



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:07 PM UTC

PDB ID : 9E1L / pdb_00009e1l
EMDB ID : EMD-47412
Title : Snf2h bound nucleosome complex - ClassA1
Authors : Malik, D.; Deshmukh, A.A.; Bilokapic, S.; Halic, M.
Deposited on : 2024-10-21
Resolution : 3.15 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:

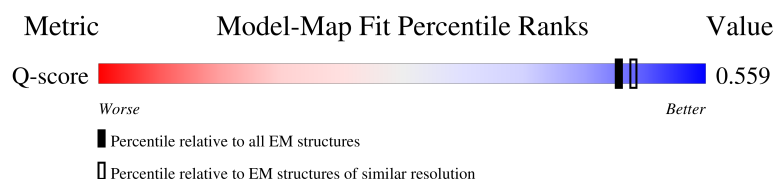
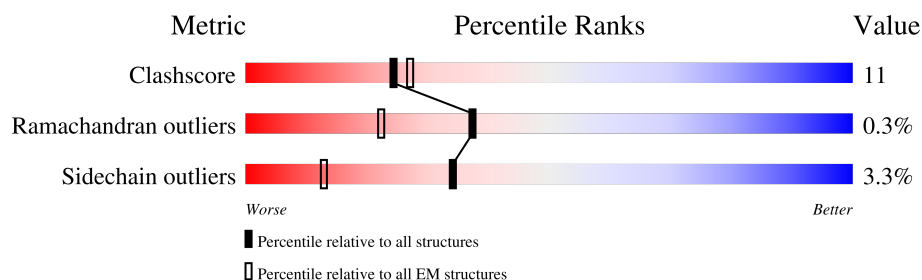
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.15 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14486 (2.65 - 3.65)

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	

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Mol	Chain	Length	Quality of chain
3	C	130	76%8%16%
3	G	130	75%8%16%
4	D	126	70%6%24%
4	H	126	68%7%24%
5	I	149	48%52%
6	J	152	50%49%
7	W	1052	11%25%16%58%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 15924 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 (149-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	149	Total	C	N	O	P	0	0
			3075	1454	580	892	149		

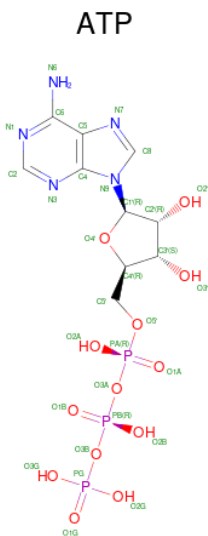
- Molecule 6 is a DNA chain called DNA (151-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	151	Total	C	N	O	P	0	0
			3077	1461	558	907	151		

- 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'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).

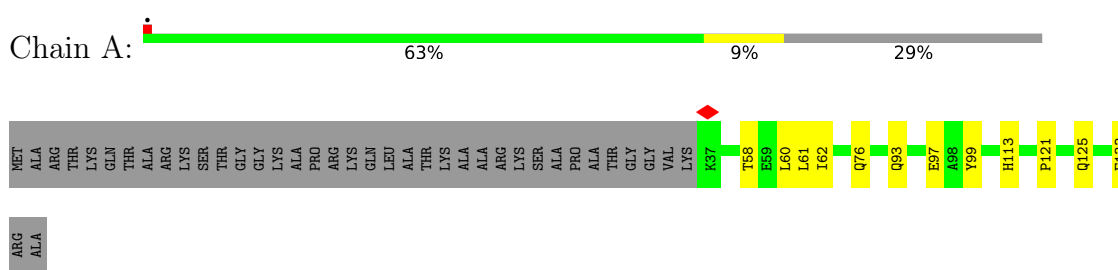


Mol	Chain	Residues	Atoms					AltConf
8	W	1	Total 31	C 10	N 5	O 13	P 3	0

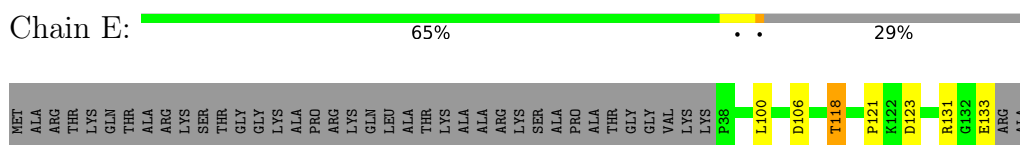
3 Residue-property plots [i](#)

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

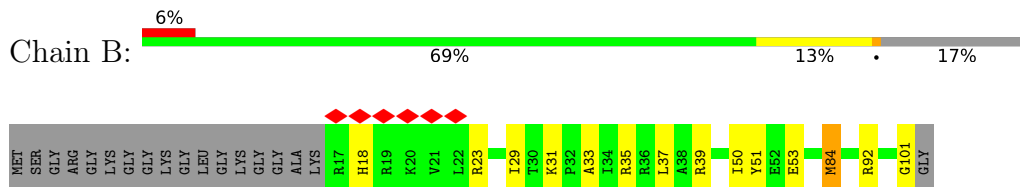
- Molecule 1: Histone H3.2



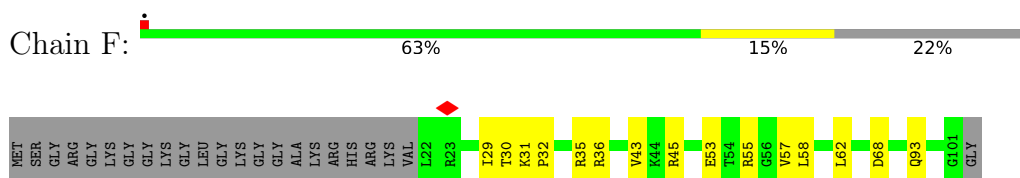
- Molecule 1: Histone H3.2



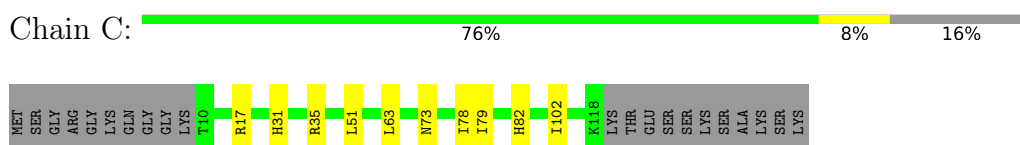
- Molecule 2: Histone H4



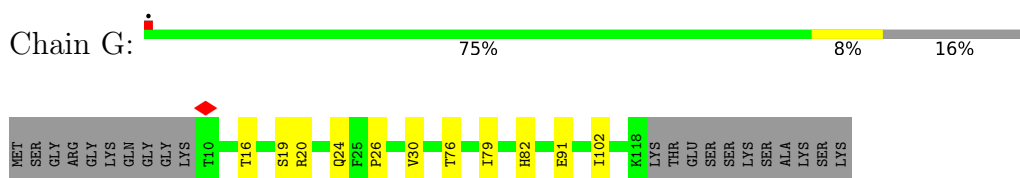
- Molecule 2: Histone H4



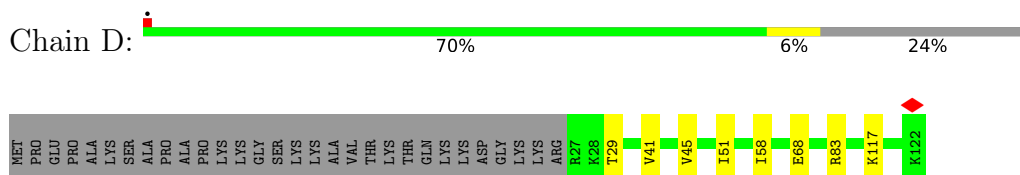
- Molecule 3: Histone H2A type 1



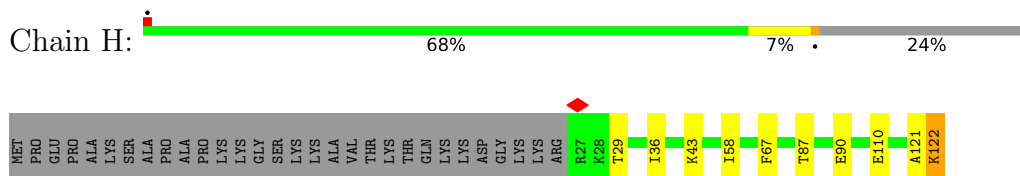
- Molecule 3: Histone H2A type 1



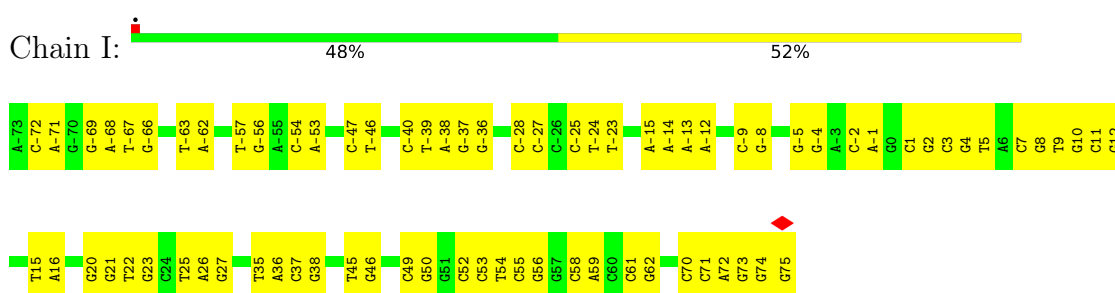
- Molecule 4: Histone H2B 1.1



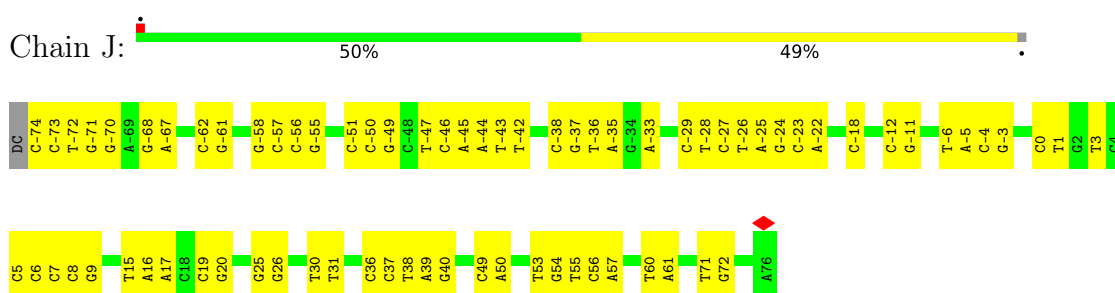
- Molecule 4: Histone H2B 1.1



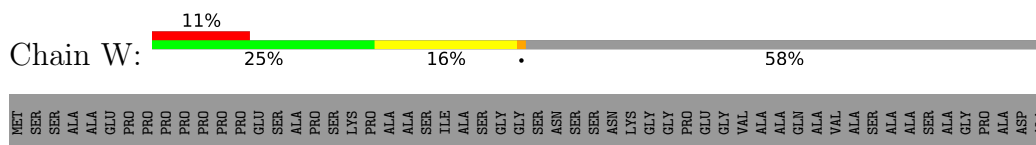
- Molecule 5: DNA (149-MER)



- Molecule 6: DNA (151-MER)



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



ILE	LYS	D182	W280	H385	Q452	L515	P583	LEU	VAL	VAL	LEU	CYS	GLU
PHE	PRO	Y183	D281	M386	L453	Y518	Q584	GLN	TYR	GLN	GLU	ASN	ASP
ASP	GLY	Q184	S286	R389	R454	C519	A589	MET	ASN	ASP	LYS	LEU	PHE
ALA	PRO	V185	F297	L393	C456	M520	R592	ARG	PHE	PHE	GLY	GLN	GLU
SER	ARG	R186	R303	R394	C457	R522	R594	HIS	GLY	PRO	LYS	ASP	ILE
PRO	ILE	W190	R395	R396	M458	R523	H594	ALA	ASP	PRO	LYS	ILE	CYS
GLY	LYS	L191	R397	R398	Y461	Y524	H596	VAL	ARG	TYR	GLY	GLY	LEU
LYS	ASP	T192	R398	A398	L462	E525	R595	HIS	ARG	ARG	GLN	ILE	LYS
LYS	GLU	S193	R399	L399	P463	E526	R596	VAL	GLY	GLY	GLY	MET	ALA
GLU	LYS	L194	E309	D399	P464	C527	R597	PHE	LYS	PHE	THR	ALA	GLY
ILE	GLN	Y195	E316	W400	D464	G527	Q598	SER	LYS	LEU	ASN	ILE	LYS
GLN	ASN	E196	N197	E401	G485	R528	T599	LEU	LYS	LEU	ILE	ILE	PHE
GLU	LEU	N197	K317	L404	G486	L529	K600	LYS	ILE	TRP	TRP	GLY	ASP
PRO	SER	T202	S318	P405	A466	D530	T601	GLY	ALA	GLY	ASN	GLY	LYS
PRO	ASP	L203	S319	P406	E467	G531	V602	SER	PHE	GLY	ASP	ARG	GLY
THR	GLY	A204	V324	K407	P468	T533	R603	ILE	THR	GLY	ALA	ALA	VAL
TYR	ASP	D205	R325	K408	G469	G532	R606	THR	TRP	ILE	ASP	ARG	PRO
GLU	TYR	E206	R207	G208	P470	T534	F607	ILE	ILE	ILE	ASP	ILE	ASP
LYS	HIS	G209	G208	G208	P471	H535	T609	GLY	PRO	GLY	GLY	GLN	GLY
GLN	ARG	G210	G209	G209	Y472	D536	D610	ASP	LYS	LYS	ILE	ILE	GLN
THR	THR	G211	G210	G210	T473	E537	N611	GLY	ARG	ARG	ALA	SER	CYS
ASP	GLY	T212	G341	G415	T474	R538	T612	ILE	GLY	GLY	GLY	ILE	ILE
ALA	GLN	L213	W348	L416	D475	Q539	D615	LEU	ARG	LYS	LYS	LYS	ASP
ASN	GLU	L218	L351	R418	H477	S541	R616	ARG	ALA	ASN	ALA	ALA	ALA
ARG	ASP	L218	L351	M419	M481	A544	R617	GLY	TYR	ARG	ARG	ASP	PRO
PHE	GLY	K222	K223	Q420	S482	F547	V618	ALA	ALA	ASN	ALA	ALA	GLY
GLU	GLY	W223	L235	L235	G483	E547	E619	LYS	ALA	GLY	ALA	ALA	THR
TYR	LEU	R224	V236	D363	R421	P548	R620	LYS	VAL	GLY	GLN	PRO	ARG
LEU	LEU	R225	P237	ASP	E422	M485	A621	LEU	ALA	LEU	VAL	ALA	ARG
LYS	THR	Y226	R226	PHE	W423	M486	E622	SER	ALA	ALA	GLY	GLN	THR
GLN	SER	R227	S361	ASP	Y424	V486	E622	MET	TYR	PHE	LYS	ILE	ALA
THR	SER	T228	S361	ASP	T425	V487	L625	ASN	ARG	ARG	GLY	LEU	MET
GLY	LYS	L235	D363	ASP	R426	L488	R626	ALA	GLY	GLY	LYS	ARG	GLY
LEU	ALA	V236	ASP	PHE	I427	D489	R627	GLY	GLY	GLY	PRO	ILE	LEU
PHE	THR	F237	ASP	ASP	L428	L491	L627	LEU	LYS	GLY	ALA	GLY	GLN
ALA	VAL	L241	SER	TRP	M429	L492	D628	LYS	VAL	VAL	ILE	VAL	ARG
HIS	VAL	L241	TRP	TRP	K430	P493	V631	MET	SER	SER	ILE	ILE	CYS
PHE	CYS	R249	ASP	ASP	ASP	K494	Q633	GLY	GLY	GLY	GLY	GLY	THR
ILE	T166	R249	PHE	ASP	ILE	L495	Q633	LEU	PRO	PRO	LEU	ASN	ASN
GLN	R167	R250	ASP	ASP	ILE	L496	Q634	ARG	GLY	LYS	VAL	ASP	GLY
PRO	F168	D170	THR	THR	ILE	E497	G634	SER	ALA	ALA	ASP	ALA	THR
ALA	E169	S171	ASN	ASN	ILE	G498	G634	LEU	LYS	LYS	GLY	ALA	ALA
GLN	D170	P172	CYS	CYS	ALA	S500	R501	ARG	PRO	PRO	VAL	VAL	GLN
LYS	S171	P172	LEU	LEU	ALA	R501	V502	THR	ARG	ARG	THR	THR	THR
THR	P172	P172	GLY	GLY	LYS	L503	L503	LEU	PRO	PRO	ASP	ASP	PRO
PRO	S173	C259	GLY	GLY	LYS	F504	F504	LEU	LYS	LYS	THR	THR	THR
SER	K176	D275	K379	MET	ASP	F505	F505	ASN	LYS	LYS	ASN	ASN	SER
PRO	W177	V274	L380	ASP	R443	S506	D572	GLY	GLY	GLY	GLY	GLY	PRO
LEU	G178	L276	T381	M444	R445	Q507	V573	ILE	ILE	ILE	ILE	ILE	LEU
LYS	K179	L276	E382	R446	M508	M508	V574	SER	GLY	GLY	GLY	GLY	GLY
MET	L180	P277	R383	L446	T509	R510	L576	ASP	GLY	GLY	GLY	GLY	GLY
	R181		L384	M448	V511	D513	Y577	GLU	ASP	ASP	ASP	ASP	ASP
				I449	I514	I514	N582	MET	GLU	GLU	GLU	GLU	GLU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23600	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	31.336	Depositor
Minimum map value	-0.429	Depositor
Average map value	-0.017	Depositor
Map value standard deviation	0.274	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: ATP

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	0.20	0/811	0.31	0/1088
1	E	0.20	0/802	0.28	0/1076
2	B	0.20	0/687	0.30	0/921
2	F	0.21	0/648	0.33	0/868
3	C	0.19	0/847	0.27	0/1144
3	G	0.19	0/847	0.29	0/1144
4	D	0.19	0/757	0.29	0/1018
4	H	0.20	0/767	0.34	0/1029
5	I	0.30	0/3454	0.44	0/5334
6	J	0.32	0/3447	0.41	0/5313
7	W	0.24	0/3733	0.48	0/5041
All	All	0.26	0/16800	0.40	0/23976

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	799	0	838	9	0
1	E	790	0	826	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	679	0	717	9	0
2	F	641	0	684	11	0
3	C	837	0	891	6	0
3	G	837	0	891	10	0
4	D	746	0	764	6	0
4	H	756	0	786	10	0
5	I	3075	0	1671	59	0
6	J	3077	0	1695	54	0
7	W	3656	0	3730	153	0
8	W	31	0	12	2	0
All	All	15924	0	13505	310	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 11.

The worst 5 of 310 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:424:TYR:CE1	7:W:453:LEU:HD11	1.64	1.30
7:W:424:TYR:CE1	7:W:453:LEU:CD1	2.45	0.99
7:W:596:ILE:HB	8:W:1101:ATP:O3'	1.63	0.98
7:W:535:HIS:O	7:W:538:ARG:HG2	1.63	0.97
7:W:404:LEU:HD11	7:W:596:ILE:HA	1.56	0.85

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	95/136 (70%)	90 (95%)	5 (5%)	0	100	100
1	E	94/136 (69%)	88 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	83/103 (81%)	81 (98%)	2 (2%)	0	100	100
2	F	78/103 (76%)	75 (96%)	3 (4%)	0	100	100
3	C	107/130 (82%)	105 (98%)	2 (2%)	0	100	100
3	G	107/130 (82%)	102 (95%)	5 (5%)	0	100	100
4	D	94/126 (75%)	93 (99%)	1 (1%)	0	100	100
4	H	94/126 (75%)	92 (98%)	2 (2%)	0	100	100
7	W	438/1052 (42%)	400 (91%)	35 (8%)	3 (1%)	18	49
All	All	1190/2042 (58%)	1126 (95%)	61 (5%)	3 (0%)	37	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	W	454	ARG
7	W	455	LYS
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	85/111 (77%)	84 (99%)	1 (1%)	63	74
1	E	84/111 (76%)	83 (99%)	1 (1%)	63	74
2	B	69/79 (87%)	65 (94%)	4 (6%)	18	46
2	F	66/79 (84%)	65 (98%)	1 (2%)	57	72
3	C	85/102 (83%)	83 (98%)	2 (2%)	43	66
3	G	85/102 (83%)	83 (98%)	2 (2%)	43	66
4	D	80/106 (76%)	79 (99%)	1 (1%)	61	73
4	H	82/106 (77%)	79 (96%)	3 (4%)	30	58
7	W	409/939 (44%)	390 (95%)	19 (5%)	24	53
All	All	1045/1735 (60%)	1011 (97%)	34 (3%)	34	60

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	W	514	ILE
7	W	547	GLU
7	W	602	VAL
4	H	29	THR
3	G	76	THR

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

Mol	Chain	Res	Type
3	G	110	ASN
7	W	197	ASN
7	W	539	GLN
1	E	39	HIS
1	A	93	GLN

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	ATP	W	1101	-	32,33,33	0.34	0	48,52,52	0.32	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
8	ATP	W	1101	-	-	4/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

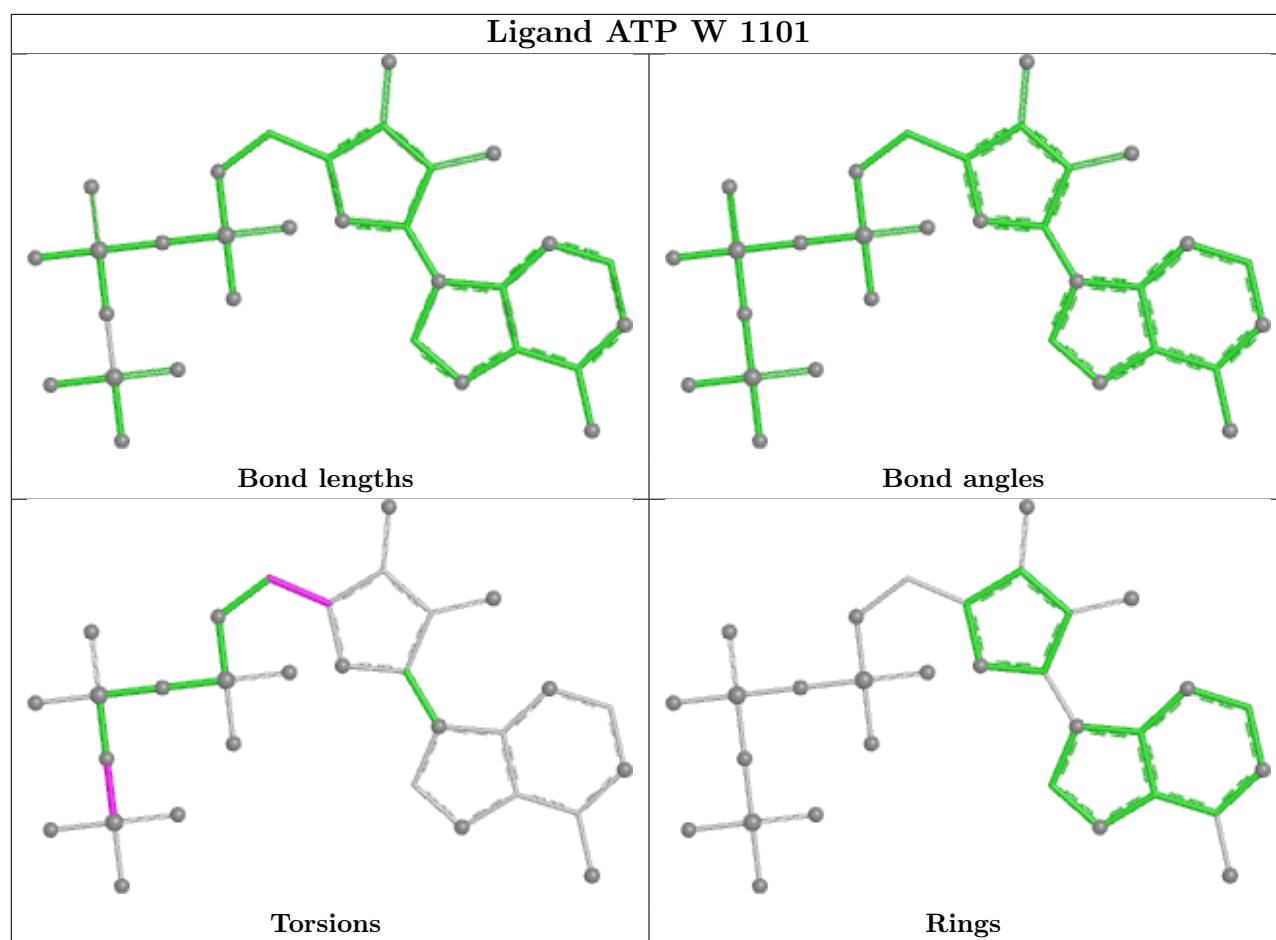
Mol	Chain	Res	Type	Atoms
8	W	1101	ATP	PB-O3B-PG-O2G
8	W	1101	ATP	O4'-C4'-C5'-O5'
8	W	1101	ATP	C3'-C4'-C5'-O5'
8	W	1101	ATP	PB-O3B-PG-O3G

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	W	1101	ATP	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.

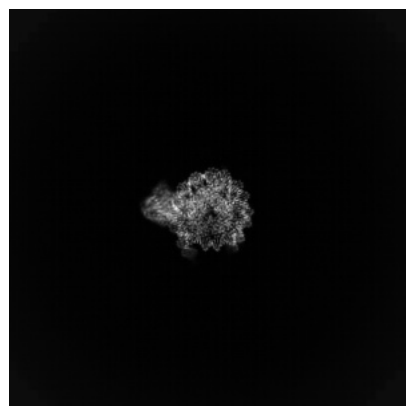
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47412. 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](#)

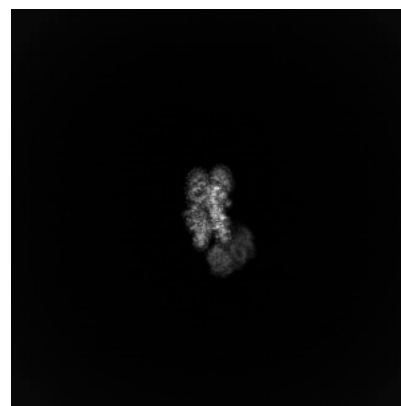
6.1.1 Primary map



X

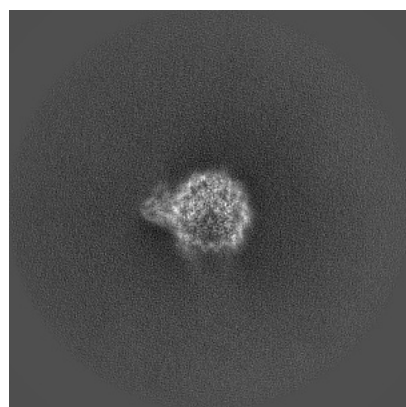


Y

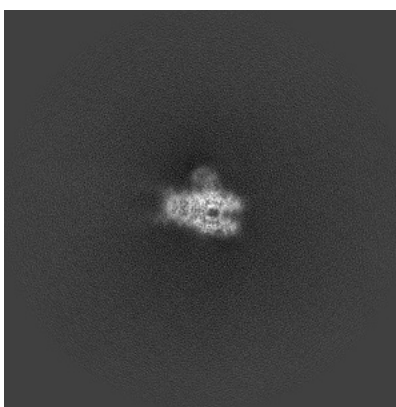


Z

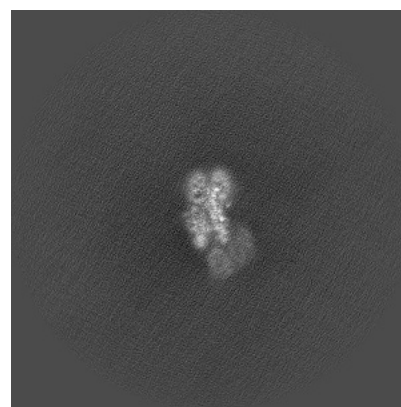
6.1.2 Raw map



X



Y

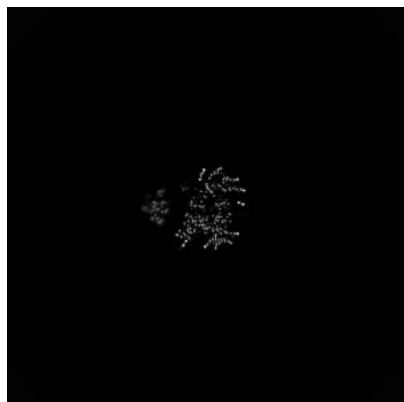


Z

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

6.2 Central slices [i](#)

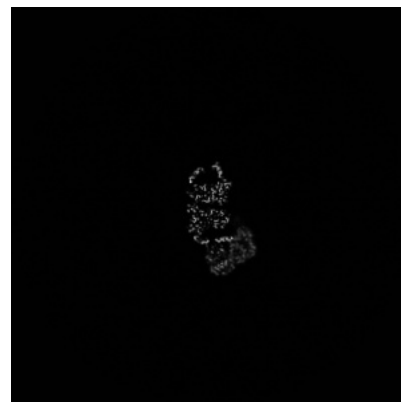
6.2.1 Primary map



X Index: 248

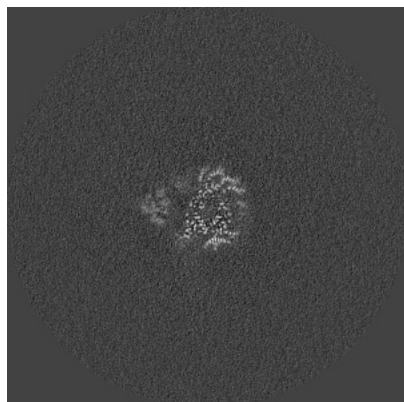


Y Index: 248

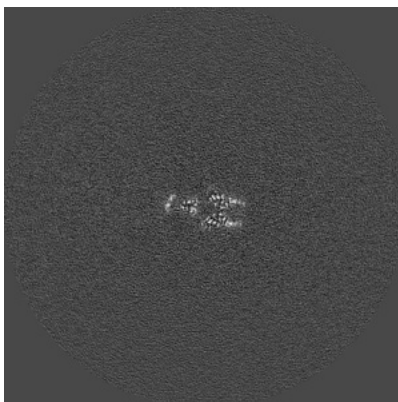


Z Index: 248

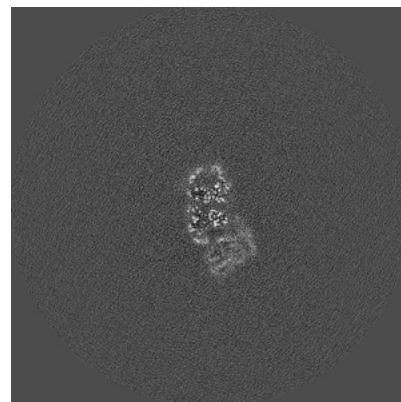
6.2.2 Raw map



X Index: 192



Y Index: 192

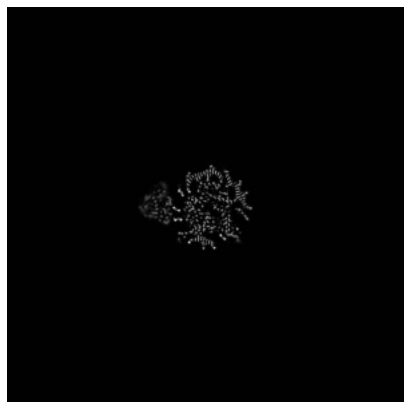


Z Index: 192

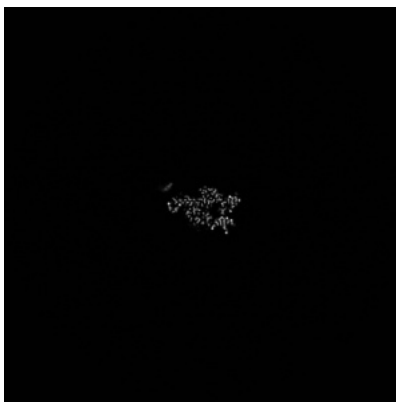
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

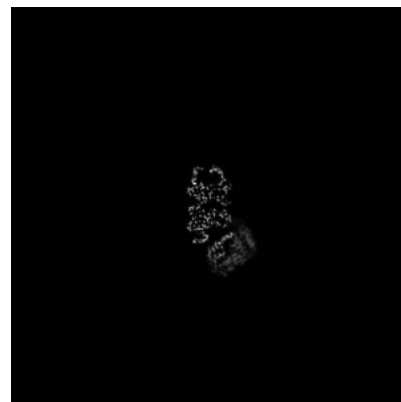
6.3.1 Primary map



X Index: 255

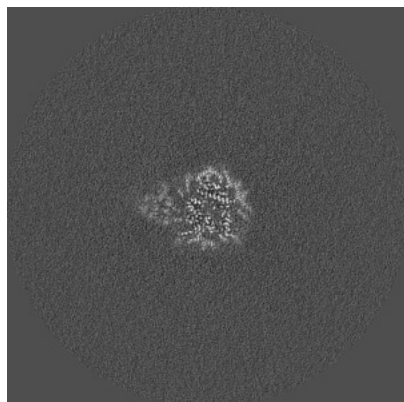


Y Index: 274

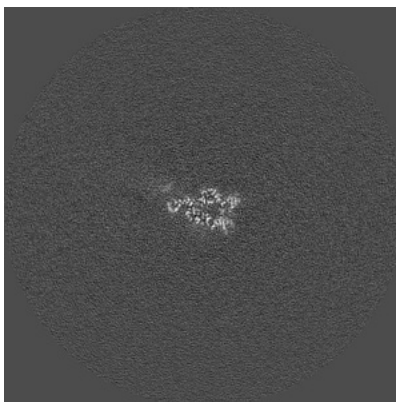


Z Index: 251

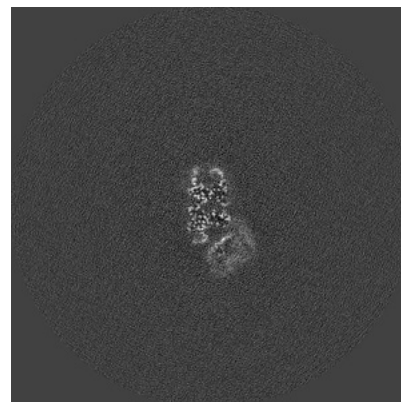
6.3.2 Raw map



X Index: 196



Y Index: 211

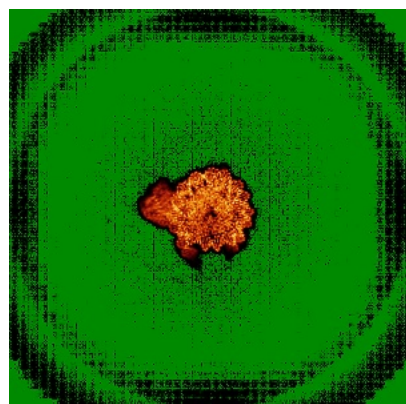


Z Index: 194

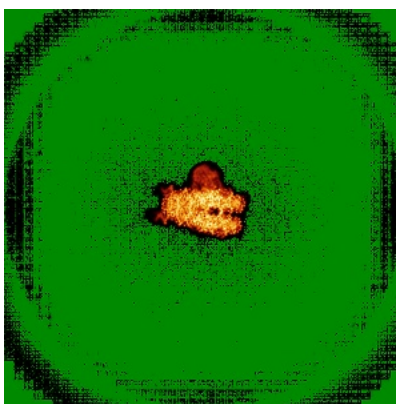
The images above show the largest variance slices of the map in three orthogonal directions.

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

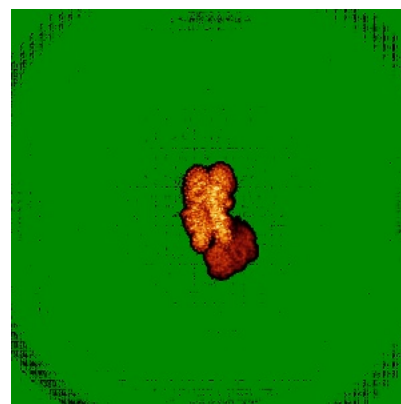
6.4.1 Primary map



X

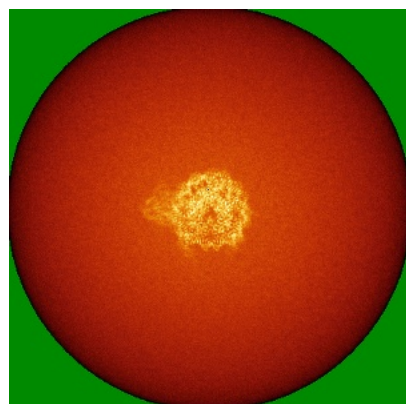


Y

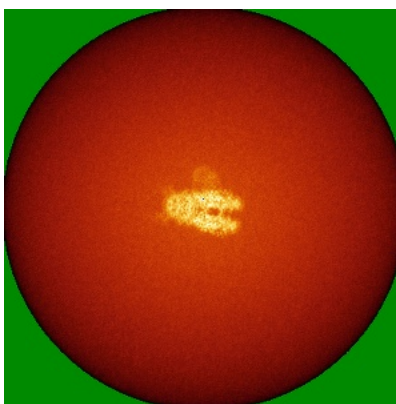


Z

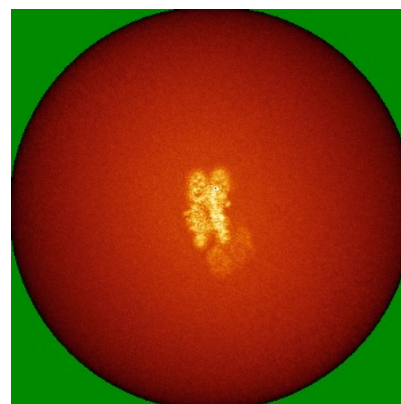
6.4.2 Raw map



X



Y

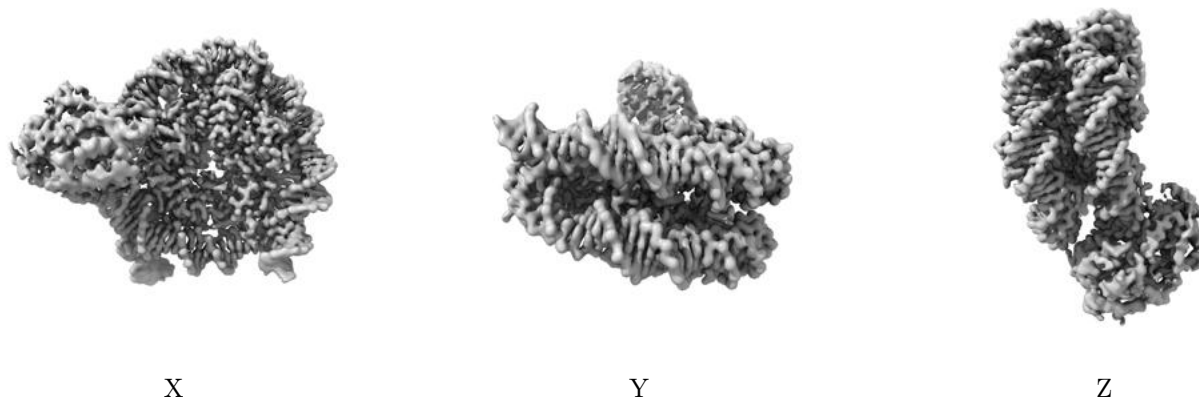


Z

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.

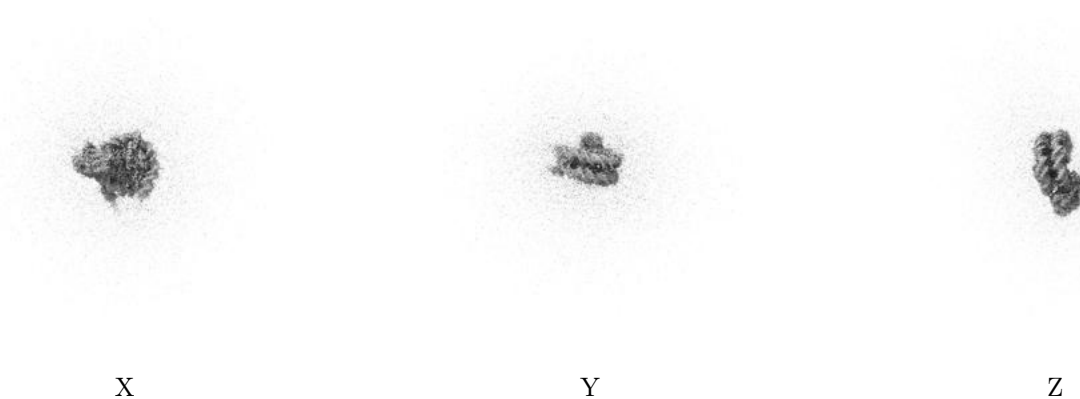
6.5 Orthogonal surface views [i](#)

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.

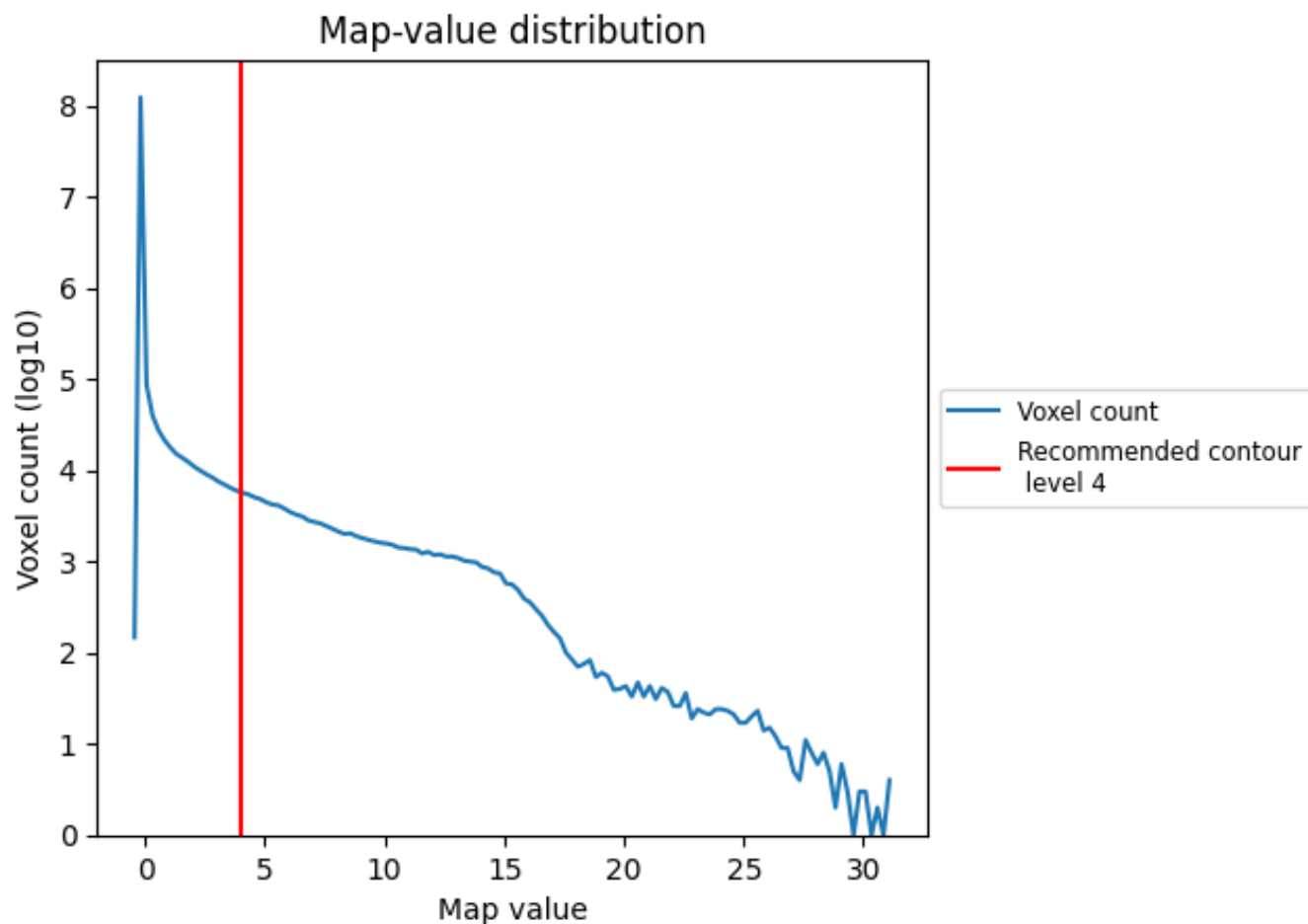
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

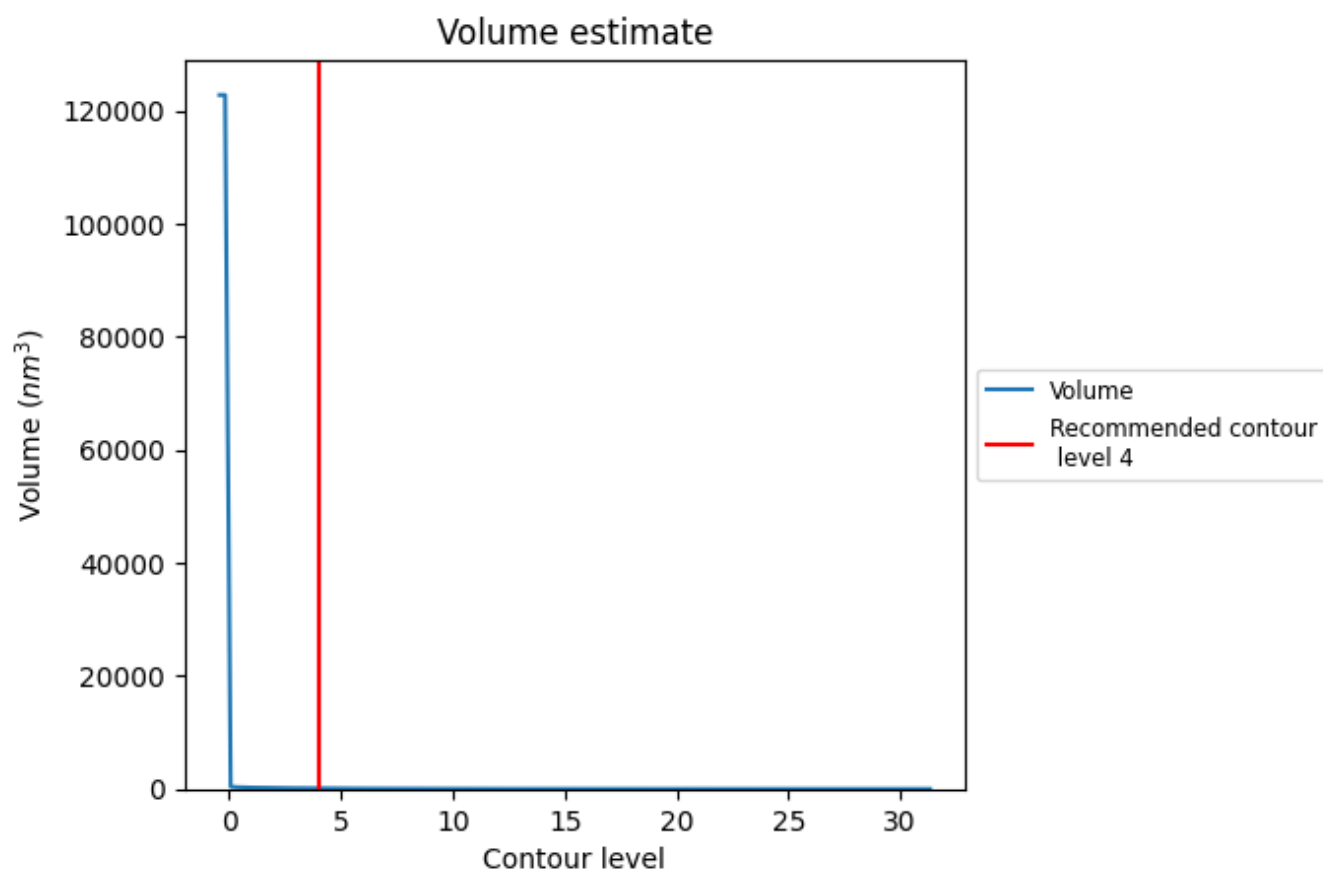
This section contains the results of statistical analysis of the map.

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.

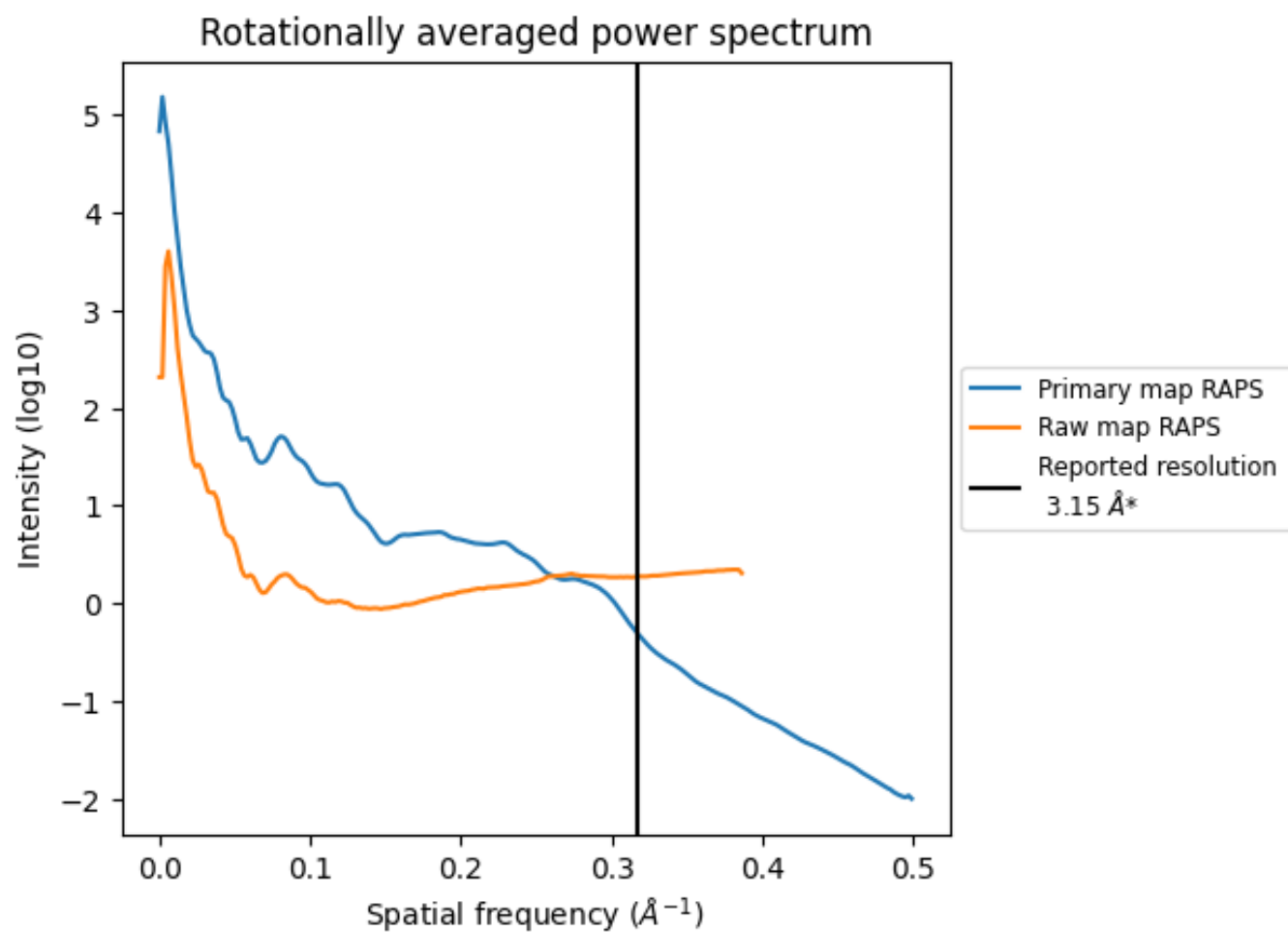
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 105 nm^3 ; this corresponds to an approximate mass of 94 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 ⓘ

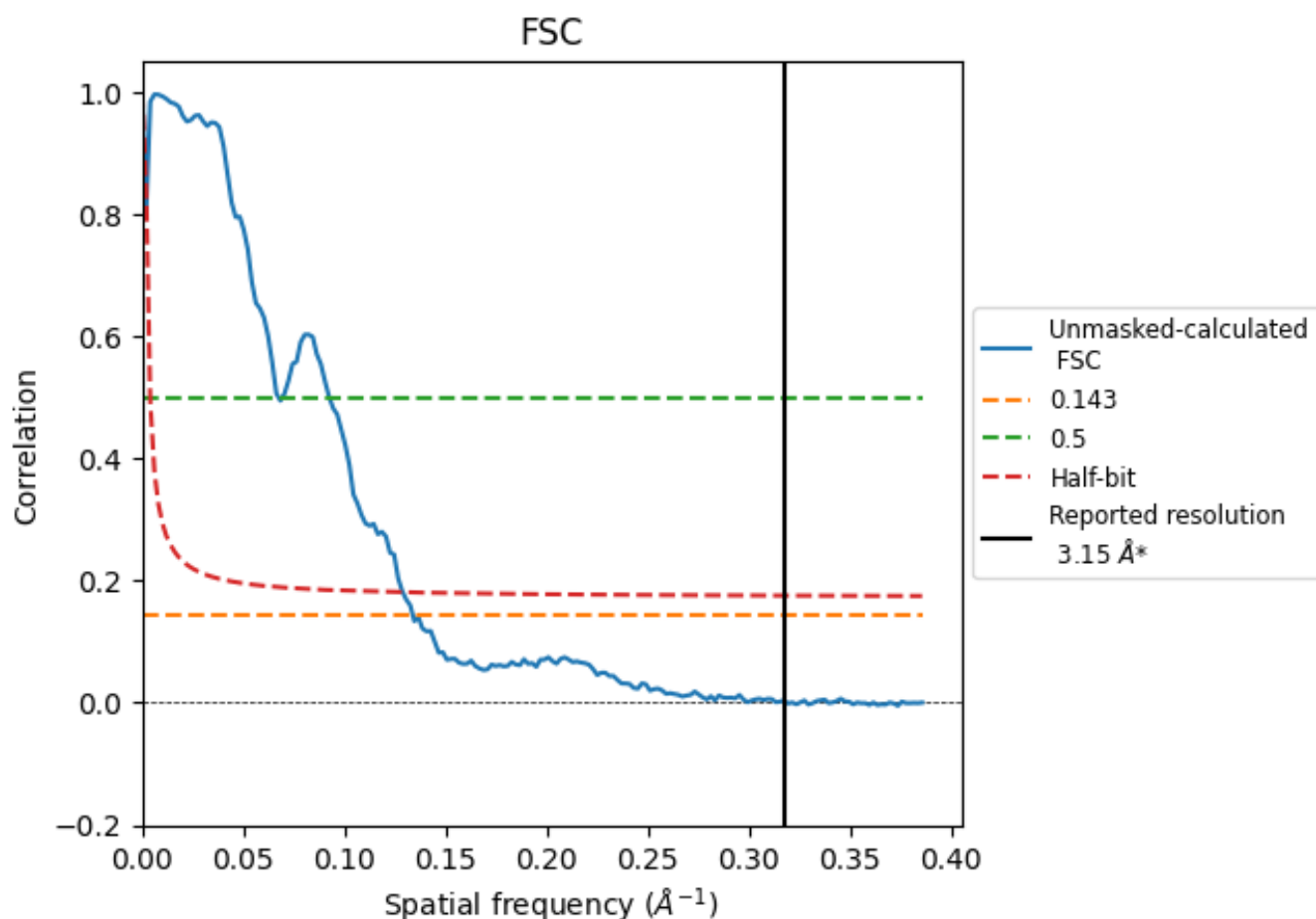


*Reported resolution corresponds to spatial frequency of 0.317 $\text{\AA}^{-1}$

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 0.317 Å⁻¹

8.2 Resolution estimates [i](#)

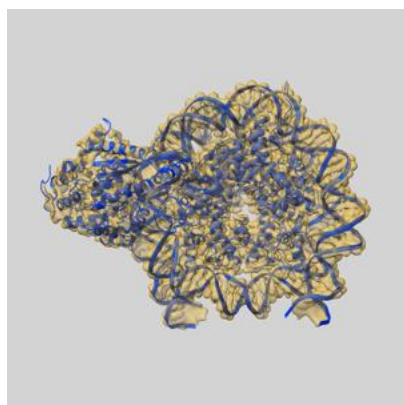
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.15	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.47	14.86	476.19

*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 7.47 differs from the reported value 3.15 by more than 10 %

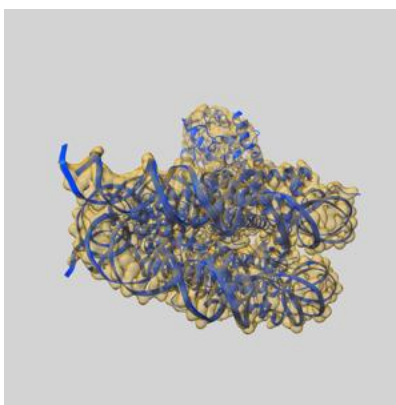
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47412 and PDB model 9E1L. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

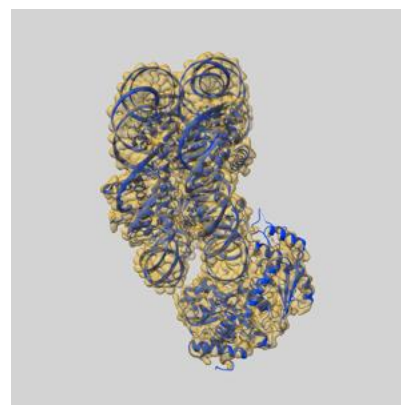
9.1 Map-model overlay [i](#)



X



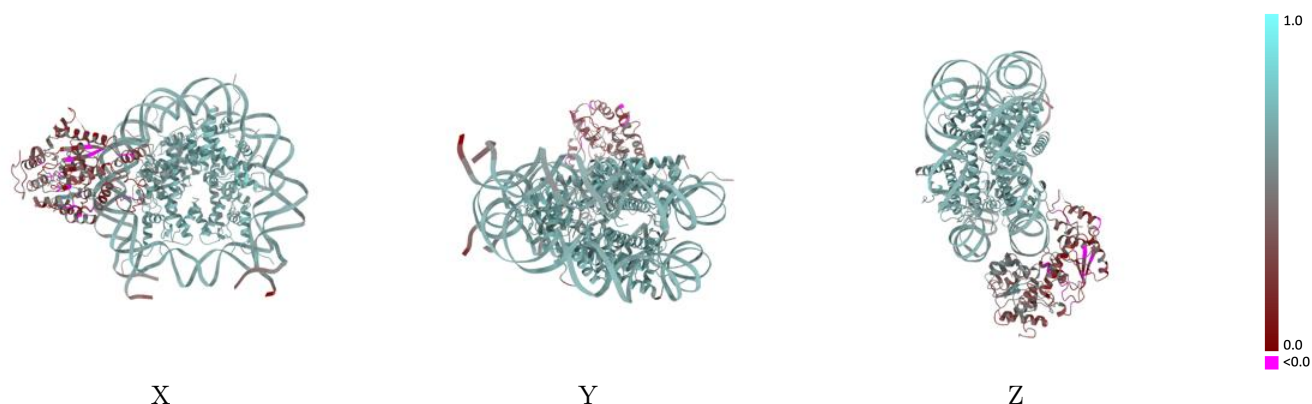
Y



Z

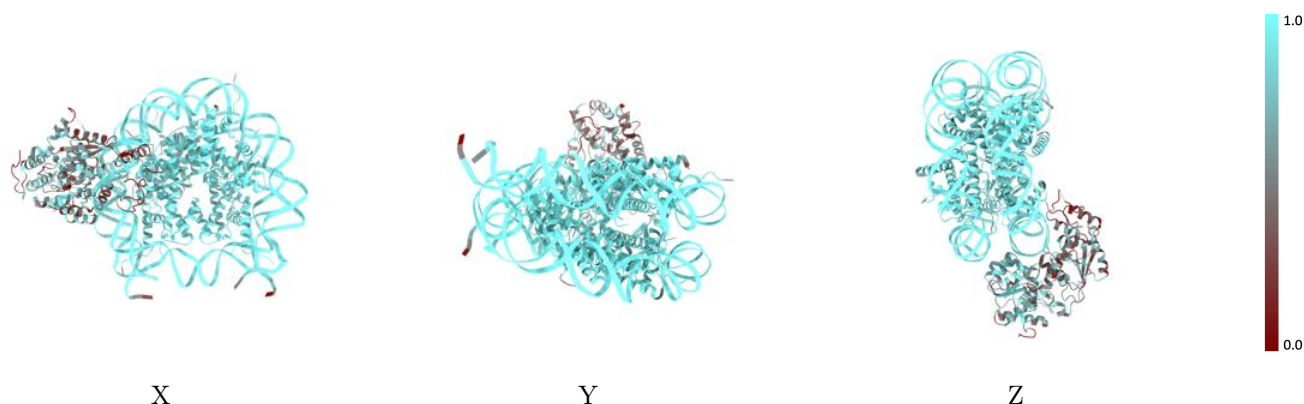
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



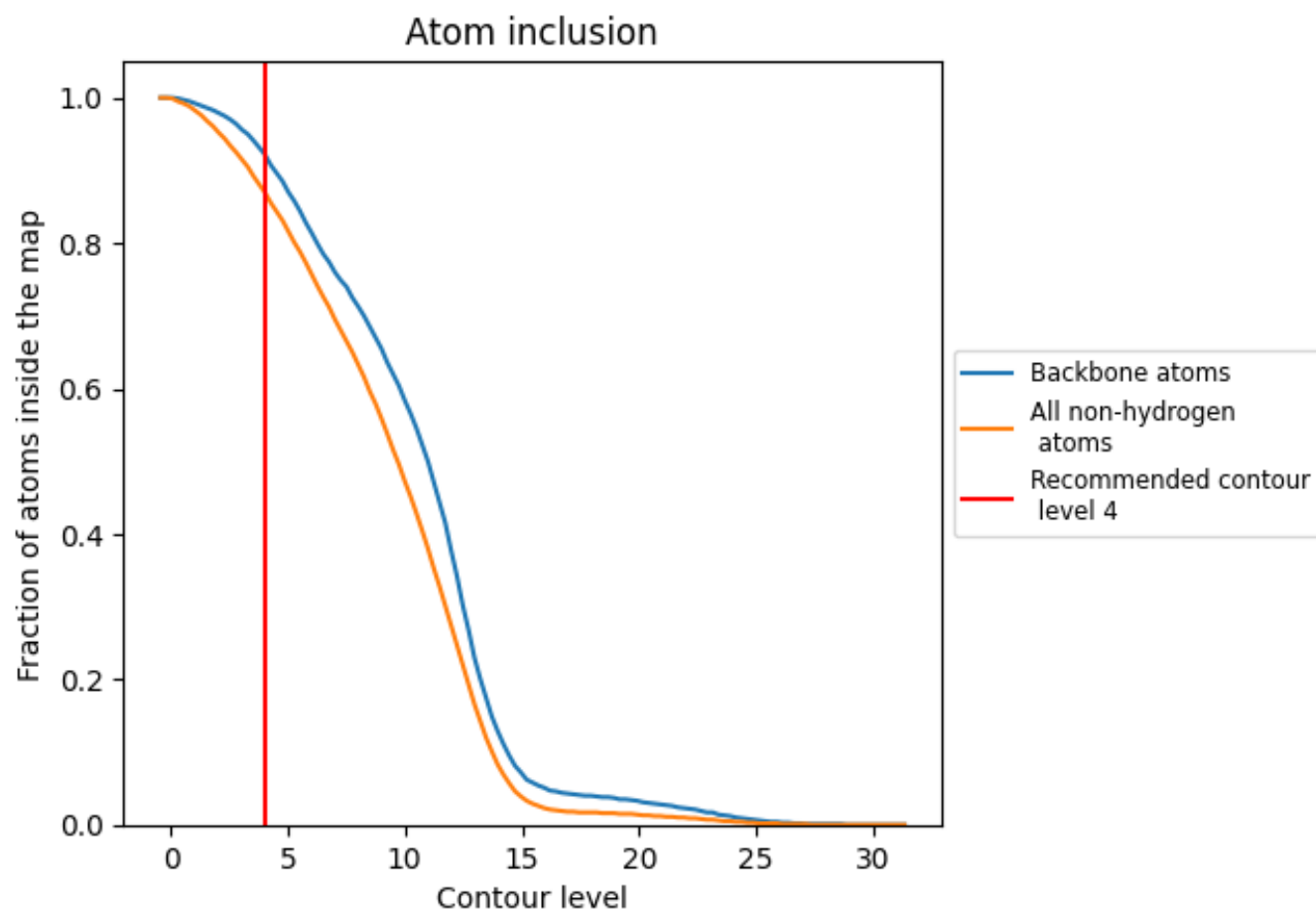
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 92% of all backbone atoms, 87% 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	0.8710	0.5590
A	0.9610	0.6620
B	0.9150	0.6370
C	0.9620	0.6630
D	0.9600	0.6600
E	0.9780	0.6630
F	0.9630	0.6650
G	0.9670	0.6560
H	0.9460	0.6550
I	0.9700	0.6050
J	0.9650	0.6030
W	0.5640	0.3210

1.0

0.0

<0.0