



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 02:57 AM UTC

PDB ID : 9KHX / pdb_00009khx
EMDB ID : EMD-62358
Title : Neck structure of Escherichia phage Mu
Authors : Zhou, J.Q.; Liu, H.R.
Deposited on : 2024-11-11
Resolution : 3.40 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:

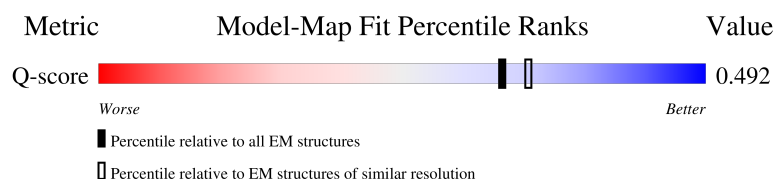
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.40 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.



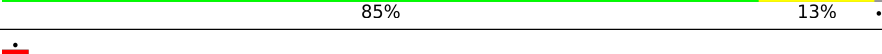
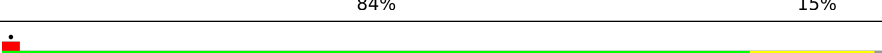
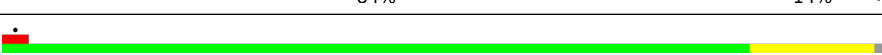
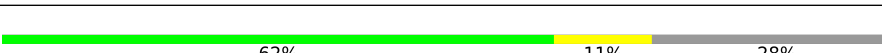
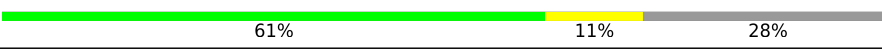
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	141	
1	B	141	
1	C	141	
1	D	141	

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Mol	Chain	Length	Quality of chain
1	E	141	 84% 14%
1	F	141	 85% 13%
1	G	141	 84% 14%
1	H	141	 86% 13%
1	I	141	 85% 13%
1	J	141	 84% 15%
1	K	141	 84% 14%
1	L	141	 84% 14%
2	M	512	 62% 11% 28%
2	N	512	 61% 11% 28%
2	O	512	 62% 11% 28%
2	P	512	 61% 11% 28%
2	Q	512	 62% 11% 28%
2	R	512	 61% 11% 28%
2	S	512	 62% 11% 28%
2	T	512	 61% 11% 28%
2	U	512	 61% 11% 28%
2	V	512	 62% 10% 28%
2	W	512	 61% 11% 28%
2	X	512	 62% 10% 28%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 47772 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 Gene product J.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		
1	B	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		
1	C	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		
1	D	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		
1	E	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		
1	F	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		
1	G	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		
1	H	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		
1	I	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		
1	J	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		
1	K	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		
1	L	139	Total	C	N	O	S	0	0
			1090	683	191	213	3		

- Molecule 2 is a protein called Portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	369	Total	C	N	O	S	0	0
			2891	1818	512	544	17		
2	M	369	Total	C	N	O	S	0	0
			2891	1818	512	544	17		
2	N	369	Total	C	N	O	S	0	0
			2891	1818	512	544	17		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	369	Total 2891	C 1818	N 512	O 544	S 17	0	0
2	P	369	Total 2891	C 1818	N 512	O 544	S 17	0	0
2	Q	369	Total 2891	C 1818	N 512	O 544	S 17	0	0
2	R	369	Total 2891	C 1818	N 512	O 544	S 17	0	0
2	S	369	Total 2891	C 1818	N 512	O 544	S 17	0	0
2	T	369	Total 2891	C 1818	N 512	O 544	S 17	0	0
2	U	369	Total 2891	C 1818	N 512	O 544	S 17	0	0
2	V	369	Total 2891	C 1818	N 512	O 544	S 17	0	0
2	W	369	Total 2891	C 1818	N 512	O 544	S 17	0	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: Gene product J

Chain A: 



- Molecule 1: Gene product J

Chain B: 



- Molecule 1: Gene product J

Chain C: 



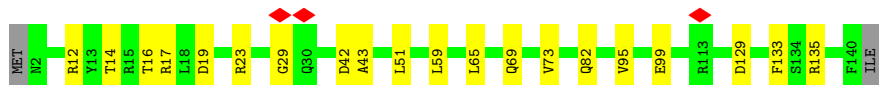
- Molecule 1: Gene product J

Chain D: 



- Molecule 1: Gene product J

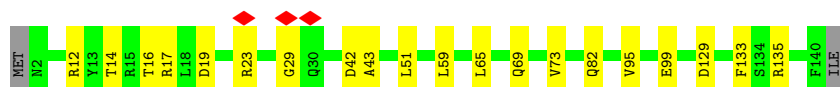
Chain E: 



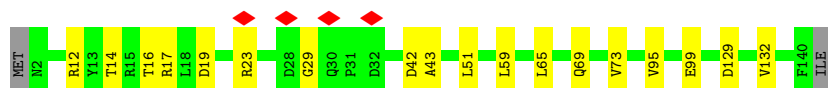
• Molecule 1: Gene product J

Chain F:  85% 13%

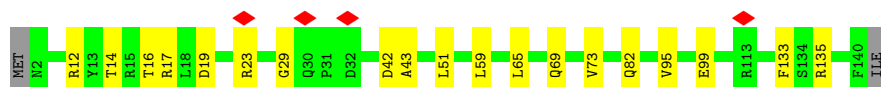
• Molecule 1: Gene product J

Chain G:  84% 14%

• Molecule 1: Gene product J

Chain H:  86% 13%

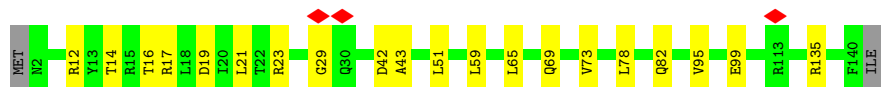
• Molecule 1: Gene product J

Chain I:  85% 13%

• Molecule 1: Gene product J

Chain J:  84% 15%

• Molecule 1: Gene product J

Chain K:  84% 14%

• Molecule 1: Gene product J

Chain L:  84% 14%

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

• Molecule 2: Portal protein

Chain O:  62% 11% 28%

ALA	ALA	ALA	ASP	HIS	GLU	ASP	TRP	GLN	ARG	SER	VAL	PRO	LEU	LEU	LYS	PRO	VAL	PHE	SER	VAL	LEU	LYS	ASP	GLY	PRO	ALA	GLU	ALA	GLU	LEU	ILE	ASP	MET	ASN	LYS	ALA	ALA	SER	SER	LEU	TYR	PRO	GLN	GLN	MET	ASN	LYS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	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• Molecule 2: Portal protein

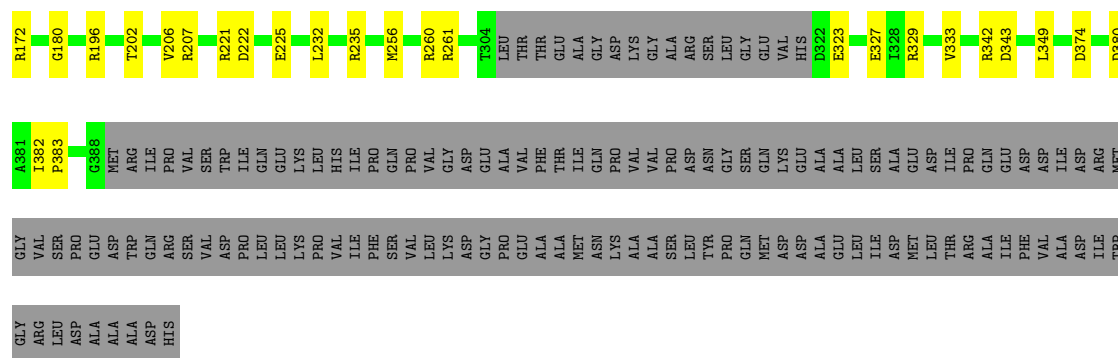
Chain P:  61% 11% 28%

GLY	ARG	LEU	ASP	ALA	ALA	ALA	ASP	HIS	GLY	VAL	SER	PRO	GLU	ASP	TRP	ILE	GLN	LEU	LEU	LYS	PRO	VAL	VAL	ASP	PRO	GLN	ASP	GLY	ALA	ALA	ASP	GLY	LEU	ILE	ASP	MET	LEU	ASP	ALA	ALA	ALA	ASP	THR	ILE	ALA	ALA	LYS	GLY	ASP	GLY	PRO	ALA	VAL	PHE	THR	ILE	ASN	GLN	LYS	ALA	ALA	ALA	SER	THR	TYR	ALA	GLY	LEU	ALA	ALA	ASP	MET	GLN	SER	LEU	ARG	ALA	VAL	HIS	T202	R196	G180	R172	A159	MET																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						

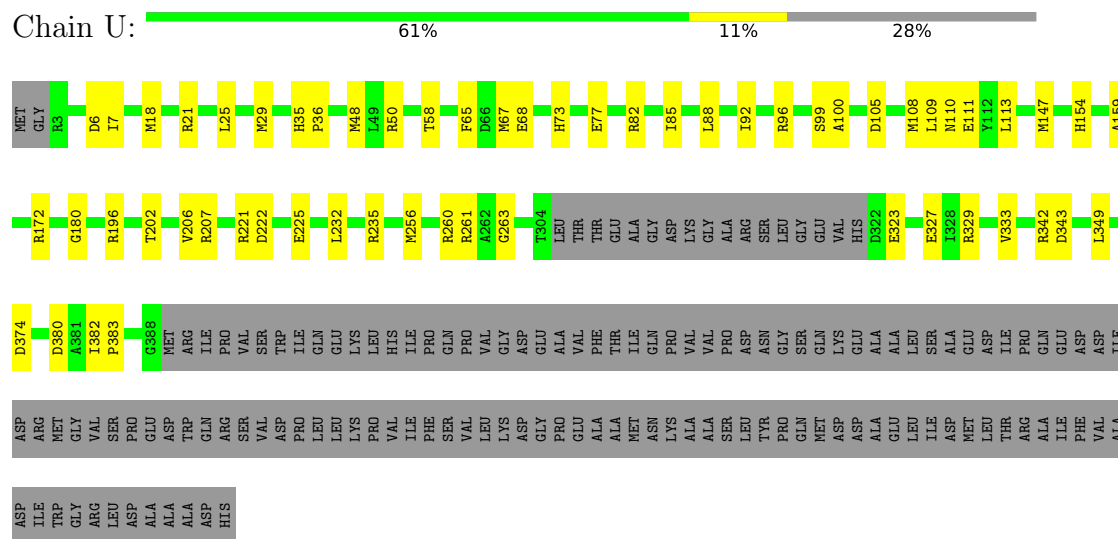
• Molecule 2: Portal protein

Chain Q:  62% 11% 28%

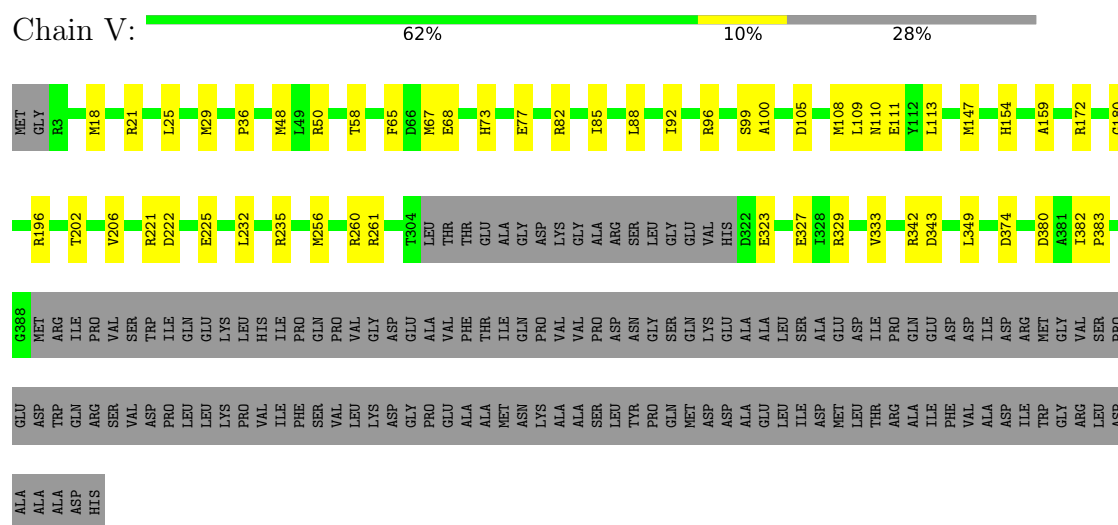
R196	T202	V206	R207	R221	D222	E225	R235	M256	R260	R261	A262	G263	T304	LEU	THR	THR	GLU	ALA	GLY	ASP	LYS	GLY	ALA	ARG	SER	LEU	GLY	GLU	VAL	HIS	D322	E323	E327	I328	R329	V333	R342	D343	L349	D374	D380	A381	I382	P383
MET	GLY	R3	M18	R21	H35	P36	M48	T58	F65	D66	M67	E68	H73	E77	R82	I85	L88	I92	R96	S99	A100	D105	M108	L109	M110	E111	Y112	L113	E140	M147	V151	H154	A159	R172	G180									



- Molecule 2: Portal protein



- Molecule 2: Portal protein



- Molecule 2: Portal protein



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55035	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	20.088	Depositor
Minimum map value	-9.255	Depositor
Average map value	0.014	Depositor
Map value standard deviation	1.391	Depositor
Recommended contour level	3	Depositor
Map size ($\text{\AA}$)	489.6, 489.6, 489.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.36, 1.36, 1.36	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.10	0/1112	0.25	0/1517
1	B	0.10	0/1112	0.25	0/1517
1	C	0.10	0/1112	0.25	0/1517
1	D	0.10	0/1112	0.25	0/1517
1	E	0.10	0/1112	0.25	0/1517
1	F	0.10	0/1112	0.25	0/1517
1	G	0.10	0/1112	0.25	0/1517
1	H	0.10	0/1112	0.25	0/1517
1	I	0.10	0/1112	0.25	0/1517
1	J	0.10	0/1112	0.25	0/1517
1	K	0.10	0/1112	0.25	0/1517
1	L	0.10	0/1112	0.25	0/1517
2	M	0.10	0/2950	0.26	0/3985
2	N	0.10	0/2950	0.26	0/3985
2	O	0.10	0/2950	0.26	0/3985
2	P	0.10	0/2950	0.26	0/3985
2	Q	0.10	0/2950	0.26	0/3985
2	R	0.10	0/2950	0.26	0/3985
2	S	0.10	0/2950	0.26	0/3985
2	T	0.10	0/2950	0.26	0/3985
2	U	0.10	0/2950	0.26	0/3985
2	V	0.10	0/2950	0.26	0/3985
2	W	0.10	0/2950	0.26	0/3985
2	X	0.10	0/2950	0.26	0/3985
All	All	0.10	0/48744	0.26	0/66024

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	1090	0	1069	15	0
1	B	1090	0	1069	15	0
1	C	1090	0	1069	16	0
1	D	1090	0	1069	17	0
1	E	1090	0	1069	15	0
1	F	1090	0	1069	15	0
1	G	1090	0	1069	15	0
1	H	1090	0	1069	13	0
1	I	1090	0	1069	14	0
1	J	1090	0	1069	15	0
1	K	1090	0	1069	14	0
1	L	1090	0	1069	14	0
2	M	2891	0	2825	37	0
2	N	2891	0	2825	37	0
2	O	2891	0	2825	35	0
2	P	2891	0	2825	39	0
2	Q	2891	0	2825	39	0
2	R	2891	0	2825	40	0
2	S	2891	0	2825	39	0
2	T	2891	0	2825	39	0
2	U	2891	0	2825	41	0
2	V	2891	0	2825	37	0
2	W	2891	0	2825	39	0
2	X	2891	0	2825	33	0
All	All	47772	0	46728	554	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 554 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:E:42:ASP:OD2	1:F:12:ARG:NH2	2.25	0.69
1:K:42:ASP:OD2	1:L:12:ARG:NH2	2.30	0.65
1:D:23:ARG:NH1	1:D:29:GLY:O	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:23:ARG:NH1	1:E:29:GLY:O	2.30	0.65
1:C:23:ARG:NH1	1:C:29:GLY:O	2.30	0.65

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	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
1	B	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
1	C	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
1	D	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
1	E	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
1	F	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
1	G	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
1	H	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
1	I	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
1	J	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
1	K	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
1	L	137/141 (97%)	135 (98%)	2 (2%)	0	100	100
2	M	365/512 (71%)	361 (99%)	4 (1%)	0	100	100
2	N	365/512 (71%)	361 (99%)	4 (1%)	0	100	100
2	O	365/512 (71%)	361 (99%)	4 (1%)	0	100	100
2	P	365/512 (71%)	362 (99%)	3 (1%)	0	100	100
2	Q	365/512 (71%)	361 (99%)	4 (1%)	0	100	100
2	R	365/512 (71%)	361 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	S	365/512 (71%)	361 (99%)	4 (1%)	0	100	100
2	T	365/512 (71%)	361 (99%)	4 (1%)	0	100	100
2	U	365/512 (71%)	361 (99%)	4 (1%)	0	100	100
2	V	365/512 (71%)	361 (99%)	4 (1%)	0	100	100
2	W	365/512 (71%)	362 (99%)	3 (1%)	0	100	100
2	X	365/512 (71%)	361 (99%)	4 (1%)	0	100	100
All	All	6024/7836 (77%)	5954 (99%)	70 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	118/120 (98%)	118 (100%)	0	100	100
1	B	118/120 (98%)	118 (100%)	0	100	100
1	C	118/120 (98%)	118 (100%)	0	100	100
1	D	118/120 (98%)	118 (100%)	0	100	100
1	E	118/120 (98%)	118 (100%)	0	100	100
1	F	118/120 (98%)	118 (100%)	0	100	100
1	G	118/120 (98%)	118 (100%)	0	100	100
1	H	118/120 (98%)	118 (100%)	0	100	100
1	I	118/120 (98%)	118 (100%)	0	100	100
1	J	118/120 (98%)	118 (100%)	0	100	100
1	K	118/120 (98%)	118 (100%)	0	100	100
1	L	118/120 (98%)	118 (100%)	0	100	100
2	M	297/418 (71%)	297 (100%)	0	100	100
2	N	297/418 (71%)	297 (100%)	0	100	100
2	O	297/418 (71%)	297 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	P	297/418 (71%)	297 (100%)	0	100	100
2	Q	297/418 (71%)	297 (100%)	0	100	100
2	R	297/418 (71%)	297 (100%)	0	100	100
2	S	297/418 (71%)	297 (100%)	0	100	100
2	T	297/418 (71%)	297 (100%)	0	100	100
2	U	297/418 (71%)	297 (100%)	0	100	100
2	V	297/418 (71%)	297 (100%)	0	100	100
2	W	297/418 (71%)	297 (100%)	0	100	100
2	X	297/418 (71%)	297 (100%)	0	100	100
All	All	4980/6456 (77%)	4980 (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 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	T	184	GLN
2	U	184	GLN
2	W	184	GLN
2	V	184	GLN
2	P	184	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 ⓘ

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.

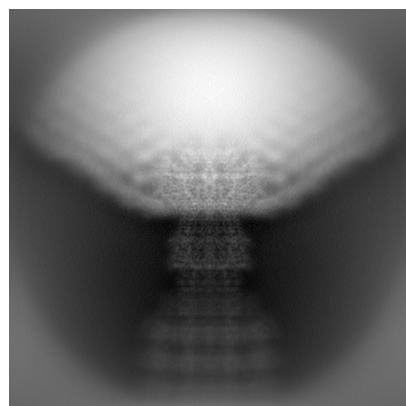
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62358. These allow visual inspection of the internal detail of the map and identification of artifacts.

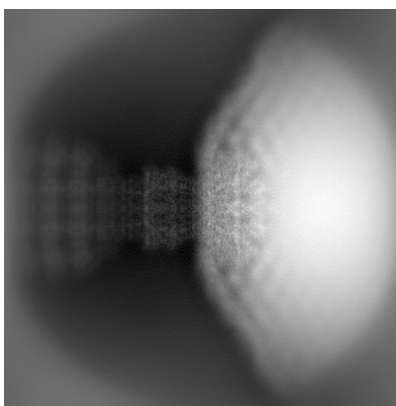
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

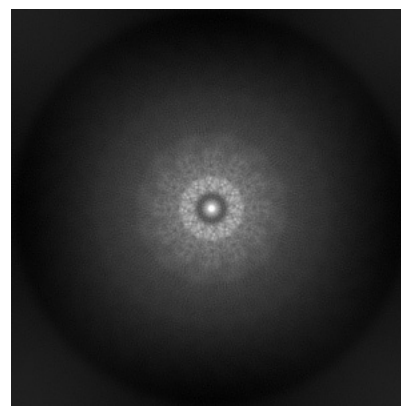
6.1.1 Primary map



X

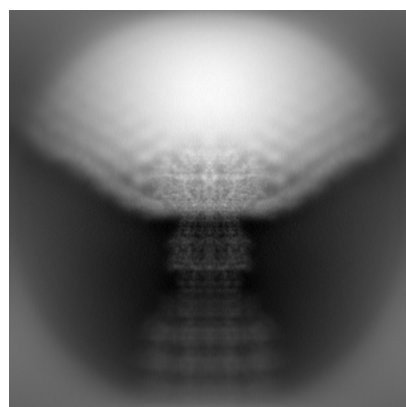


Y

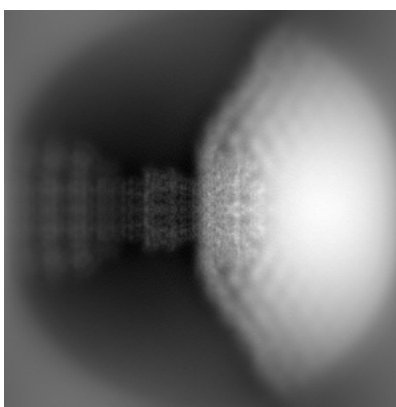


Z

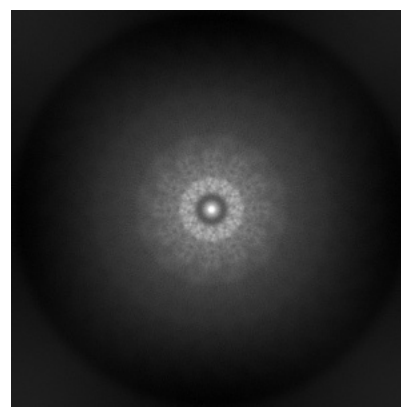
6.1.2 Raw map



X



Y

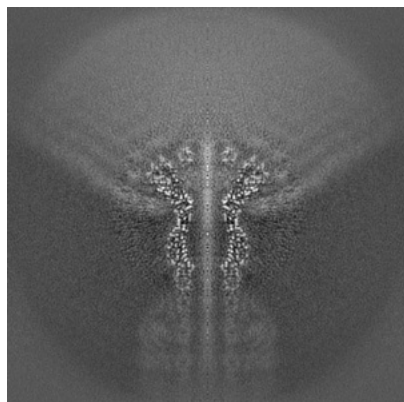


Z

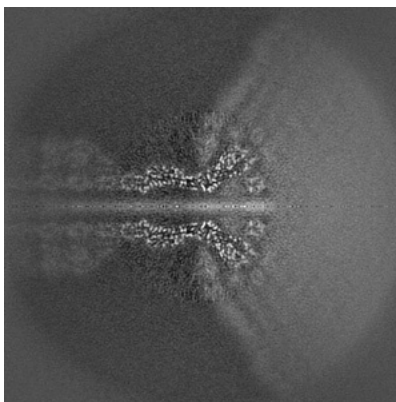
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

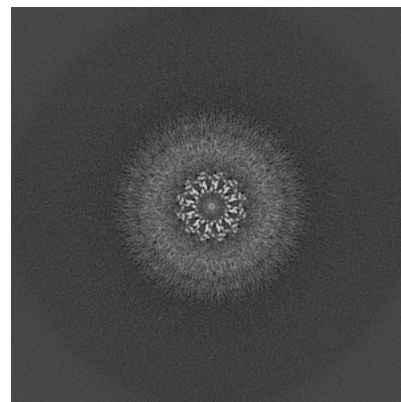
6.2.1 Primary map



X Index: 180

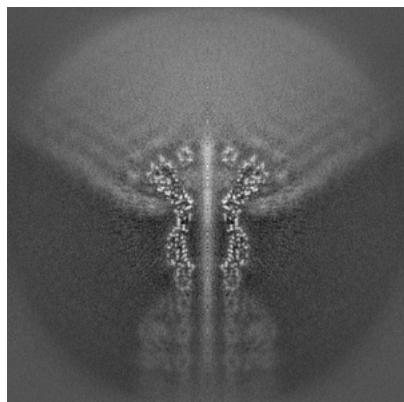


Y Index: 180

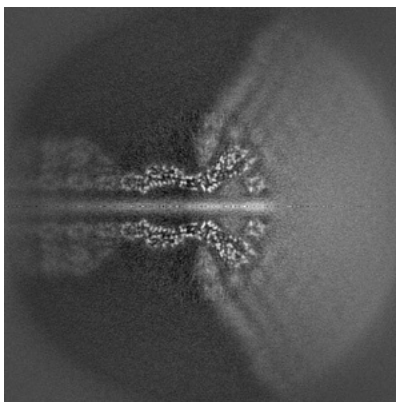


Z Index: 180

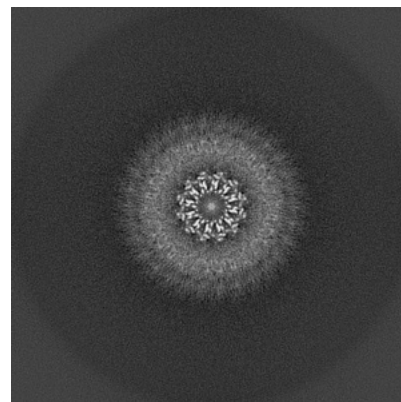
6.2.2 Raw map



X Index: 180



Y Index: 180

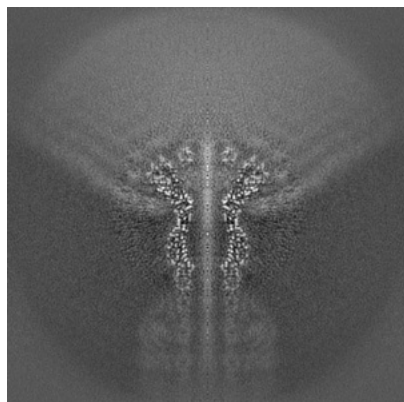


Z Index: 180

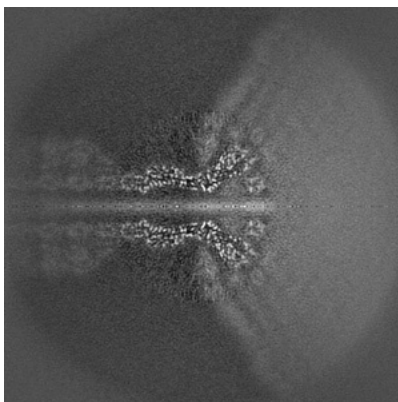
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

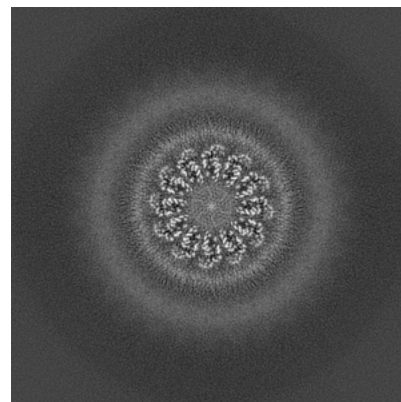
6.3.1 Primary map



X Index: 180

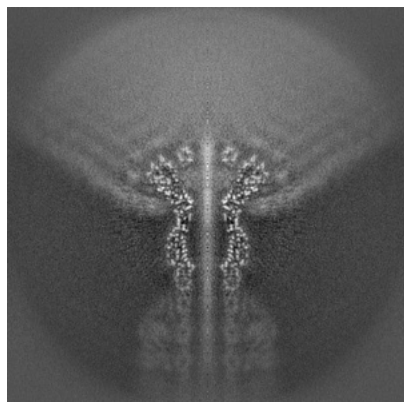


Y Index: 180

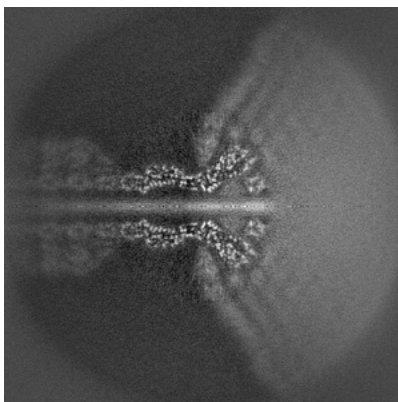


Z Index: 210

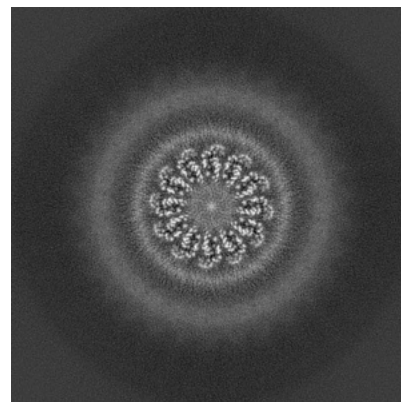
6.3.2 Raw map



X Index: 180



Y Index: 180

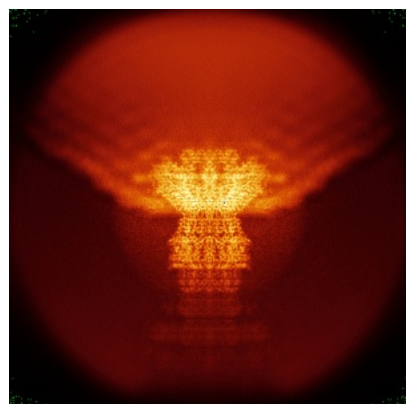


Z Index: 210

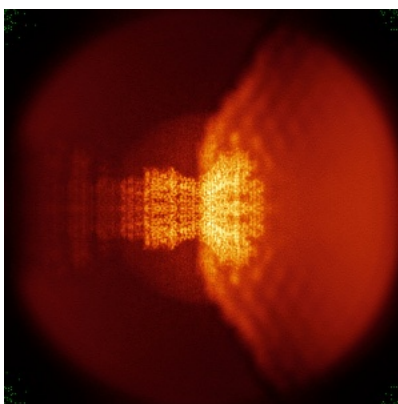
The images above show the largest variance slices of the map in three orthogonal directions.

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

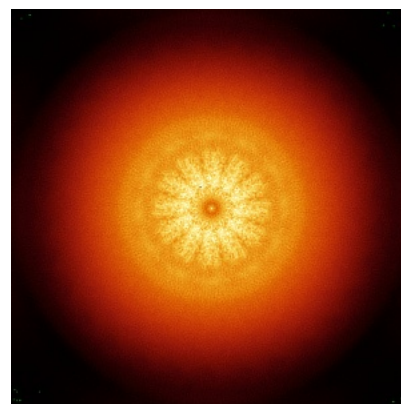
6.4.1 Primary map



X

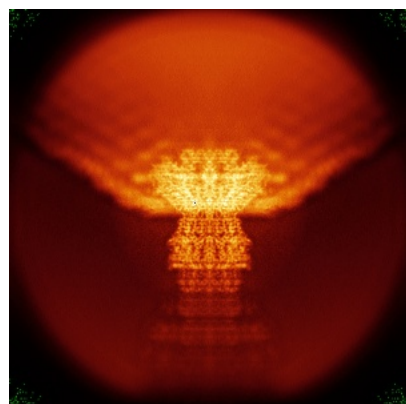


Y

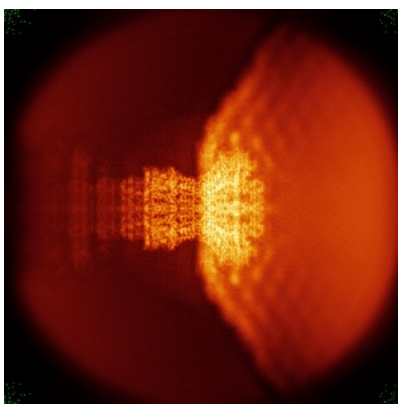


Z

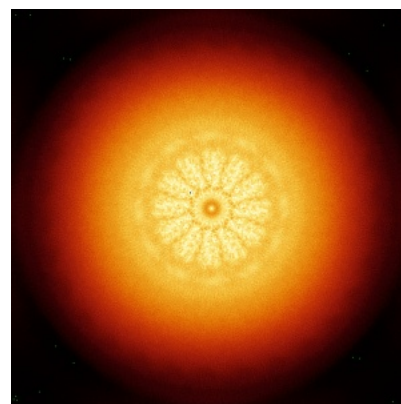
6.4.2 Raw map



X



Y

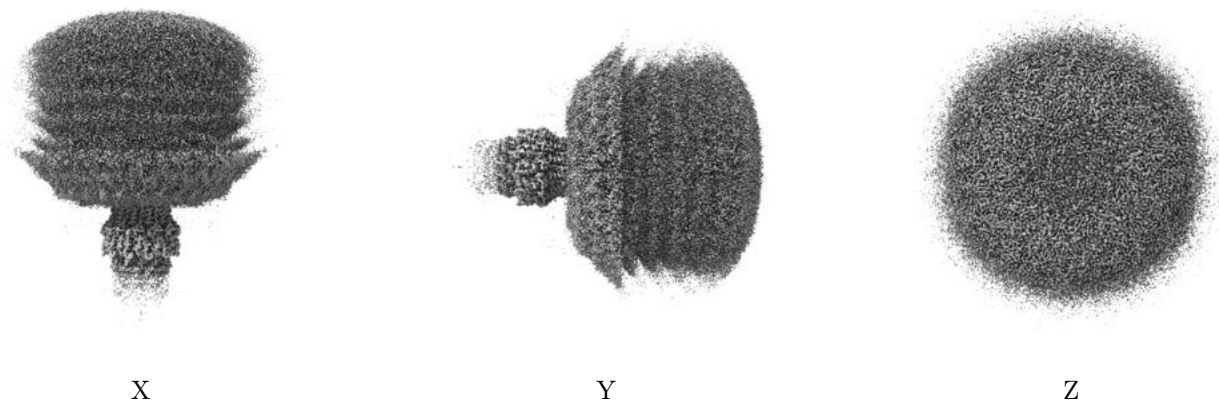


Z

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.

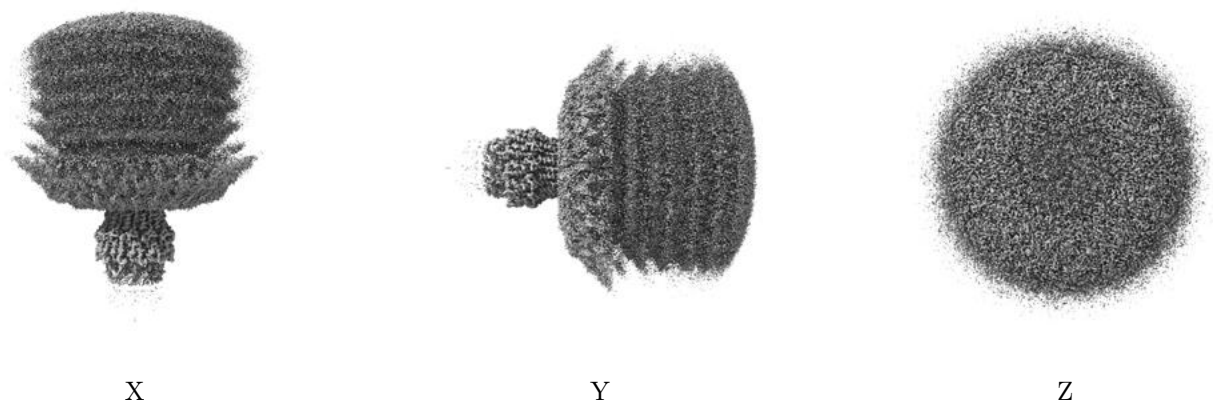
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

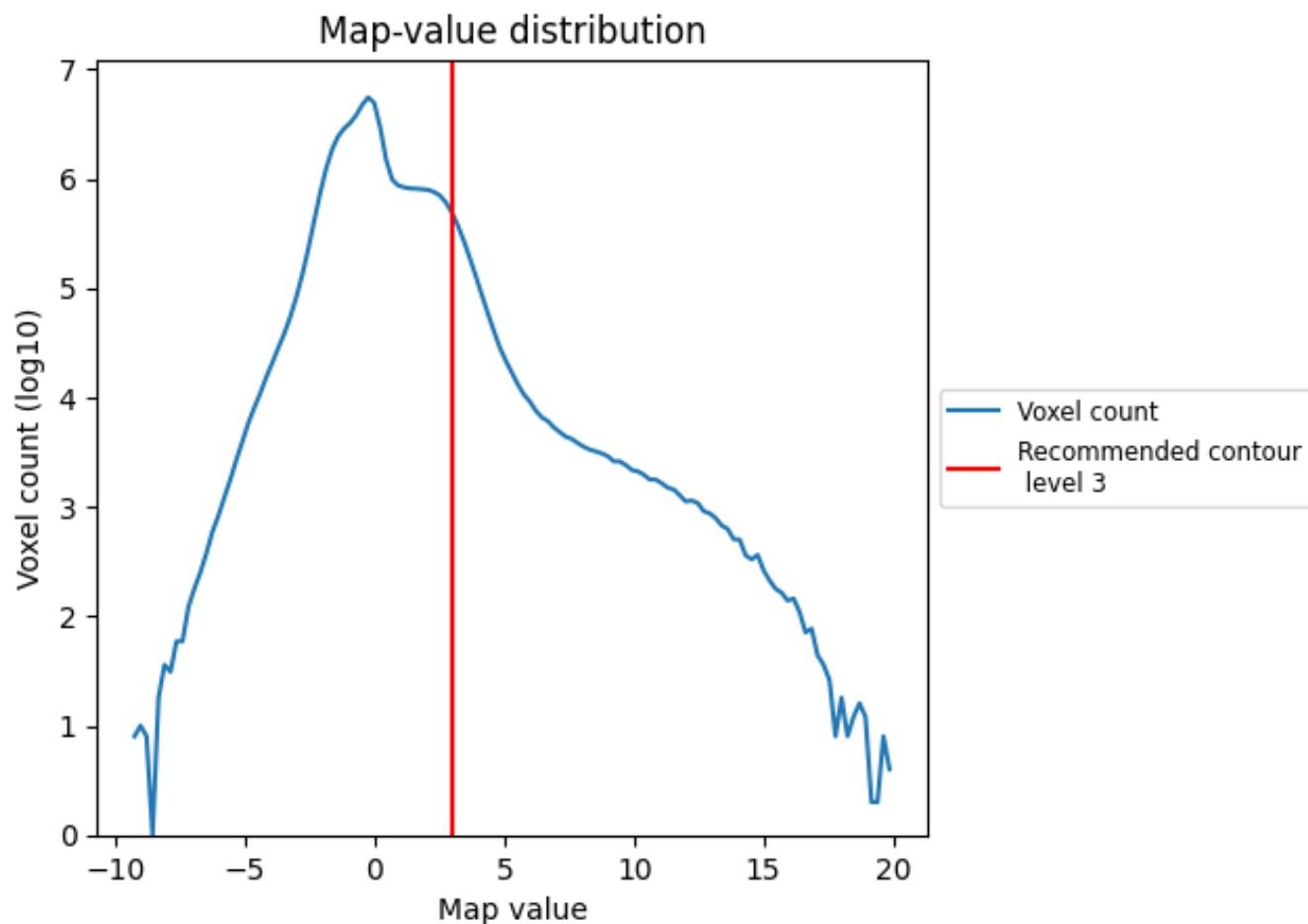
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

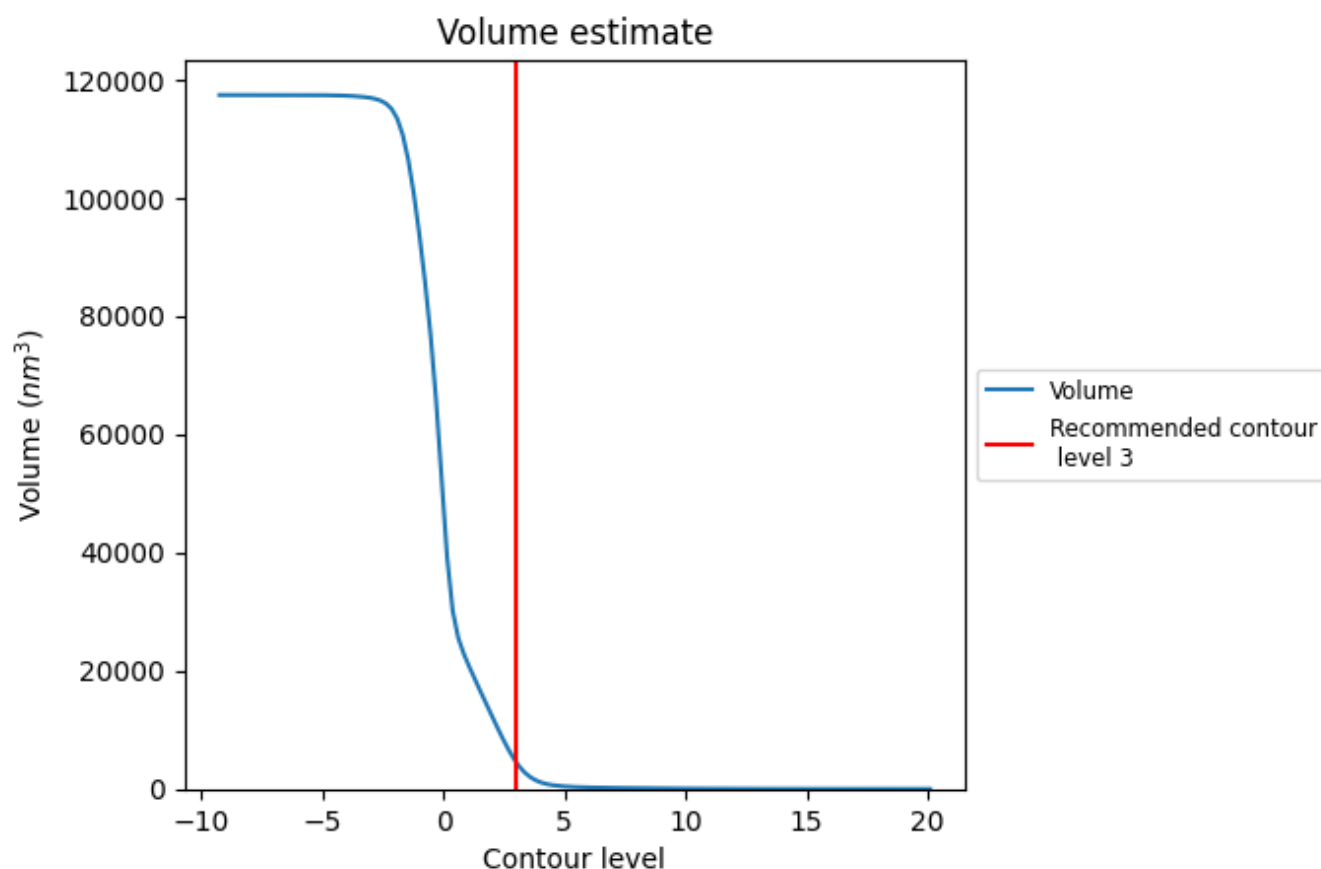
This section contains the results of statistical analysis of the map.

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.

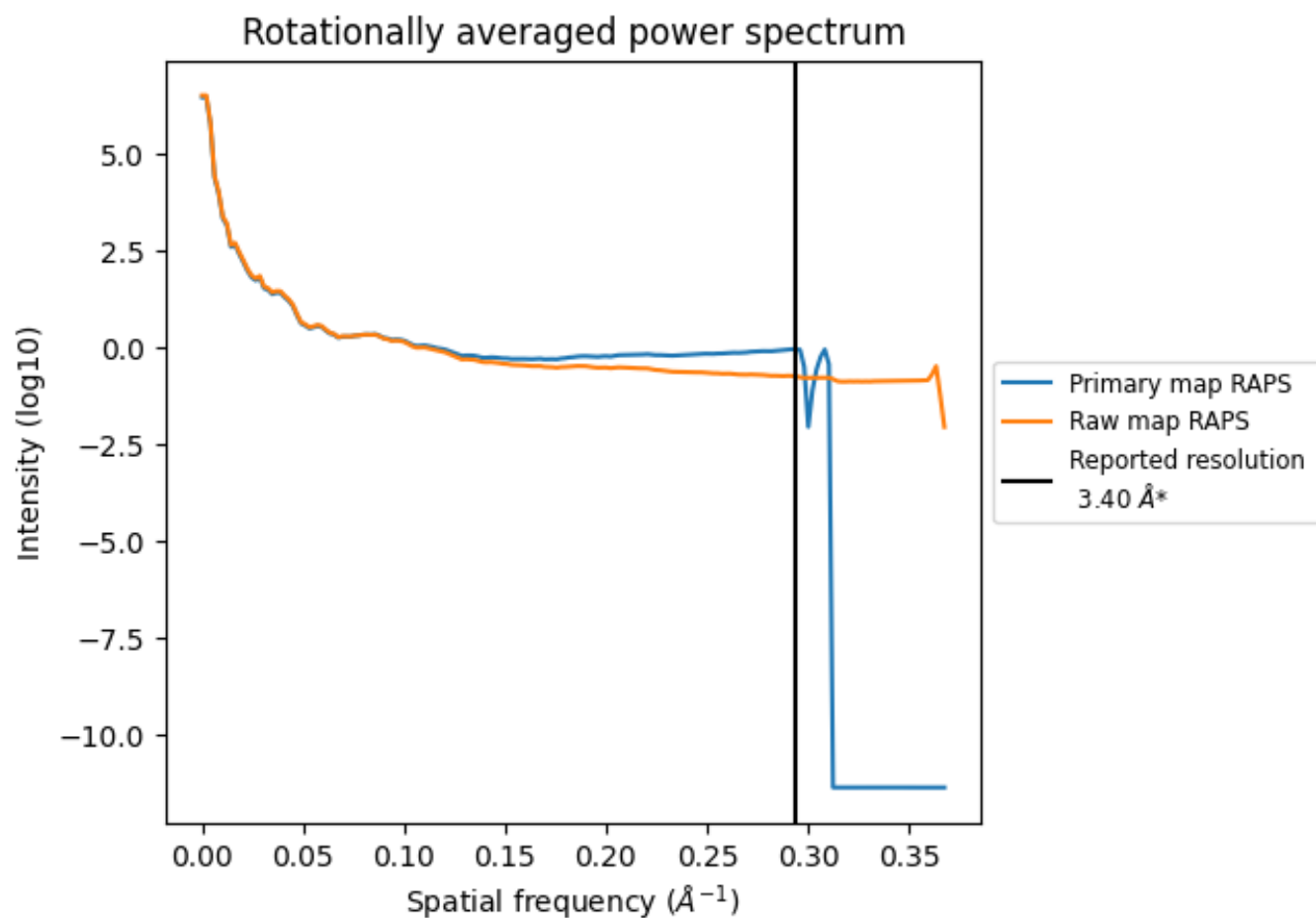
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4530 nm³; this corresponds to an approximate mass of 4092 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 ⓘ

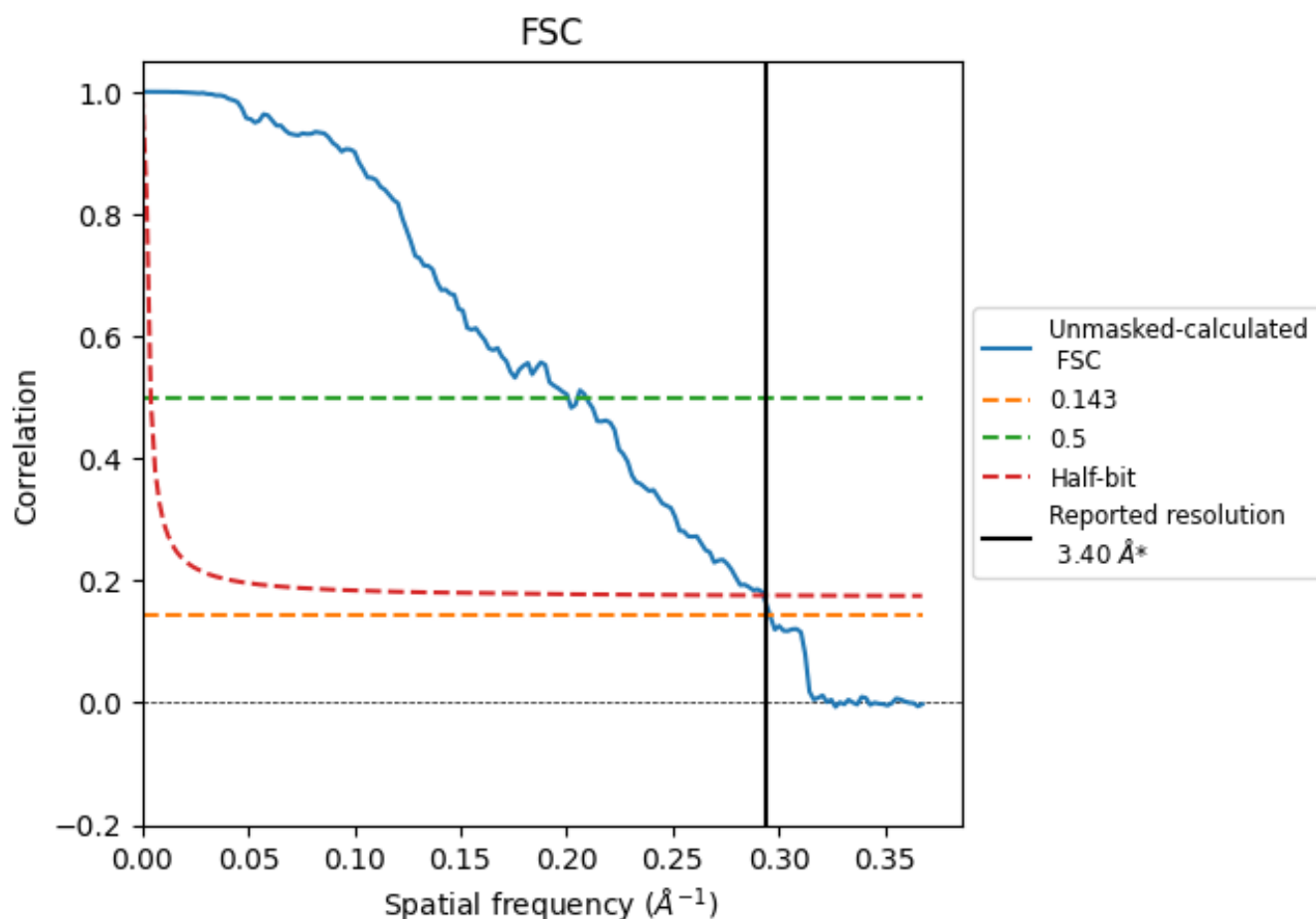


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

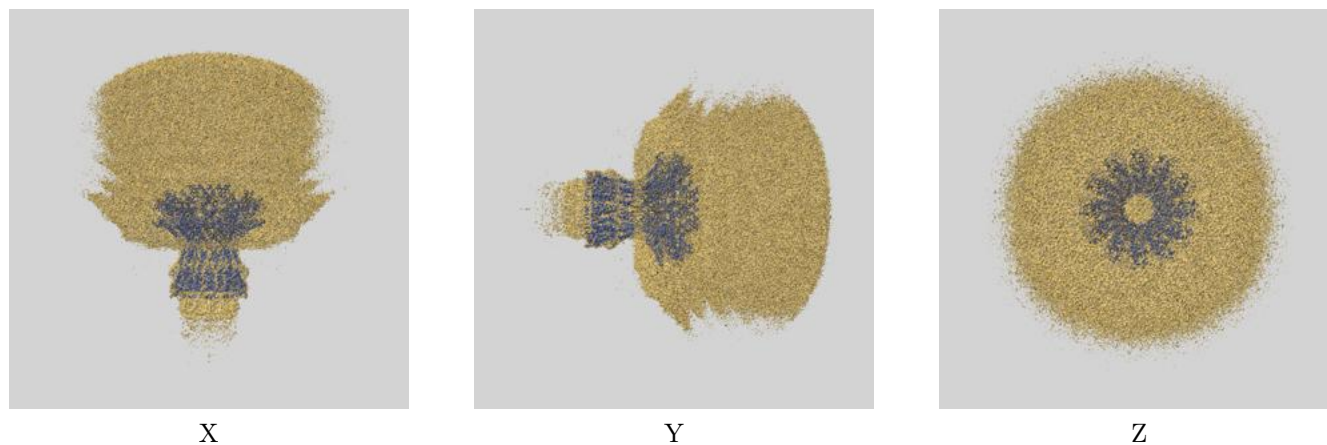
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.38	4.99	3.42

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

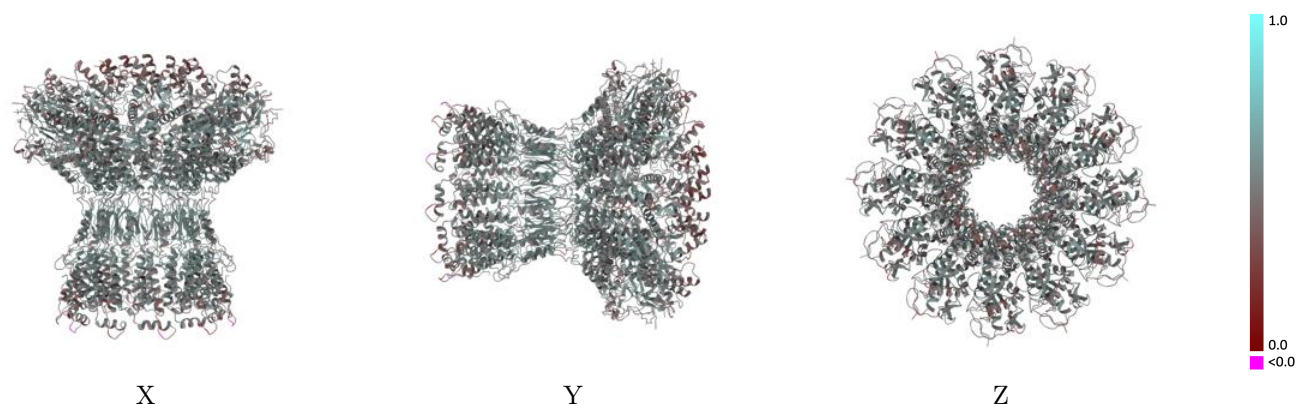
This section contains information regarding the fit between EMDB map EMD-62358 and PDB model 9KHX. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



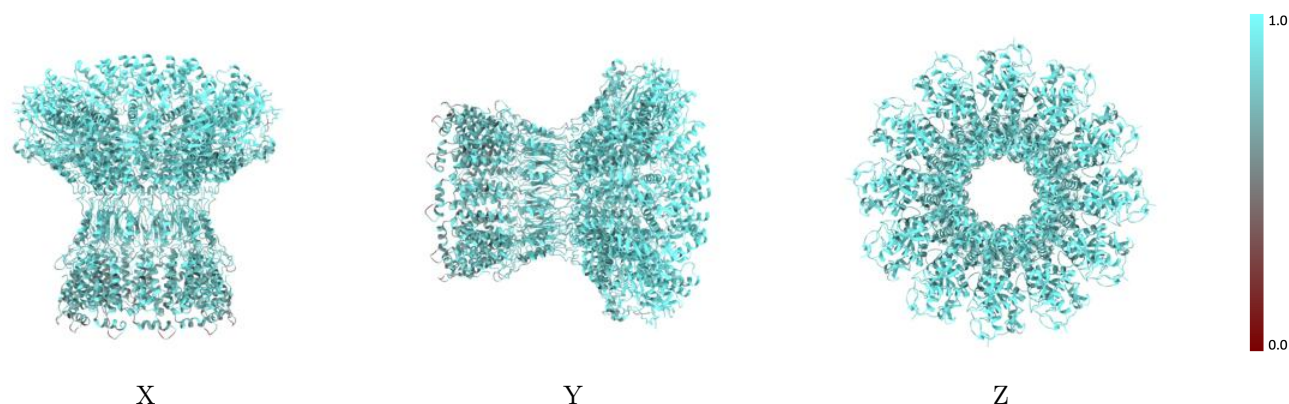
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



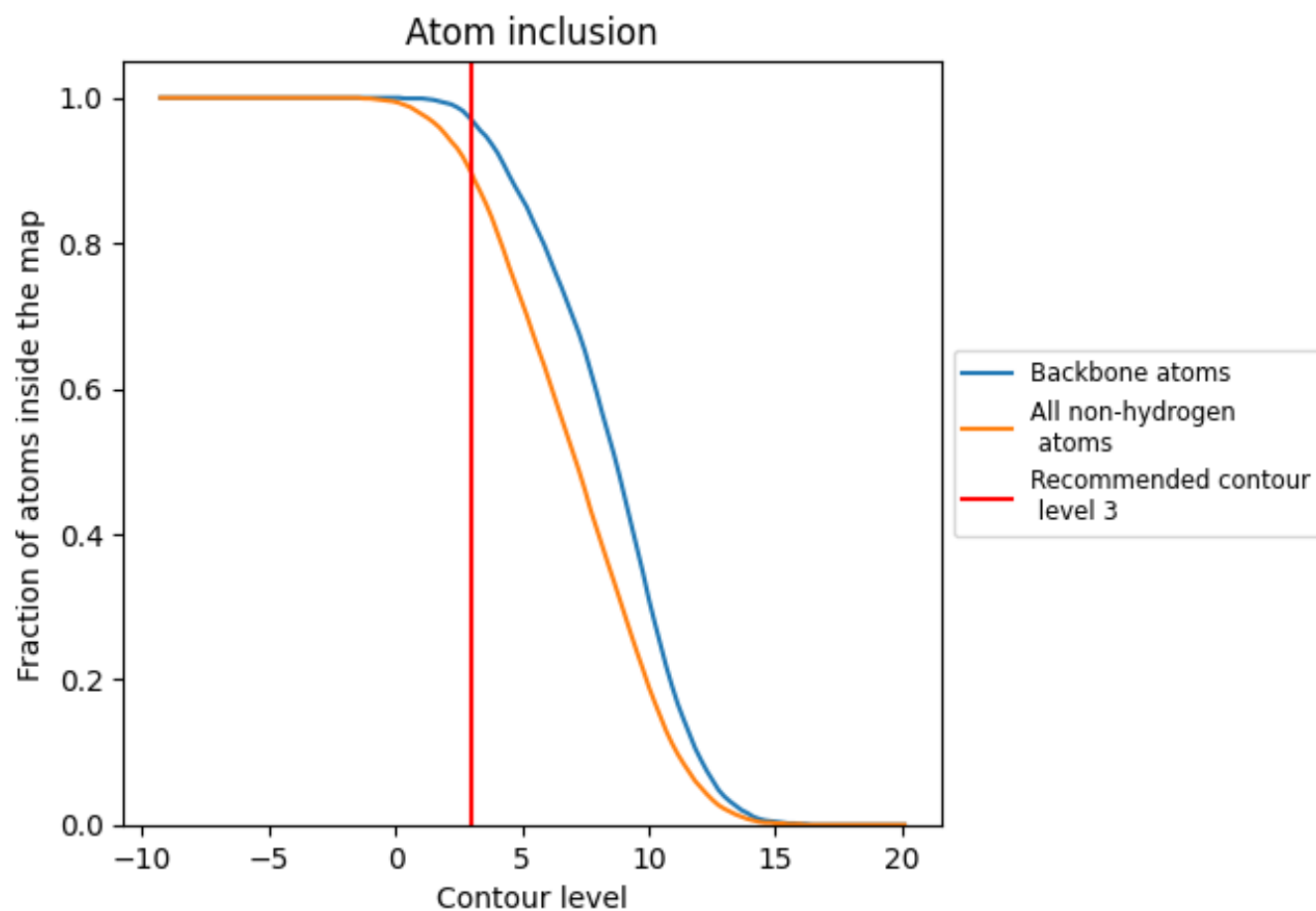
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8970	 0.4920
A	 0.8290	 0.4980
B	 0.8030	 0.4760
C	 0.8120	 0.4980
D	 0.8010	 0.4760
E	 0.8230	 0.5000
F	 0.8110	 0.4740
G	 0.8250	 0.5000
H	 0.8060	 0.4780
I	 0.8120	 0.4990
J	 0.8070	 0.4790
K	 0.8190	 0.5000
L	 0.8130	 0.4770
M	 0.9310	 0.4990
N	 0.9240	 0.4880
O	 0.9330	 0.4980
P	 0.9260	 0.4910
Q	 0.9320	 0.4970
R	 0.9230	 0.4910
S	 0.9320	 0.5000
T	 0.9240	 0.4890
U	 0.9330	 0.4970
V	 0.9250	 0.4910
W	 0.9320	 0.4970
X	 0.9240	 0.4900

