



wwPDB EM Validation Summary Report ⓘ

Sep 9, 2026 – 04:36 PM EDT

PDB ID : 9ZMM / pdb_00009zmm
EMDB ID : EMD-74422
Title : CryoEM structure of Ku heterodimer bound to N7 nucleosome
Authors : Lu, W.; He, Y.
Deposited on : 2025-12-10
Resolution : 3.89 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.dev133
MolProbity : 4-5-2 with Phenix2.0
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) : 2.50

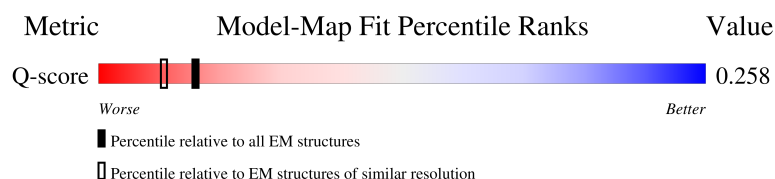
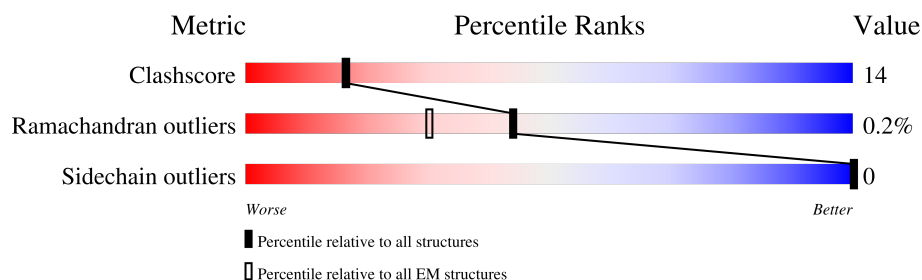
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.89 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	8712 (3.39 - 4.39)

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	I	154	51% 49%
2	J	154	36% 64%
3	A	101	74% 26%
3	E	101	63% 34% .

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Mol	Chain	Length	Quality of chain
4	B	87	
4	F	87	
5	C	229	
5	G	229	
6	D	99	
6	H	99	
7	K	504	
8	L	536	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 39210 atoms, of which 18450 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 DNA chain called DNA (154-mer).

Mol	Chain	Residues	Atoms						AltConf	Trace
1	I	154	Total	C	H	N	O	P	0	0
			4903	1503	1729	591	926	154		

- Molecule 2 is a DNA chain called DNA (154-mer).

Mol	Chain	Residues	Atoms						AltConf	Trace
2	J	154	Total	C	H	N	O	P	0	0
			4866	1491	1729	573	920	153		

- Molecule 3 is a protein called Histone H3.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	E	98	Total	C	H	N	O	S	0	0
			1654	509	846	156	140	3		
3	A	101	Total	C	H	N	O	S	0	0
			1716	526	883	161	143	3		

- Molecule 4 is a protein called Histone H4.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	F	83	Total	C	H	N	O	S	0	0
			1372	418	710	129	114	1		
4	B	87	Total	C	H	N	O	S	0	0
			1461	442	758	142	118	1		

- Molecule 5 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	115	Total	C	H	N	O	0	0
			1828	552	948	175	153		
5	C	108	Total	C	H	N	O	0	0
			1728	525	896	163	144		

- Molecule 6 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	H	99	Total	C	H	N	O	S	0	0
			1614	493	829	146	144	2		
6	D	99	Total	C	H	N	O	S	0	0
			1613	493	828	146	144	2		

- Molecule 7 is a protein called X-ray repair cross-complementing protein 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	K	490	Total	C	H	N	O	S	0	0
			8002	2533	4047	671	734	17		

- Molecule 8 is a protein called X-ray repair cross-complementing protein 5.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	L	526	Total	C	H	N	O	S	0	0
			8450	2693	4245	704	785	23		

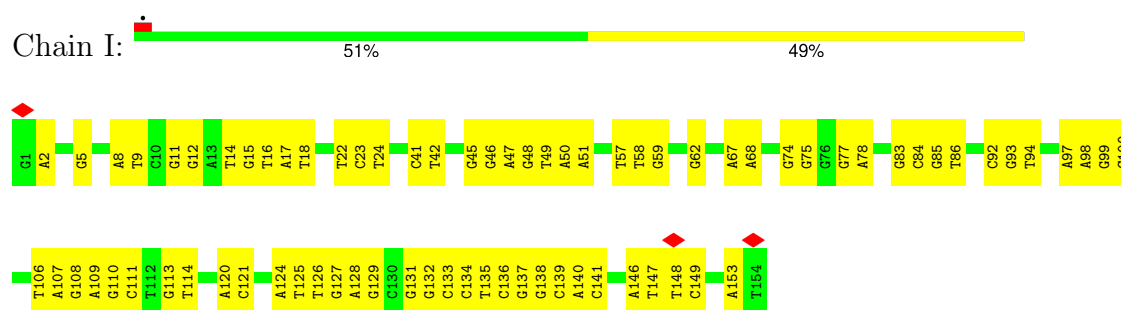
- Molecule 9 is water.

Mol	Chain	Residues	Atoms			AltConf
9	F	1	Total	H	O	0
			3	2	1	

3 Residue-property plots

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

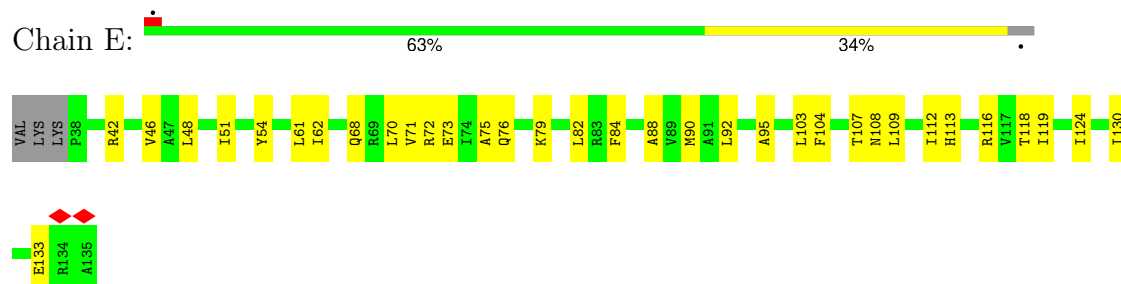
• Molecule 1: DNA (154-mer)



• Molecule 2: DNA (154-mer)

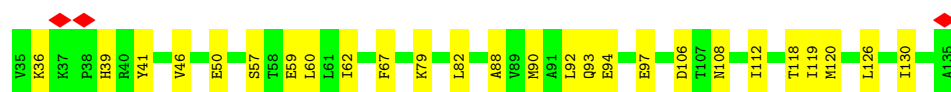


• Molecule 3: Histone H3

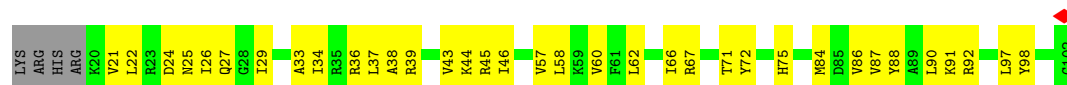


• Molecule 3: Histone H3





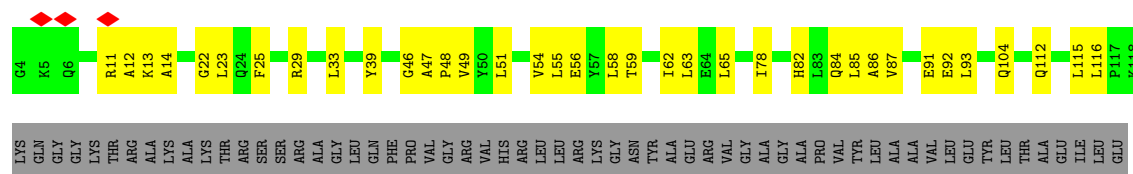
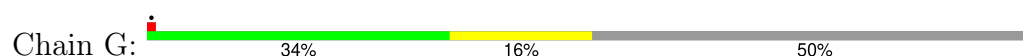
- Molecule 4: Histone H4



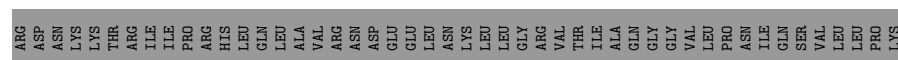
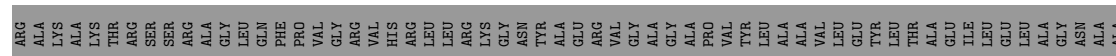
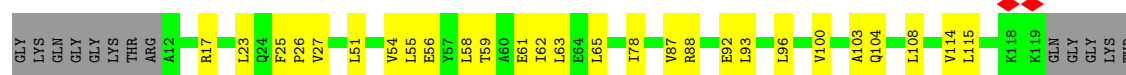
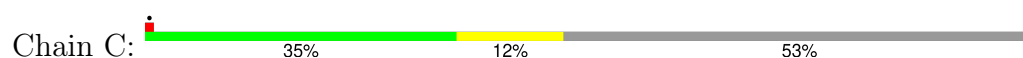
- Molecule 4: Histone H4



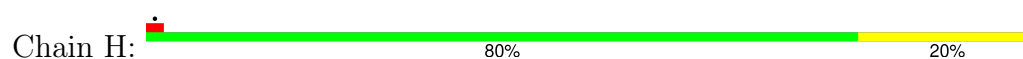
- Molecule 5: Histone H2A



- Molecule 5: Histone H2A



- Molecule 6: Histone H2B



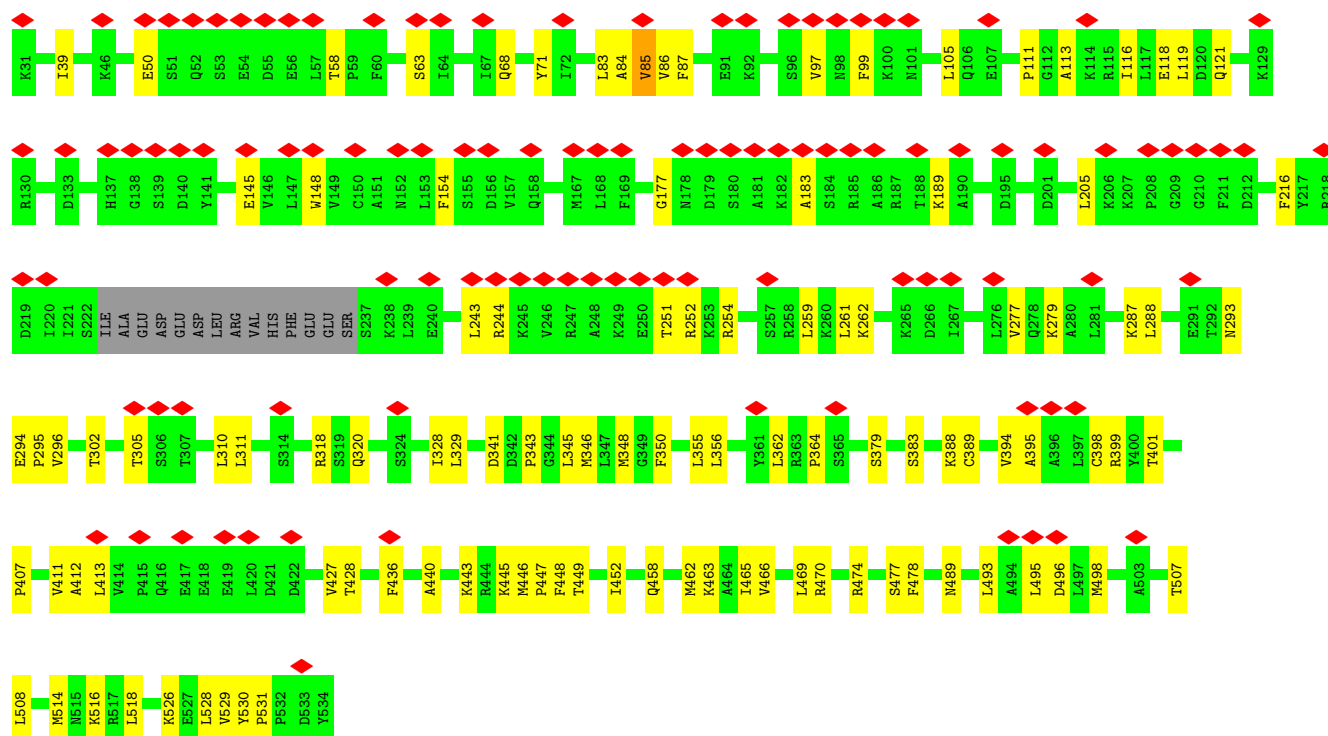
- Molecule 6: Histone H2B

Chain D:  66% 34%



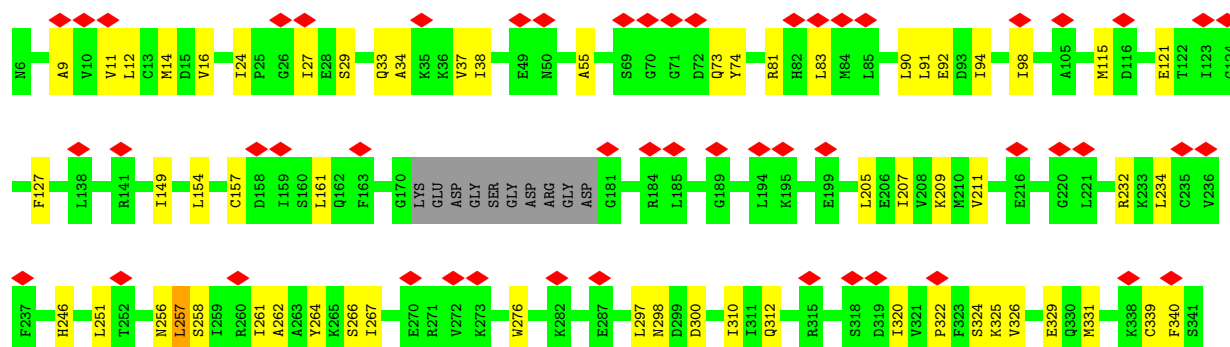
- Molecule 7: X-ray repair cross-complementing protein 6

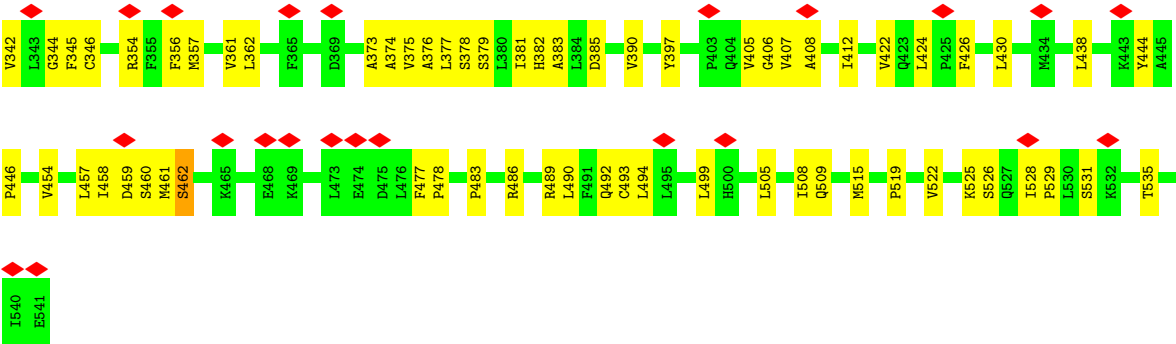
Chain K:  22% 75% 22%



- Molecule 8: X-ray repair cross-complementing protein 5

Chain L:  14% 75% 23%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81691	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.397	Depositor
Minimum map value	-0.142	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	238.08, 238.08, 238.08	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.93, 0.93, 0.93	Depositor

5 Model quality

5.1 Standard geometry

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	I	0.26	0/3563	0.50	0/5502
2	J	0.26	0/3516	0.50	0/5420
3	A	0.23	0/845	0.41	0/1132
3	E	0.23	0/820	0.43	0/1099
4	B	0.24	0/711	0.40	0/948
4	F	0.26	0/669	0.50	0/894
5	C	0.22	0/842	0.37	0/1135
5	G	0.21	0/890	0.38	0/1197
6	D	0.23	0/796	0.46	0/1065
6	H	0.22	0/796	0.41	0/1065
7	K	0.17	0/4032	0.44	0/5429
8	L	0.15	0/4292	0.41	1/5791 (0.0%)
All	All	0.22	0/21772	0.45	1/30677 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
8	L	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	L	378	SER	N-CA-C	-6.88	103.56	112.23

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	L	266	SER	Peptide

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	I	3174	1729	1730	73	0
2	J	3137	1729	1729	101	0
3	A	833	883	880	31	0
3	E	808	846	846	34	0
4	B	703	758	755	31	0
4	F	662	710	709	50	0
5	C	832	896	895	29	0
5	G	880	948	945	30	0
6	D	785	828	825	38	0
6	H	785	829	825	27	0
7	K	3955	4047	4042	112	0
8	L	4205	4245	4239	115	0
9	F	1	2	0	0	0
All	All	20760	18450	18420	550	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 14.

The worst 5 of 550 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:K:462:MET:HE1	8:L:379:SER:O	1.76	0.85
6:H:74:ALA:HB1	6:H:86:ILE:HD11	1.58	0.84
7:K:462:MET:HE3	8:L:383:ALA:HB2	1.59	0.82
7:K:443:LYS:HA	8:L:267:ILE:HD12	1.64	0.78
7:K:440:ALA:CB	8:L:234:LEU:HD21	2.14	0.76

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	
3	A	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
3	E	96/101 (95%)	90 (94%)	6 (6%)	0	100	100
4	B	85/87 (98%)	79 (93%)	6 (7%)	0	100	100
4	F	81/87 (93%)	75 (93%)	6 (7%)	0	100	100
5	C	106/229 (46%)	102 (96%)	4 (4%)	0	100	100
5	G	113/229 (49%)	105 (93%)	8 (7%)	0	100	100
6	D	97/99 (98%)	91 (94%)	6 (6%)	0	100	100
6	H	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
7	K	486/504 (96%)	430 (88%)	55 (11%)	1 (0%)	43	74
8	L	522/536 (97%)	475 (91%)	44 (8%)	3 (1%)	21	55
All	All	1782/2072 (86%)	1637 (92%)	141 (8%)	4 (0%)	44	74

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	K	85	VAL
8	L	257	LEU
8	L	462	SER
8	L	27	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	
3	A	88/88 (100%)	88 (100%)	0	100	100
3	E	85/88 (97%)	85 (100%)	0	100	100
4	B	72/72 (100%)	72 (100%)	0	100	100
4	F	68/72 (94%)	68 (100%)	0	100	100
5	C	85/178 (48%)	85 (100%)	0	100	100
5	G	89/178 (50%)	89 (100%)	0	100	100
6	D	85/85 (100%)	85 (100%)	0	100	100
6	H	85/85 (100%)	85 (100%)	0	100	100
7	K	444/458 (97%)	444 (100%)	0	100	100
8	L	473/481 (98%)	473 (100%)	0	100	100
All	All	1574/1785 (88%)	1574 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
8	L	411	HIS
8	L	496	HIS
7	K	110	ASN
7	K	137	HIS
7	K	176	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

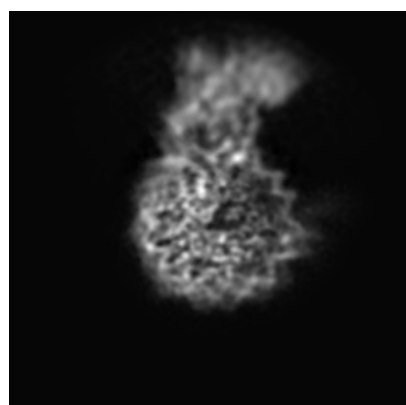
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74422. These allow visual inspection of the internal detail of the map and identification of artifacts.

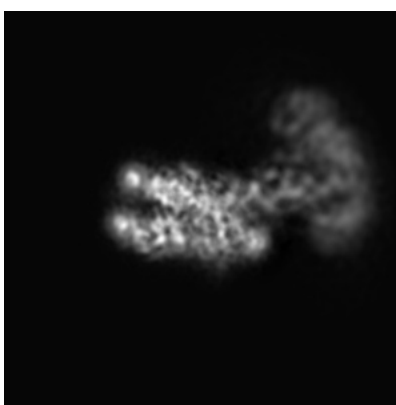
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

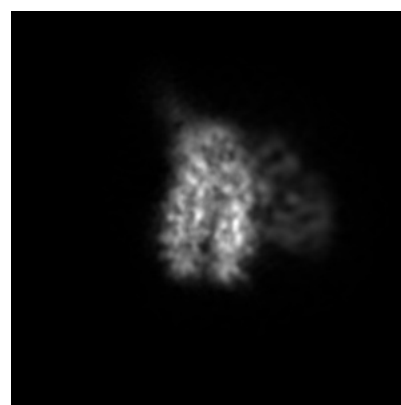
6.1.1 Primary map



X



Y

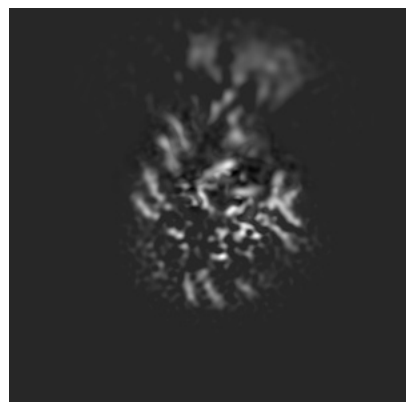


Z

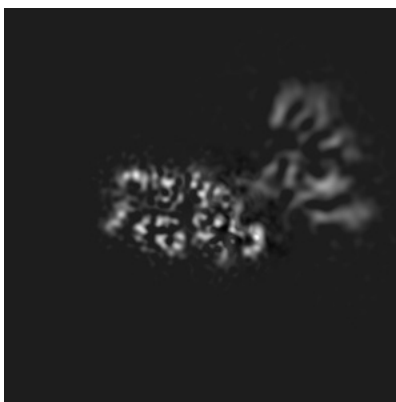
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

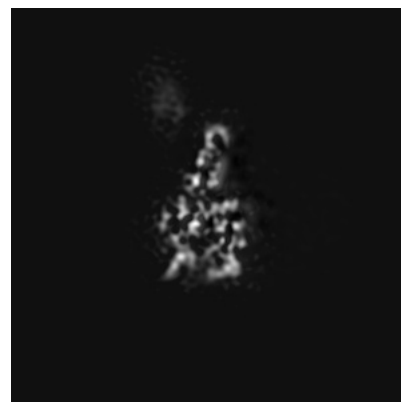
6.2.1 Primary map



X Index: 128



Y Index: 128

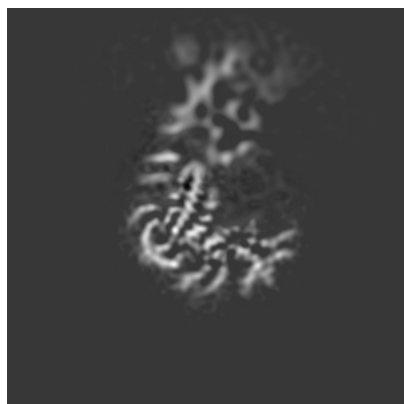


Z Index: 128

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

6.3 Largest variance slices [i](#)

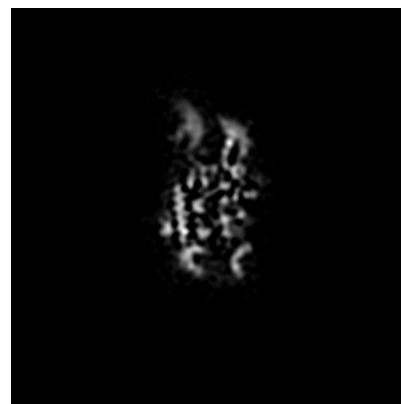
6.3.1 Primary map



X Index: 143



Y Index: 112



Z Index: 99

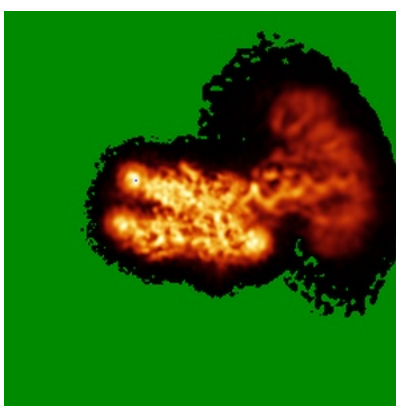
The images above show the largest variance slices of the map in three orthogonal directions.

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

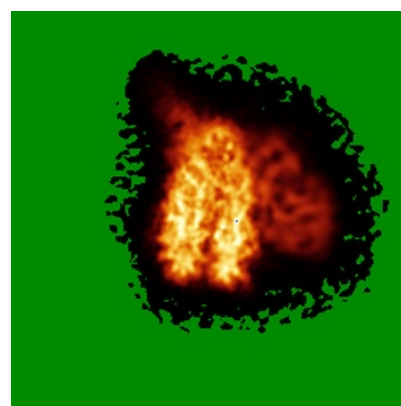
6.4.1 Primary map



X



Y

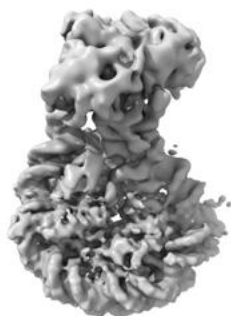


Z

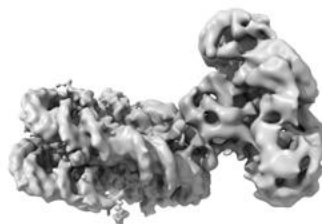
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

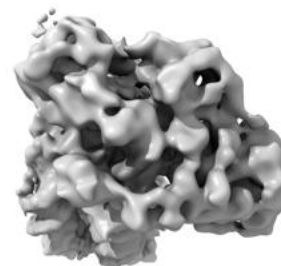
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

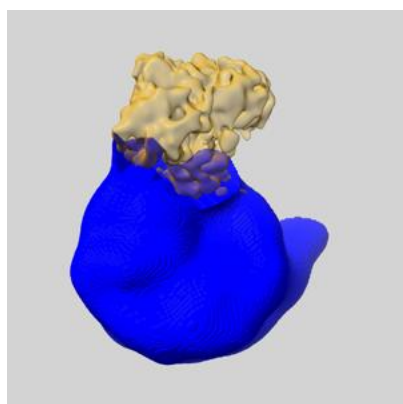
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

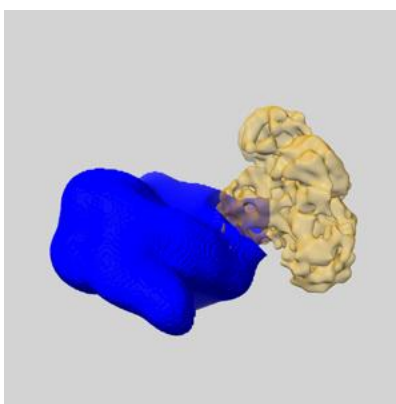
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

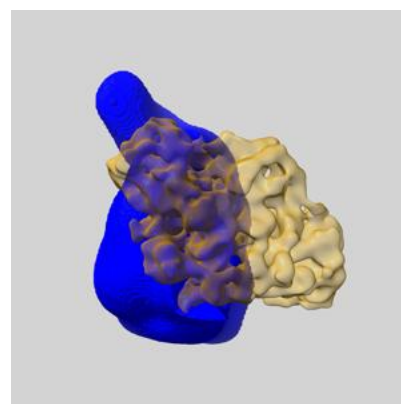
6.6.1 emd_74422_msk_2.map [i](#)



X

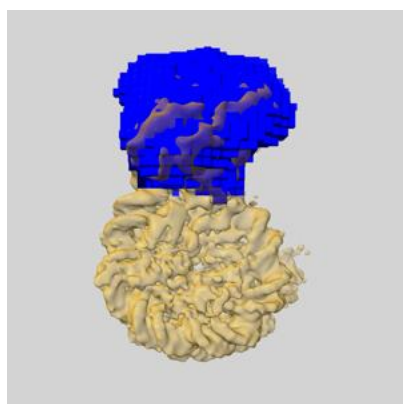


Y

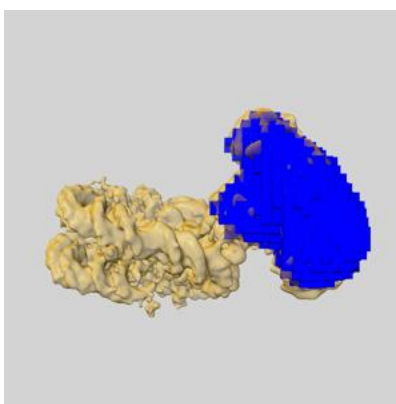


Z

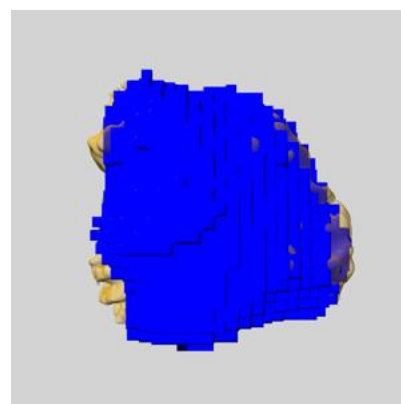
6.6.2 emd_74422_msk_1.map [i](#)



X



Y

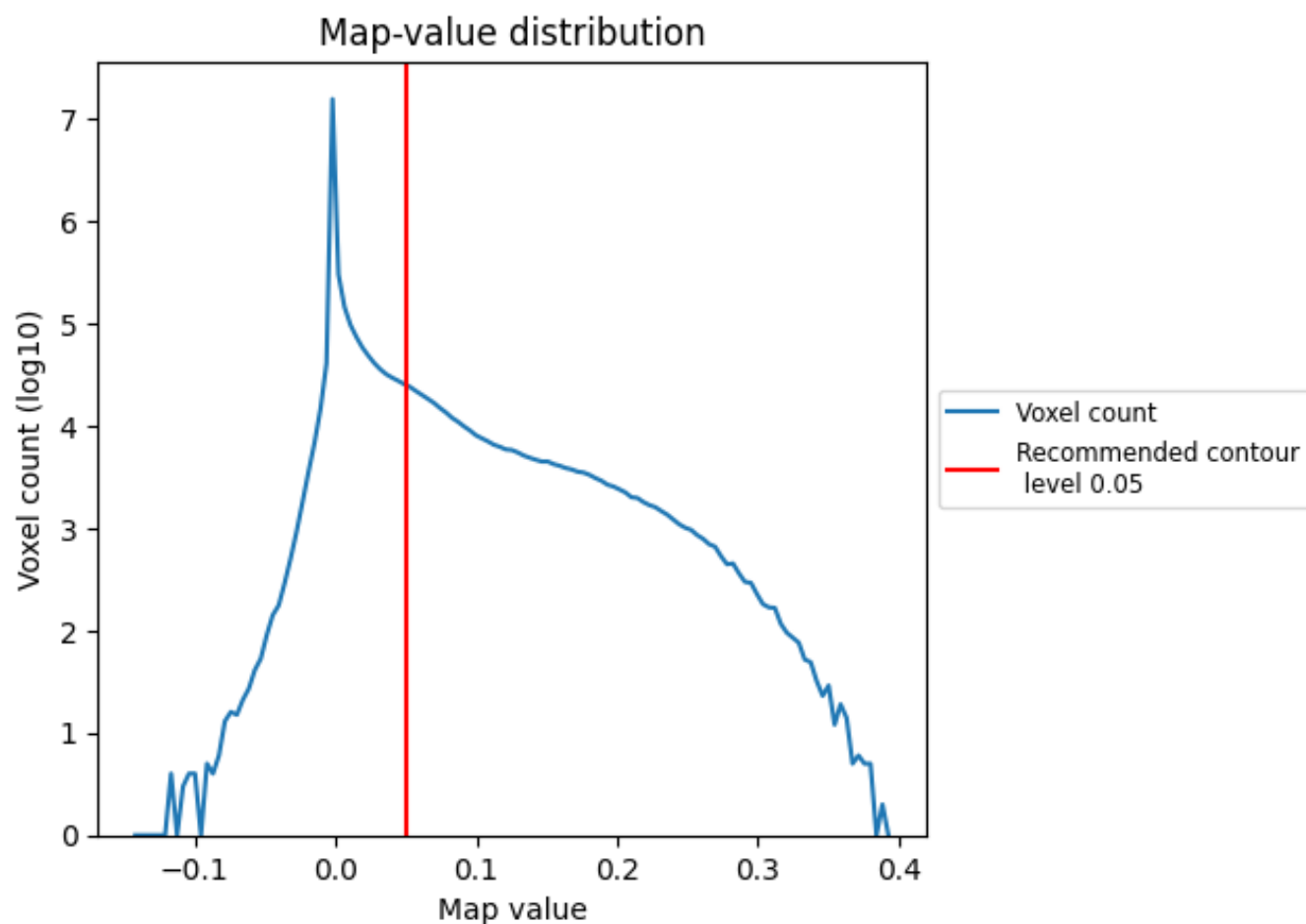


Z

7 Map analysis [i](#)

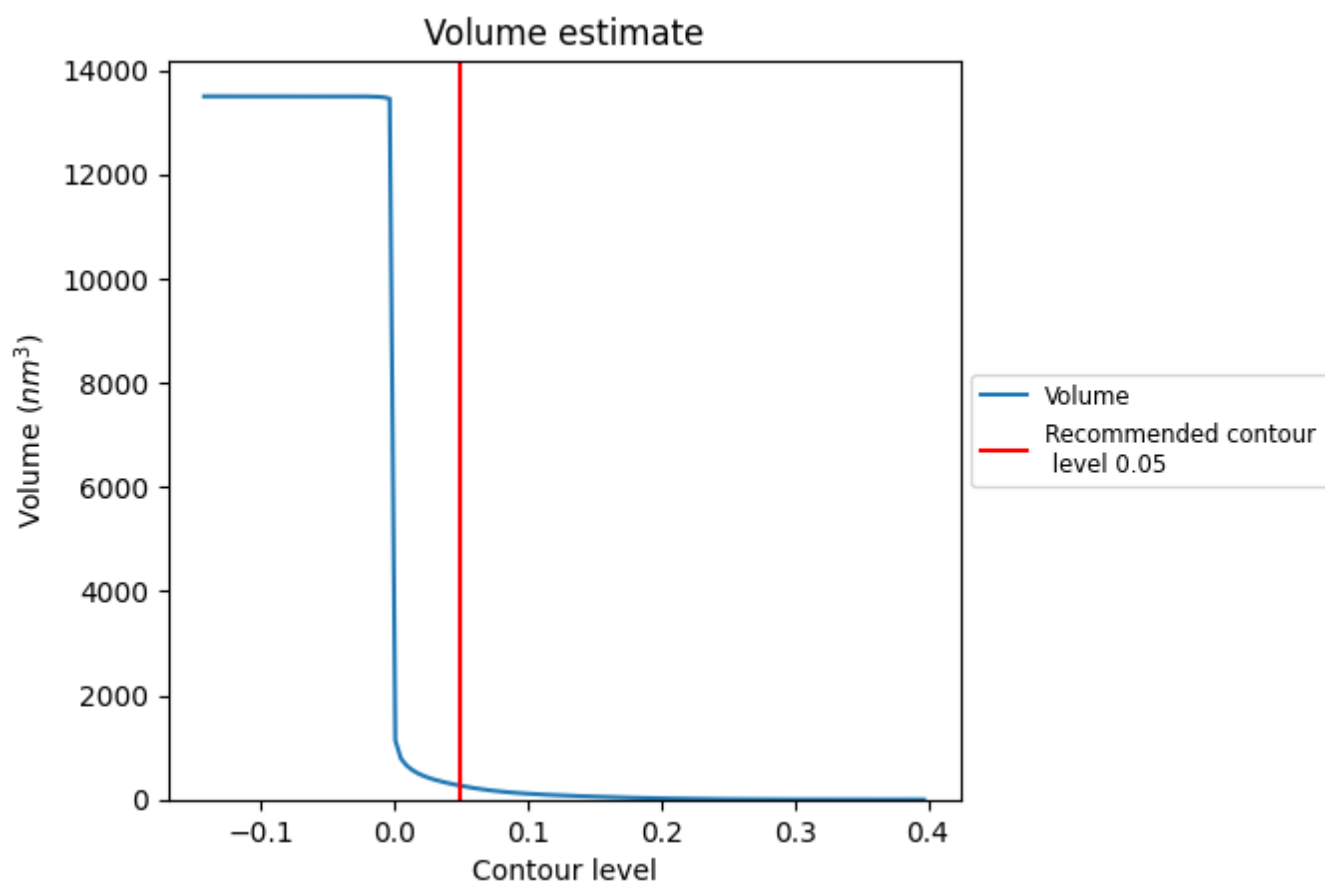
This section contains the results of statistical analysis of the map.

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.

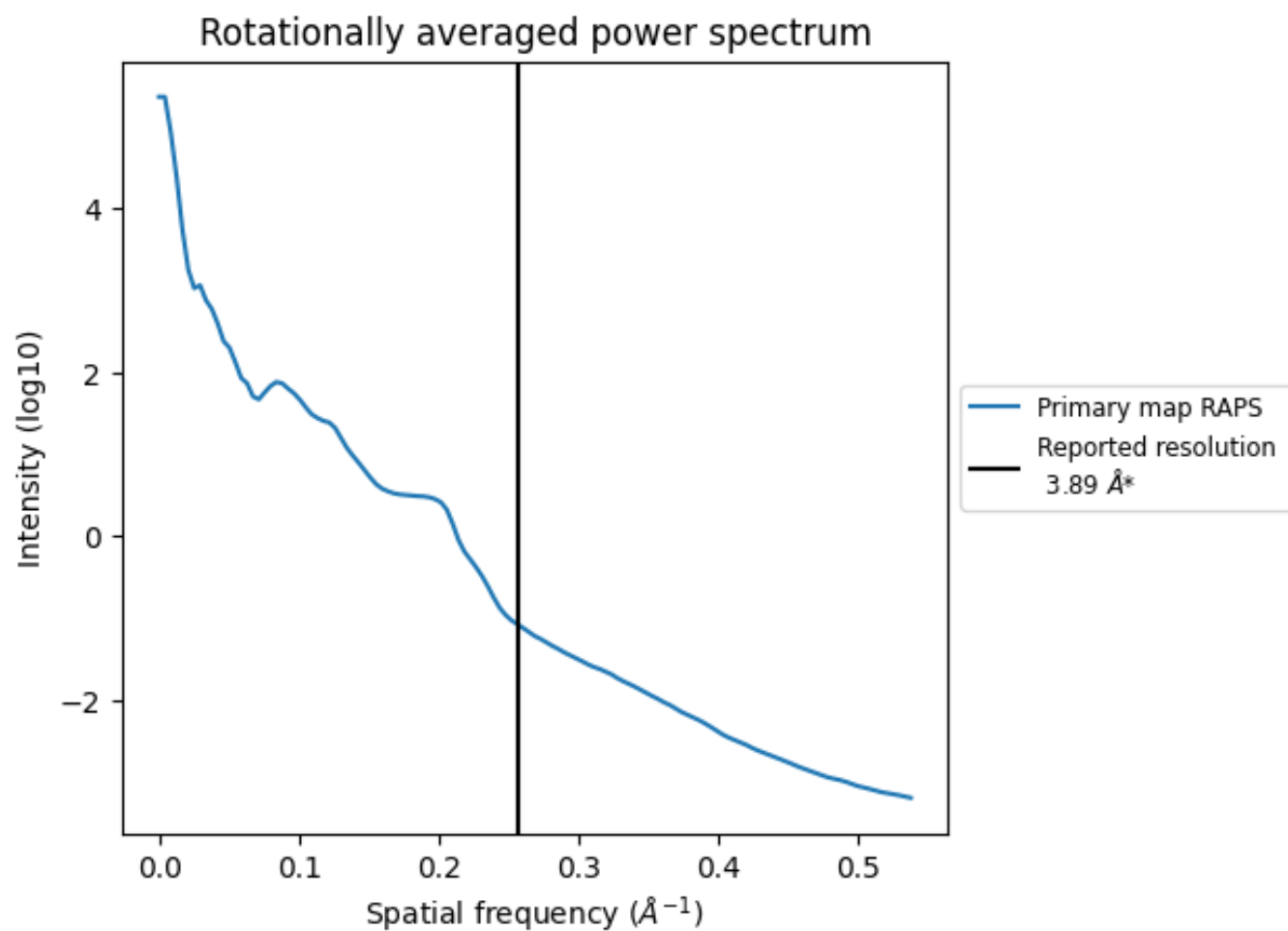
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 264 nm³; this corresponds to an approximate mass of 239 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 0.257 Å⁻¹

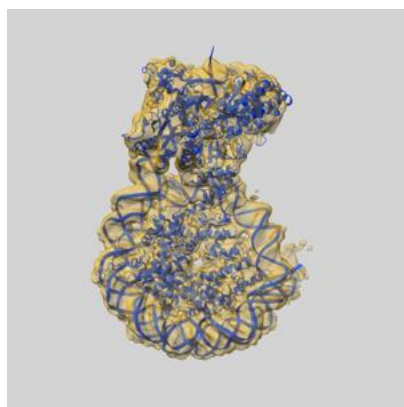
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

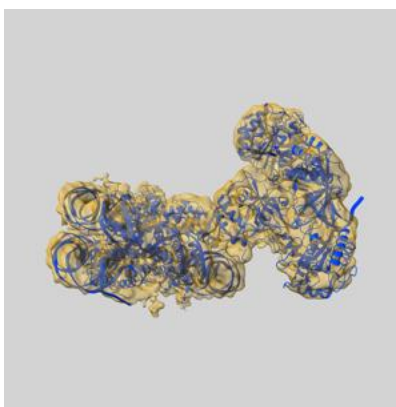
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-74422 and PDB model 9ZMM. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

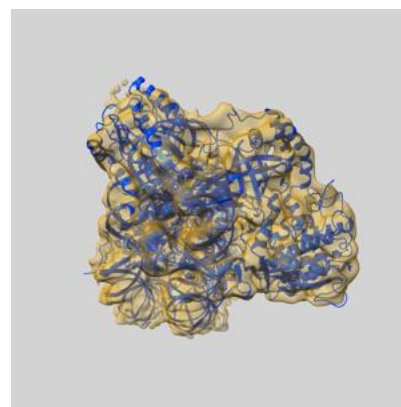
9.1 Map-model overlay [i](#)



X



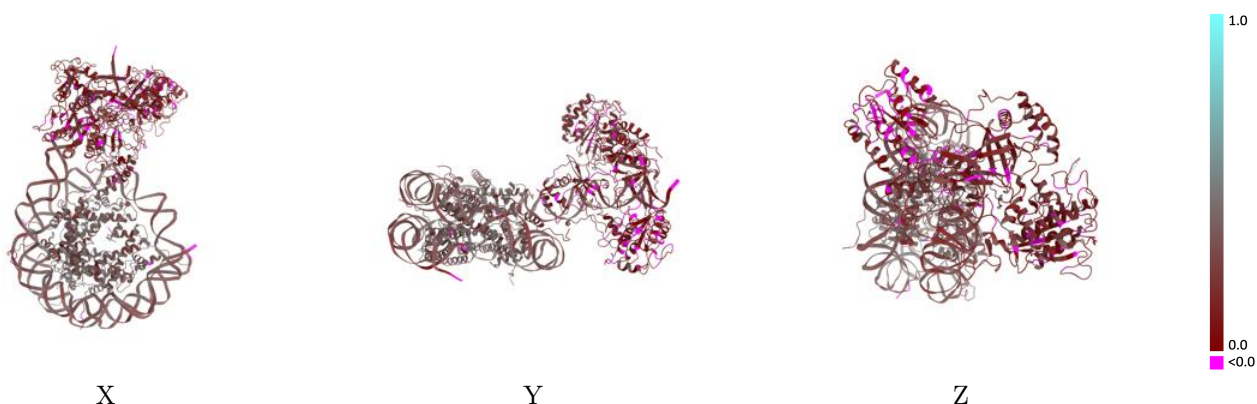
Y



Z

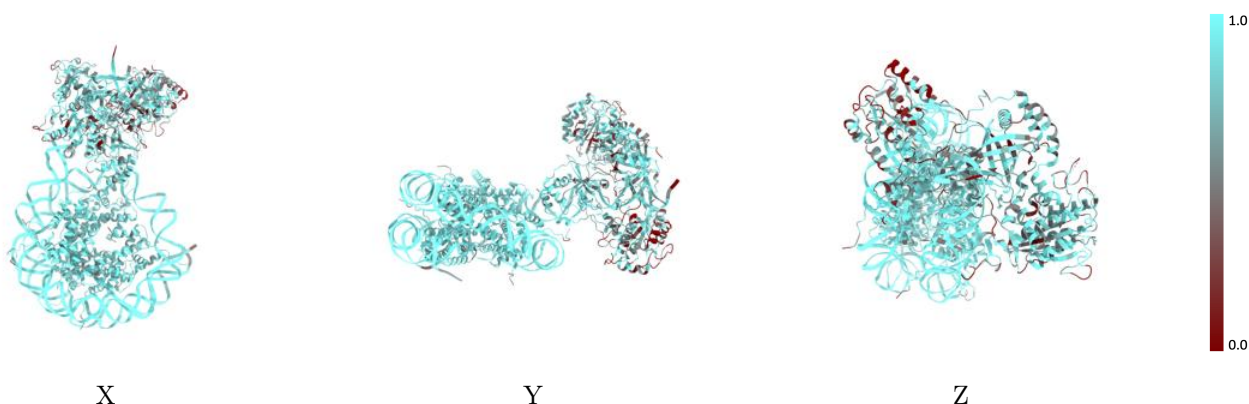
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



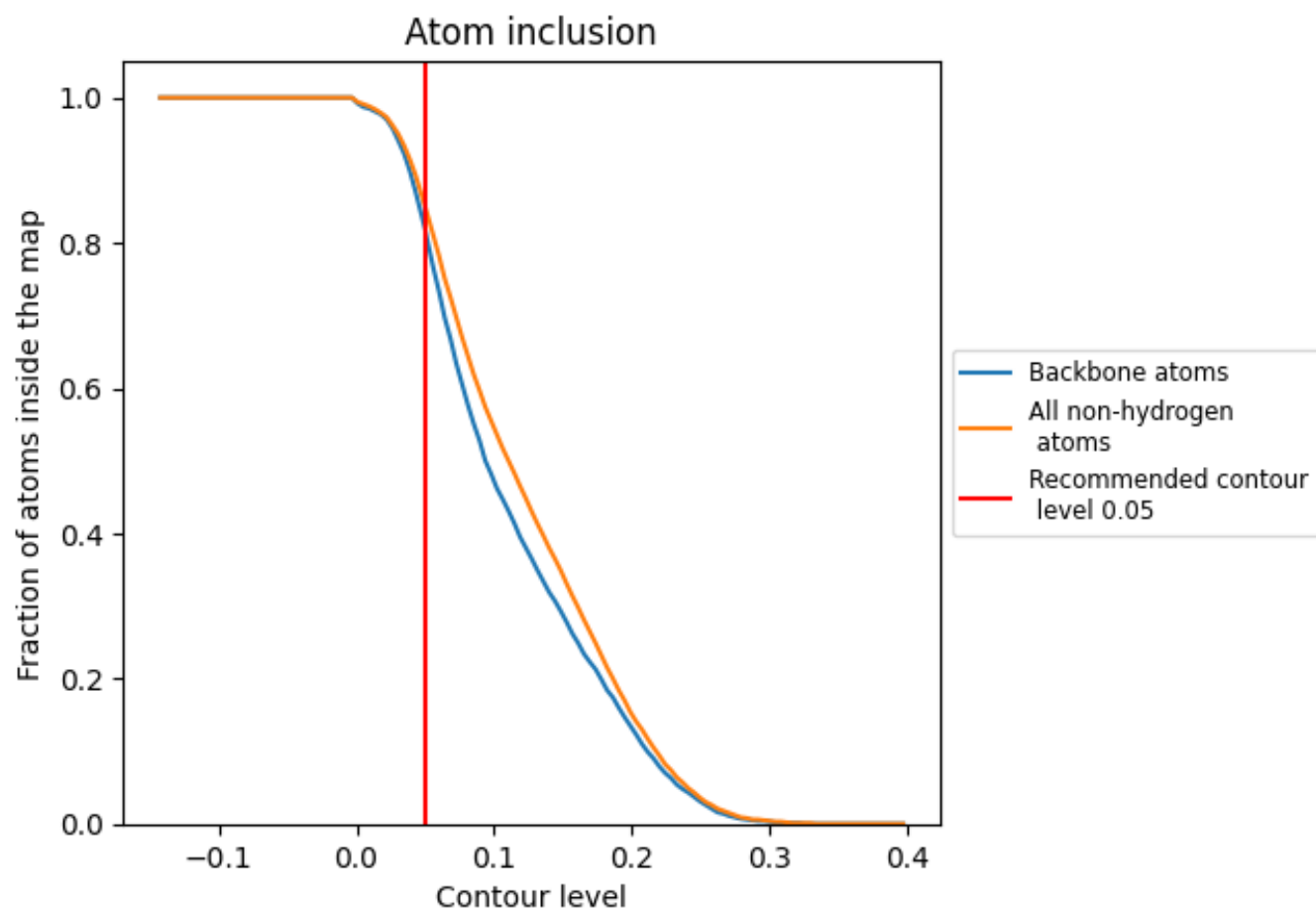
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion ⓘ



At the recommended contour level, 82% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8500	0.2580
A	0.9260	0.3360
B	0.9170	0.3580
C	0.9190	0.3790
D	0.9190	0.3560
E	0.8930	0.3450
F	0.9150	0.3680
G	0.9250	0.3500
H	0.9210	0.3340
I	0.9590	0.3010
J	0.9760	0.3130
K	0.6550	0.1360
L	0.6980	0.1610

1.0

0.0

<0.0