



## wwPDB EM Validation Summary Report ⓘ

May 19, 2025 – 11:08 AM EDT

PDB ID : 9E1P / pdb\_00009e1p  
EMDB ID : EMD-47416  
Title : Snf2h bound nucleosome complex - ClassB2  
Authors : Malik, D.; Deshmukh, A.A.; Bilokapic, S.; Halic, M.  
Deposited on : 2024-10-21  
Resolution : 3.25 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.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) : 2.43.1

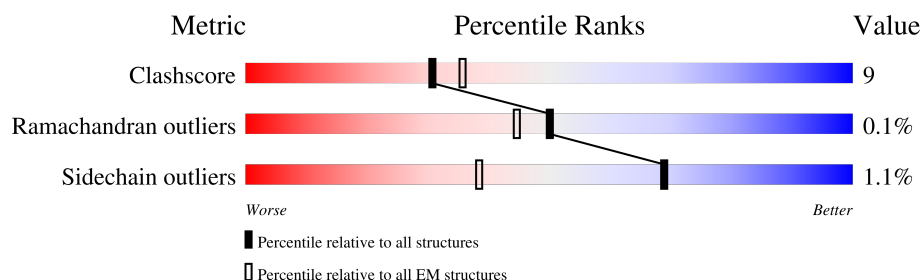
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.25 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	136	
1	E	136	
2	B	103	
2	F	103	
3	C	130	
3	G	130	
4	D	126	
4	H	126	

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Mol	Chain	Length	Quality of chain
5	I	152	<div><div></div><div>43%</div><div>55%</div><div></div></div>
6	J	152	<div><div></div><div>54%</div><div>45%</div><div></div></div>
7	W	1052	<div><div>5%</div><div>31%</div><div>11%</div><div>58%</div><div></div></div>

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 16007 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 Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	97	Total	C	N	O	S	1	0
			807	510	156	138	3		
1	E	96	Total	C	N	O	S	0	0
			790	499	151	137	3		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	85	Total	C	N	O	S	0	0
			679	428	135	115	1		
2	F	80	Total	C	N	O	S	0	0
			641	405	125	110	1		

- Molecule 3 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	109	Total	C	N	O	0	0
			837	526	165	146		
3	G	109	Total	C	N	O	0	0
			837	526	165	146		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	99	ARG	GLY	conflict	UNP P06897
C	123	SER	ALA	conflict	UNP P06897
G	99	ARG	GLY	conflict	UNP P06897
G	123	SER	ALA	conflict	UNP P06897

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	96	Total	C	N	O	S	0	0
			746	469	134	141	2		
4	H	96	Total	C	N	O	S	0	0
			756	475	138	141	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	29	THR	SER	engineered mutation	UNP P02281
H	29	THR	SER	engineered mutation	UNP P02281

- Molecule 5 is a DNA chain called DNA (152-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	152	Total	C	N	O	P	0	0
			3135	1482	591	910	152		

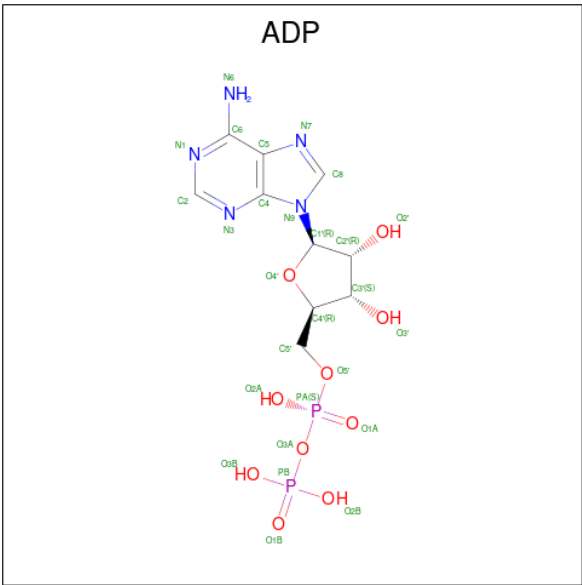
- Molecule 6 is a DNA chain called DNA (152-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	152	Total	C	N	O	P	0	0
			3096	1470	561	913	152		

- Molecule 7 is a protein called SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	W	444	Total	C	N	O	S	0	0
			3656	2340	643	650	23		

- Molecule 8 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).

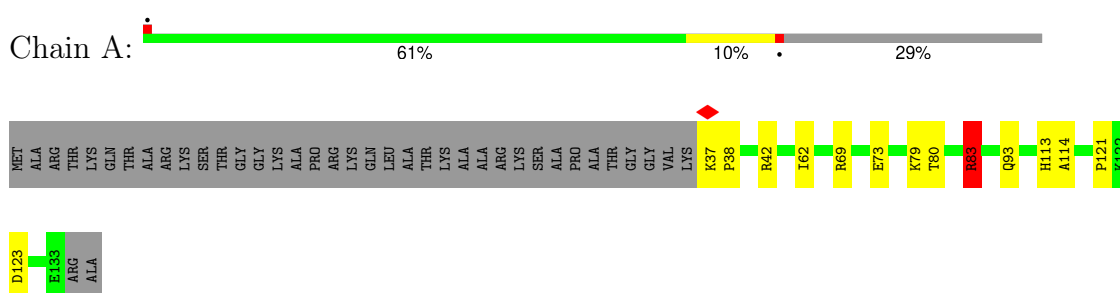


Mol	Chain	Residues	Atoms					AltConf
8	W	1	Total	C	N	O	P	0
			27	10	5	10	2	

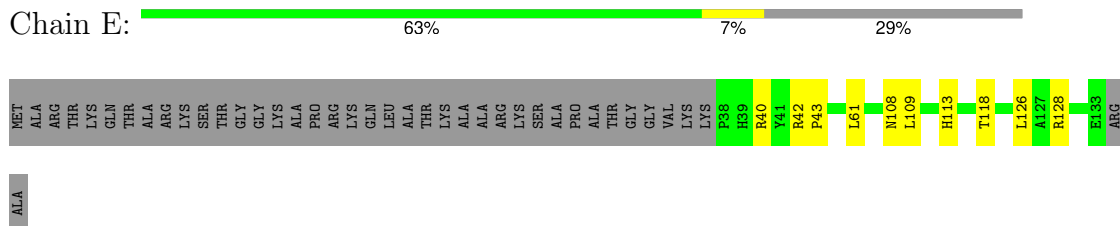
### 3 Residue-property plots [i](#)

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.

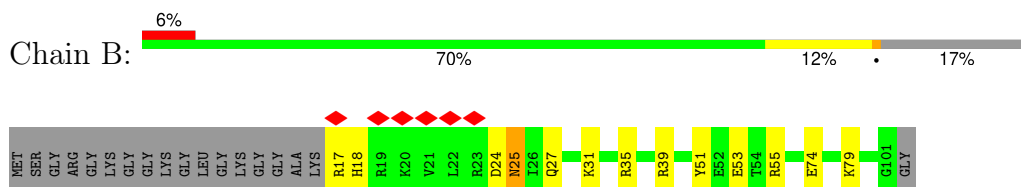
#### • Molecule 1: Histone H3.2



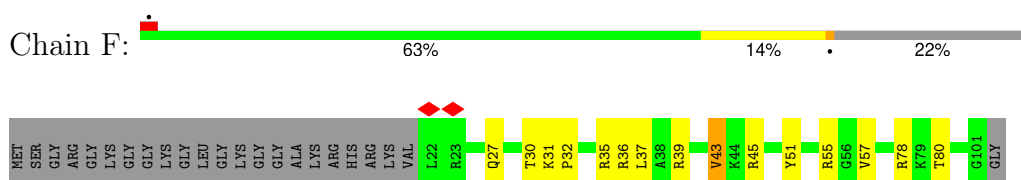
#### • Molecule 1: Histone H3.2



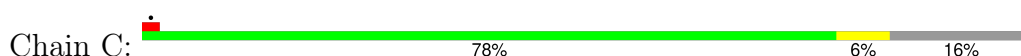
#### • Molecule 2: Histone H4

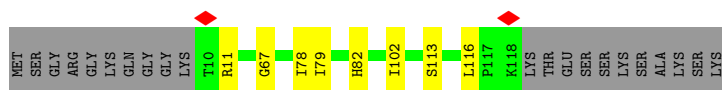


#### • Molecule 2: Histone H4

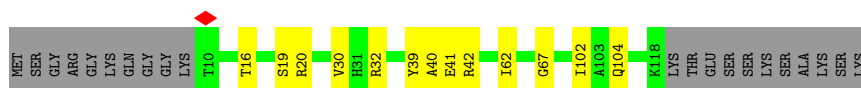


#### • Molecule 3: Histone H2A type 1

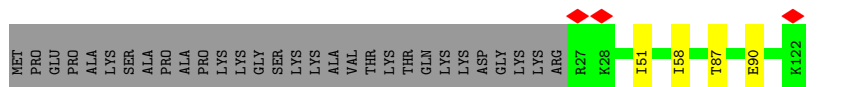




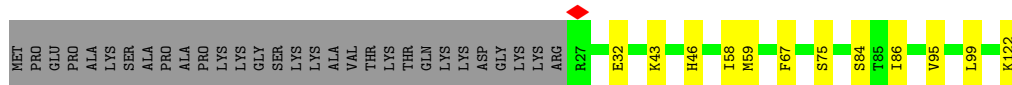
- Molecule 3: Histone H2A type 1



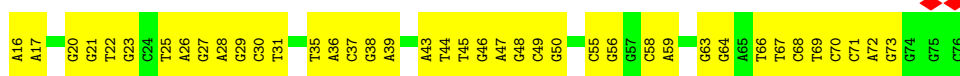
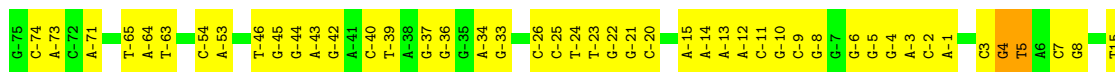
- Molecule 4: Histone H2B 1.1



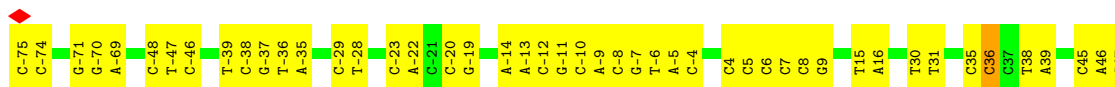
- Molecule 4: Histone H2B 1.1



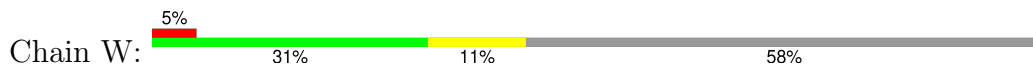
- Molecule 5: DNA (152-MER)



- Molecule 6: DNA (152-MER)



- Molecule 7: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family A member 5



MET	ILE	LYS	Q184	K298	R394	P493	R606	GLY	ASN	PRO	GLY	LEU	PRO	GLY	LEU	PRO	GLN
SER	PHE	PRO	V185	W302	R395	K494	F607	ALA	TYR	ARG	ARG	ASP	ASP	THR	THR	ASP	THR
ALA	ASP	GLY	R186	R302	R395	K495	T608	LYS	ALA	ASN	ALA	LYS	ASN	LYS	LYS	ASP	PHE
ALA	ASP	ARG	G187	R303	R395	K496	T609	THR	VAL	PRO	LYS	GLU	PRO	ASP	GLU	GLU	LYS
GLU	SER	PRO	L188	Y304	K397	K496	D610	ALA	ASP	LEU	ALA	ALA	LEU	ALA	ALA	ALA	ALA
PRO	GLY	ILE	N189	L305	A398	E497	N611	GLU	TYR	PRO	GLU	VAL	PRO	ASP	ASP	ASP	ASP
PRO	GLY	LYS	I192	I307	D399	S500	T612	MET	PHE	ASN	ASN	LEU	ASN	ILE	ILE	ILE	TYR
PRO	LYS	LYS	T202	K314	V400	L515	V618	GLU	ARG	ALA	ALA	GLU	ALA	ALA	ALA	ALA	ALA
PRO	GLN	ASP	G205	H315	E401	M520	D628	LYS	GLU	ALA	ALA	GLU	ALA	ALA	ALA	ALA	ALA
PRO	GLN	ASN	E206	E316	K402	R521	Q634	SER	ARG	LEU	LEU	SER	GLN	GLN	GLN	GLN	GLN
GLU	GLN	LEU	M207	R325	L404	R522	Q634	MET	GLY	GLY	GLY	GLU	GLY	GLY	GLY	GLY	GLY
SER	GLU	LEU	G208	K328	S403	Y524	Q634	LYS	GLY	GLY	GLY	GLU	GLY	GLY	GLY	GLY	GLY
PRO	ALA	LEU	L209	T329	L404	E525	T612	VAL	SER	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
SER	ASP	VAL	G210	T330	L404	L529	T612	ASP	ASP	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
PRO	THR	GLY	L213	L340	M429	G531	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
PRO	TYR	ASP	G220	L340	K430	P534	T612	LYS	LYS	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
ALA	GLU	TYR	Y221	E346	R430	R538	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ALA	GLU	HIS	R226	L347	ILE	ILE	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
SER	THR	ARG	N227	W348	ASP	ILE	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLY	ASP	GLN	I228	L354	ILE	ILE	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLY	ARG	GLN	M233	D357	LYS	LYS	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ASN	ALA	GLU	V234	R361	GLY	GLY	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
SER	ARG	ASP	L235	A362	LYS	LYS	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
SER	PHE	GLU	K238	D363	MET	MET	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ASN	TYR	LEU	L241	ASP	ASP	ASP	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLY	LEU	LEU	M245	PHE	ASP	ASP	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
PRO	GLY	THR	K249	TRP	TRP	TRP	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLU	GLN	SER	L255	ASP	ASP	ASP	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLY	THR	LYS	R256	PHE	PHE	PHE	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
VAL	ALA	ALA	S257	ASN	ASN	ASN	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ALA	ALA	ASN	I261	CYS	CYS	CYS	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLN	VAL	VAL	G262	LEU	LEU	LEU	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
VAL	PHE	CYS	D263	GLY	GLY	GLY	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
SER	ILE	ALA	D273	Q377	Q378	Q379	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ALA	ALA	ALA	E169	R167	R168	R169	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
SER	ALA	ALA	G170	F167	F168	F169	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLY	GLY	GLY	S173	T166	T167	T168	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
PRO	PRO	PRO	W177	CYS	CYS	CYS	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ASP	THR	THR	G178	VAL	VAL	VAL	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ALA	SER	SER	K179	E169	E169	E169	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLU	PRO	PRO	L180	D170	D170	D170	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
MET	GLU	GLU	R181	G173	G173	G173	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLU	LEU	LEU	K182	E173	E173	E173	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLU	MET	MET	Y183	D182	D182	D182	T612	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16200	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 ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	30.600	Depositor
Minimum map value	-0.316	Depositor
Average map value	-0.022	Depositor
Map value standard deviation	0.273	Depositor
Recommended contour level	4	Depositor
Map size (Å)	497.0, 497.0, 497.0	wwPDB
Map dimensions	497, 497, 497	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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	0.34	0/822	0.42	2/1102 (0.2%)
1	E	0.18	0/802	0.28	0/1076
2	B	0.21	0/687	0.39	0/921
2	F	0.18	0/648	0.30	0/868
3	C	0.16	0/847	0.24	0/1144
3	G	0.15	0/847	0.27	0/1144
4	D	0.14	0/757	0.29	0/1018
4	H	0.15	0/767	0.27	0/1029
5	I	0.28	0/3521	0.43	2/5437 (0.0%)
6	J	0.27	0/3468	0.45	1/5345 (0.0%)
7	W	0.17	0/3733	0.35	0/5041
All	All	0.23	0/16899	0.38	5/24125 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	4	DG	C2'-C3'-O3'	-9.65	97.02	111.50
5	I	5	DT	C4'-C3'-O3'	-5.77	101.34	110.00
1	A	83[A]	ARG	CA-C-O	5.52	126.66	120.70
1	A	83[B]	ARG	CA-C-O	5.52	126.66	120.70
6	J	36	DC	C2'-C3'-O3'	-5.16	103.76	111.50

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	A	807	0	851	11	0
1	E	790	0	826	12	0
2	B	679	0	717	11	0
2	F	641	0	684	11	0
3	C	837	0	891	7	0
3	G	837	0	891	15	0
4	D	746	0	764	3	0
4	H	756	0	786	13	0
5	I	3135	0	1704	67	0
6	J	3096	0	1706	57	0
7	W	3656	0	3730	86	0
8	W	27	0	12	7	0
All	All	16007	0	13562	255	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 255 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)
7:W:238:LYS:NZ	7:W:261:ILE:HD11	1.63	1.12
7:W:238:LYS:HZ2	7:W:261:ILE:HD11	1.29	0.88
7:W:238:LYS:HZ1	7:W:261:ILE:HD11	1.39	0.84
7:W:455:LYS:HB2	7:W:462:LEU:HD12	1.65	0.78
5:I:4:DG:H2"	5:I:5:DT:H71	1.65	0.78

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	96/136 (71%)	93 (97%)	3 (3%)	0	100	100
1	E	94/136 (69%)	90 (96%)	4 (4%)	0	100	100
2	B	83/103 (81%)	81 (98%)	2 (2%)	0	100	100
2	F	78/103 (76%)	76 (97%)	2 (3%)	0	100	100
3	C	107/130 (82%)	106 (99%)	1 (1%)	0	100	100
3	G	107/130 (82%)	103 (96%)	4 (4%)	0	100	100
4	D	94/126 (75%)	92 (98%)	2 (2%)	0	100	100
4	H	94/126 (75%)	93 (99%)	1 (1%)	0	100	100
7	W	438/1052 (42%)	405 (92%)	32 (7%)	1 (0%)	44	71
All	All	1191/2042 (58%)	1139 (96%)	51 (4%)	1 (0%)	50	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	W	566	ILE

### 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	A	86/111 (78%)	83 (96%)	3 (4%)	31	56
1	E	84/111 (76%)	84 (100%)	0	100	100
2	B	69/79 (87%)	67 (97%)	2 (3%)	37	61
2	F	66/79 (84%)	65 (98%)	1 (2%)	60	75
3	C	85/102 (83%)	85 (100%)	0	100	100
3	G	85/102 (83%)	84 (99%)	1 (1%)	67	79
4	D	80/106 (76%)	80 (100%)	0	100	100
4	H	82/106 (77%)	82 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	W	409/939 (44%)	403 (98%)	6 (2%)	60	75
All	All	1046/1735 (60%)	1033 (99%)	13 (1%)	69	79

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	W	207	MET
7	W	256	ARG
7	W	591	ASP
7	W	391	PHE
7	W	515	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
7	W	598	GLN
7	W	184	GLN
4	H	44	GLN
1	E	108	ASN
4	H	79	HIS

### 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](#)

1 ligand is 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	$\# Z  > 2$
8	ADP	W	1101	-	24,29,29	0.88	0	29,45,45	1.15	2 (6%)

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
8	ADP	W	1101	-	-	1/12/32/32	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	W	1101	ADP	N3-C2-N1	-3.51	123.91	128.67
8	W	1101	ADP	C4-C5-N7	-2.56	106.63	109.34

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	W	1101	ADP	C4'-C5'-O5'-PA

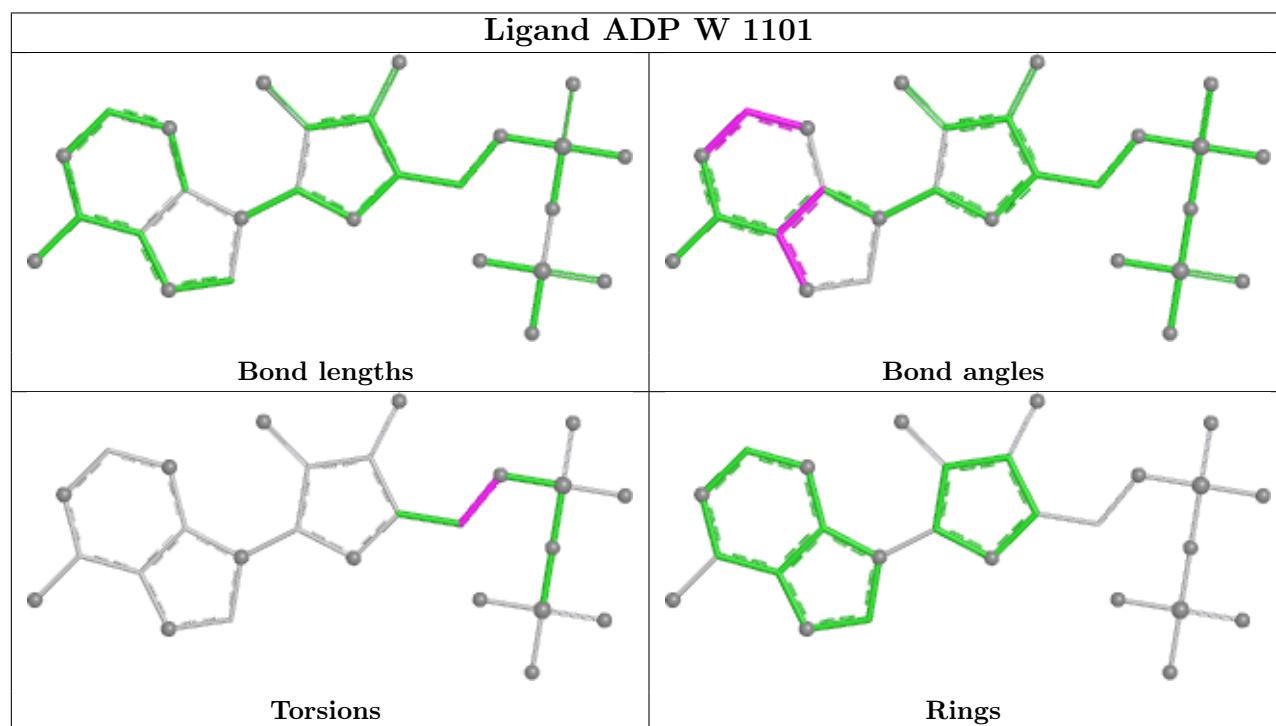
There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	W	1101	ADP	7	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.

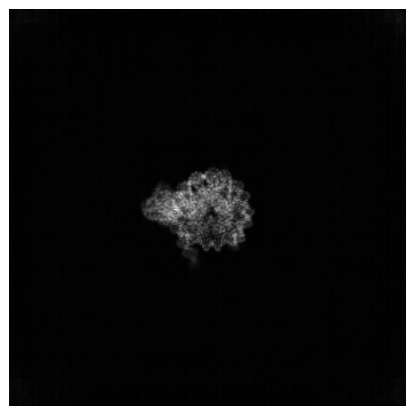
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47416. These allow visual inspection of the internal detail of the map and identification of artifacts.

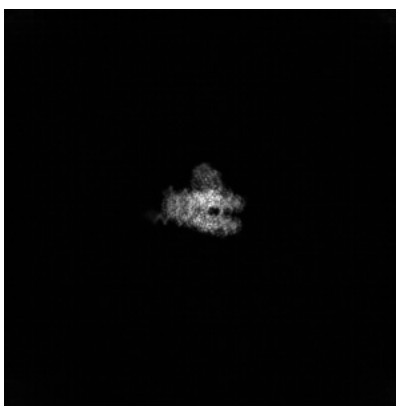
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

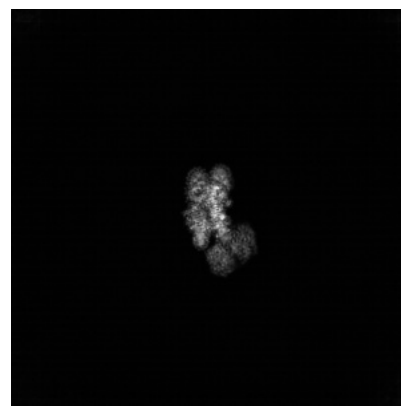
#### 6.1.1 Primary map



X

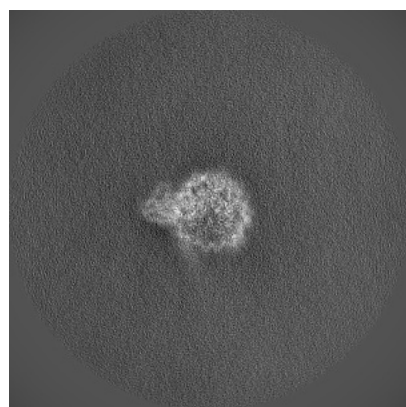


Y

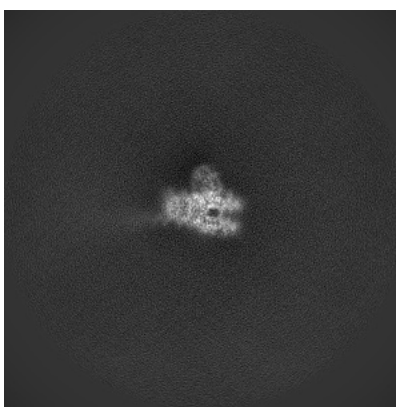


Z

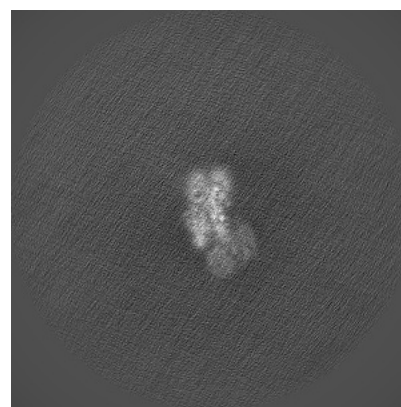
#### 6.1.2 Raw map



X



Y

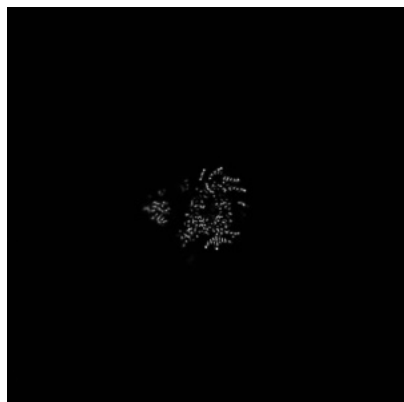


Z

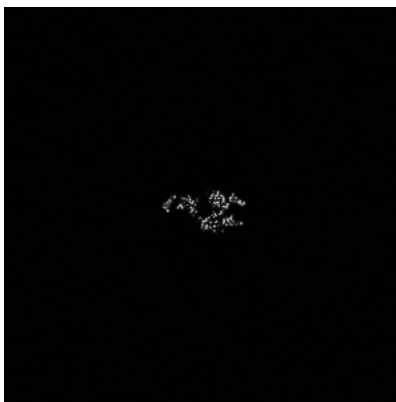
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

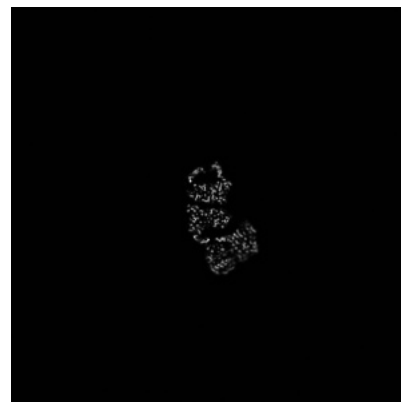
### 6.2.1 Primary map



X Index: 248

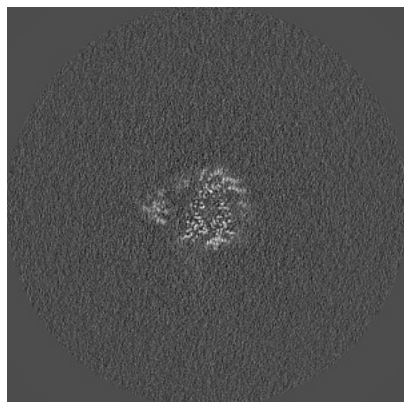


Y Index: 248

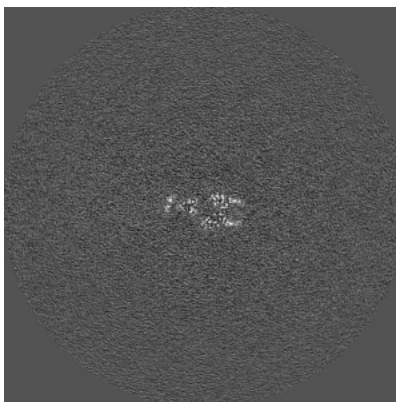


Z Index: 248

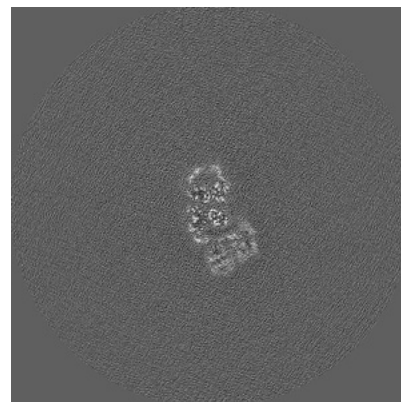
### 6.2.2 Raw map



X Index: 192



Y Index: 192

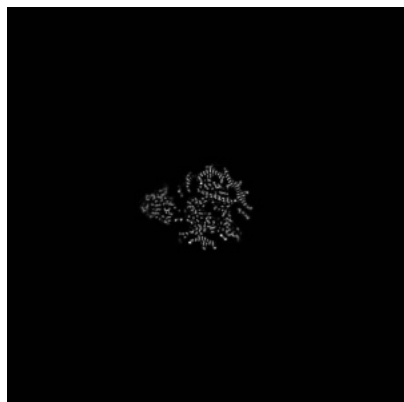


Z Index: 192

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

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

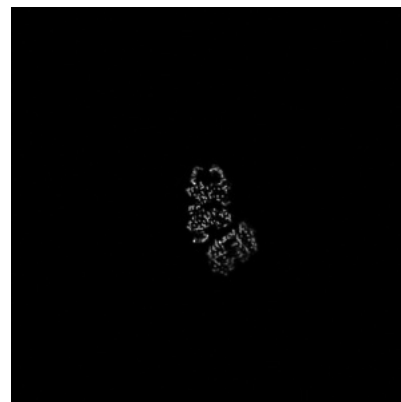
### 6.3.1 Primary map



X Index: 254

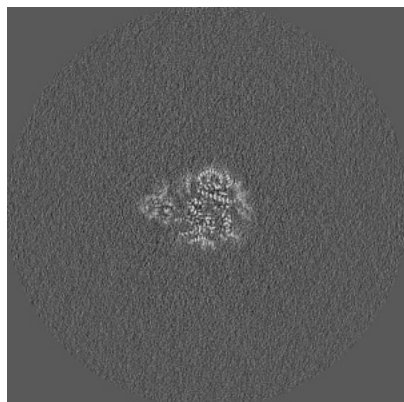


Y Index: 274

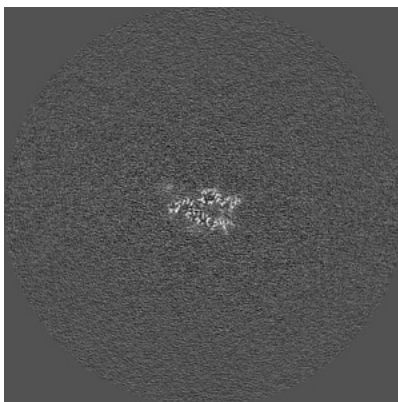


Z Index: 251

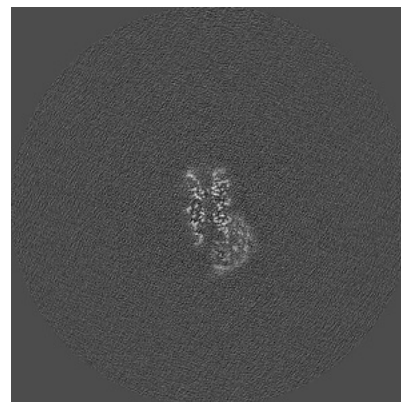
### 6.3.2 Raw map



X Index: 196



Y Index: 211



Z Index: 198

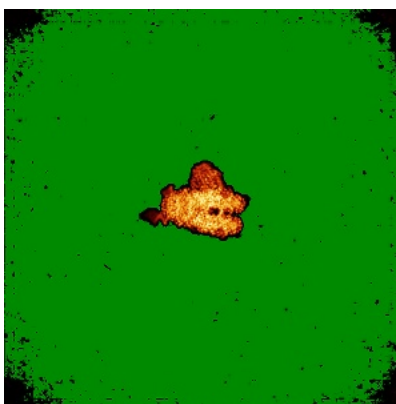
The images above show the largest variance slices of the map in three orthogonal directions.

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

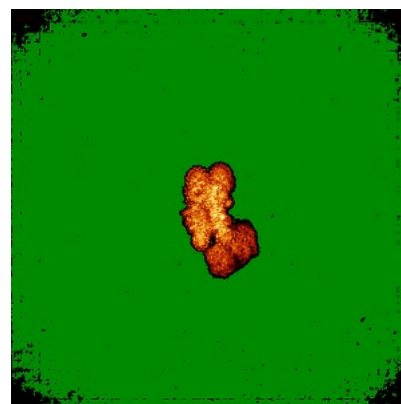
### 6.4.1 Primary map



X

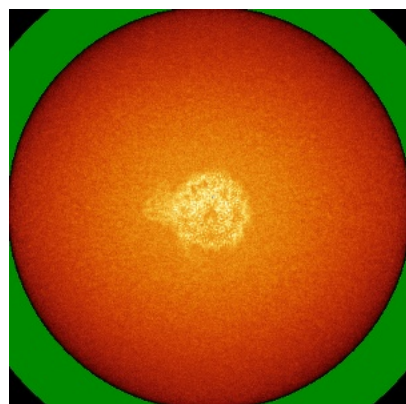


Y

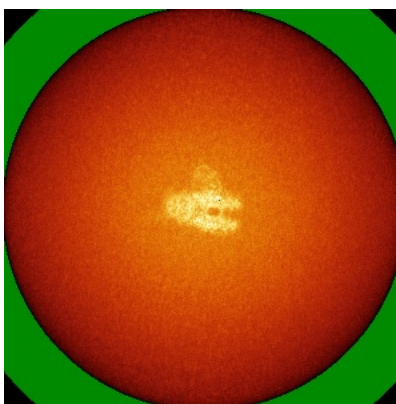


Z

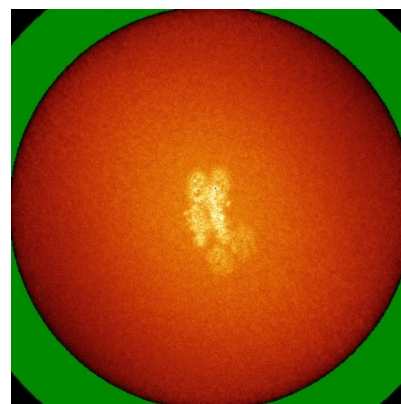
### 6.4.2 Raw map



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.

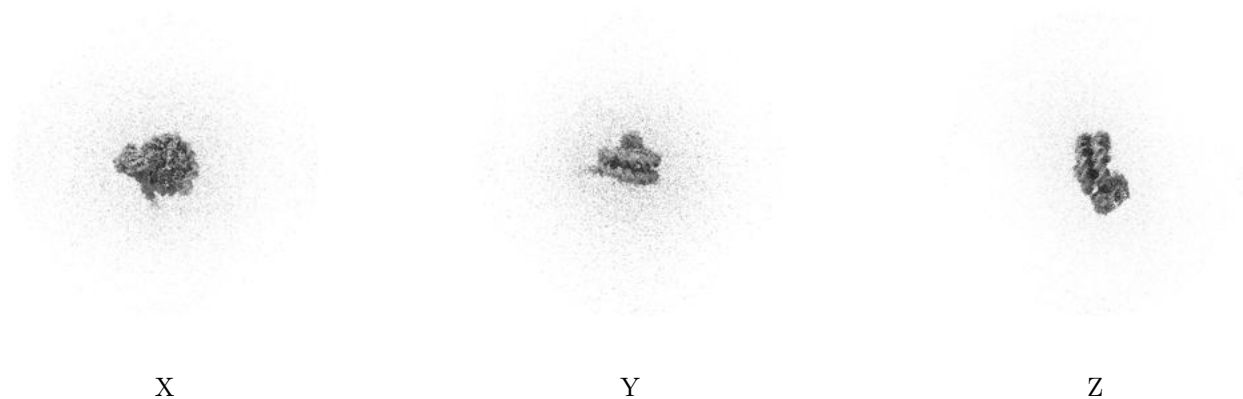
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. 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.

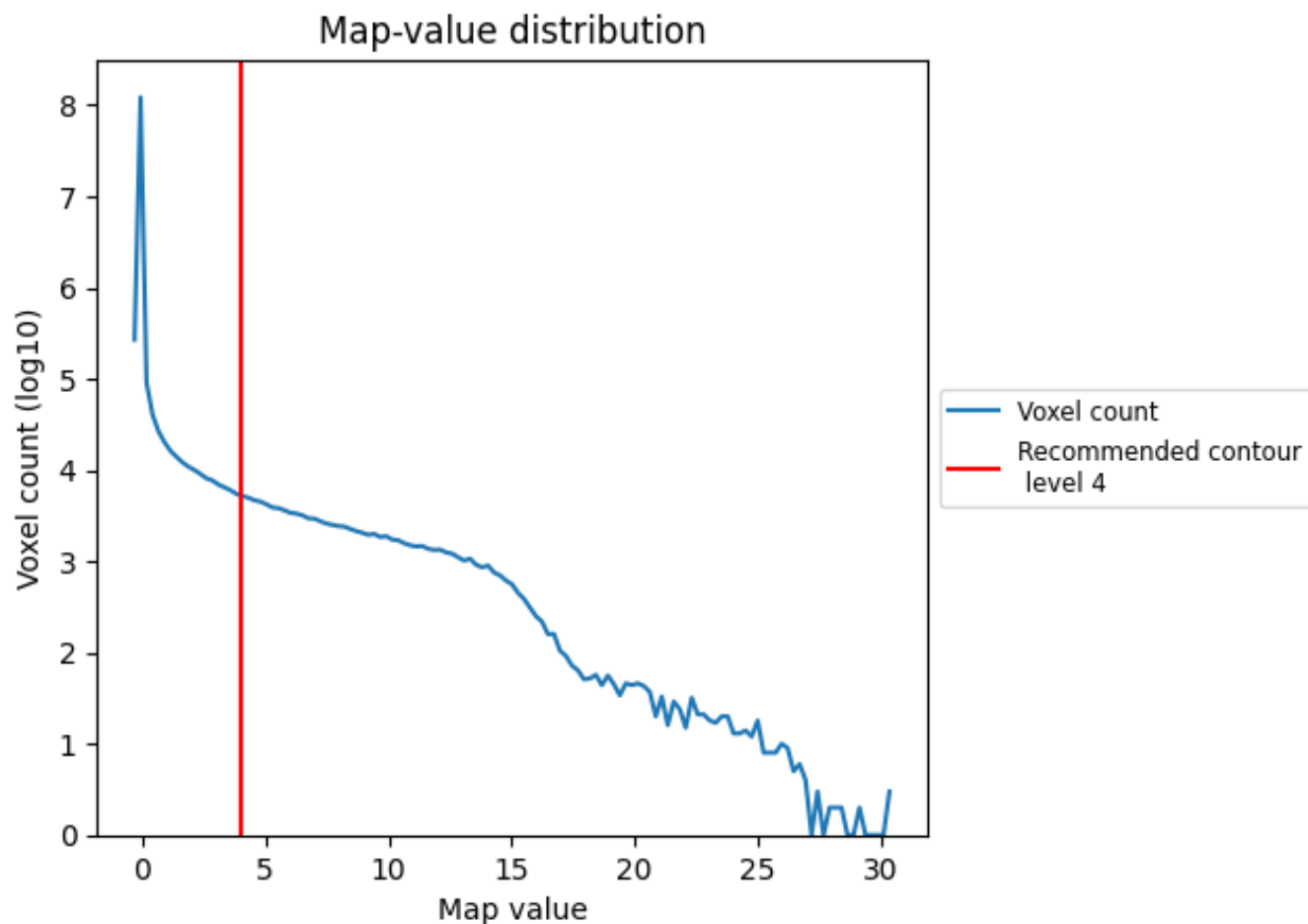
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

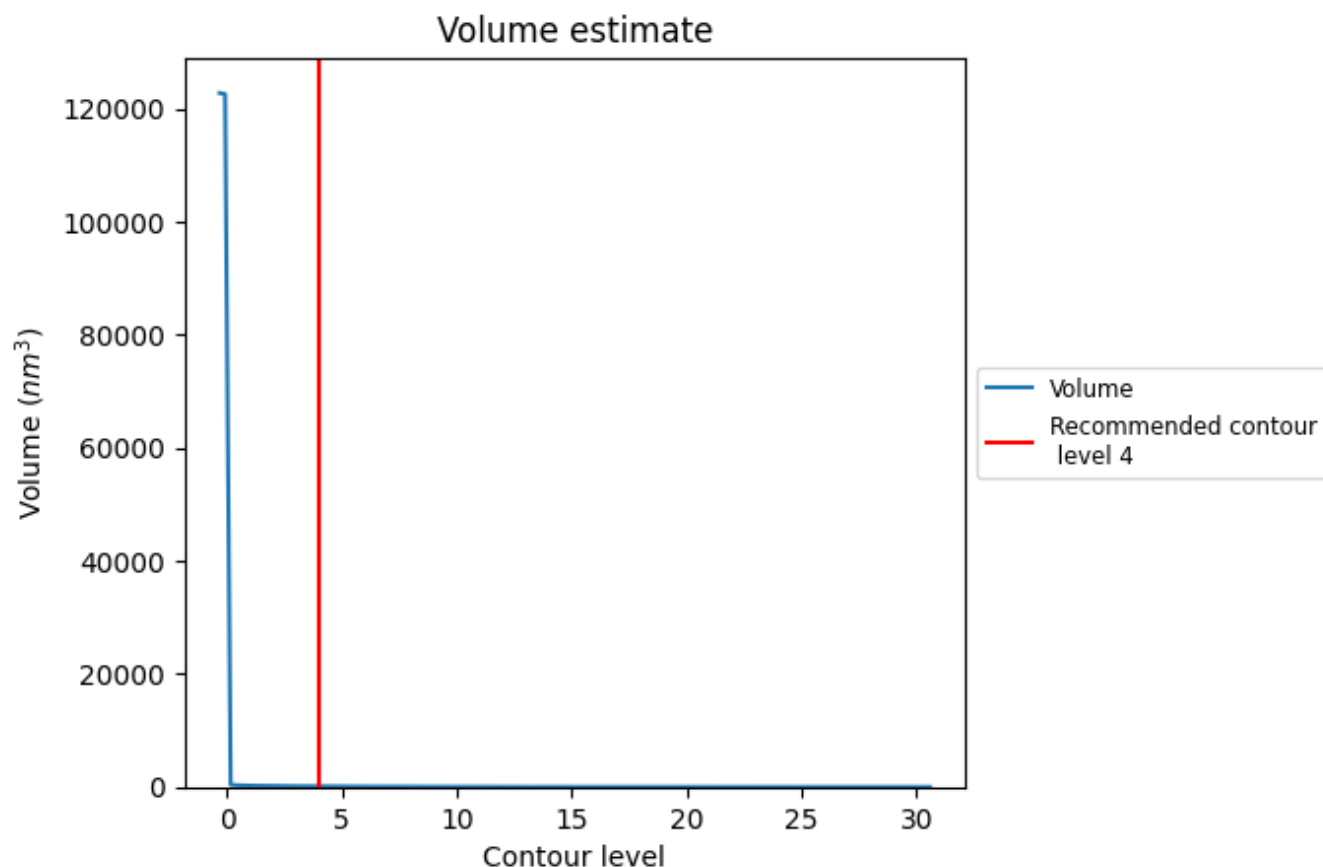
This section contains the results of statistical analysis of the map.

### 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.

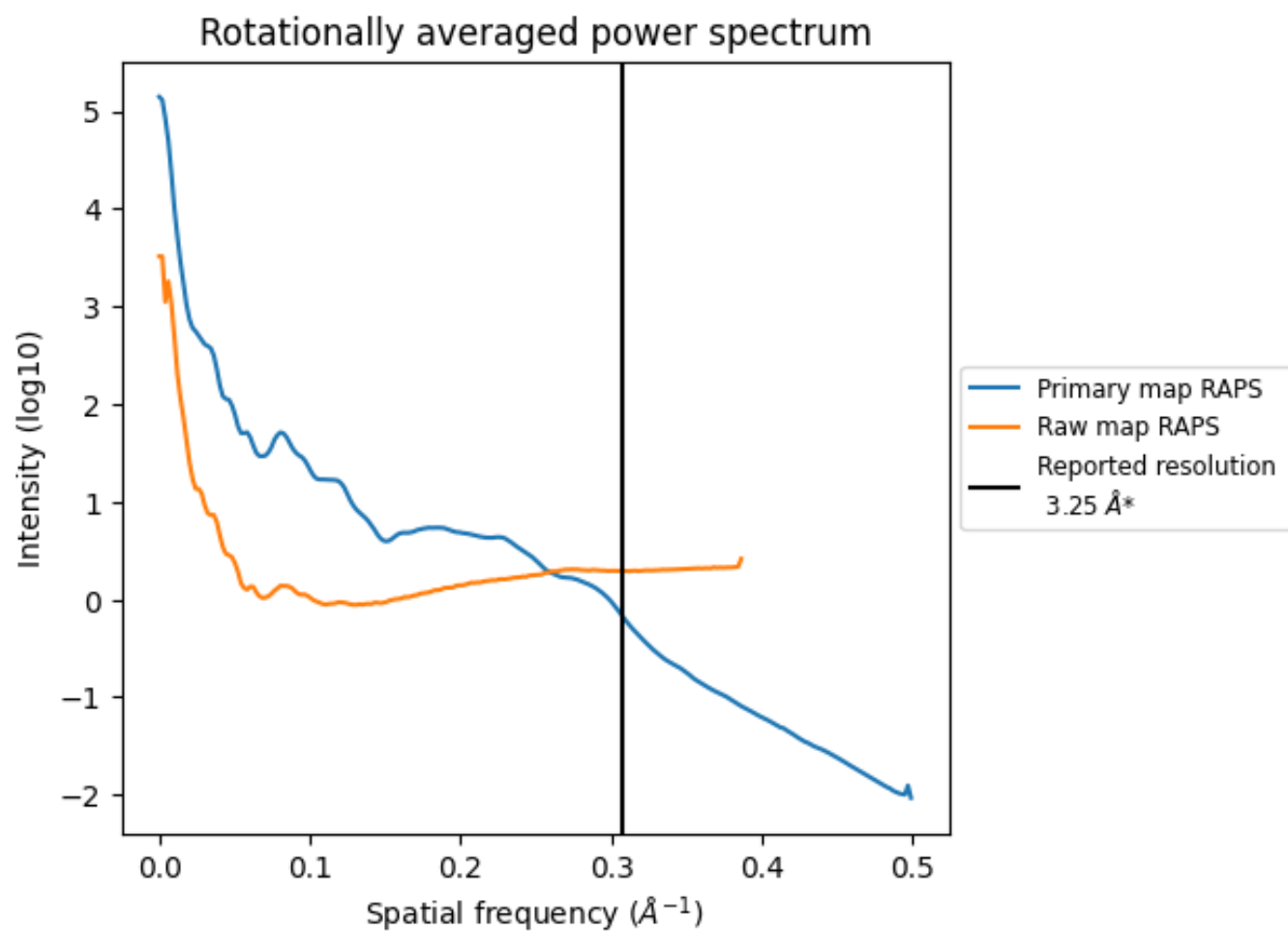
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 107  $\text{nm}^3$ ; this corresponds to an approximate mass of 97 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 ⓘ

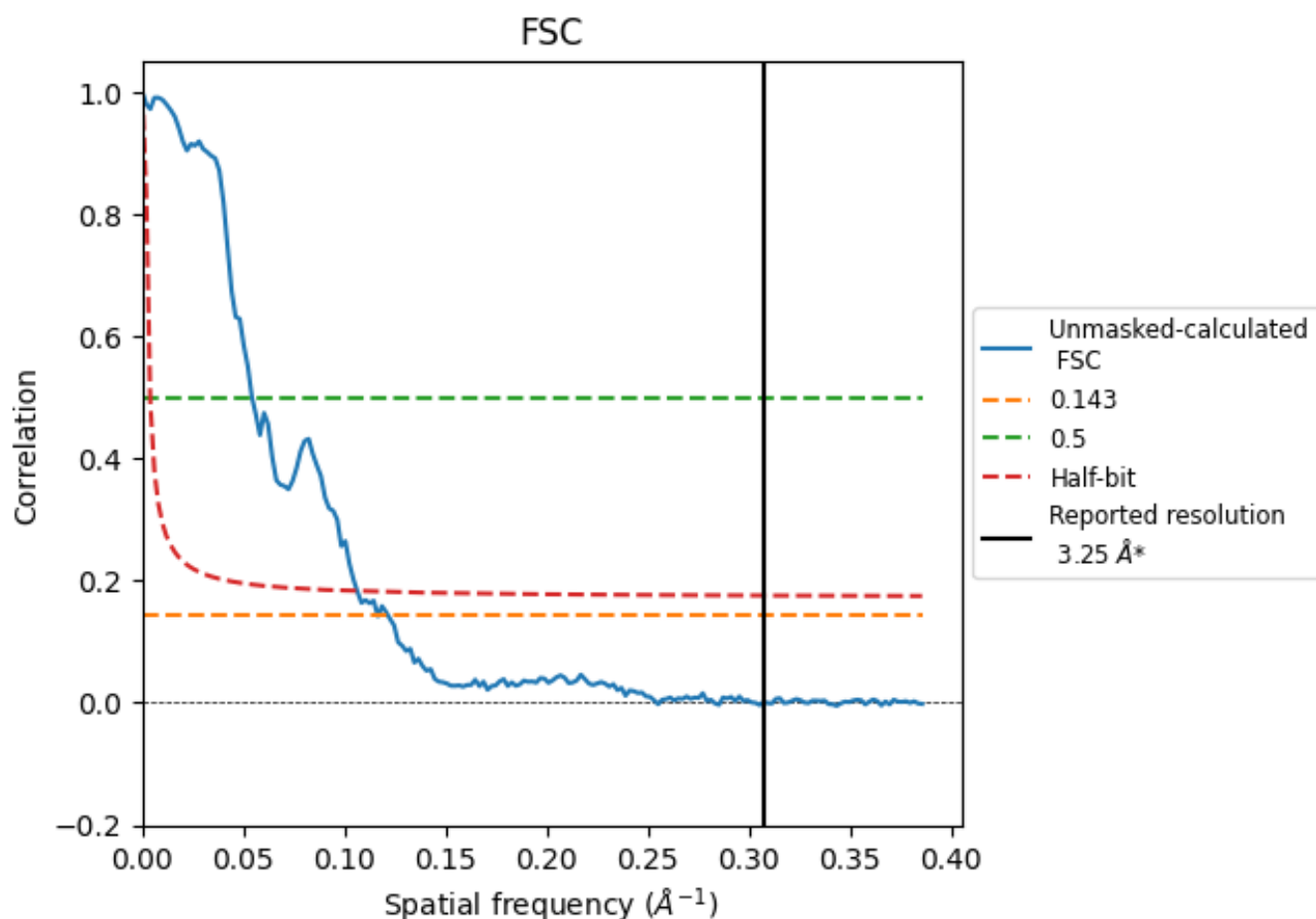


\*Reported resolution corresponds to spatial frequency of 0.308 Å<sup>-1</sup>

## 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 0.308 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

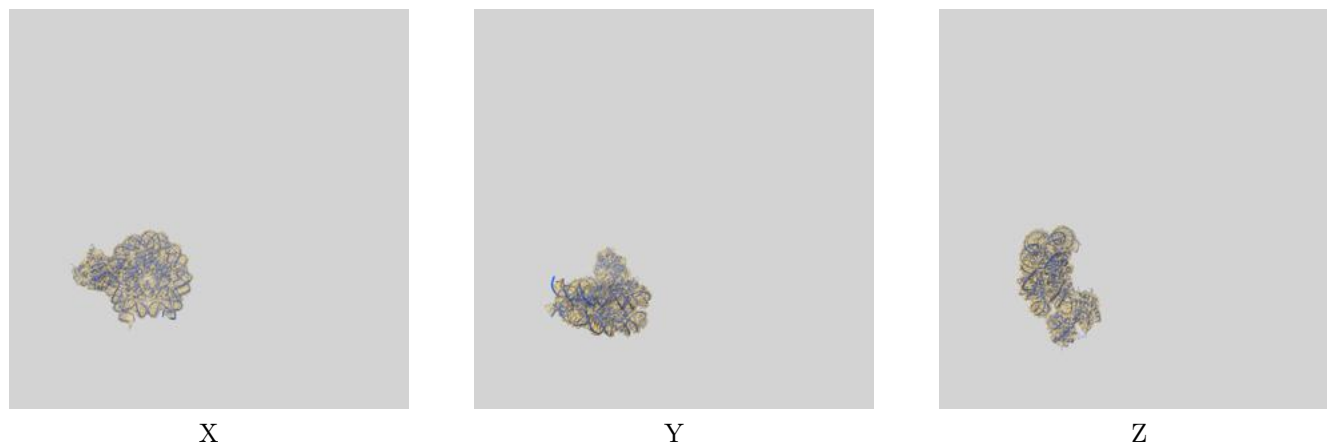
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.25	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.60	18.45	9.41

\*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 8.60 differs from the reported value 3.25 by more than 10 %

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

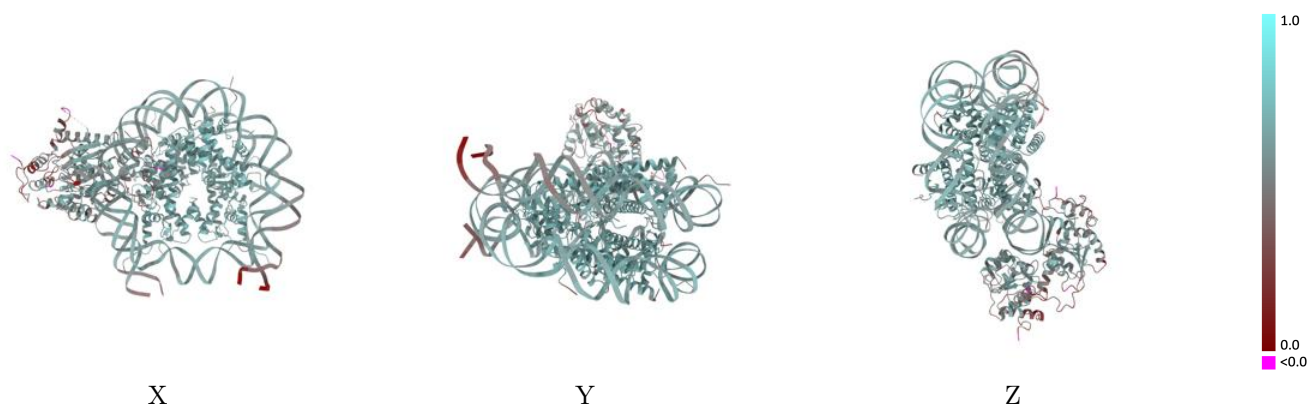
This section contains information regarding the fit between EMDB map EMD-47416 and PDB model 9E1P. Per-residue inclusion information can be found in section [3](#) on page [7](#).

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



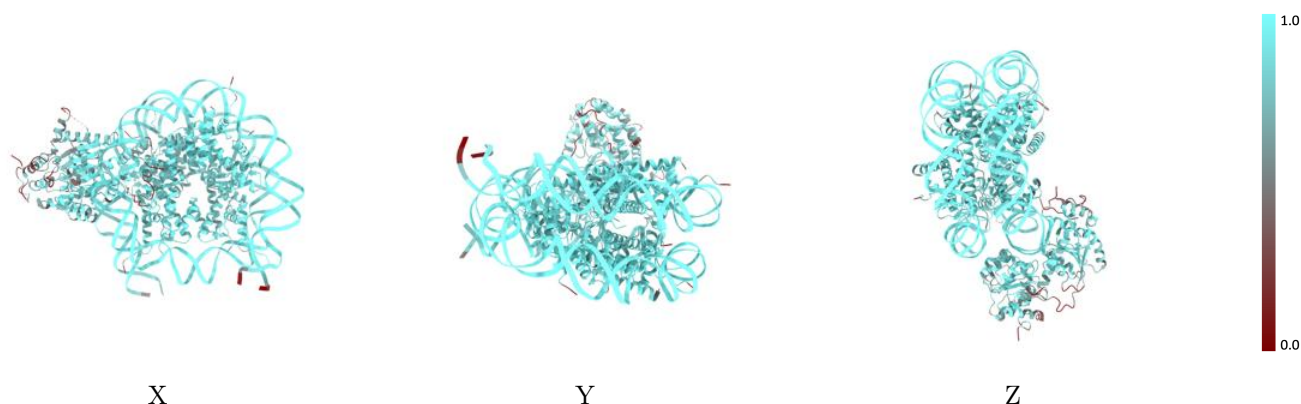
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



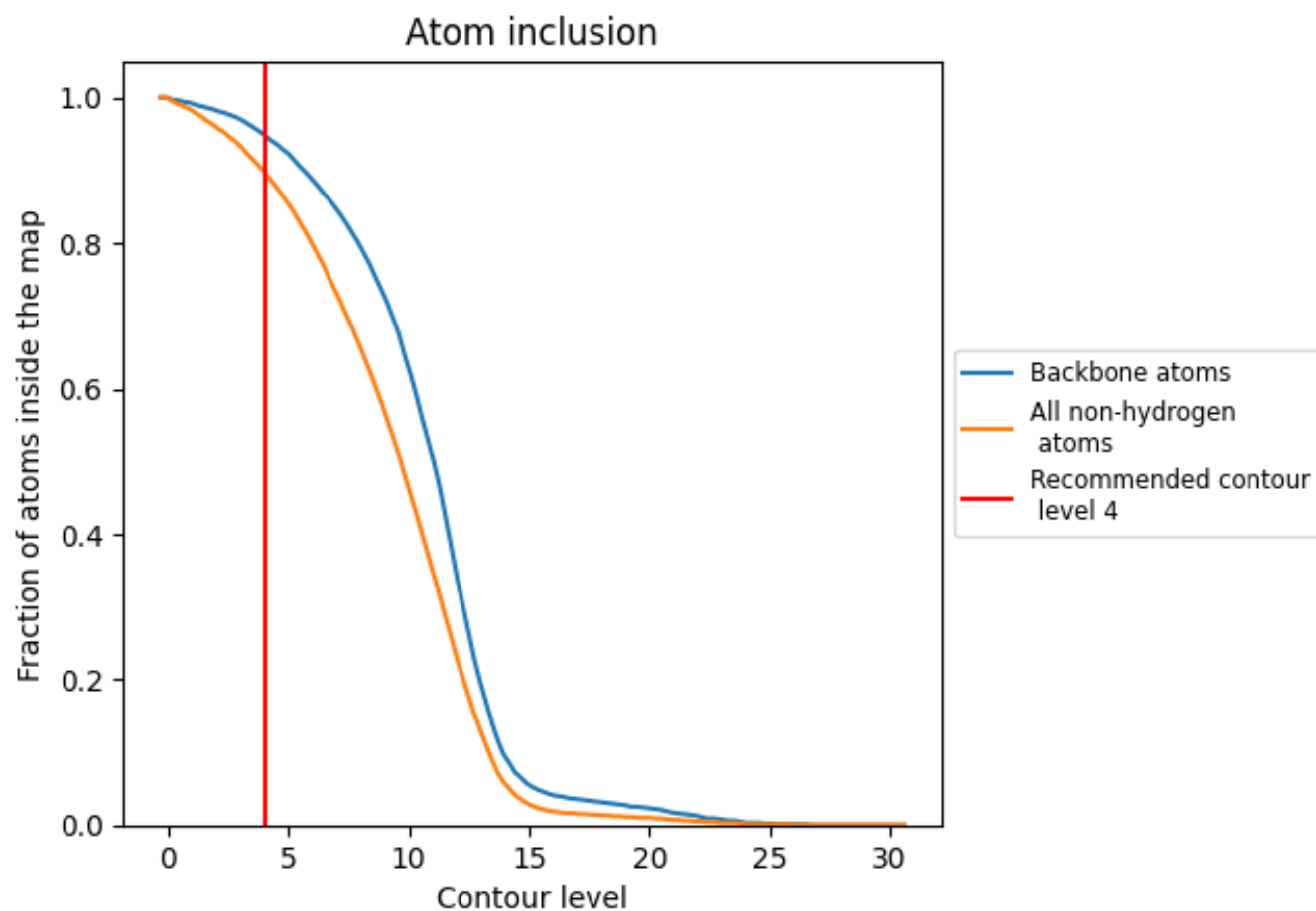
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 90% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8980</div>	<div><div></div>0.5760</div>
A	<div><div></div>0.9420</div>	<div><div></div>0.6420</div>
B	<div><div></div>0.9020</div>	<div><div></div>0.6300</div>
C	<div><div></div>0.9420</div>	<div><div></div>0.6430</div>
D	<div><div></div>0.9340</div>	<div><div></div>0.6390</div>
E	<div><div></div>0.9590</div>	<div><div></div>0.6530</div>
F	<div><div></div>0.9530</div>	<div><div></div>0.6560</div>
G	<div><div></div>0.9400</div>	<div><div></div>0.6470</div>
H	<div><div></div>0.9290</div>	<div><div></div>0.6390</div>
I	<div><div></div>0.9510</div>	<div><div></div>0.5670</div>
J	<div><div></div>0.9560</div>	<div><div></div>0.5740</div>
W	<div><div></div>0.7350</div>	<div><div></div>0.4730</div>

1.0

0.0

<0.0