



# wwPDB EM Validation Summary Report ⓘ

Apr 20, 2026 – 01:03 PM EDT

PDB ID : 9Z05 / pdb\_00009z05  
EMDB ID : EMD-73694  
Title : Structure of human lymphoid-specific helicase HELLS in its auto-inhibitory state (D3)  
Authors : Kaur, G.; Horton, J.R.; Cheng, X.  
Deposited on : 2025-10-31  
Resolution : 2.86 Å(reported)  
Based on initial model : .

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:

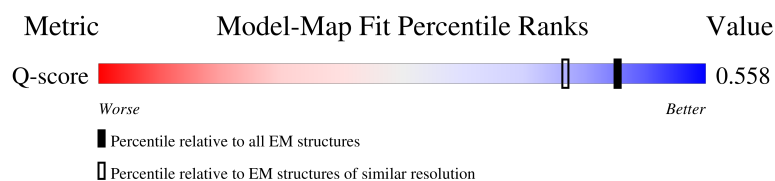
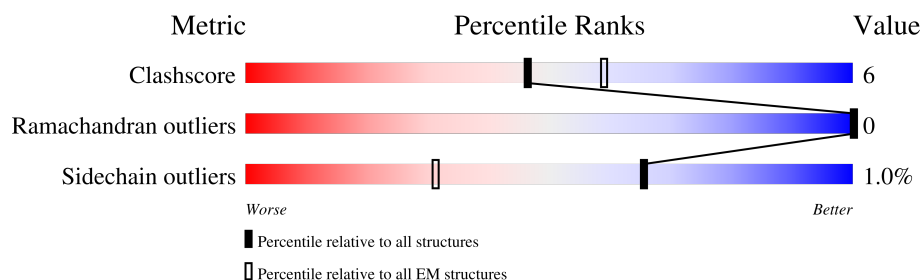
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 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 2.86 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	12017 ( 2.36 - 3.36 )

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	838	 32% 7% 61%
1	B	838	 32% 6% 61%
1	C	838	 32% 7% 61%
1	D	838	 32% 6% 61%

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Mol	Chain	Length	Quality of chain
1	E	838	 32%7%61%
1	F	838	 32%6%61%

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15960 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 Lymphoid-specific helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	324	Total 2660	C 1703	N 465	O 475	S 17	2	0
1	B	324	Total 2660	C 1703	N 465	O 475	S 17	2	0
1	C	324	Total 2660	C 1703	N 465	O 475	S 17	2	0
1	D	324	Total 2660	C 1703	N 465	O 475	S 17	2	0
1	E	324	Total 2660	C 1703	N 465	O 475	S 17	2	0
1	F	324	Total 2660	C 1703	N 465	O 475	S 17	2	0

### 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: Lymphoid-specific helicase



- Molecule 1: Lymphoid-specific helicase





[illegible]

- Molecule 1: Lymphoid-specific helicase

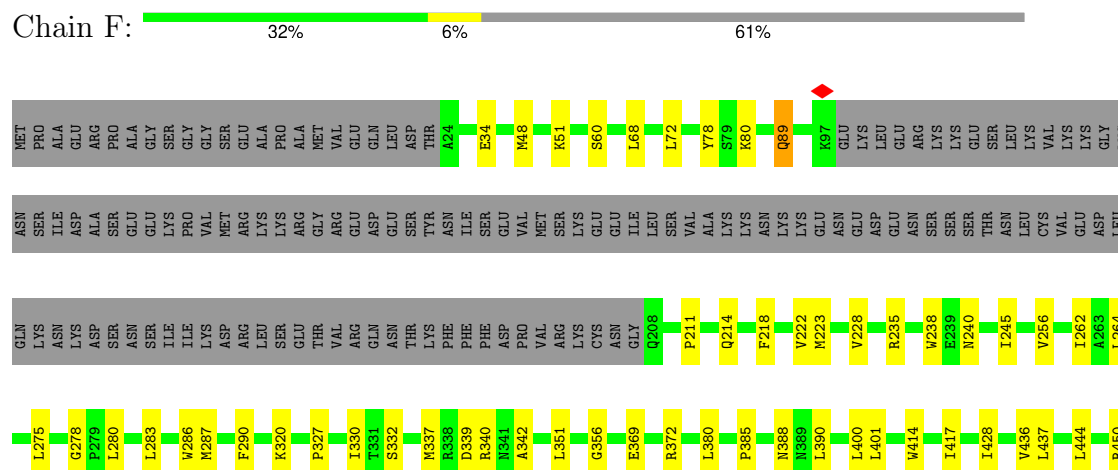
Chain D:  32% 6% 61%

GLY	LYS	LEU	GLY	PRO	ARG	GLY	TYR	GLY	TYR	LEU	LEU	L275	GLN	ASN	MET
LYS	MET	ASN	PHE	SER	ASP	TYR	SER	GLY	SER	GLY	VAL	L276	LYS	SER	PRO
ILE	GLY	LEU	LEU	ASP	PHE	ILE	ILE	PRO	ILE	VAL	PRO	G278	ASN	ILE	ALA
ILE	ASN	LEU	LEU	LEU	SER	ASP	ASP	PRO	ASP	ARG	LYS	P279	LYS	ASP	ARG
PHE	LYS	ASN	GLN	SER	SER	GLN	ASP	LYS	ASP	ARG	LYS	L280	SER	SER	PRO
LYS	ASN	ALA	ALA	ARG	ARG	VAL	PHE	ARG	PHE	GLY	ARG		ASN	GLY	ALA
ILE	ILE	ASP	LEU	LEU	LEU	THR	PRO	GLN	PRO	GLY	GLY	W286	SER	GLY	GLY
LEU	LEU	ASP	ASP	ASP	GLY	GLN	ASN	VAL	ASN	VAL	VAL	M287	ILE	LYS	SER
GLY	GLY	ASP	GLY	GLY	GLY	VAL	GLY	VAL	GLY	VAL	VAL		ILE	PRO	GLY
ASN	ASN	PRO	CYS	SER	SER	PHE	LEU	CYS	LEU	VAL	TYR	F290	LYS	VAL	GLY
SER	SER	LYS	HIS	MET	MET	LYS	GLY	GLY	GLY	TYR	ALA	F291	ASP	SER	GLY
GLY	GLY	GLY	ARG	SER	SER	ILE	LYS	ILE	LYS	ALA	ALA	R292	ARG	MET	SER
ASP	ASP	LEU	ILE	TYR	TYR	ASP	LEU	PRO	LEU	PRO	PRO		LEU	ARG	GLY
PRO	PRO	GLY	GLY	SER	GLY	GLY	GLY	ILE	ILE	LEU	LEU	K320	SER	LYS	PRO
PRO	PRO	LEU	GLY	GLY	ARG	GLY	GLN	SER	GLN	LYS	LYS	P327	THR	GLY	ALA
GLY	GLY	LEU	LEU	GLY	GLY	VAL	ILE	ILE	ILE	LYS	GLN		THR	GLY	MET
CYS	CYS	GLY	LYS	LYS	LYS	THR	GLN	GLN	GLN	GLN	GLN	I330	ARG	VAL	GLY
LEU	LEU	VAL	ASN	ASN	ASN	PRO	PRO	GLY	PRO	GLY	GLY	T331	GLN	ASP	GLN
PHE	PHE	ARG	ARG	VAL	MET	GLY	GLY	ILE	GLY	PHE	ILE	S332	ASN	GLY	LEU
		TYR	SER	SER	SER	LYS	ASP	TYR	ASP	TYR	THR	M337	LYS	TYR	THR
		GLY	PHE	PHE	PHE	PHE	ARG	ARG	ARG	THR	THR		PHE	ASN	A24
		ARG	ASN	ASN	ASN	ILE	GLY	GLY	GLY	ALA	ALA	R340	THR	ASN	E24
		ILE	THR	THR	THR	ILE	ARG	ARG	ARG	ILE	ILE		PHE	SER	E34
		LYS	ASP	ASP	ASP	LEU	ALA	VAL	ALA	VAL	VAL	L343	PRO	VAL	M48
		ALA	PRO	PRO	PRO	ASP	VAL	VAL	VAL	ASN	ASN		VAL	MET	K51
		GLY	ASN	GLY	GLY	ARG	VAL	ARG	VAL	ARG	ARG	W348	VAL	SER	K51
		SER	THR	VAL	VAL	MET	GLY	GLY	GLY	THR	THR		ARG	SER	K51
		ARG	ILE	PHE	PHE	LEU	VAL	ILE	VAL	ILE	ILE	L351	LYS	LYS	S60
		GLY	ASP	ILE	ILE	PRO	ASN	ASN	ASN	ALA	ALA		CYS	GLY	S60
		LYS	PHE	PHE	PHE	GLY	ILE	GLN	ILE	ASN	ASN	G356	ASN	GLY	L68
		VAL	VAL	LEU	LEU	LEU	PRO	PRO	PRO	MET	MET		GLY	ILE	L68
		ILE	ILE	VAL	VAL	LYS	VAL	VAL	VAL	PHE	PHE	E369	G208	LEU	L72
		SER	SER	SER	SER	LYS	GLY	GLY	GLY	GLY	GLY		THR	SER	L72
		ASP	THR	THR	THR	ARG	SER	ARG	SER	SER	SER	R372	P211	VAL	K80
		LYS	ARG	ARG	ARG	GLY	GLY	GLY	GLY	GLY	GLY		ALA	ALA	K80
		ASP	ALA	ALA	ALA	HIS	GLY	VAL	GLY	GLY	GLY	N377	Q214	LYS	F81
		LEU	GLY	GLY	GLY	LYS	ASN	ASN	ASN	LYS	LYS		G220	LYS	L82
		GLY	ALA	GLY	GLY	VAL	LEU	LEU	LEU	GLY	GLY	L380	G220	ASN	L82
		LEU	LYS	LEU	LEU	LEU	LYS	LEU	LYS	THR	THR		G221	LYS	Q89
		LEU	ARG	ILE	ILE	LEU	LEU	ILE	ILE	ILE	ILE	N388	V222	LYS	K97
		ASP	GLY	ASN	ASN	PHE	GLN	GLN	GLN	GLY	GLY	N389	M223	GLY	K97
		ASP	GLY	LEU	LEU	GLY	ASN	ASN	ASN	LEU	LEU	L390	V228	ASN	GLY
		SER	THR	THR	THR	MET	MET	MET	MET	THR	THR		V228	ASP	LYS
		ASP	ALA	ALA	ALA	THR	MET	MET	MET	THR	THR	L400	R235	GLY	LYS
		LEU	ILE	ILE	ILE	SER	LEU	GLY	GLY	GLY	GLY	W414	W238	GLY	LEU
		ILE	ASP	ASP	ASP	MET	LEU	ARG	ARG	PRO	PRO		W238	SER	ARG
		ASP	THR	THR	THR	LEU	ARG	GLY	GLY	ARG	ARG	I417	E239	SER	LYS
		GLN	VAL	VAL	VAL	ASP	LYS	LYS	LYS	LYS	LYS	N240	G241	SER	GLY
		MET	ILE	ILE	ILE	ILE	CYS	CYS	CYS	ARG	ARG	I428	I242	THR	SER
		ASN	ILE	ILE	ILE	LEU	CYS	CYS	CYS	ARG	ARG		I242	ASN	LEU
		ALA	TYR	TYR	TYR	MET	ASN	ASN	ASN	THR	THR	V436	I245	LEU	SER
		SER	ASP	ASP	ASP	ASP	HIS	HIS	HIS	ARG	ARG	L437	I245	CYS	VAL
		GLY	SER	SER	SER	TYR	PRO	PRO	PRO	LYS	LYS		I245	VAL	LYS
		PRO	ASP	ASP	ASP	TYR	CYS	CYS	CYS	SER	SER	L444	I262	GLY	LYS
		ILE	TRP	TRP	TRP	ILE	HIS	HIS	HIS	LEU	LEU		I262	ASP	LYS
		ASN	ASN	ASN	ASN	LEU	LEU	LEU	LEU	ILE	ILE	V437	I264	GLY	GLY
		SER	SER	SER	SER	THR	THR	THR	THR	ASN	ASN		I264	LEU	GLY

- Molecule 1: Lymphoid-specific helicase



- Molecule 1: Lymphoid-specific helicase





PRO	ILE	LYS	GLY	ASN	TRP	ASP	CYS	TYR	SER	V456
LYS	ILE	ASN	SER	ASN	TRP	ASP	ILE	ILE	ASN	A457
GLY	GLY	PRO	ARG	GLY	ARG	ASP	GLY	GLY	TYR	LEU
LYS	LEU	GLN	ASP	PHE	ASP	PHE	ASP	PRO	LYS	VAL
MET	ASN	SER	ASN	ASN	ASN	ASN	ILE	ILE	ASP	PRO
GLY	SER	GLN	PHE	GLN	GLN	ALA	ARG	VAL	PHE	ARG
ILE	ILE	PHE	ASN	ASN	ASN	GLN	LEU	THR	PRO	GLY
LEU	LEU	ASP	LEU	ASP	ASP	GLN	GLN	THR	ASN	VAL
GLU	ASP	ARG	GLY	GLY	GLY	GLY	GLY	GLU	GLU	VAL
ASN	ASN	PRO	CYS	SER	SER	SER	MET	PHE	LEU	VAL
SER	SER	LYS	HIS	ARG	ILE	ILE	TYR	ASP	LYS	ALA
GLY	GLU	GLY	GLY	GLY	GLY	GLY	TYR	ILE	GLY	ALA
ASP	ASN	ILE	GLY	GLY	GLY	GLY	SER	GLU	ILE	PRO
SER	SER	MET	ASN	GLY	GLY	GLY	SER	GLU	ILE	LEU
SER	SER	GLU	GLN	GLN	GLN	GLN	GLY	GLU	SER	SER
PRO	PRO	LEU	LEU	THR	THR	THR	ARG	GLN	LYS	GLY
GLY	GLY	LEU	LEU	GLY	GLY	GLY	GLY	VAL	ILE	LYS
CYS	CYS	LEU	LEU	PRO	PRO	PRO	LYS	THR	GLN	GLN
LEU	LEU	SER	SER	VAL	VAL	VAL	ASN	ASN	PRO	GLY
PHE	PHE	ARG	ARG	VAL	VAL	VAL	MET	SER	GLU	ILE
		ASP	ASP	VAL	VAL	VAL	HIS	GLY	VAL	PHE
		TYR	TYR	TYR	TYR	TYR	SER	LYS	ASP	TYR
		GLU	GLU	ARG	ARG	ARG	PHE	PHE	ARG	ALA
		ARG	ARG	LEU	LEU	LEU	ASN	LEU	GLY	ALA
		GLY	GLY	VAL	VAL	VAL	THR	ILE	ARG	ILE
		ILE	ILE	THR	THR	THR	THR	LEU	ALA	VAL
		LYS	LYS	ASN	ASN	ASN	PRO	ASP	VAL	ASN
		GLY	GLY	GLY	GLY	GLY	GLY	ARG	VAL	ARG
		SER	SER	THR	THR	THR	VAL	MET	GLY	THR
		ARG	ARG	ILE	PHE	PHE	LEU	VAL	ILE	ILE
		GLY	GLY	ASP	GLN	GLN	ILE	PRO	ASN	ALA
		LYS	LYS	GLY	GLY	GLY	PHE	GLY	ASN	ALA
		VAL	VAL	LYS	LYS	LYS	LEU	LEU	SER	SER
		ASP	ASP	GLY	THR	THR	THR	ARG	SER	GLY
		ASP	LYS	LYS	ARG	ARG	ALA	GLY	GLY	THR
		ASP	ASP	ALA	ALA	ALA	ALA	HIS	VAL	SER
		LEU	LEU	ALA	GLY	GLY	LYS	LYS	ASN	GLY
		GLY	GLY	ALA	GLY	GLY	VAL	VAL	LEU	LEU
		LEU	LEU	LYS	GLY	GLY	LEU	LEU	LYS	THR
		LEU	LEU	ARG	ILE	ILE	ILE	PHE	GLN	GLY
		LEU	LEU	LYS	LYS	LYS	ASN	SER	ASN	LEU
		ASP	ASP	GLY	GLY	GLY	LEU	THR	GLN	GLY
		ASP	ASP	ALA	ALA	ALA	ALA	THR	ILE	THR
		ILE	ILE	ILE	ILE	ILE	ALA	SER	LEU	GLY
		ASP	HIS	THR	ASP	ASP	THR	MET	ARG	ARG
		GLN	LYS	VAL	VAL	VAL	VAL	LEU	LEU	PRO
		MET	ASN	ASN	ILE	ILE	ILE	ILE	LYS	LYS
		ASN	ASN	PHE	ILE	ILE	ILE	CYS	CYS	ARG
		ALA	PHE	ASN	THR	THR	THR	ASN	THR	THR
		SER	LYS	LYS	ASP	ASP	ASP	HIS	ARG	ARG

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D3	Depositor
Number of particles used	337161	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 ( $e^-/\text{\AA}^2$ )	58.51	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.156	Depositor
Minimum map value	-2.125	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.066	Depositor
Recommended contour level	0.113	Depositor
Map size (Å)	317.568, 317.568, 317.568	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82699996, 0.82699996, 0.82699996	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	A	0.13	0/2722	0.25	0/3673
1	B	0.13	0/2722	0.25	0/3673
1	C	0.13	0/2722	0.25	0/3673
1	D	0.13	0/2722	0.25	0/3673
1	E	0.13	0/2722	0.26	0/3673
1	F	0.14	0/2722	0.27	0/3673
All	All	0.13	0/16332	0.26	0/22038

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

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	2660	0	2680	37	0
1	B	2660	0	2680	32	0
1	C	2660	0	2680	38	0
1	D	2660	0	2680	34	0
1	E	2660	0	2680	36	0
1	F	2660	0	2680	34	0
All	All	15960	0	16080	194	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 6.

The worst 5 of 194 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:34:GLU:HG3	1:E:280:LEU:HD22	1.66	0.77
1:A:280:LEU:HD22	1:D:34:GLU:HG3	1.67	0.77
1:C:280:LEU:HD22	1:E:34:GLU:HG3	1.66	0.77
1:B:34:GLU:HG3	1:F:280:LEU:HD22	1.70	0.73
1:F:337:MET:HA	1:F:369:GLU:HG2	1.71	0.72

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	322/838 (38%)	317 (98%)	5 (2%)	0	100	100
1	B	322/838 (38%)	318 (99%)	4 (1%)	0	100	100
1	C	322/838 (38%)	319 (99%)	3 (1%)	0	100	100
1	D	322/838 (38%)	318 (99%)	4 (1%)	0	100	100
1	E	322/838 (38%)	318 (99%)	4 (1%)	0	100	100
1	F	322/838 (38%)	318 (99%)	4 (1%)	0	100	100
All	All	1932/5028 (38%)	1908 (99%)	24 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	288/768 (38%)	285 (99%)	3 (1%)	68	83
1	B	288/768 (38%)	285 (99%)	3 (1%)	68	83
1	C	288/768 (38%)	284 (99%)	4 (1%)	59	78
1	D	288/768 (38%)	287 (100%)	1 (0%)	86	93
1	E	288/768 (38%)	284 (99%)	4 (1%)	59	78
1	F	288/768 (38%)	286 (99%)	2 (1%)	76	87
All	All	1728/4608 (38%)	1711 (99%)	17 (1%)	65	83

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	456	VAL
1	F	456	VAL
1	C	91	LEU
1	C	303	HIS
1	C	456	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	344	GLN
1	F	374	ASN
1	C	70	HIS
1	C	344	GLN
1	D	344	GLN

### 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 [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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.

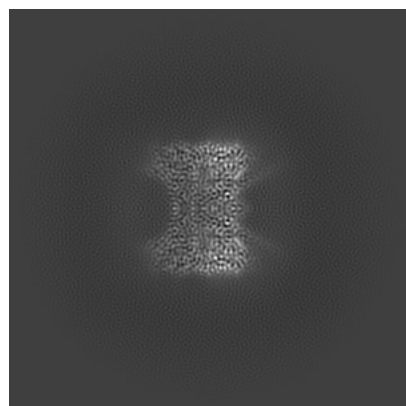
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73694. These allow visual inspection of the internal detail of the map and identification of artifacts.

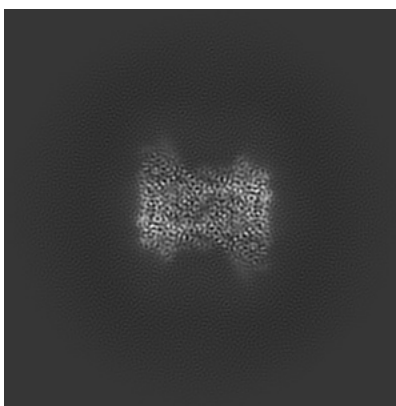
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

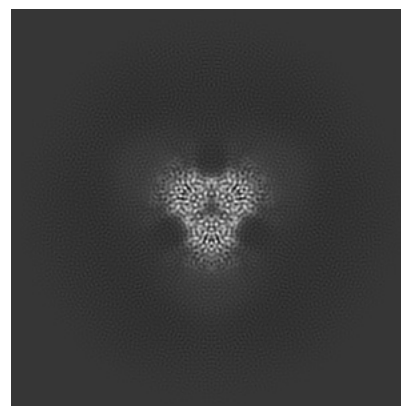
#### 6.1.1 Primary map



X

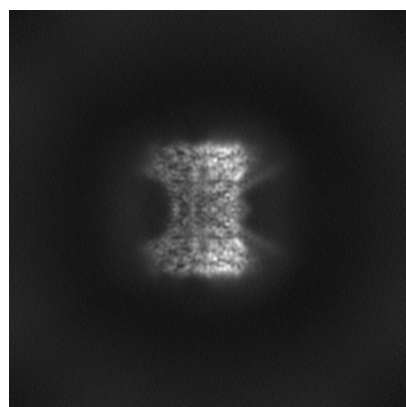


Y

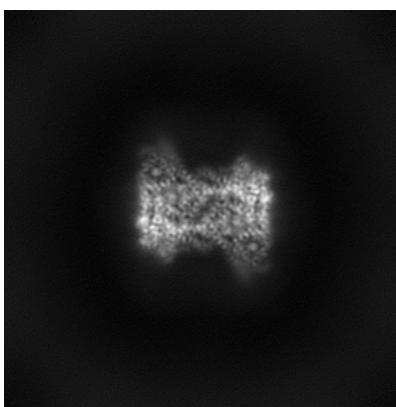


Z

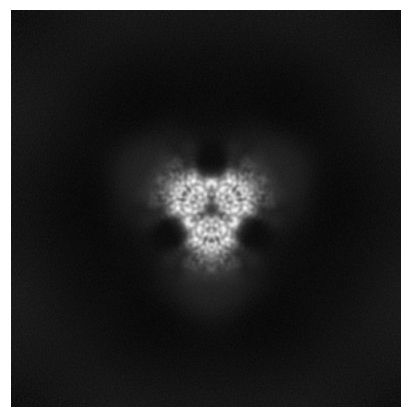
#### 6.1.2 Raw map



X



Y

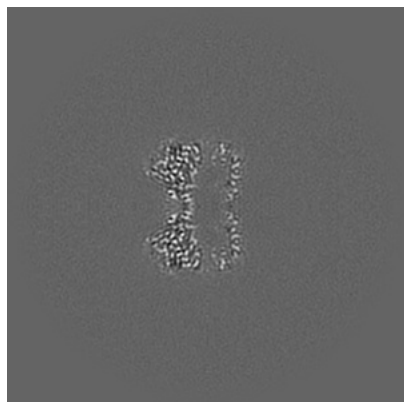


Z

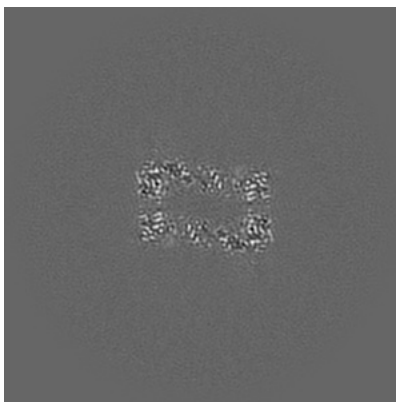
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

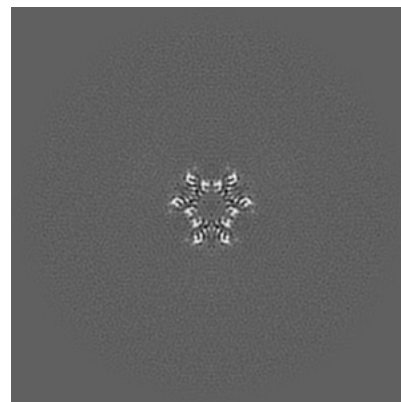
### 6.2.1 Primary map



X Index: 192

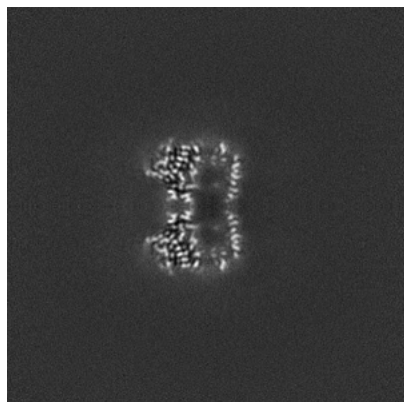


Y Index: 192

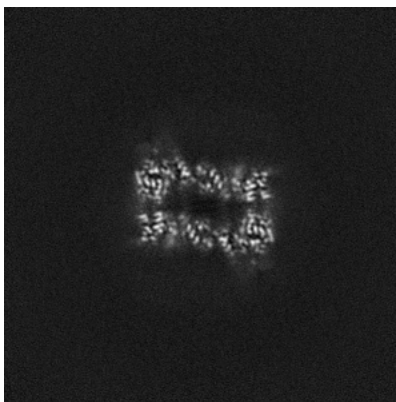


Z Index: 192

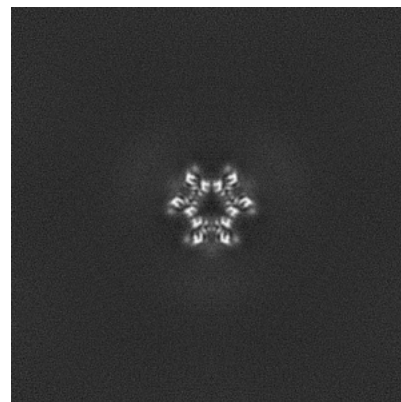
### 6.2.2 Raw map



X Index: 192



Y Index: 192



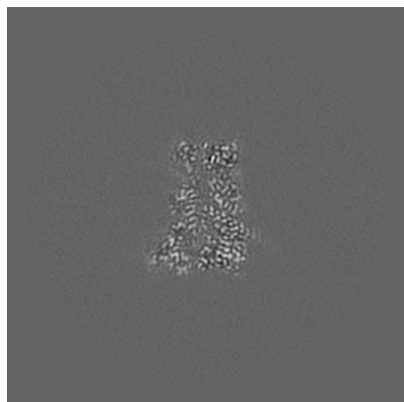
Z Index: 192

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

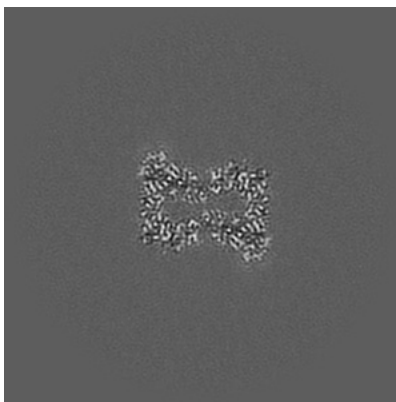


## 6.3 Largest variance slices [i](#)

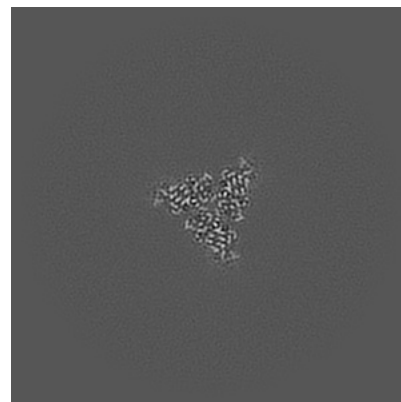
### 6.3.1 Primary map



X Index: 175

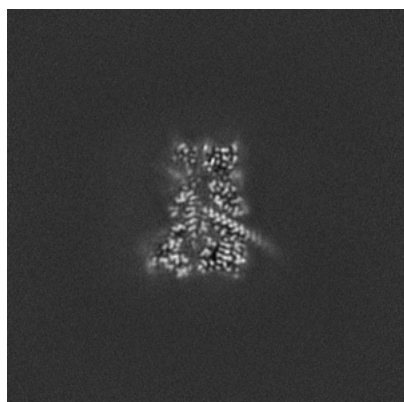


Y Index: 208

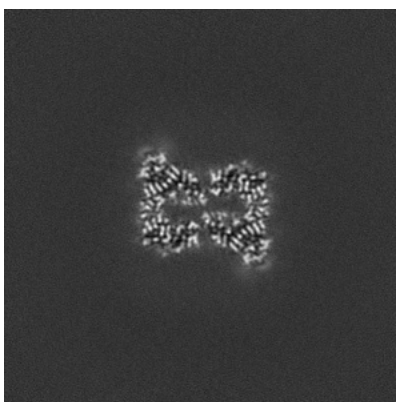


Z Index: 239

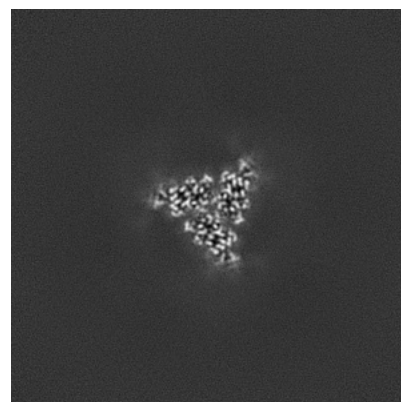
### 6.3.2 Raw map



X Index: 175



Y Index: 208

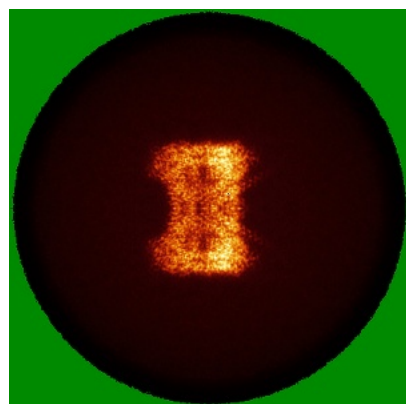


Z Index: 239

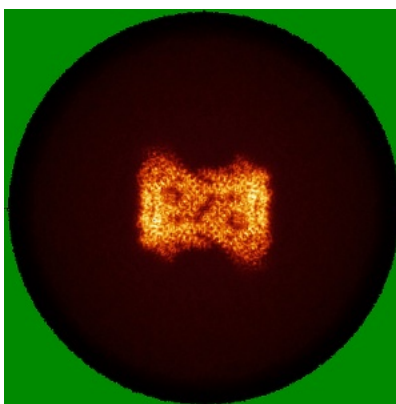
The images above show the largest variance slices of the map in three orthogonal directions.

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

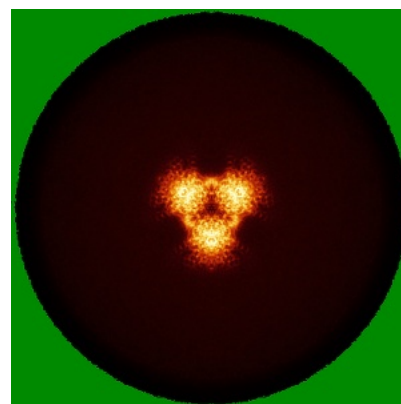
### 6.4.1 Primary map



X

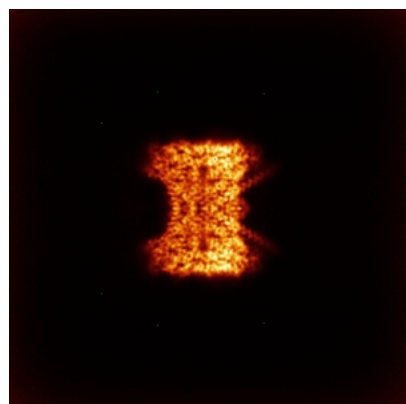


Y

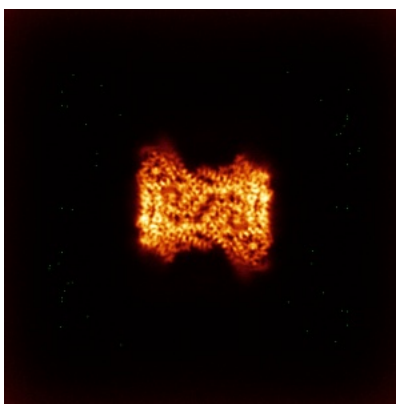


Z

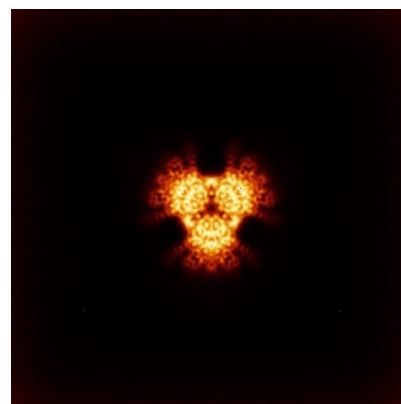
### 6.4.2 Raw map



X



Y

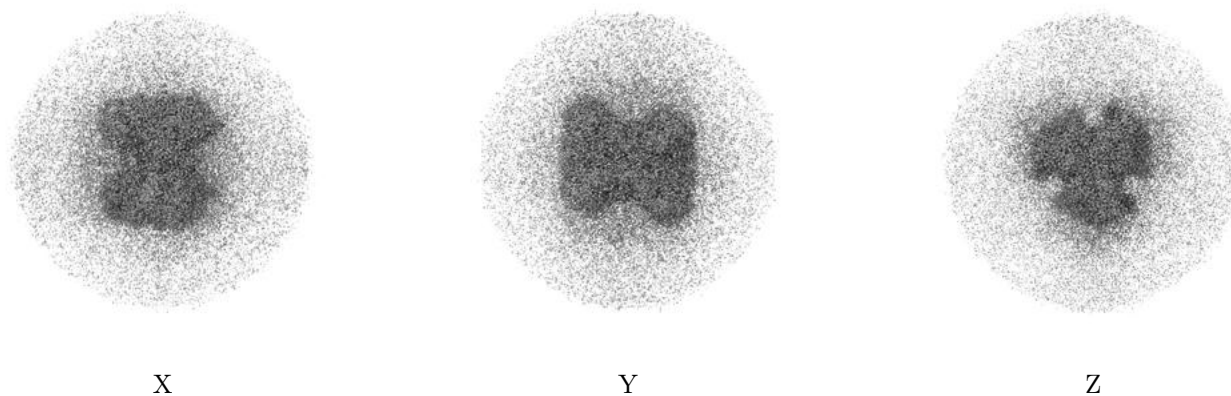


Z

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.

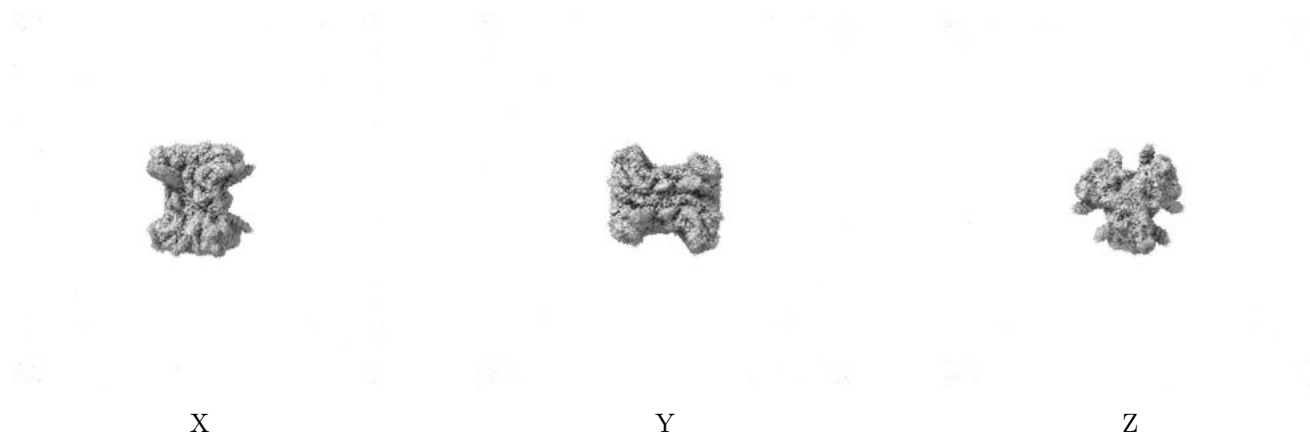
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.113. 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.

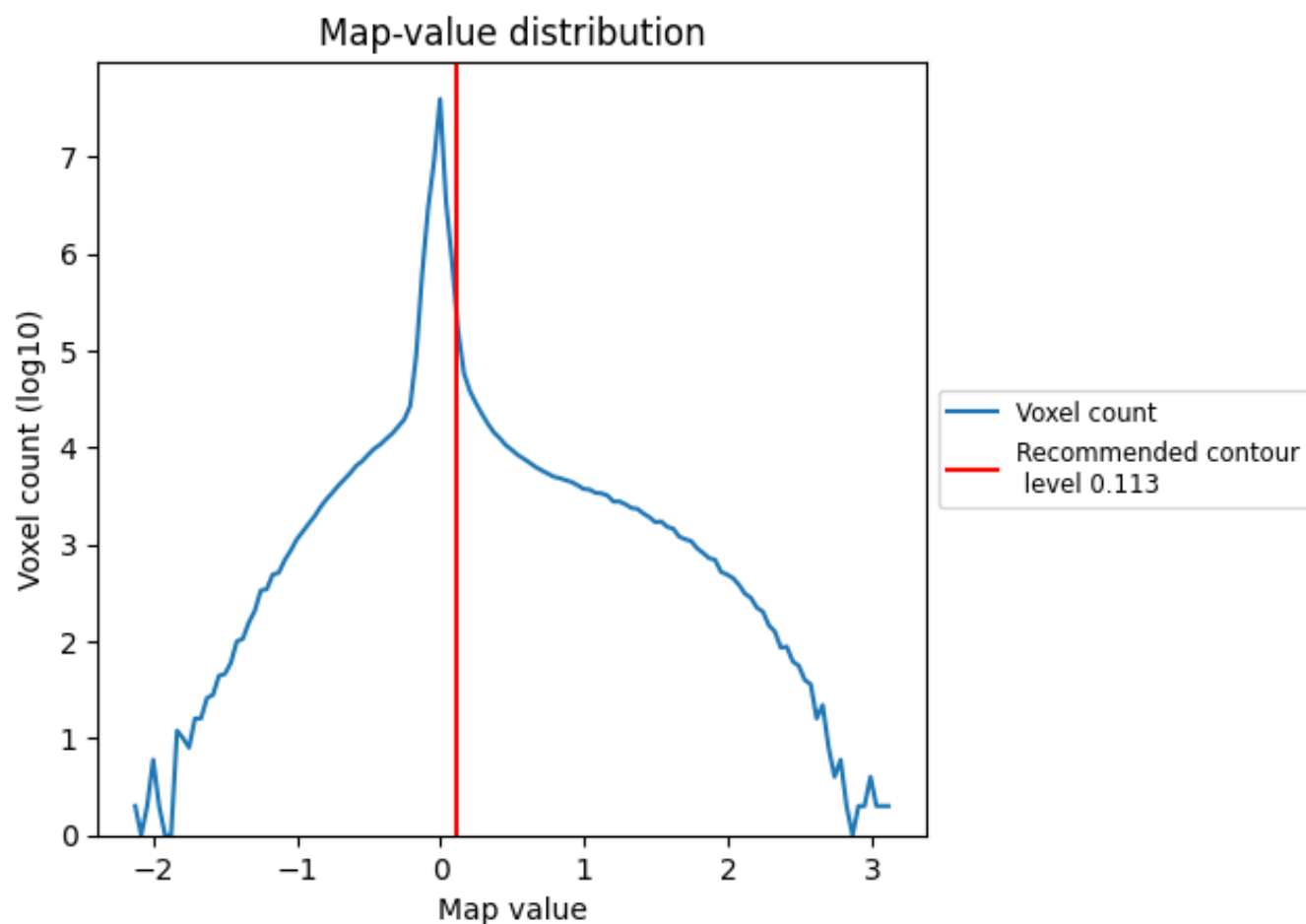
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

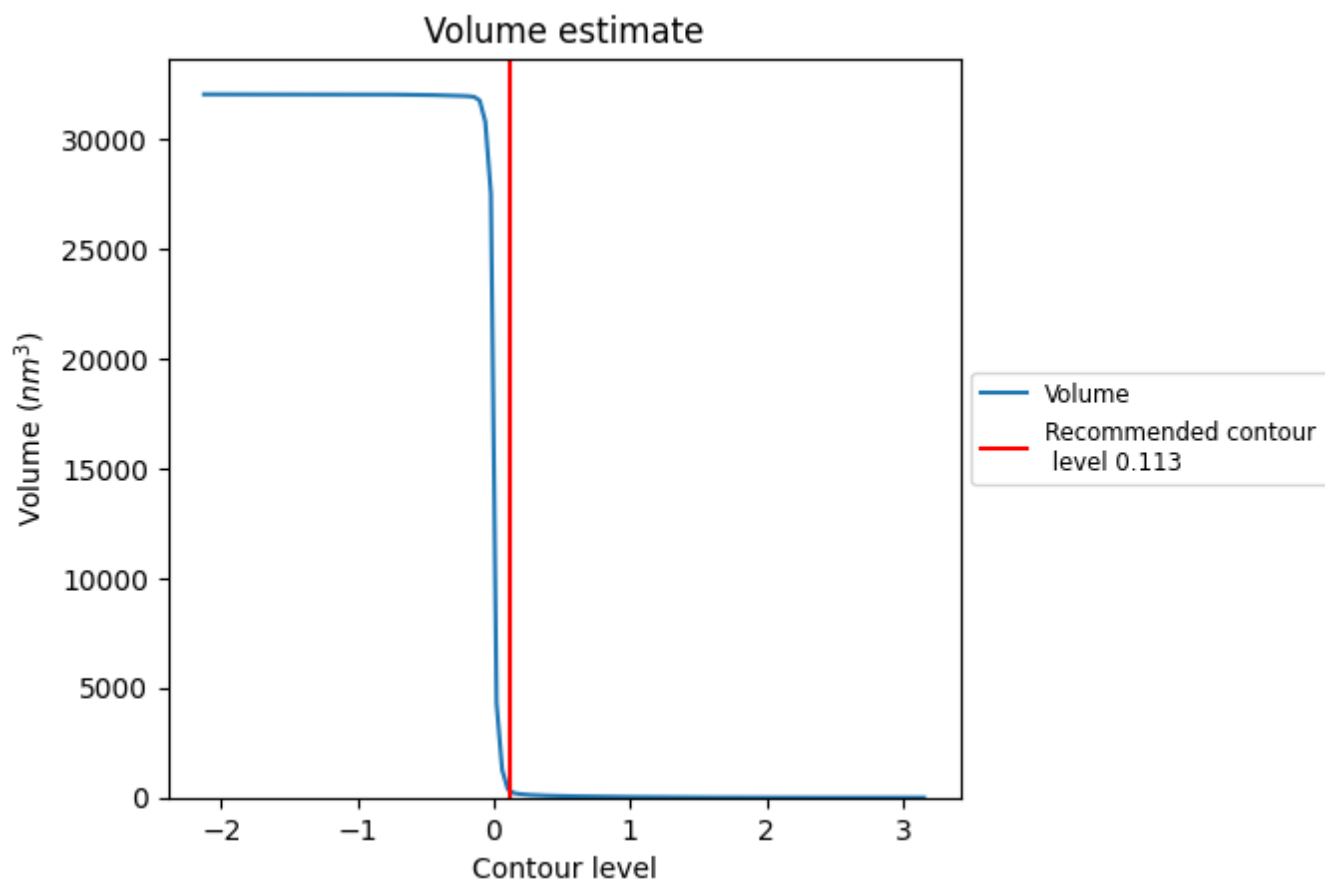
This section contains the results of statistical analysis of the map.

### 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.

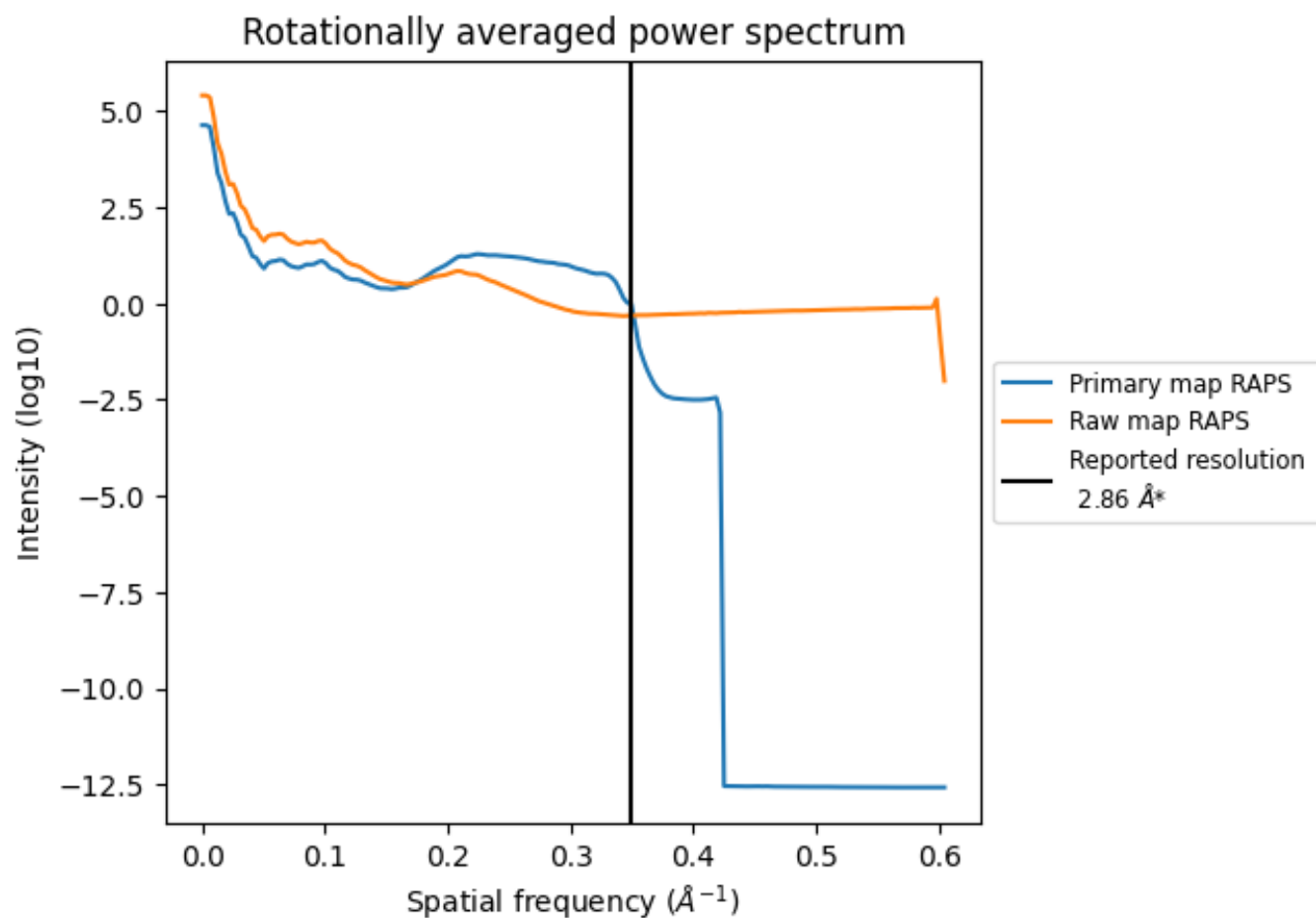
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 342 nm<sup>3</sup>; this corresponds to an approximate mass of 309 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 ⓘ

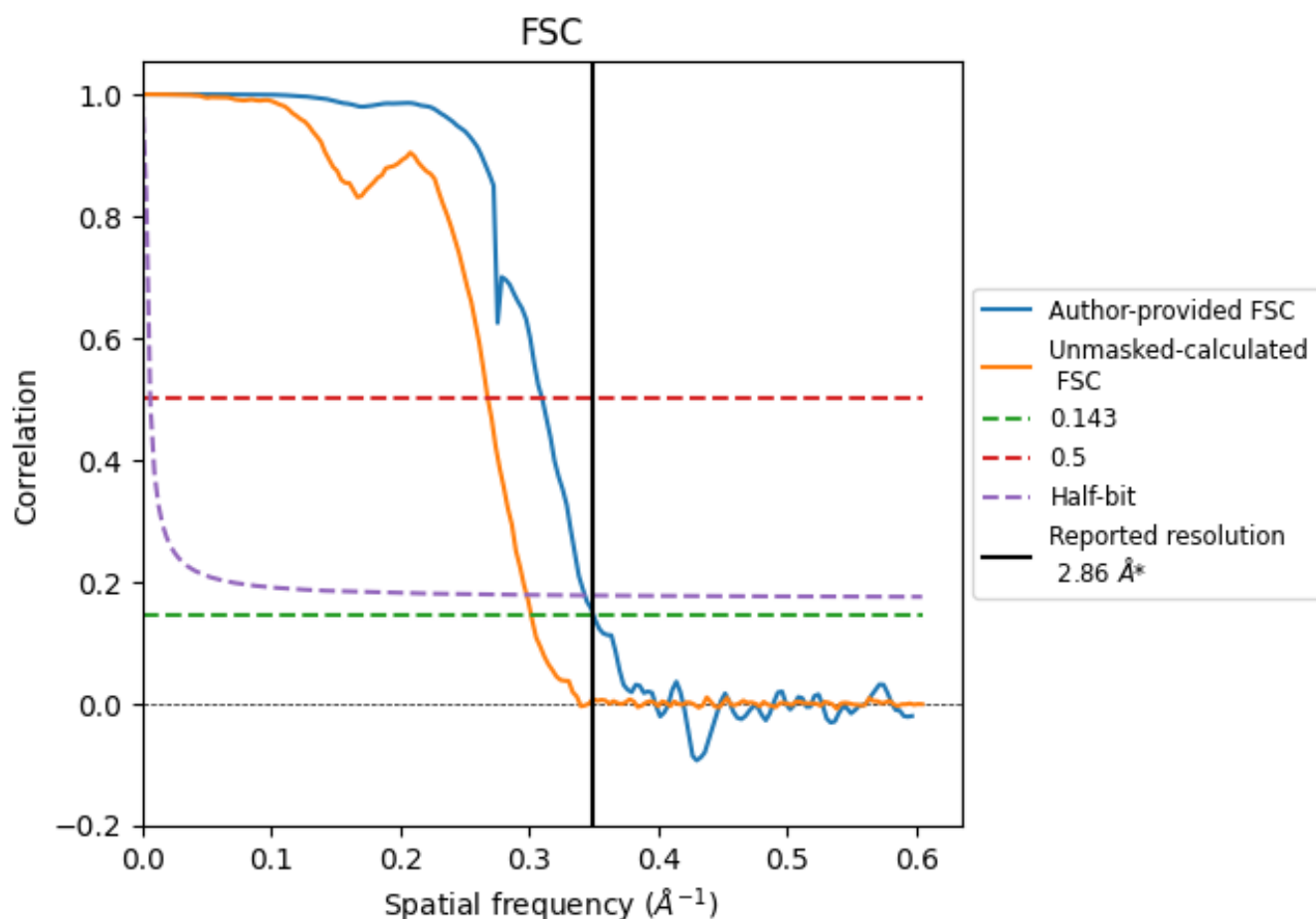


\*Reported resolution corresponds to spatial frequency of 0.350  $\text{\AA}^{-1}$

## 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  $0.350 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.86	-	-
Author-provided FSC curve	2.86	3.22	2.91
Unmasked-calculated*	3.31	3.73	3.35

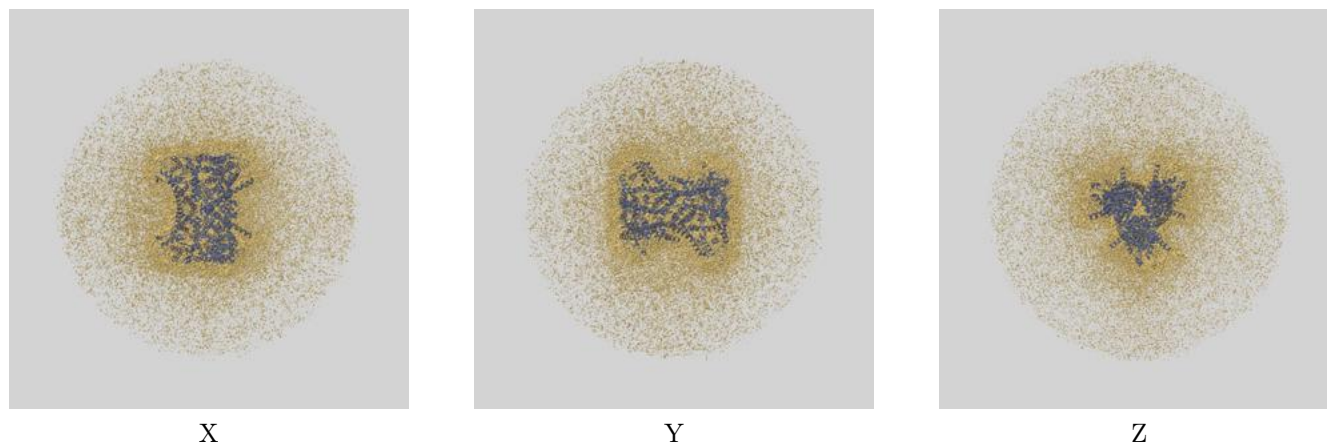
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.31 differs from the reported value 2.86 by more than 10 %



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

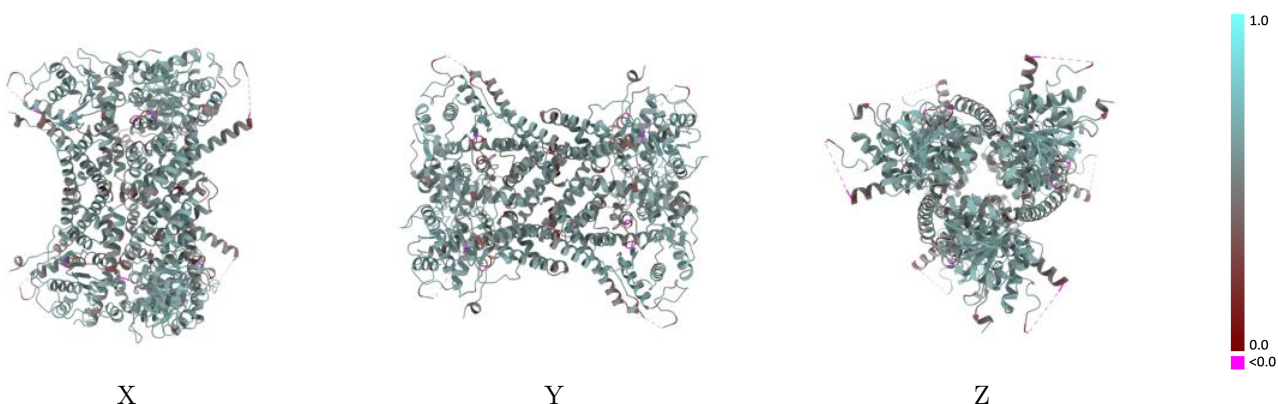
This section contains information regarding the fit between EMDB map EMD-73694 and PDB model 9Z05. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

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



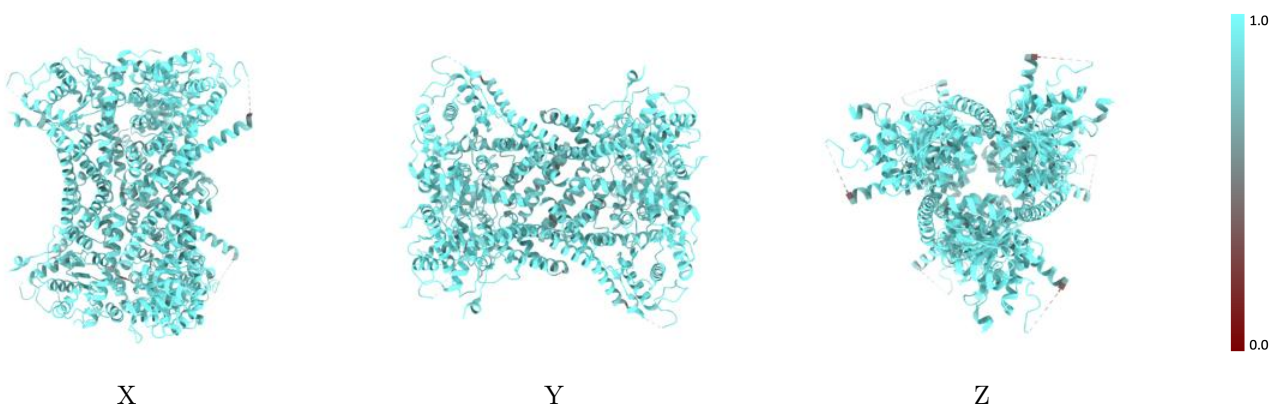
The images above show the 3D surface view of the map at the recommended contour level 0.113 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



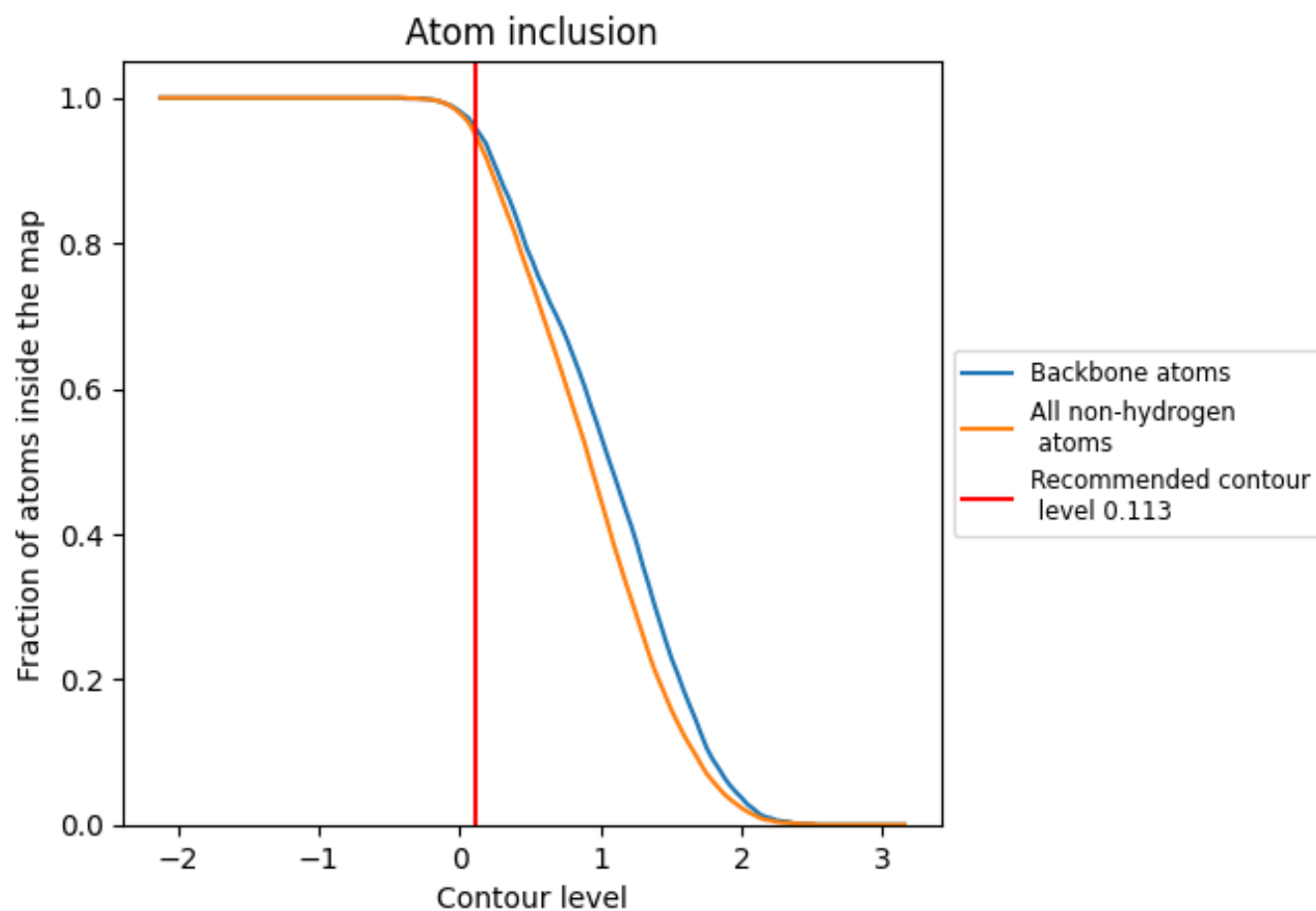
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.113).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.113) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.9480	<div><div></div></div> 0.5580
A	<div><div></div></div> 0.9410	<div><div></div></div> 0.5570
B	<div><div></div></div> 0.9540	<div><div></div></div> 0.5600
C	<div><div></div></div> 0.9520	<div><div></div></div> 0.5580
D	<div><div></div></div> 0.9470	<div><div></div></div> 0.5570
E	<div><div></div></div> 0.9510	<div><div></div></div> 0.5580
F	<div><div></div></div> 0.9430	<div><div></div></div> 0.5560

1.0

0.0

<0.0