



wwPDB EM Validation Summary Report ⓘ

May 25, 2025 – 10:26 PM EDT

PDB ID : 9E1Q / pdb_00009e1q
EMDB ID : EMD-47417
Title : Snf2h bound nucleosome complex - ClassB3
Authors : Malik, D.; Deshmukh, A.A.; Bilokapic, S.; Halic, M.
Deposited on : 2024-10-21
Resolution : 3.10 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.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

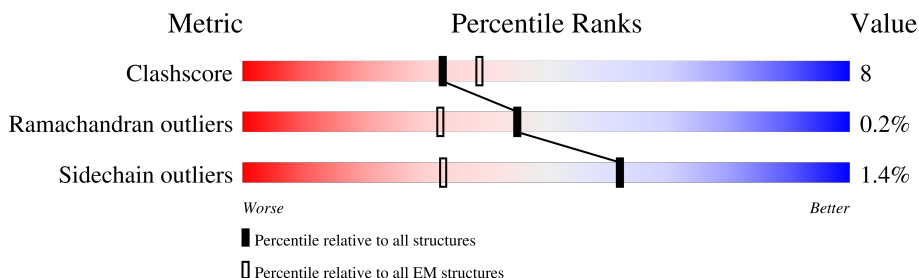
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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 ≥ 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>51%</div><div>48%</div><div></div></div>
6	J	152	<div><div></div><div>43%</div><div>57%</div><div></div></div>
7	W	1052	<div><div></div><div>32%</div><div>10%</div><div>58%</div><div></div></div>

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 15999 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	0	0
			799	505	153	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: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).

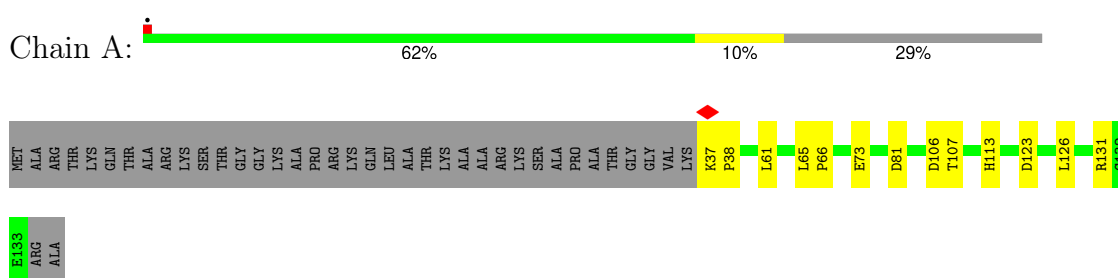


Mol	Chain	Residues	Atoms					AltConf
8	W	1	Total	C	N	O	P	0
			27	10	5	10	2	

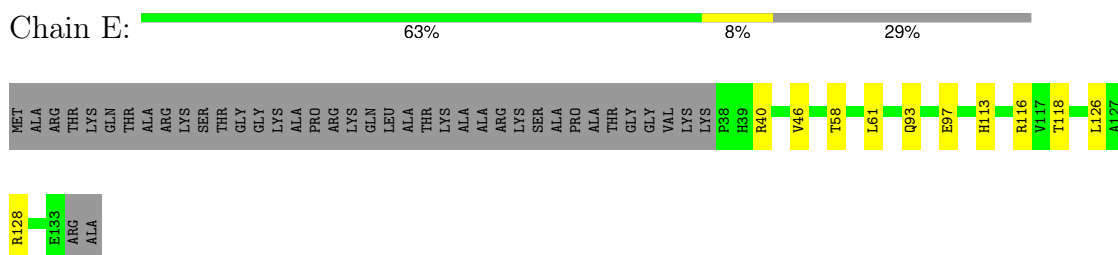
3 Residue-property plots [i](#)

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.

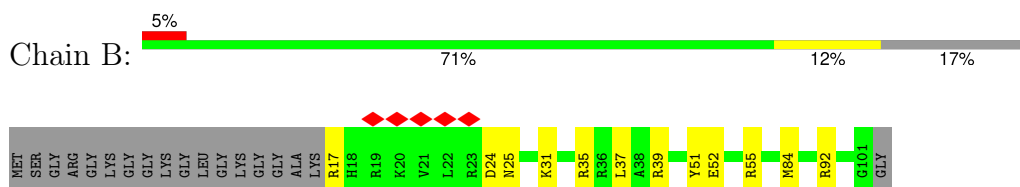
- Molecule 1: Histone H3.2



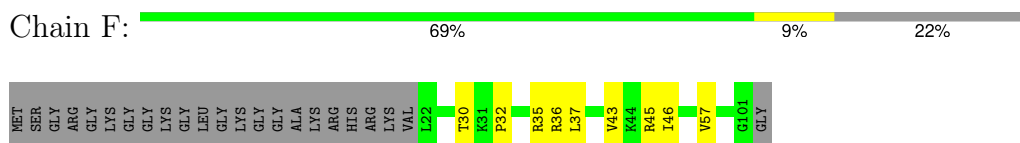
- Molecule 1: Histone H3.2



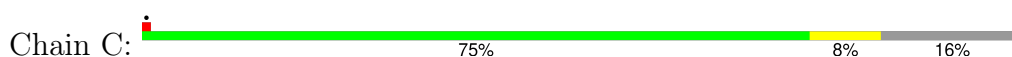
- Molecule 2: Histone H4



- Molecule 2: Histone H4



- Molecule 3: Histone H2A type 1

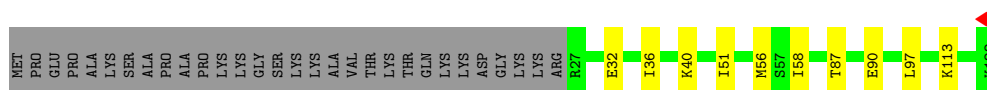




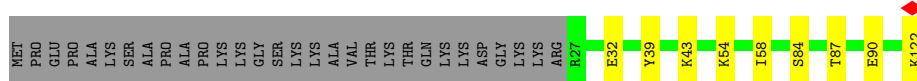
- Molecule 3: Histone H2A type 1



- 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	TLE	LYS	L194	R303	K430	C527	LYS	TLE	LEU	TRP	GLU	ASP
SER	PHE	PRO	L194	Y304	ASP	Y545	GLU	ALA	GLU	ASN	ARG	LYS
ALA	ASP	GLY	N200	V306	ILE	Y545	SER	PHE	LYS	LYS	GLY	GLU
ALA	ALA	ARG	G201	A310	ASP	K552	ILE	THR	ILE	ARG	THR	GLU
PRO	SER	ARG	I202	E326	ILE	M556	THR	ILE	PHE	ASN	PHE	PRO
PRO	PRO	ILE	E206	E326	ASN	L557	ASP	GLU	TYR	GLN	GLN	ILE
PRO	LYS	LYS	M207	T329	SER	S558	GLU	PRO	ARG	PHE	ARG	ARG
PRO	GLN	ASP	G208	T329	ALA	R560	ILE	PRO	LYS	ILE	ILE	ARG
PRO	LYS	GLU	L209	L334	GLY	R560	THR	LYS	THR	LYS	THR	ILE
PRO	GLU	LYS	G210	L334	LYS	L564	ILE	ALA	ILE	ALA	GLY	ILE
GLU	GLN	ASN	K211	T336	MET	G585	LEU	ARG	TYR	GLU	TYR	ILE
SER	GLN	LEU	T215	L340	ASP	I586	GLU	ARG	ILE	ASN	GLU	ARG
ALA	PRO	LEU	L218	L354	K443	D580	LYS	LYS	LYS	LYS	LYS	LYS
PRO	PRO	SER	L219	L355	M444	W581	GLY	ALA	ALA	ASP	ALA	ALA
LYS	THR	GLY	G220	L447	R445	V585	ALA	TYR	ASN	ASP	VAL	LYS
PRO	TYR	ASP	M222	N360	L447	F607	THR	ALA	LYS	ILE	VAL	THR
ALA	GLU	ARG	H224	A362	L449	R616	GLU	ALA	ALA	ILE	ALA	ALA
ALA	GLU	ARG	H224	D363	L450	R620	GLU	ALA	ALA	ARG	ALA	ALA
SER	THR	THR	P229	P361	M451	D628	GLU	GLN	GLN	GLY	GLN	PRO
GLY	THR	GLN	P231	P361	Q452	D628	LEU	ALA	ALA	GLY	ALA	ALA
GLY	THR	GLN	F248	P361	L453	G634	LEU	ALA	ALA	GLY	ALA	ALA
ASN	THR	GLN	R249	ASP	R454	G634	LEU	ALA	ALA	GLY	ALA	ALA
SER	THR	GLN	R250	THR	K455	G634	LEU	ALA	ALA	GLY	ALA	ALA
SER	THR	GLN	R256	THR	L462	G634	LEU	ALA	ALA	GLY	ALA	ALA
LYS	THR	GLN	S257	THR	E467	G634	LEU	ALA	ALA	GLY	ALA	ALA
GLY	THR	GLN	L260	THR	P468	G634	LEU	ALA	ALA	GLY	ALA	ALA
PRO	THR	GLN	E265	THR	G469	G634	LEU	ALA	ALA	GLY	ALA	ALA
GLU	THR	GLN	Q266	THR	P470	G634	LEU	ALA	ALA	GLY	ALA	ALA
SER	THR	GLN	R267	THR	P471	G634	LEU	ALA	ALA	GLY	ALA	ALA
VAL	THR	GLN	A268	THR	D475	G634	LEU	ALA	ALA	GLY	ALA	ALA
ALA	THR	GLN	V271	THR	V479	G634	LEU	ALA	ALA	GLY	ALA	ALA
ALA	THR	GLN	R272	THR	S482	G634	LEU	ALA	ALA	GLY	ALA	ALA
VAL	THR	GLN	V274	THR	M485	G634	LEU	ALA	ALA	GLY	ALA	ALA
ALA	THR	GLN	L275	THR	V486	G634	LEU	ALA	ALA	GLY	ALA	ALA
ALA	THR	GLN	L276	THR	V487	G634	LEU	ALA	ALA	GLY	ALA	ALA
VAL	THR	GLN	G277	THR	P493	G634	LEU	ALA	ALA	GLY	ALA	ALA
ALA	THR	GLN	G278	THR	K494	G634	LEU	ALA	ALA	GLY	ALA	ALA
ALA	THR	GLN	E279	THR	L495	G634	LEU	ALA	ALA	GLY	ALA	ALA
ALA	THR	GLN	W280	THR	K496	G634	LEU	ALA	ALA	GLY	ALA	ALA
PRO	THR	GLN	G176	THR	E497	G634	LEU	ALA	ALA	GLY	ALA	ALA
ALA	THR	GLN	G176	THR	Q498	G634	LEU	ALA	ALA	GLY	ALA	ALA
ASP	THR	GLN	G179	THR	G499	G634	LEU	ALA	ALA	GLY	ALA	ALA
ALA	THR	GLN	D182	THR	R501	G634	LEU	ALA	ALA	GLY	ALA	ALA
GLU	THR	GLN	N189	THR	L512	G634	LEU	ALA	ALA	GLY	ALA	ALA
GLU	THR	GLN	W190	THR	E525	G634	LEU	ALA	ALA	GLY	ALA	ALA
MET	THR	GLN	L191	THR	Y526	G634	LEU	ALA	ALA	GLY	ALA	ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	33000	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	33.885	Depositor
Minimum map value	-0.395	Depositor
Average map value	-0.017	Depositor
Map value standard deviation	0.292	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 [i](#)

5.1 Standard geometry [i](#)

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	0.14	0/811	0.26	0/1088
1	E	0.14	0/802	0.24	0/1076
2	B	0.15	0/687	0.29	0/921
2	F	0.14	0/648	0.28	0/868
3	C	0.12	0/847	0.22	0/1144
3	G	0.13	0/847	0.25	0/1144
4	D	0.12	0/757	0.26	0/1018
4	H	0.12	0/767	0.25	0/1029
5	I	0.26	0/3521	0.44	2/5437 (0.0%)
6	J	0.23	0/3468	0.41	0/5345
7	W	0.14	0/3733	0.32	0/5041
All	All	0.19	0/16888	0.35	2/24111 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	25	DT	C2'-C3'-O3'	-5.91	102.63	111.50
5	I	-25	DC	C2'-C3'-O3'	-5.81	102.78	111.50

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	799	0	838	9	0
1	E	790	0	826	11	0
2	B	679	0	717	7	0
2	F	641	0	684	8	0
3	C	837	0	891	8	0
3	G	837	0	891	13	0
4	D	746	0	764	6	0
4	H	756	0	786	9	0
5	I	3135	0	1704	65	0
6	J	3096	0	1706	66	0
7	W	3656	0	3730	70	0
8	W	27	0	12	0	0
All	All	15999	0	13549	242	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 8.

The worst 5 of 242 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:560:ARG:HE	7:W:585:VAL:HG21	1.26	1.00
7:W:560:ARG:NE	7:W:585:VAL:HG21	1.91	0.83
7:W:455:LYS:HB2	7:W:462:LEU:HD12	1.65	0.79
7:W:167:ARG:HE	7:W:189:ASN:HB3	1.55	0.70
5:I:15:DT:H2"	5:I:16:DA:C8	2.27	0.69

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	95/136 (70%)	92 (97%)	3 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	78 (100%)	0	0	100	100
3	C	107/130 (82%)	106 (99%)	1 (1%)	0	100	100
3	G	107/130 (82%)	104 (97%)	3 (3%)	0	100	100
4	D	94/126 (75%)	91 (97%)	3 (3%)	0	100	100
4	H	94/126 (75%)	92 (98%)	2 (2%)	0	100	100
7	W	438/1052 (42%)	405 (92%)	31 (7%)	2 (0%)	25	58
All	All	1190/2042 (58%)	1139 (96%)	49 (4%)	2 (0%)	45	74

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	W	566	ILE
7	W	381	VAL

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	85/111 (77%)	85 (100%)	0	100	100
1	E	84/111 (76%)	83 (99%)	1 (1%)	67	83
2	B	69/79 (87%)	67 (97%)	2 (3%)	37	65
2	F	66/79 (84%)	65 (98%)	1 (2%)	60	80
3	C	85/102 (83%)	84 (99%)	1 (1%)	67	83
3	G	85/102 (83%)	85 (100%)	0	100	100
4	D	80/106 (76%)	79 (99%)	1 (1%)	65	82
4	H	82/106 (77%)	82 (100%)	0	100	100
7	W	409/939 (44%)	400 (98%)	9 (2%)	47	71
All	All	1045/1735 (60%)	1030 (99%)	15 (1%)	62	81

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	W	209	LEU
7	W	527	CYS
7	W	248	PHE
7	W	558	SER
7	W	396	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	75	HIS
3	G	89	ASN
4	H	81	ASN
3	C	112	GLN
1	A	108	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	0.90	0	29,45,45	1.18	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	-	-	4/12/32/32	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	-3.69	123.67	128.67
8	W	1101	ADP	C4-C5-N7	-2.65	106.54	109.34

There are no chirality outliers.

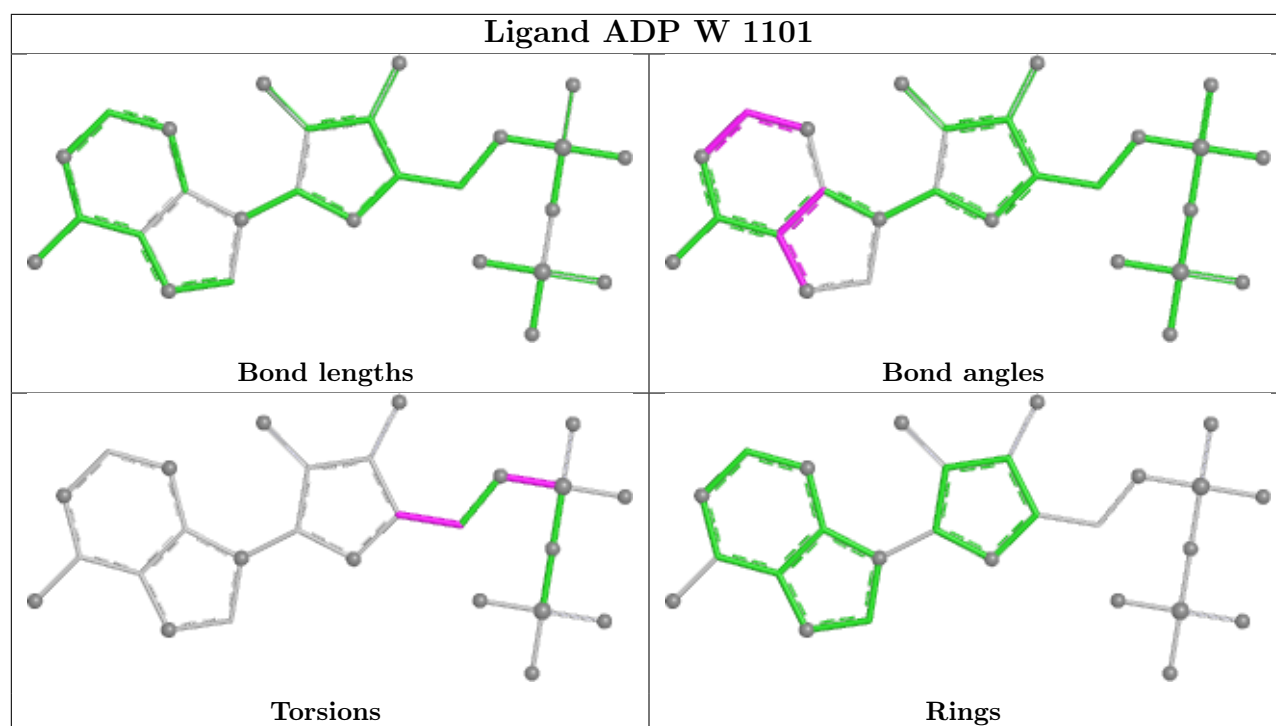
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	W	1101	ADP	C5'-O5'-PA-O3A
8	W	1101	ADP	O4'-C4'-C5'-O5'
8	W	1101	ADP	C3'-C4'-C5'-O5'
8	W	1101	ADP	C5'-O5'-PA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

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.

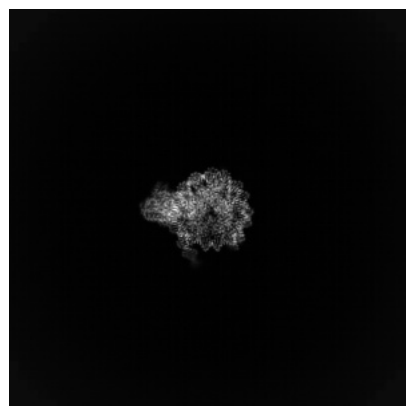
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47417. These allow visual inspection of the internal detail of the map and identification of artifacts.

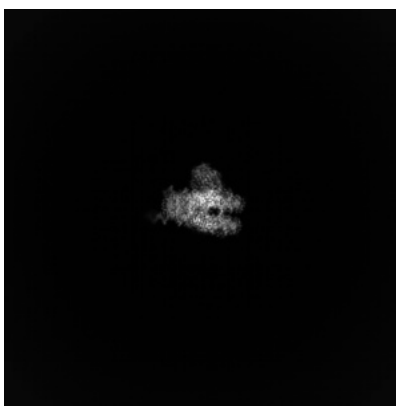
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

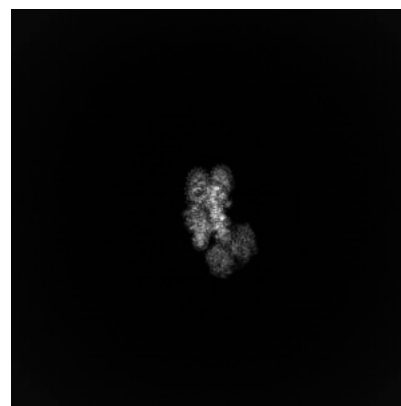
6.1.1 Primary map



X

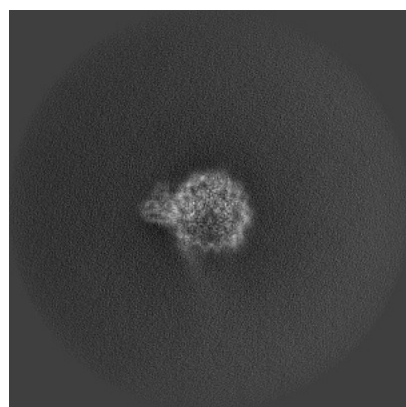


Y

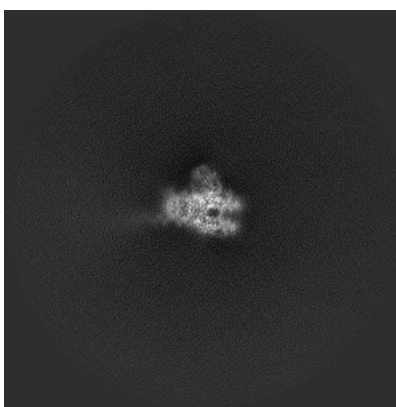


Z

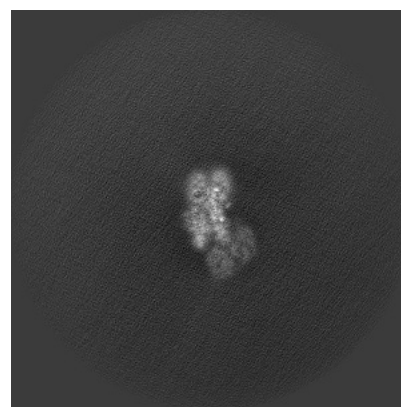
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

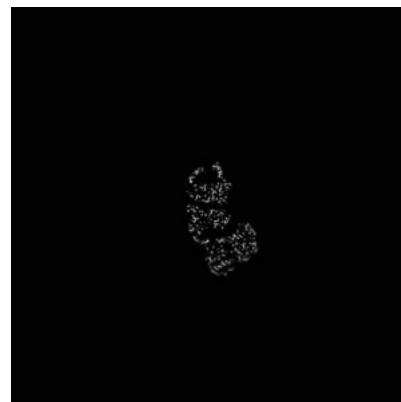
6.2.1 Primary map



X Index: 248

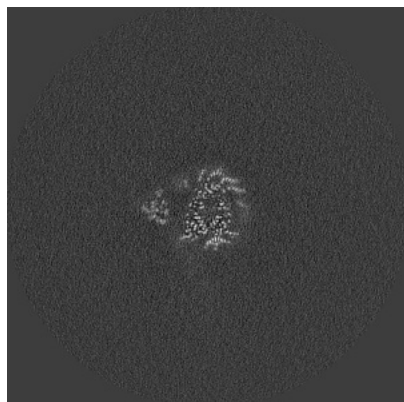


Y Index: 248



Z Index: 248

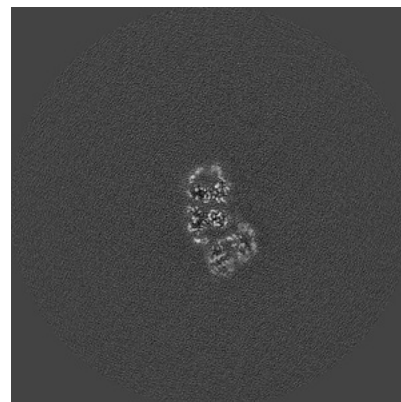
6.2.2 Raw map



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](#)

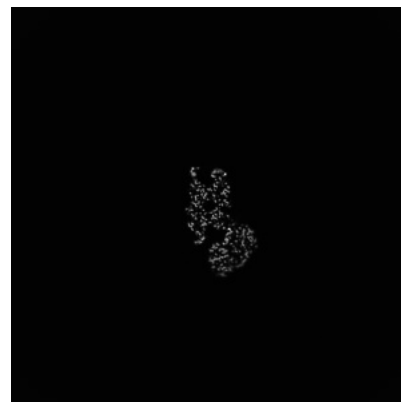
6.3.1 Primary map



X Index: 255

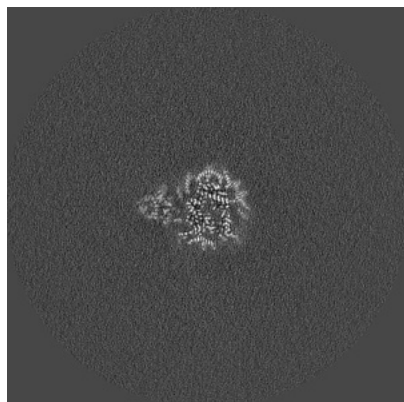


Y Index: 224

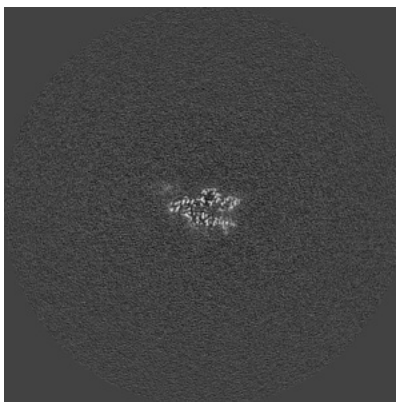


Z Index: 254

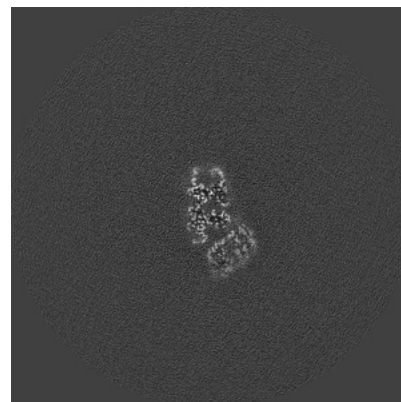
6.3.2 Raw map



X Index: 196



Y Index: 210

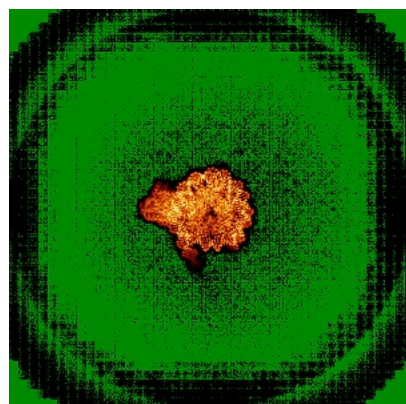


Z Index: 194

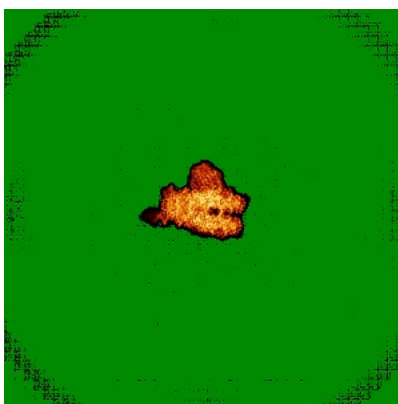
The images above show the largest variance slices of the map in three orthogonal directions.

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

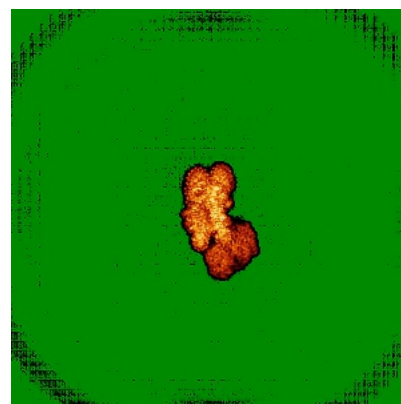
6.4.1 Primary map



X

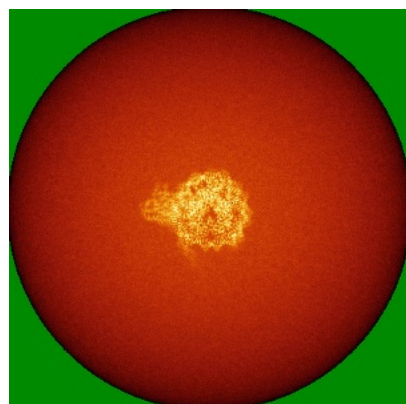


Y

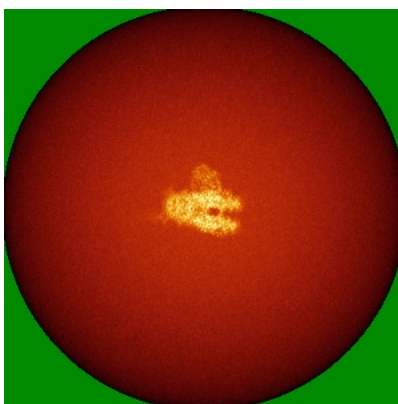


Z

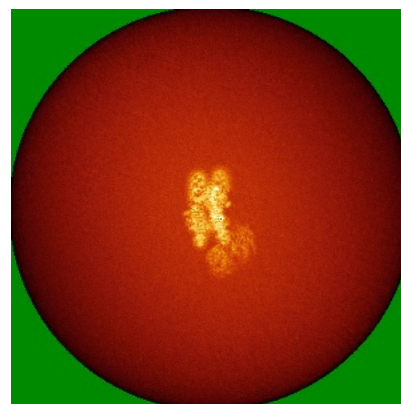
6.4.2 Raw map



X



Y

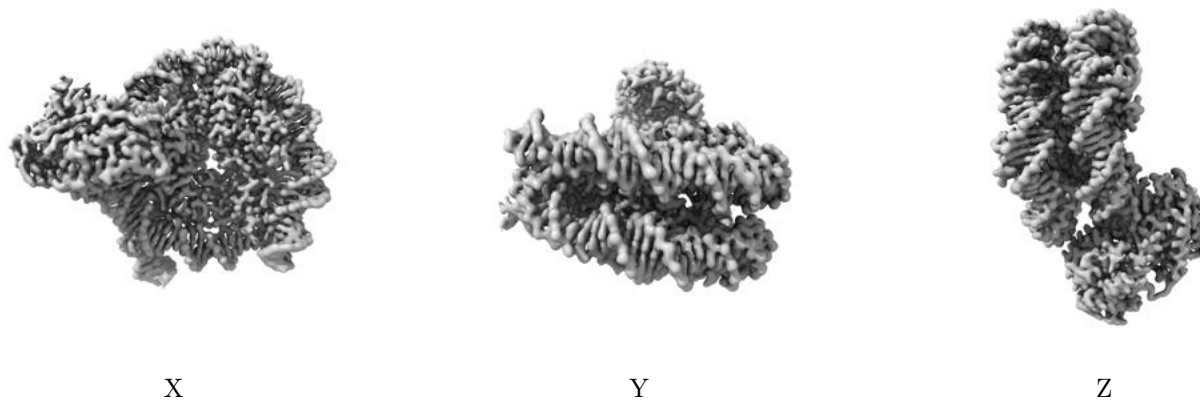


Z

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.

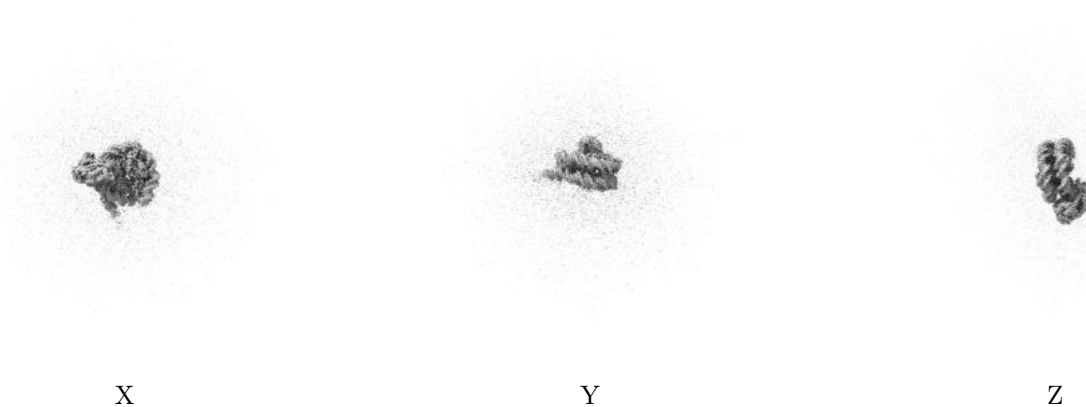
6.5 Orthogonal surface views [i](#)

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.

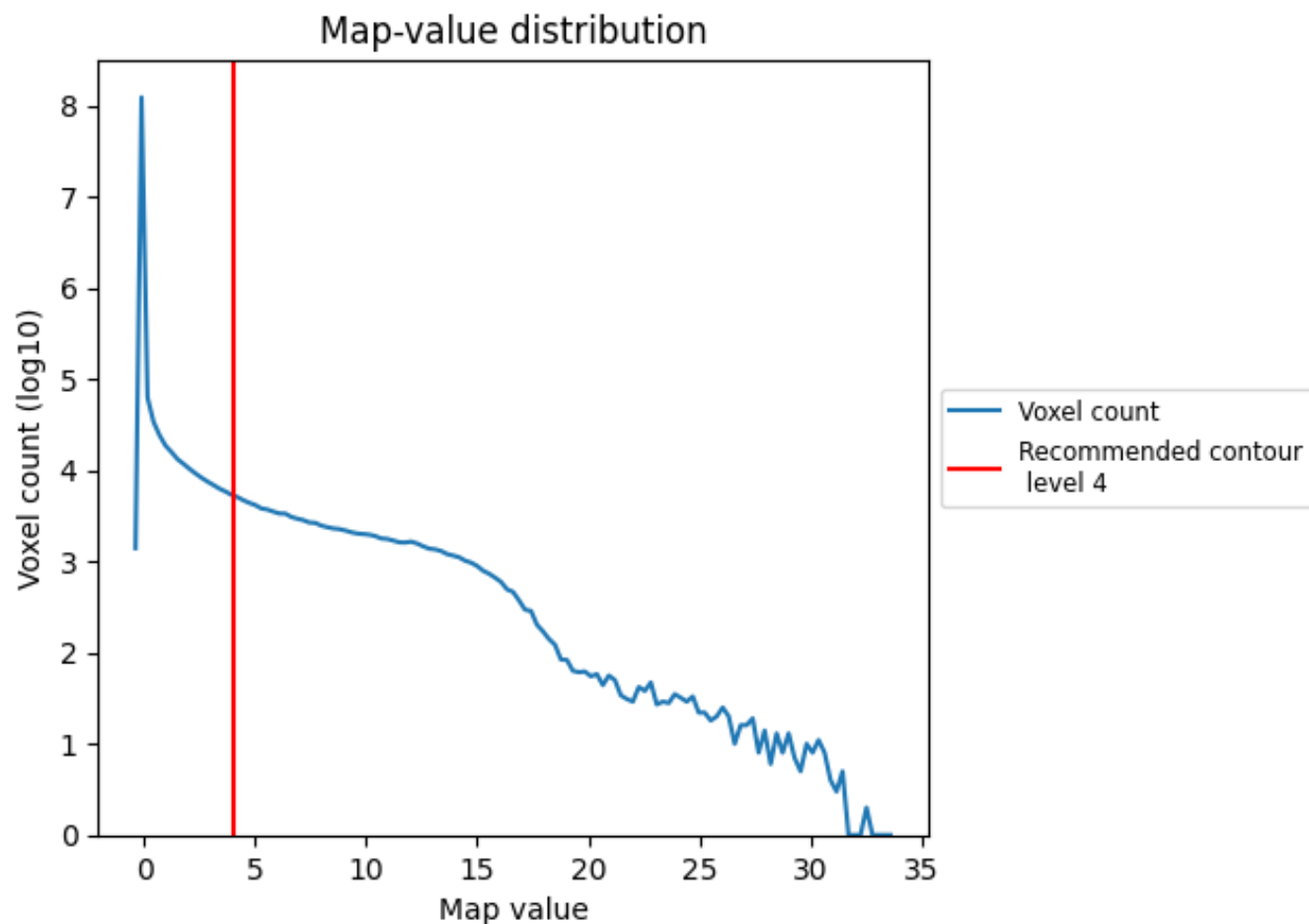
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

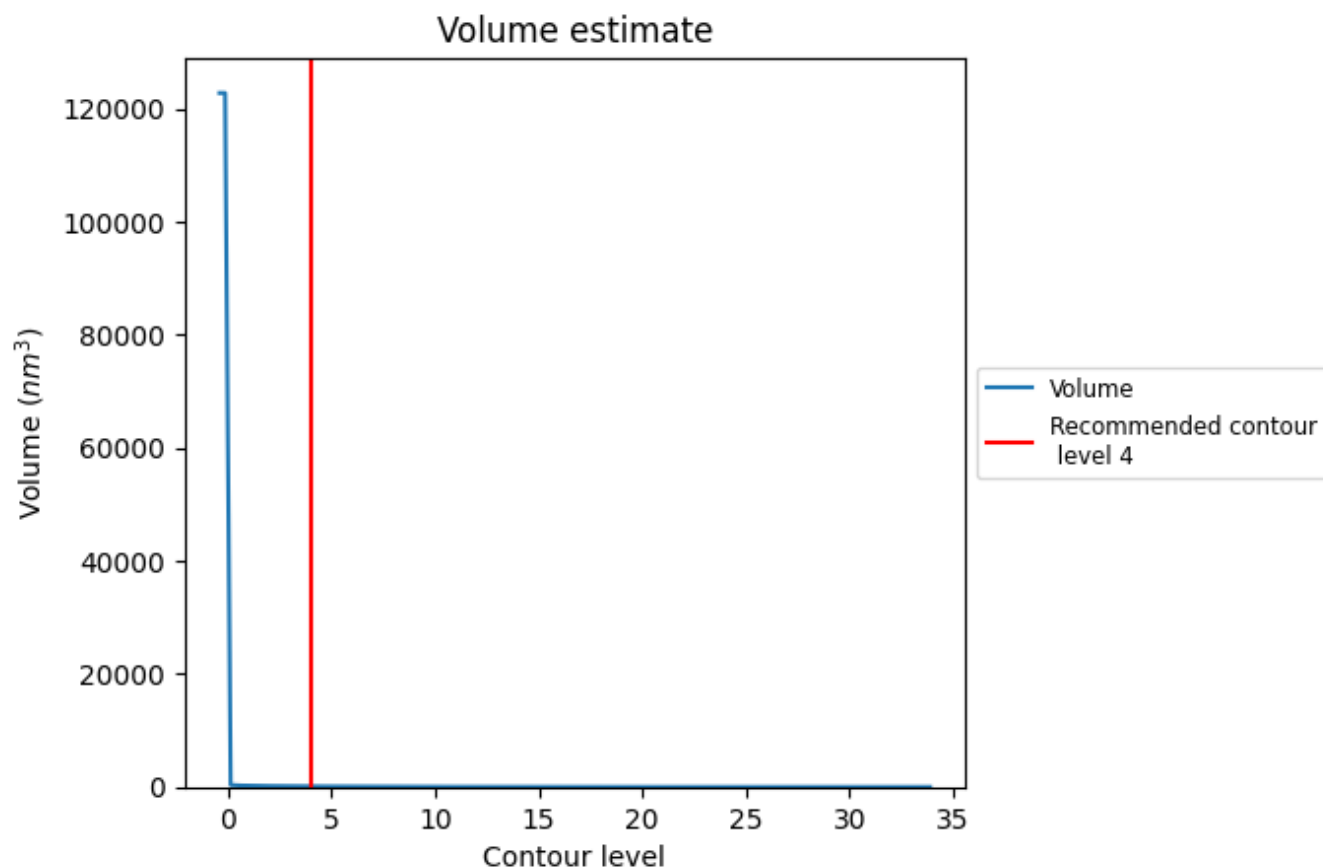
This section contains the results of statistical analysis of the map.

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.

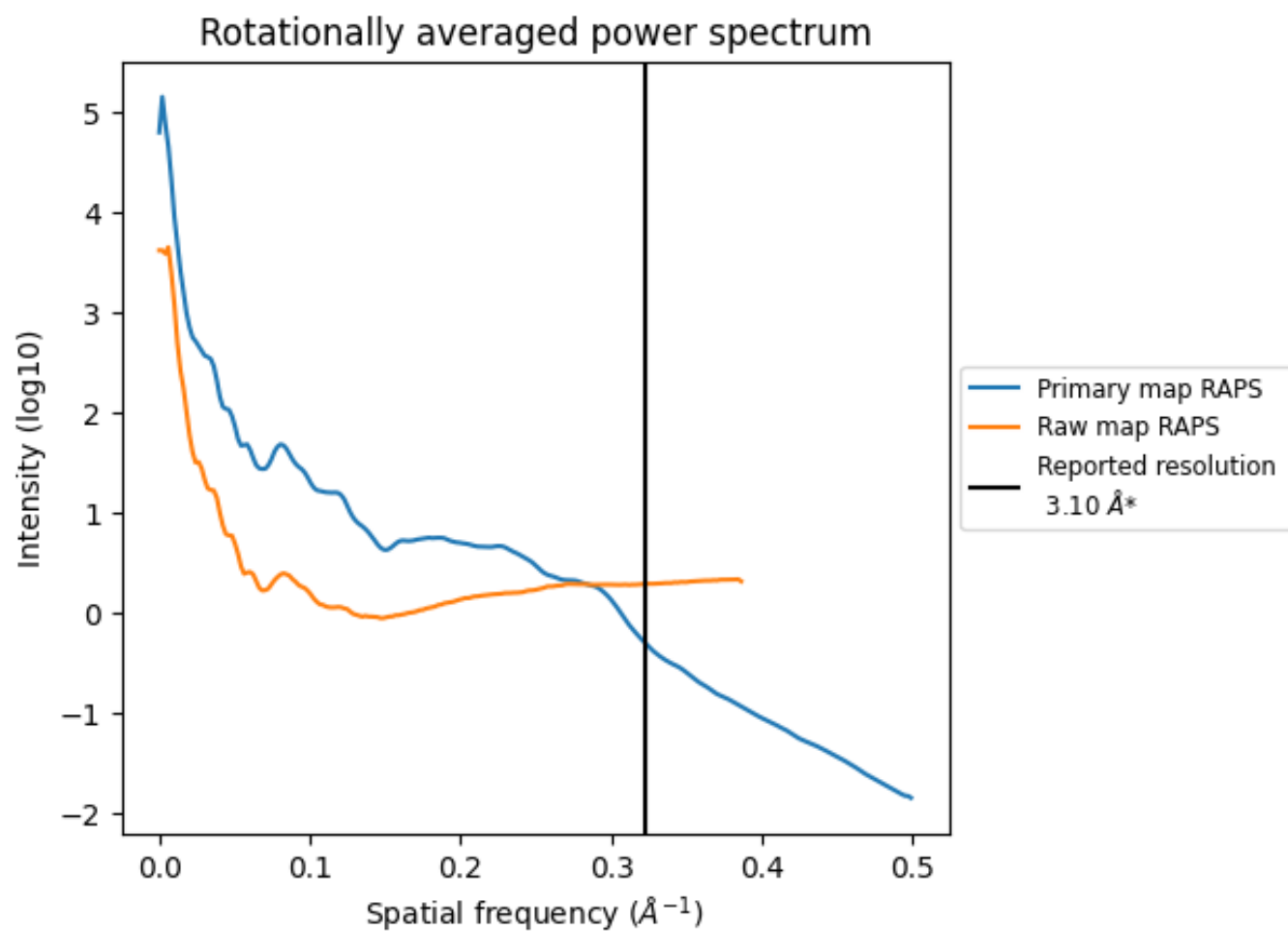
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 106 nm³; this corresponds to an approximate mass of 96 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 ⓘ

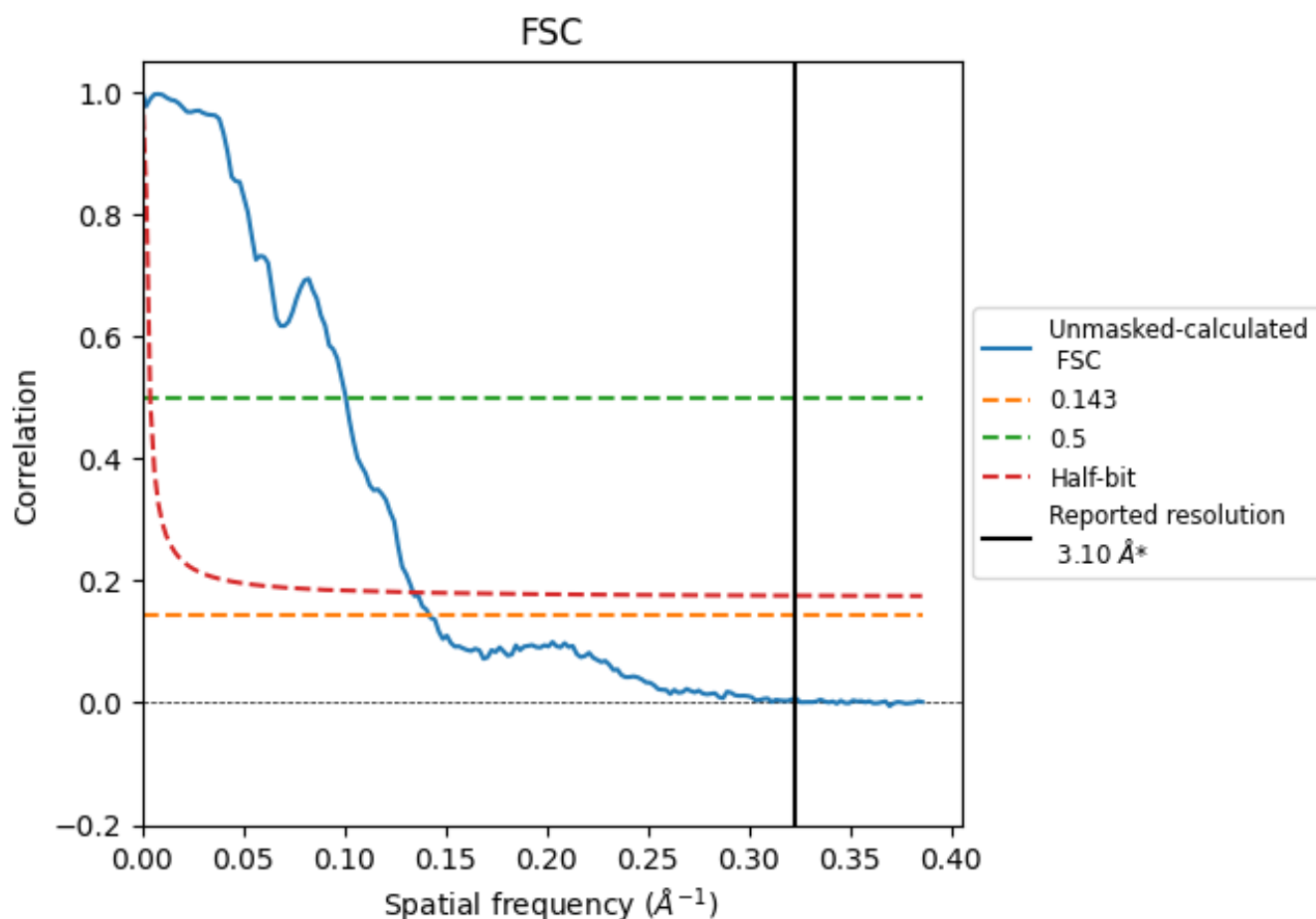


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 \AA^{-1}

8.2 Resolution estimates [i](#)

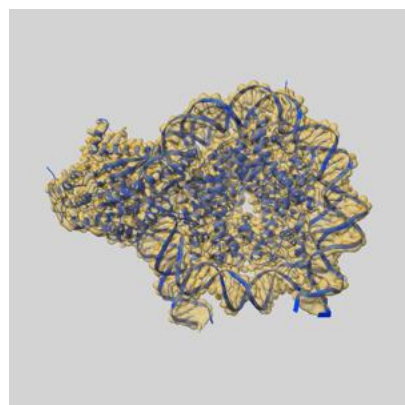
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.05	9.94	7.47

*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 7.05 differs from the reported value 3.1 by more than 10 %

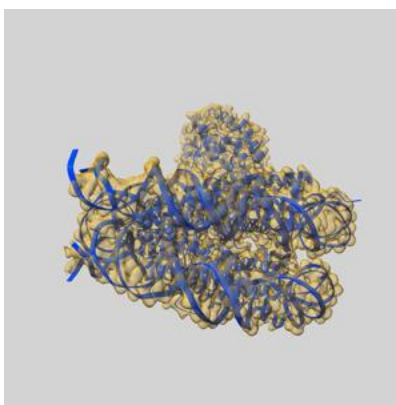
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47417 and PDB model 9E1Q. Per-residue inclusion information can be found in section [3](#) on page [7](#).

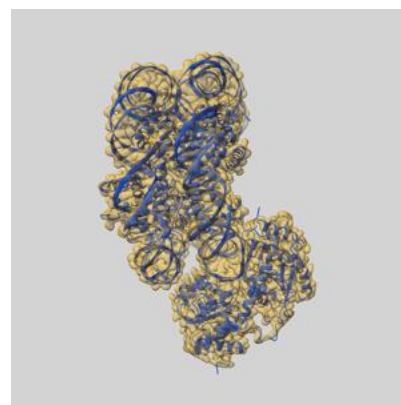
9.1 Map-model overlay [i](#)



X



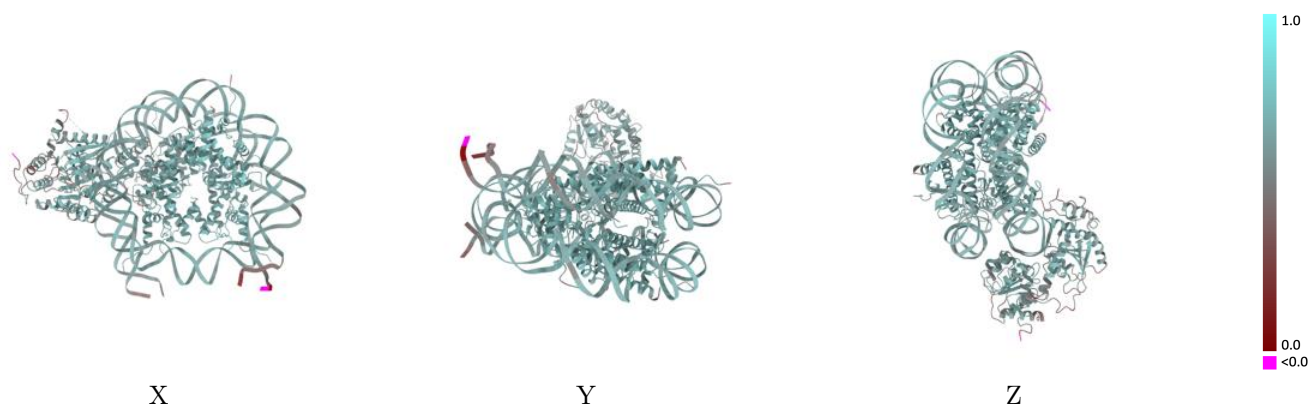
Y



Z

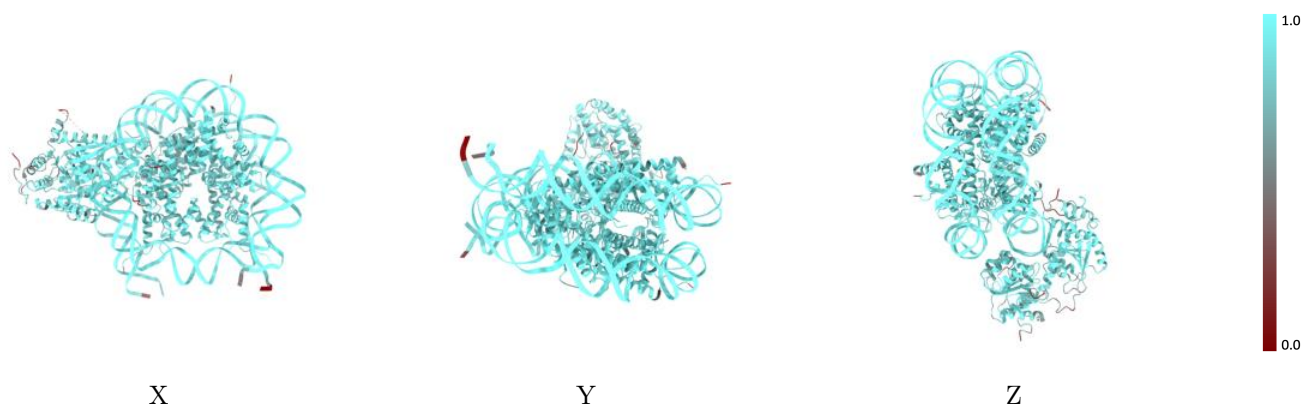
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



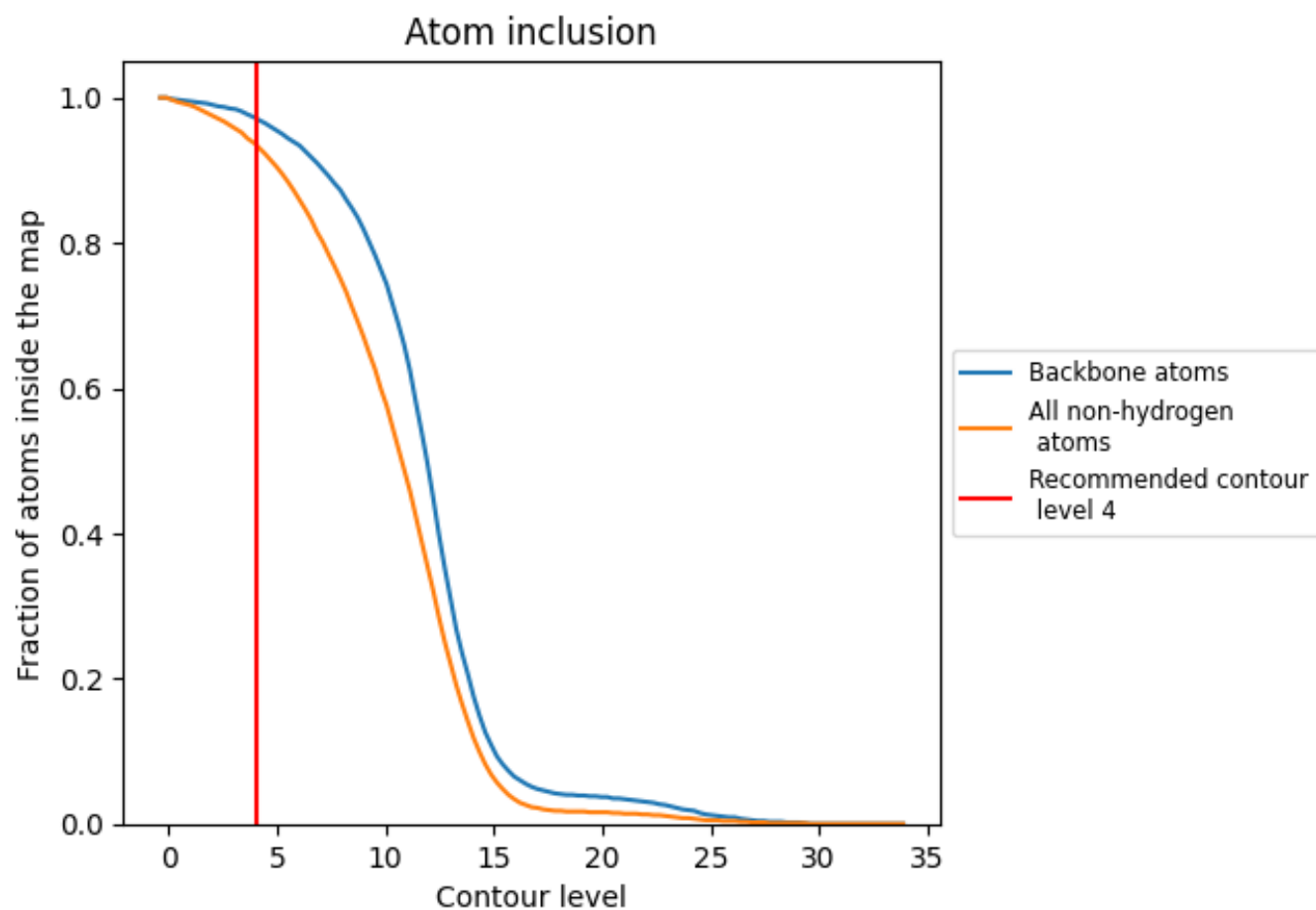
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 97% of all backbone atoms, 94% 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>0.9360</div>	<div><div></div>0.6140</div>
A	<div><div></div>0.9740</div>	<div><div></div>0.6750</div>
B	<div><div></div>0.9230</div>	<div><div></div>0.6570</div>
C	<div><div></div>0.9720</div>	<div><div></div>0.6740</div>
D	<div><div></div>0.9590</div>	<div><div></div>0.6670</div>
E	<div><div></div>0.9830</div>	<div><div></div>0.6790</div>
F	<div><div></div>0.9820</div>	<div><div></div>0.6800</div>
G	<div><div></div>0.9690</div>	<div><div></div>0.6670</div>
H	<div><div></div>0.9570</div>	<div><div></div>0.6600</div>
I	<div><div></div>0.9600</div>	<div><div></div>0.5890</div>
J	<div><div></div>0.9660</div>	<div><div></div>0.6000</div>
W	<div><div></div>0.8390</div>	<div><div></div>0.5530</div>

1.0

0.0

<0.0