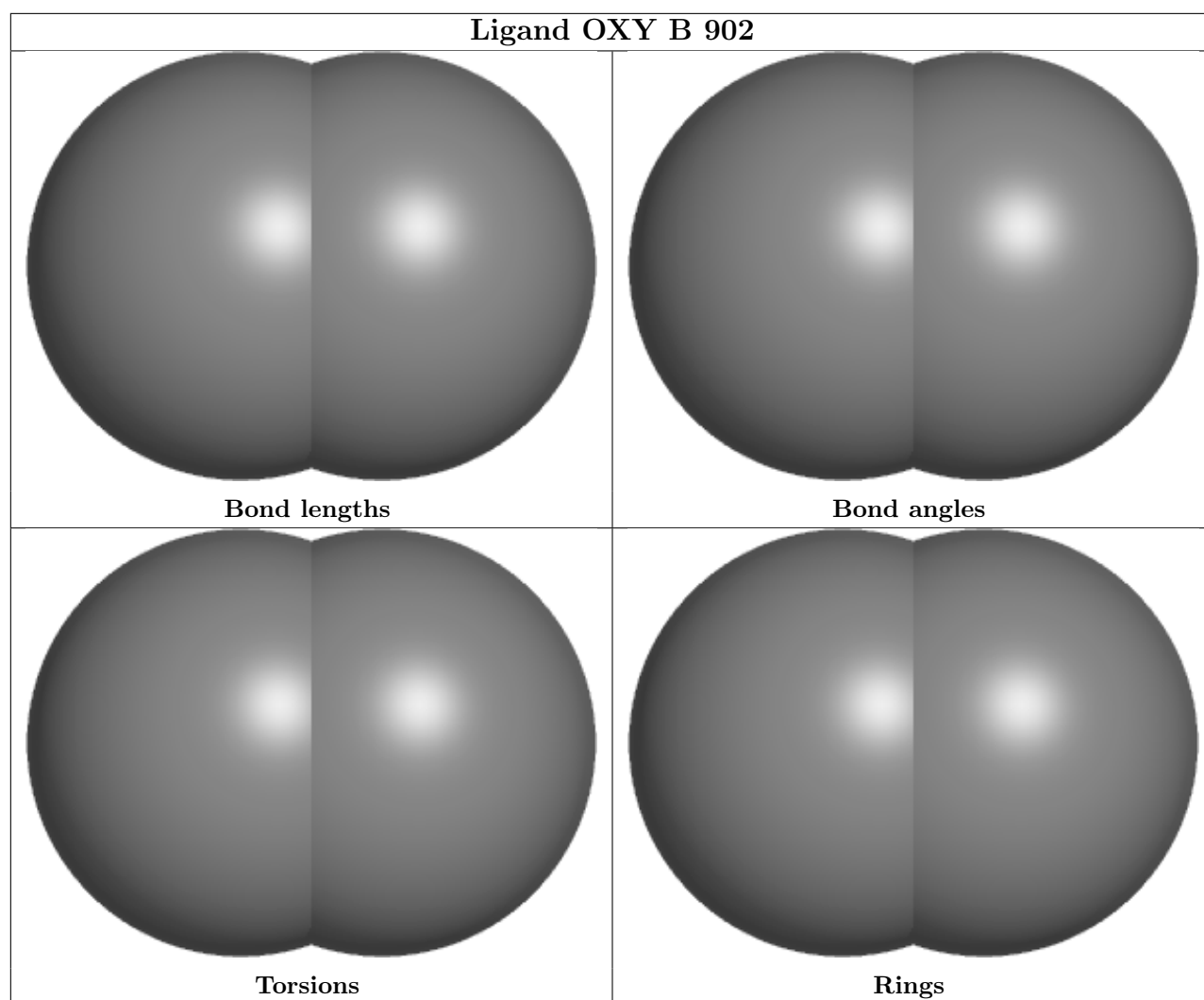
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











## 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.

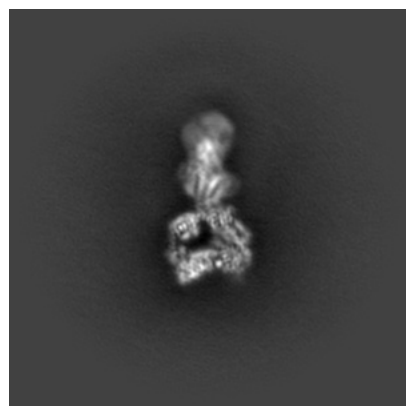
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45489. These allow visual inspection of the internal detail of the map and identification of artifacts.

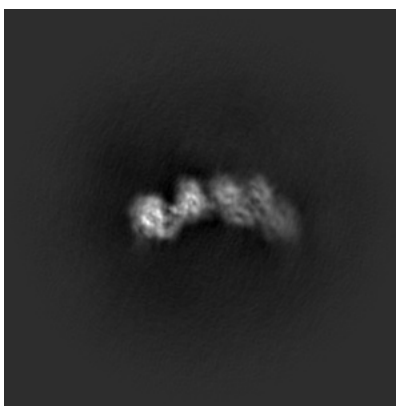
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

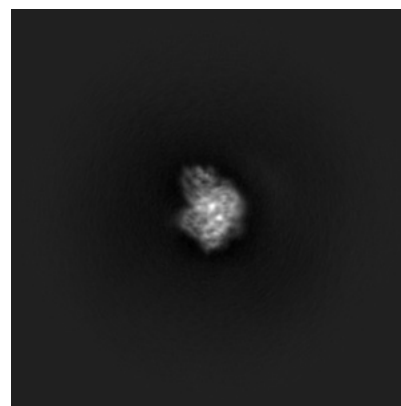
#### 6.1.1 Primary map



X

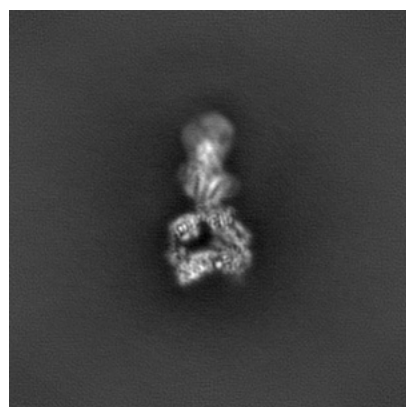


Y

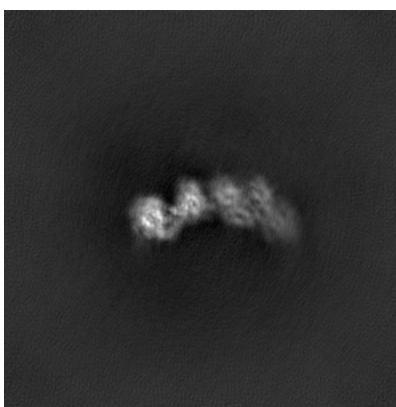


Z

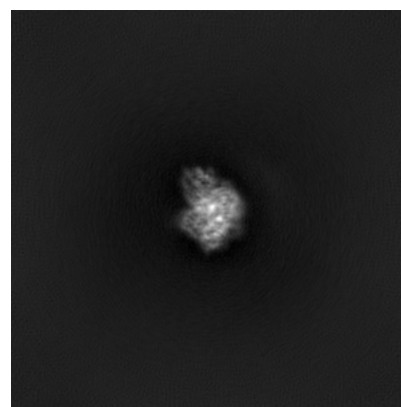
#### 6.1.2 Raw map



X



Y

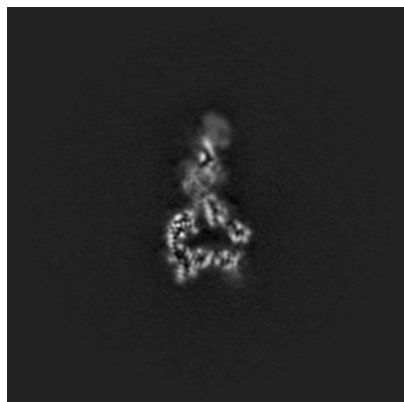


Z

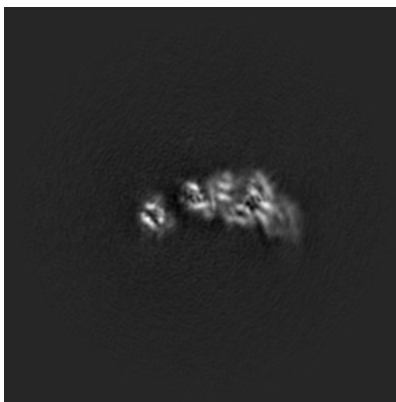
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

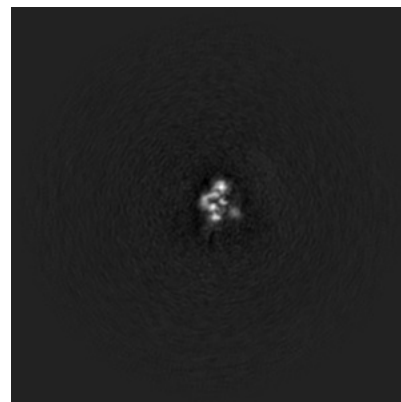
### 6.2.1 Primary map



X Index: 128

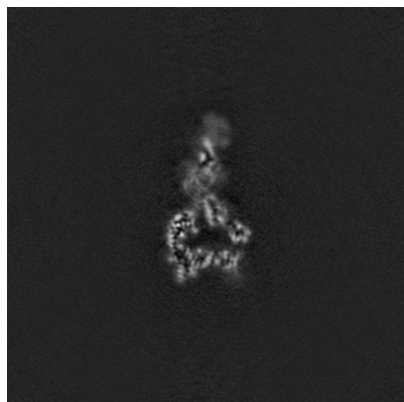


Y Index: 128

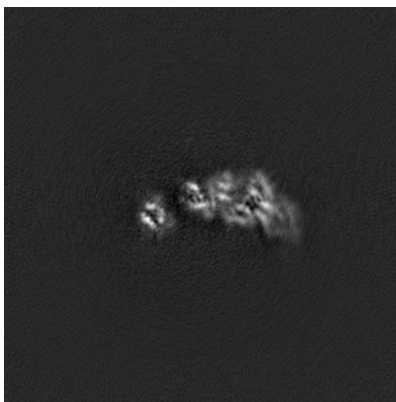


Z Index: 128

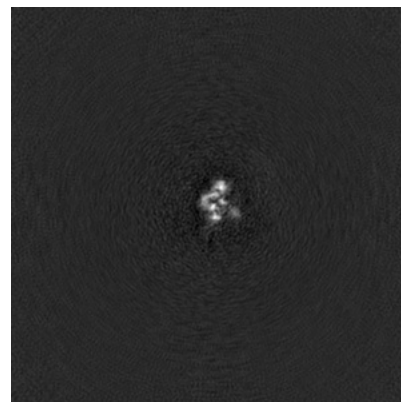
### 6.2.2 Raw map



X Index: 128



Y Index: 128

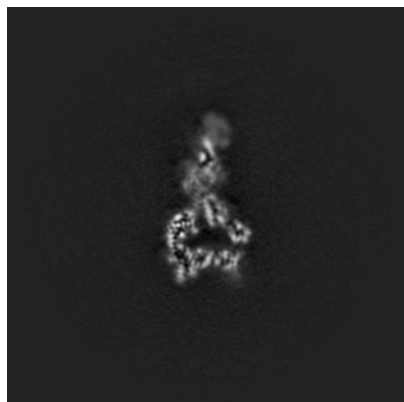


Z Index: 128

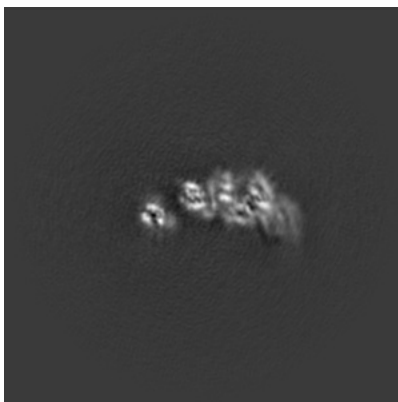
The images above show central slices of the map in three orthogonal directions.

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

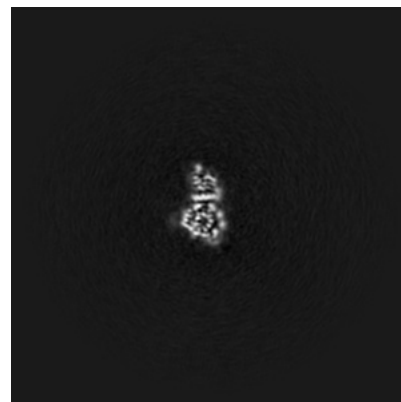
### 6.3.1 Primary map



X Index: 128

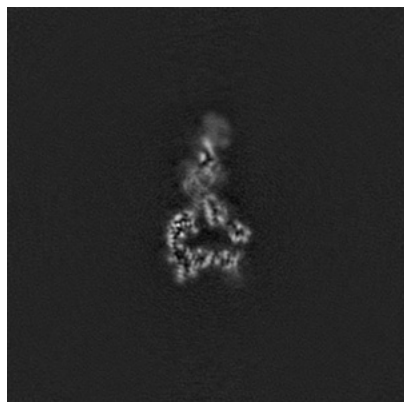


Y Index: 129

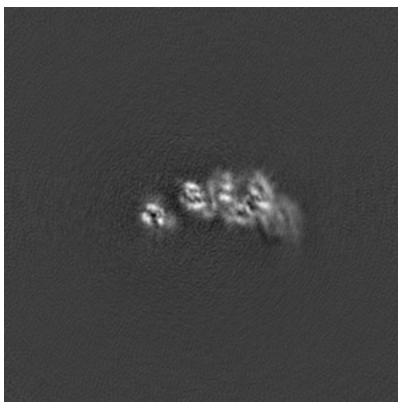


Z Index: 92

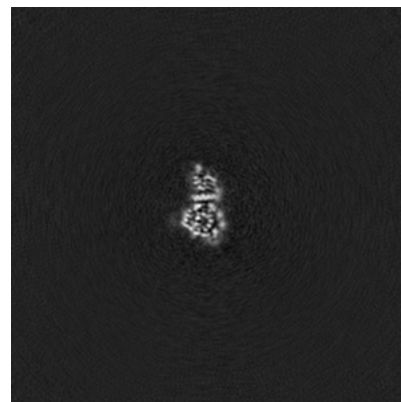
### 6.3.2 Raw map



X Index: 128



Y Index: 129



Z Index: 92

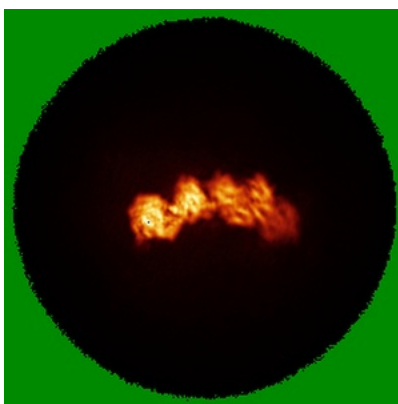
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



X

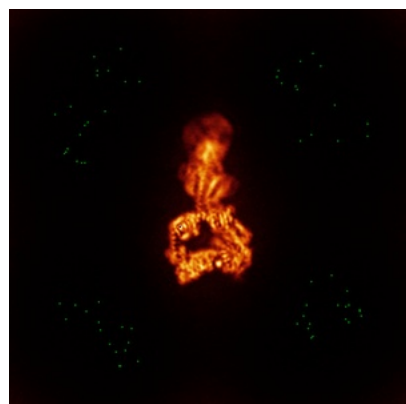


Y



Z

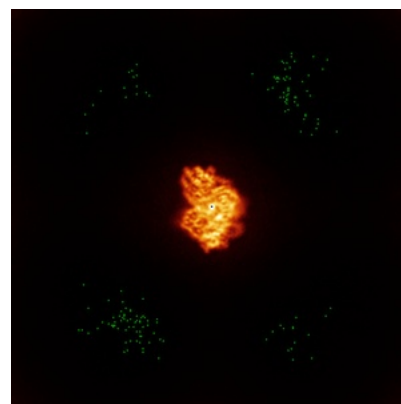
### 6.4.2 Raw map



X



Y

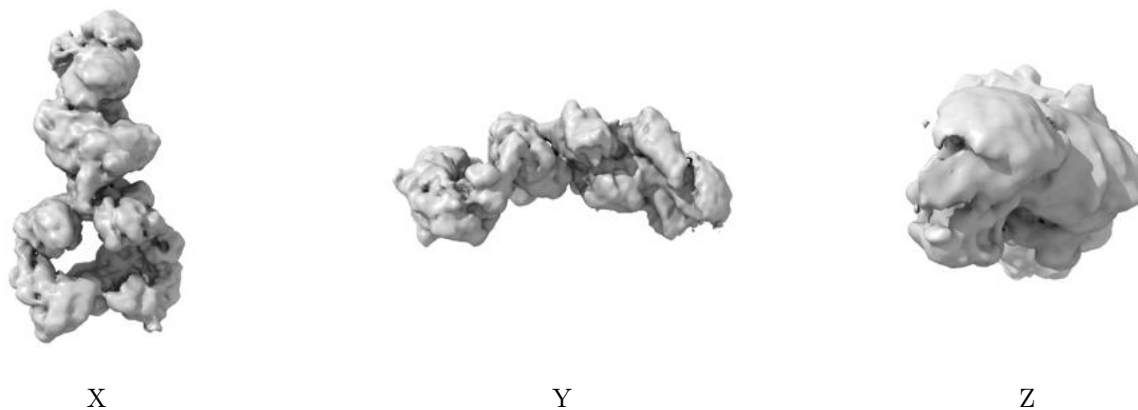


Z

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.

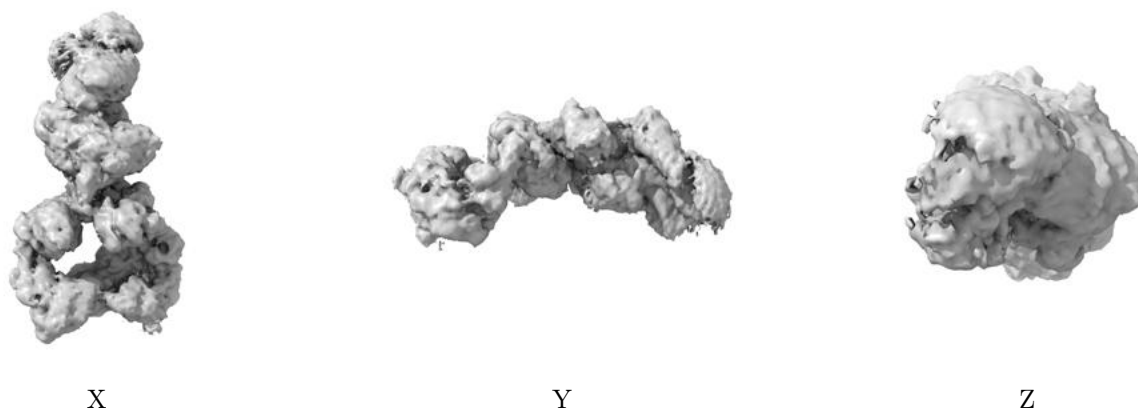
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.123. 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.

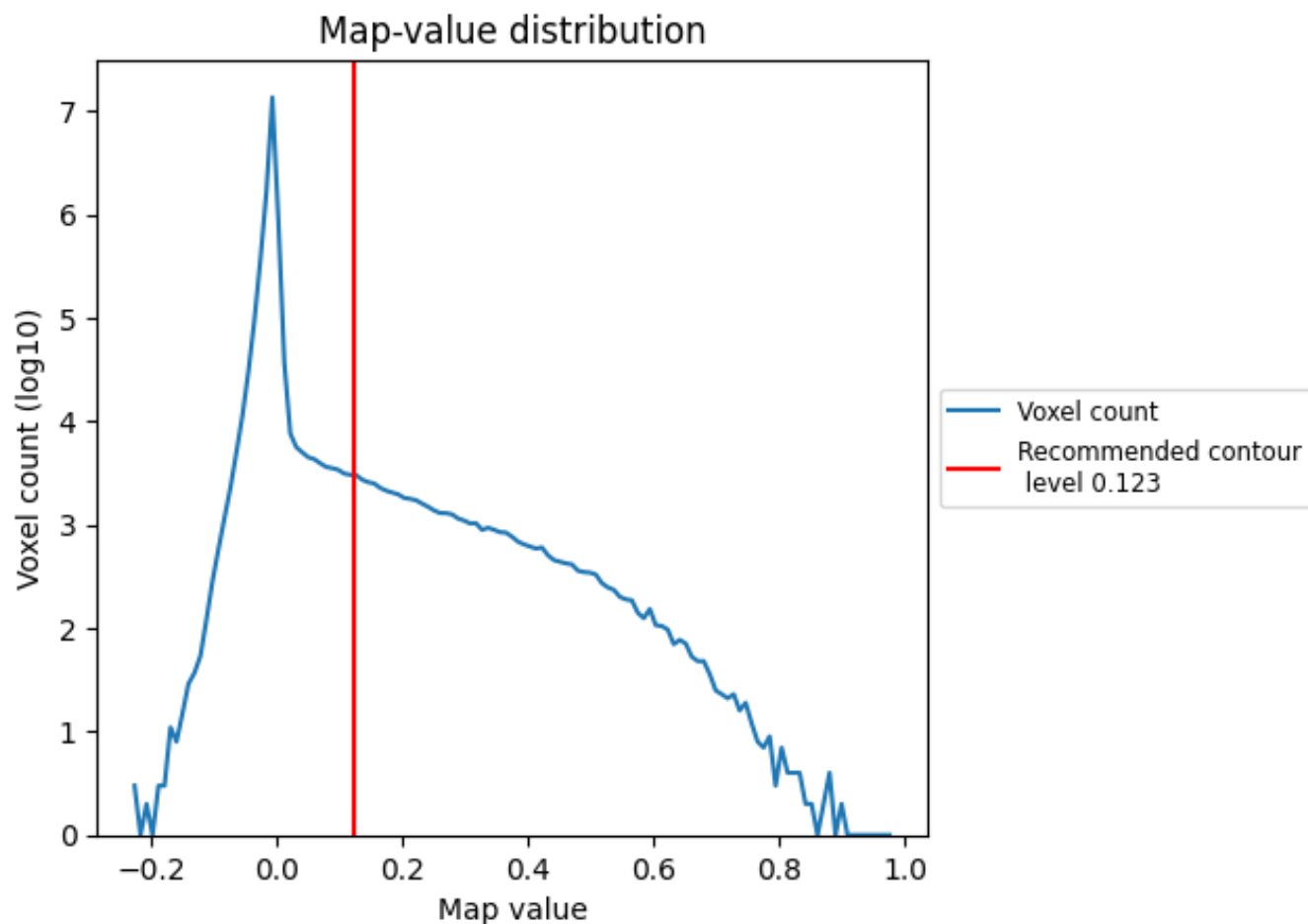
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

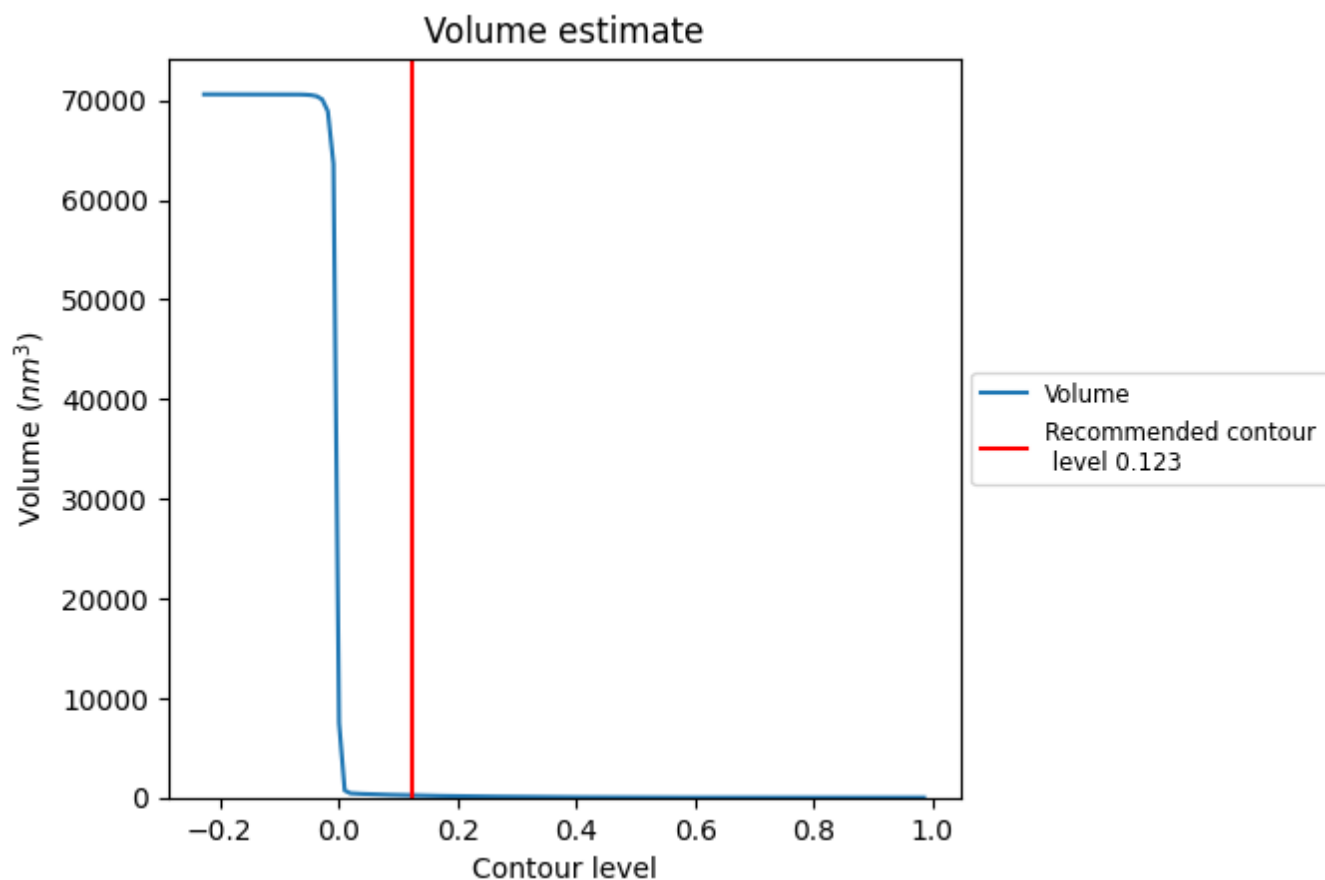
This section contains the results of statistical analysis of the map.

### 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](#)

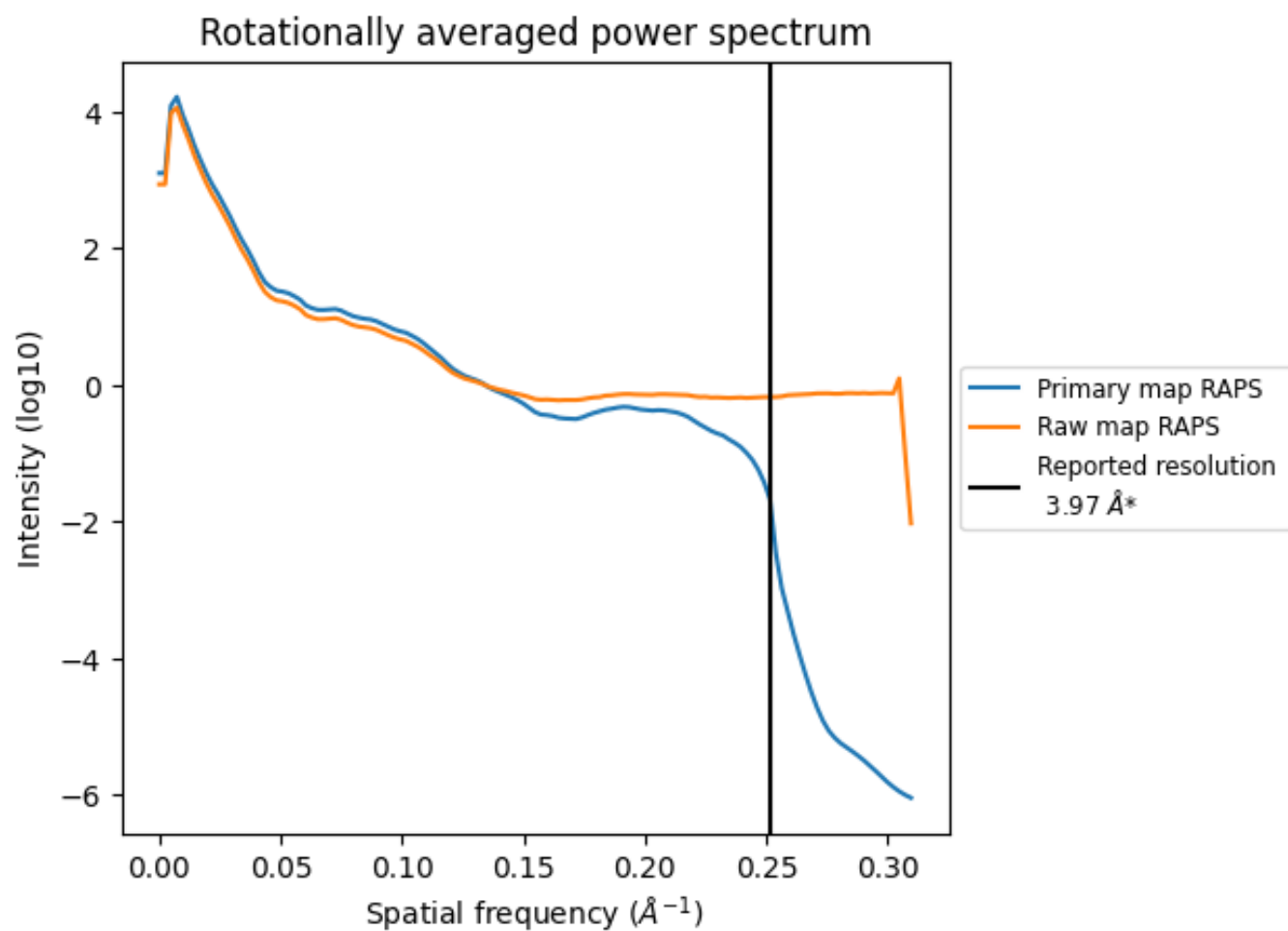


The volume at the recommended contour level is 223 nm<sup>3</sup>; this corresponds to an approximate mass of 202 kDa.

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 ⓘ

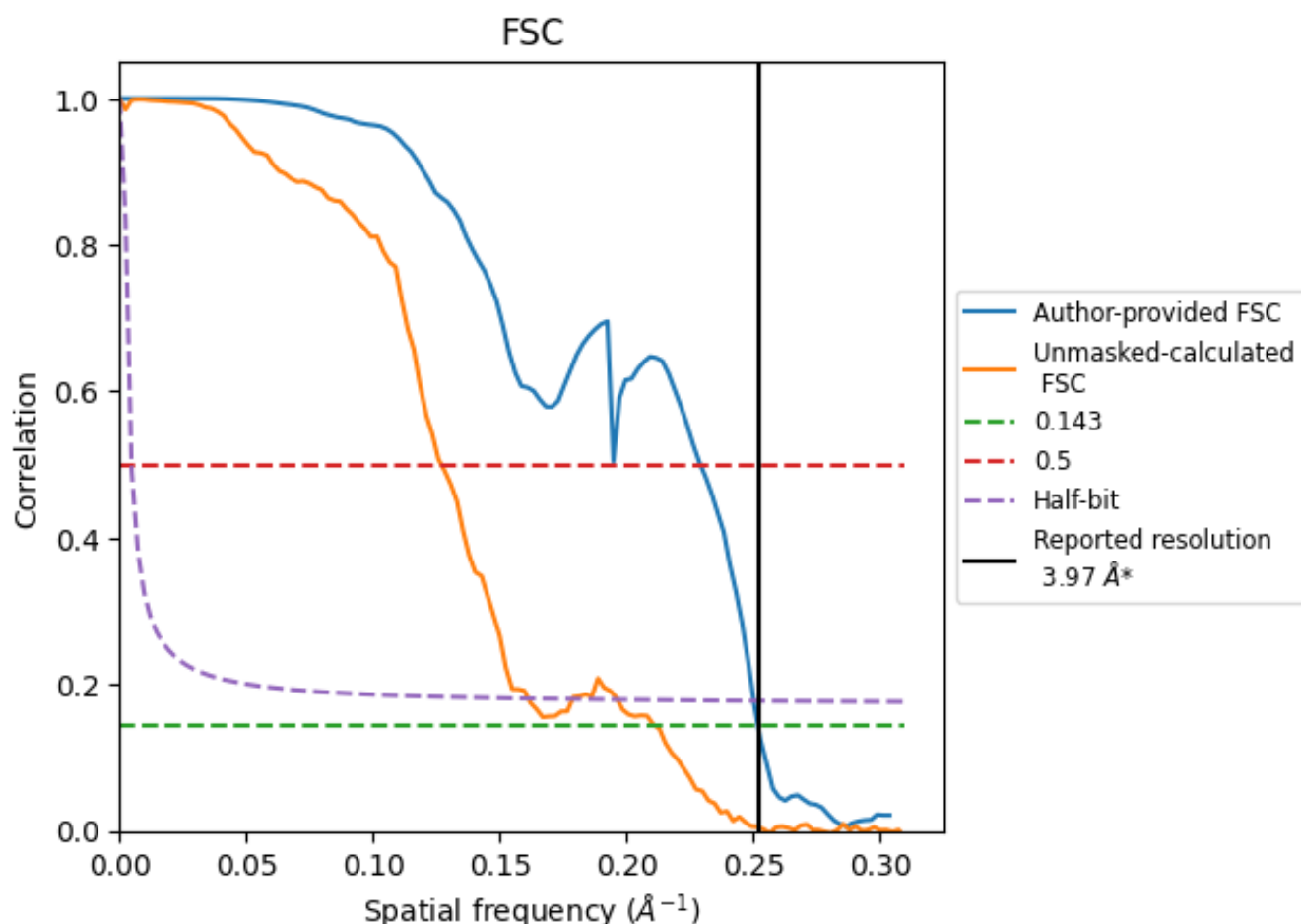


\*Reported resolution corresponds to spatial frequency of 0.252 Å<sup>-1</sup>

## 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 0.252 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

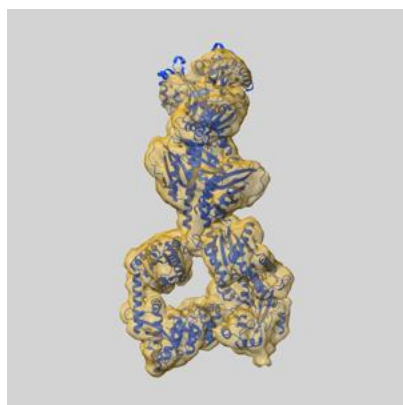
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.97	-	-
Author-provided FSC curve	3.97	4.36	4.00
Unmasked-calculated*	4.73	7.87	6.20

\*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 4.73 differs from the reported value 3.97 by more than 10 %

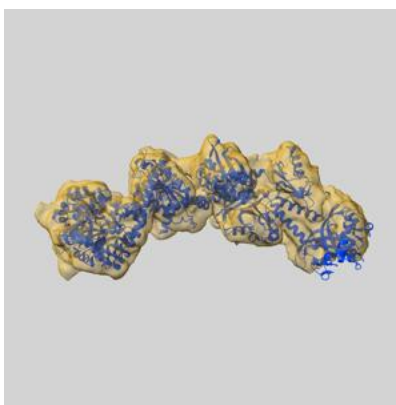
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45489 and PDB model 9CE0. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

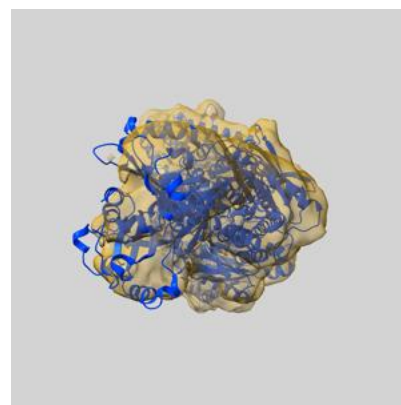
### 9.1 Map-model overlay [i](#)



X



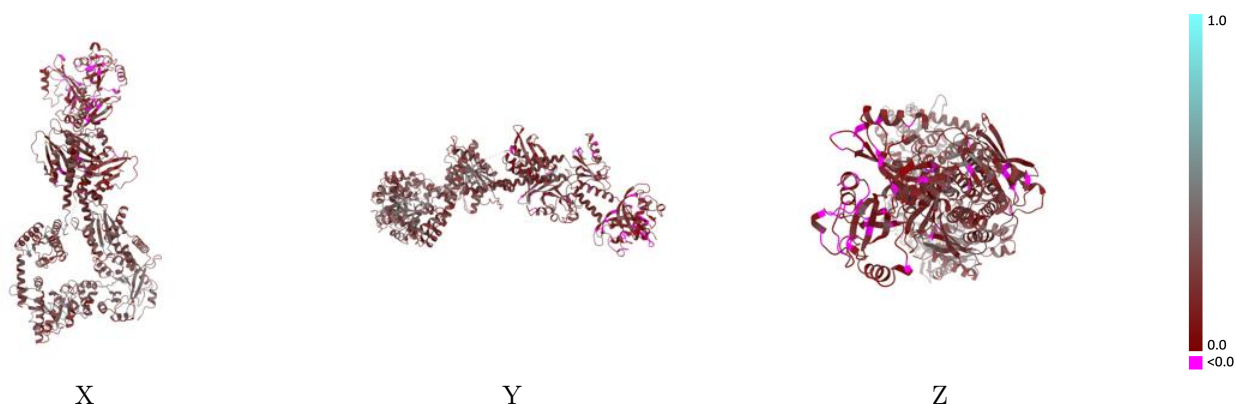
Y



Z

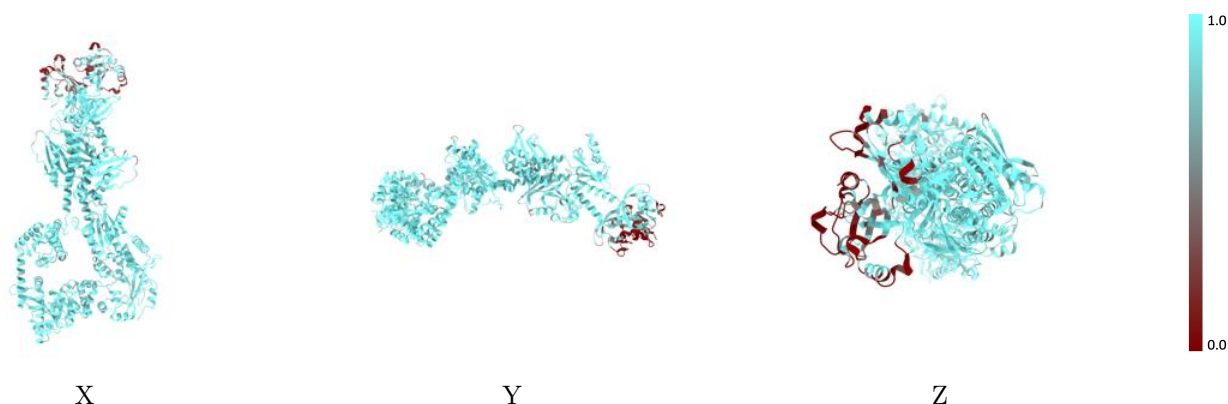
The images above show the 3D surface view of the map at the recommended contour level 0.123 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



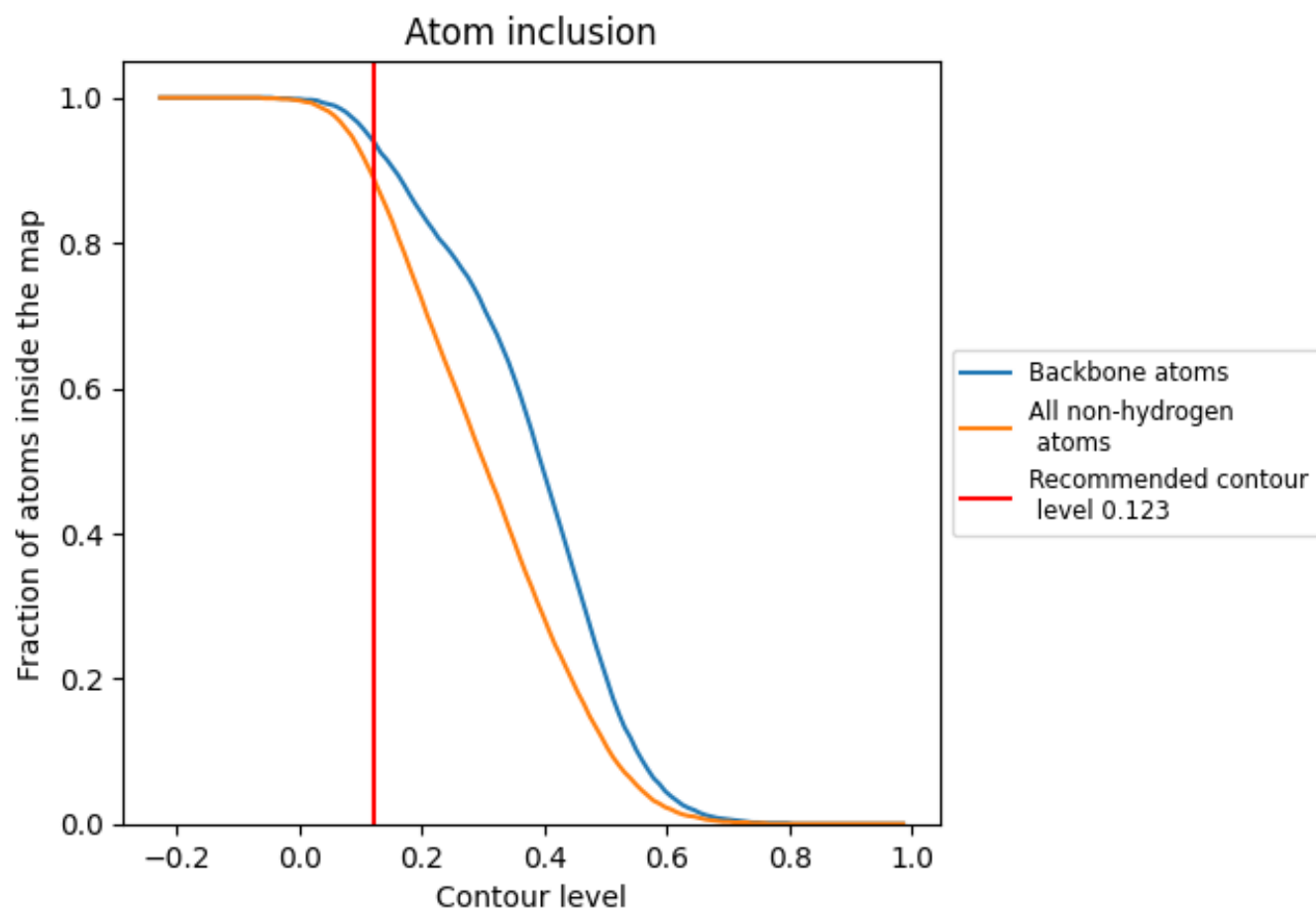
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.123).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 89% 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 (0.123) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8870	<div></div> 0.2480
A	<div></div> 0.8770	<div></div> 0.2490
B	<div></div> 0.8980	<div></div> 0.2470

