



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:56 AM UTC

PDB ID : 8CV1 / pdb_00008cv1
EMDB ID : EMD-27005
Title : ACP1-KS-AT domains of mycobacterial Pks13
Authors : Kim, S.K.; Dickinson, M.S.; Finer-Moore, J.S.; Rosenberg, O.S.; Stroud, R.M.
Deposited on : 2022-05-17
Resolution : 2.60 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

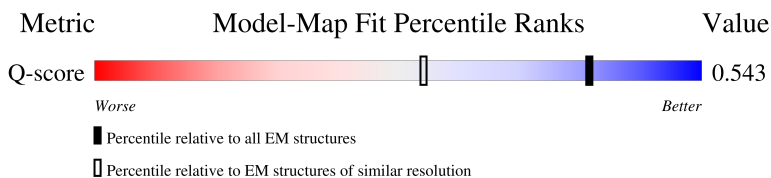
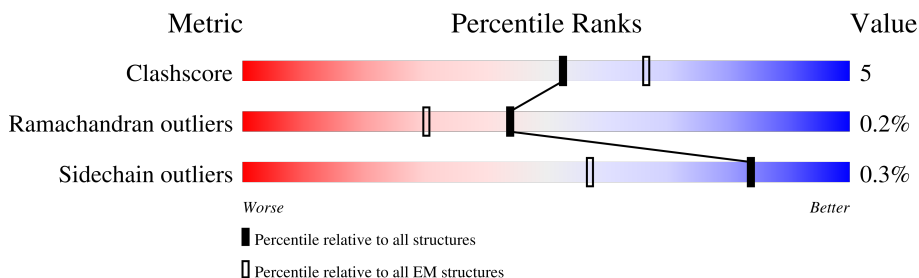
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 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	8728 (2.10 - 3.10)

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	1816	 48% 8% 44%
1	B	1816	 46% 5% 49%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14771 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 Polyketide synthase PKS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1016	Total	C	N	O	S	0	0
			7710	4833	1351	1502	24		
1	B	923	Total	C	N	O	S	0	0
			7016	4407	1238	1351	20		

- Molecule 2 is UNKNOWN LIGAND (CCD ID: UNL) (formula:) (labeled as "Ligand of Interest" by depositor).

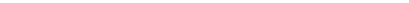
Mol	Chain	Residues	Atoms			AltConf
2	A	1	Total	C	O	0
			19	18	1	
2	B	1	Total	C	O	0
			19	18	1	

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	O	0
			2	2	
3	B	5	Total	O	0
			5	5	

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

- Molecule 1: Polyketide synthase PKS13

Chain B:  46% 5% 49%

ASN	GLY	ALA	P988	T761	VAL	L271	ALA	THR	MET
SER	ALA	ALA			GLY	V272	PHE	THR	THR
GLY	GLN	GLY	L991	E767	GLN		ARG	GLY	ASN
THR	VAL	VAL			ARG	Q276	HIS	PRO	ASN
ILE	THR	LEU	L1008	Q770	MET	G284	THR	THR	MET
GLY	LEU	ASP	L1012	Q777	ASP	E285	ILE	ARG	ARG
GLN	PRO	ALA			GLU	A296	GLU	GLU	GLN
ARG	VAL	LYS	D1017	P791	TYR	L297	SER	TRP	TRP
LEU	ALA	LEU			GLY		LEU	LEU	LEU
GLY	VAL	ALA	S1021	S798	GLU		ALA	ARG	ASN
THR	GLY	ALA			PHE	P300	THR	THR	ASN
ILE	ALA	PHE			ILE		VAL	TRP	TRP
VAL	GLY	GLN	K1047	E801	ASP	E308	ILE	VAL	VAL
GLY	VAL	GLN	GLY	Y806	GLU		ALA	ILE	VAL
ALA	ALA	ARG	ALA		ASP	A326	GLY	ASN	ASN
ALA	VAL	ALA	GLY	L813	GLU		GLY	ALA	ALA
VAL	VAL	VAL	ALA		PRO	M337	GLU	GLY	THR
GLY	GLY	PRO	L1063	R823	ALA	L372	PRO	GLU	GLY
TYR	ASP	ALA			GLU		GLU	GLN	GLN
GLU	VAL	ASN	F1074	E837	GLY	G406	PRO	SER	SER
PRO	GLU	ASN	THR		GLY	T407	GLU	GLY	ALA
GLU	GLY	ALA	GLY	R840	ASP	I408	PRO	ASP	ASP
GLY	GLY	ARG	ASP		ALA	L409	TYR	ALA	ALA
LEU	GLY	LEU	SER	E846	TYR		ASP	ILE	ILE
PRO	ALA	VAL	SER	Y847	PRO	R426	ASP	GLU	GLU
TRP	GLY	THR	ALA		SER		GLU	SER	GLY
GLU	ALA	THR	VAL	E861	TYR	H443	W137	GLY	LEU
VAL	SER	LEU	MET		ASP		R136	LEU	LEU
PRO	VAL	THR	PRO	D861	GLU	S446	R149	SER	SER
LEU	ILE	ARG	GLY		ASP			ARG	ARG
ILE	GLU	HIS	ASN	V864	TYR	D463	R154	ASP	ASP
GLU	ASP	PRO	HIS		GLY	K464	T155	ALA	VAL
LEU	ASP	GLY	VAL	D880	LEU		R207	ALA	VAL
GLY	GLU	GLY	ALA	Q861	PRO	R484	ALA	ALA	ALA
LEU	PRO	ALA	THR		PRO			MET	MET
ASP	ASP	THR	ALA	S891	GLY	F510		SER	SER
SER	PRO	VAL	GLN	E892	ILE		R219	ASP	ASP
LEU	ILE	VAL	ARG	G893		E529	GLU	ILE	ILE
MET	LEU	VAL	HIS	K894	ALA	PRO	ALA	GLU	GLU
VAL	GLN	ALA	ALA		A590	GLU	M227	ASP	ASP
VAL	ASP	ARG	VAL	A904	D671	PRO	R228	LEU	LEU
ARG	ASP	THR	TRP			PRO	S217	THR	THR
ILE	ASN	VAL	GLU	T907	H688	GLU	S218	GLY	GLY
LYS	GLU	GLU	PHE	G908	P689	LYS	P230	VAL	VAL
ASN	THR	GLU	VAL	Q909		PRO	T231	THR	THR
ARG	ALA	SER	ALA		W704	GLU		VAL	VAL
VAL	GLY	PHE	ARG	Y933		ALA		THR	THR
GLU	ALA	THR	GLY		A707	ALA		VAL	VAL
THR	GLY	LEU	LYS	E939		PRO	D229	THR	THR
ASP	MET	VAL	THR	G940	Q739	GLU	S231	GLY	GLY
PHE	GLY	TYR	ASP			LYS	1232	VAL	VAL
ASP	ALA	ASP	LEU	L960	Y744	SER	D264	THR	THR
LEU	ASP	ALA	ALA		S745	GLU		LEU	LEU
PRO	PHE	ILE	ALA	S963	E748	ALA	C267	ALA	ALA
PRO	GLN	VAL	VAL			ASP		THR	THR
ILE	LYS	ALA	VAL	Y965	D756	ALA		ALA	ALA
GLN	TRP	ARG	GLN			VAL		VAL	VAL
LEU	ASP	ASN	THR	N972		THR		THR	THR

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	39685	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45.8	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.060	Depositor
Minimum map value	-0.015	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0116	Depositor
Map size (Å)	322.31, 322.31, 322.31	wwPDB
Map dimensions	386, 386, 386	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.835, 0.835, 0.835	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: UNL

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	0.41	5/7865 (0.1%)	0.39	1/10685 (0.0%)
1	B	0.42	6/7158 (0.1%)	0.36	1/9715 (0.0%)
All	All	0.42	11/15023 (0.1%)	0.38	2/20400 (0.0%)

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	219	THR	C-O	-8.91	1.13	1.23
1	B	219	THR	C-O	-8.87	1.12	1.23
1	A	217	SER	CA-C	-6.53	1.44	1.52
1	A	218	SER	C-O	-6.37	1.15	1.24
1	B	217	SER	C-O	-6.22	1.16	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	218	SER	N-CA-C	6.14	122.17	113.02
1	B	218	SER	N-CA-C	5.86	122.40	113.61

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	7710	0	7551	107	0
1	B	7016	0	6896	51	0
2	A	19	0	0	0	0
2	B	19	0	0	0	0
3	A	2	0	0	0	0
3	B	5	0	0	0	0
All	All	14771	0	14447	155	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 5.

The worst 5 of 155 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:A:801:GLU:OE2	1:A:955:TYR:CE2	2.00	1.13
1:A:801:GLU:OE2	1:A:955:TYR:HE2	1.50	0.94
1:A:11:ARG:HG3	1:A:25:ILE:HB	1.61	0.81
1:A:7:ARG:HG2	1:A:11:ARG:HH12	1.46	0.78
1:A:8:GLU:O	1:A:12:ASN:N	2.17	0.77

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	1012/1816 (56%)	976 (96%)	34 (3%)	2 (0%)	43 66
1	B	917/1816 (50%)	892 (97%)	24 (3%)	1 (0%)	48 70
All	All	1929/3632 (53%)	1868 (97%)	58 (3%)	3 (0%)	44 66

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1052	ALA
1	A	230	PRO
1	B	230	PRO

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	799/1414 (56%)	797 (100%)	2 (0%)	86	94
1	B	725/1414 (51%)	723 (100%)	2 (0%)	86	94
All	All	1524/2828 (54%)	1520 (100%)	4 (0%)	84	94

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	231	SER
1	A	232	ILE
1	B	231	SER
1	B	232	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	700	ASN
1	B	1034	HIS
1	B	1007	GLN
1	A	978	HIS
1	B	613	GLN

5.3.3 RNA ⓘ

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](#)

Of 2 ligands modelled in this entry, 2 are unknown - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

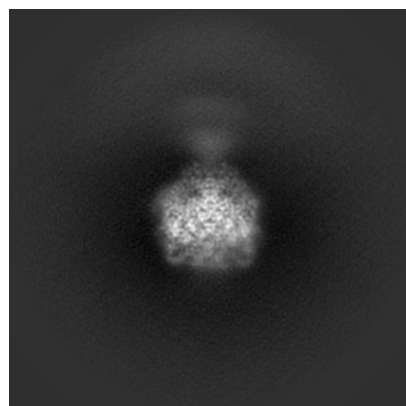
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27005. These allow visual inspection of the internal detail of the map and identification of artifacts.

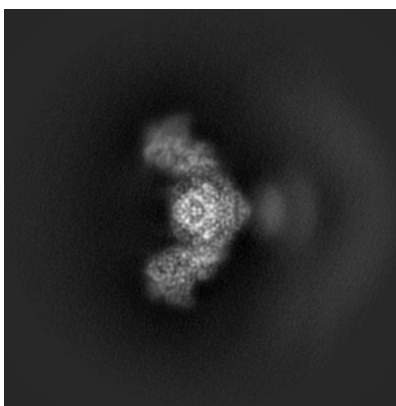
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

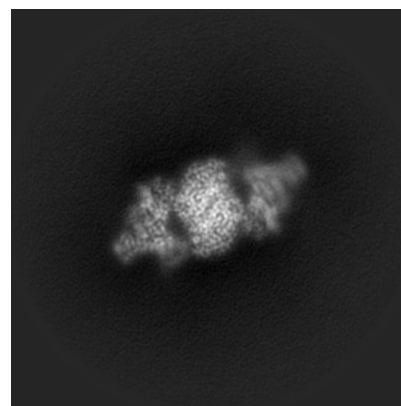
6.1.1 Primary map



X

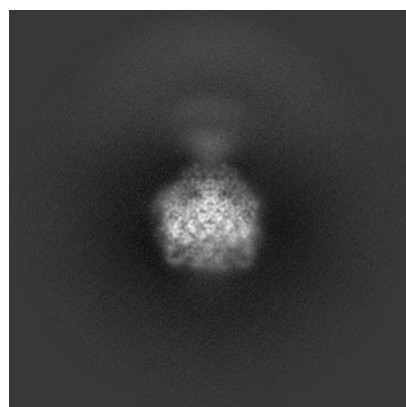


Y

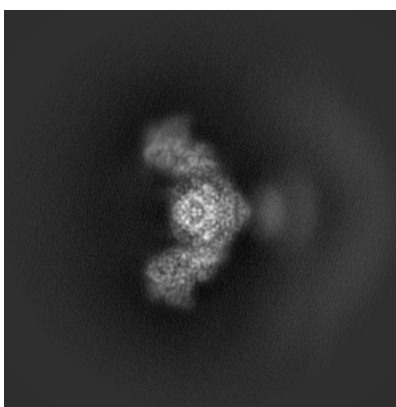


Z

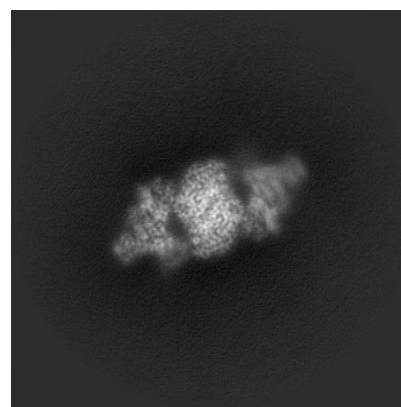
6.1.2 Raw map



X



Y

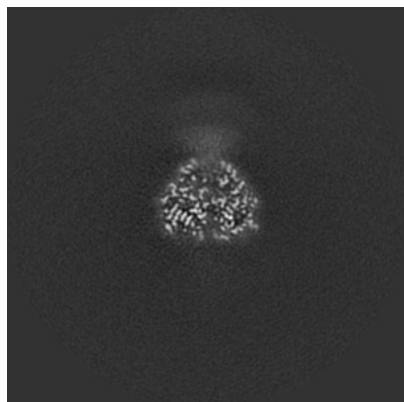


Z

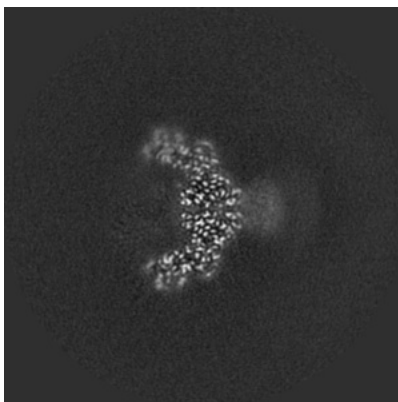
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

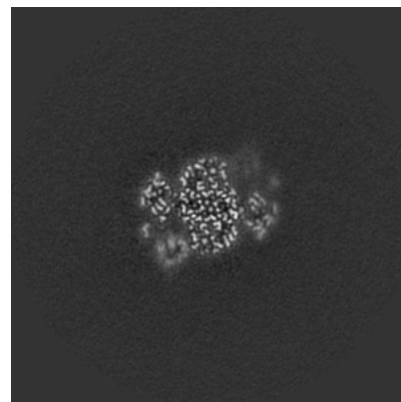
6.2.1 Primary map



X Index: 193

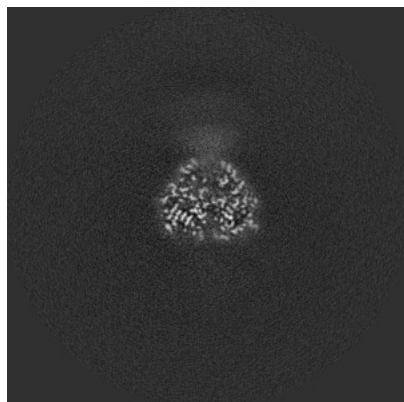


Y Index: 193

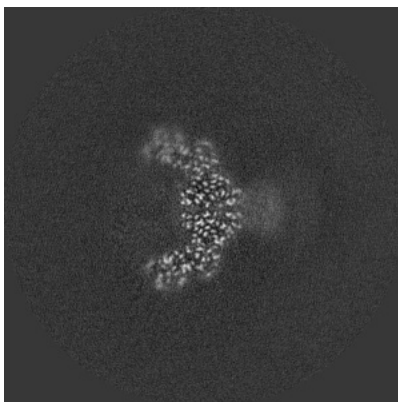


Z Index: 193

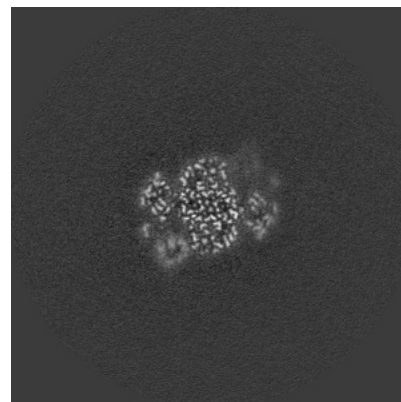
6.2.2 Raw map



X Index: 193



Y Index: 193

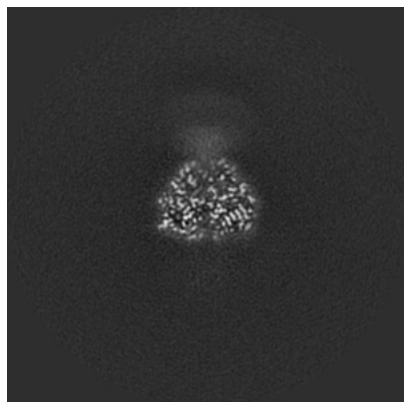


Z Index: 193

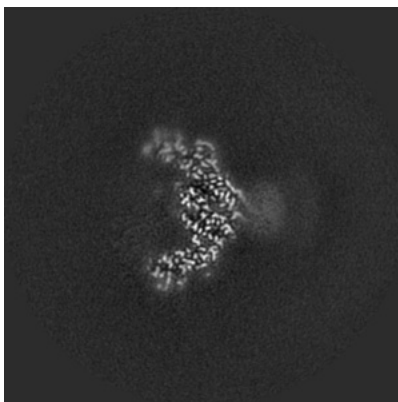
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

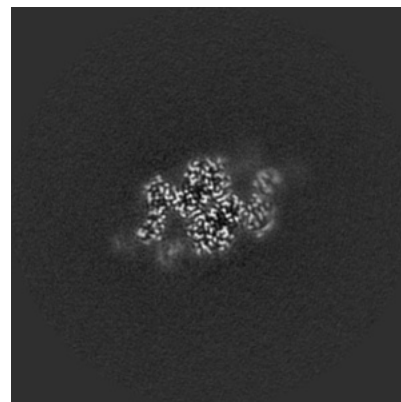
6.3.1 Primary map



X Index: 188

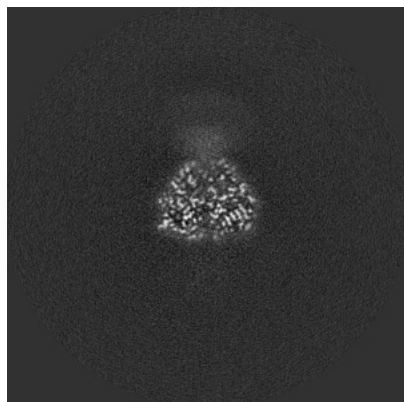


Y Index: 191

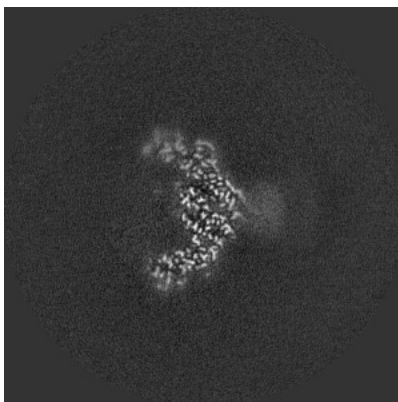


Z Index: 184

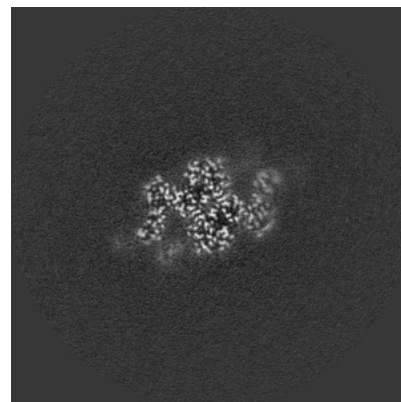
6.3.2 Raw map



X Index: 188



Y Index: 191

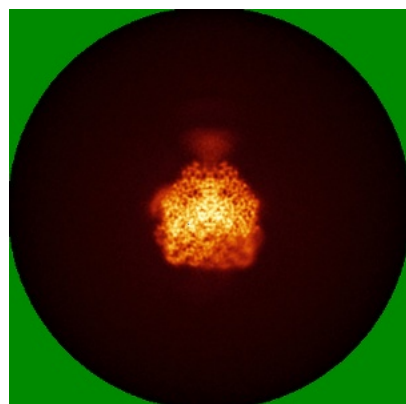


Z Index: 184

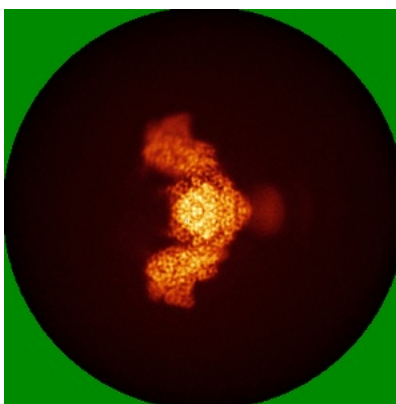
The images above show the largest variance slices of the map in three orthogonal directions.

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

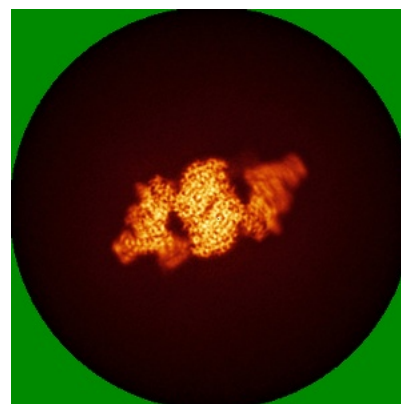
6.4.1 Primary map



X

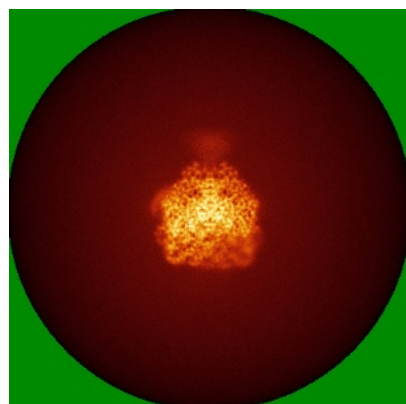


Y

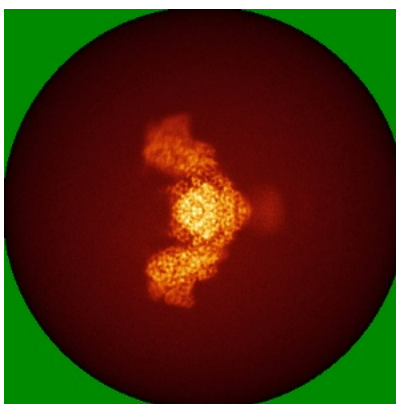


Z

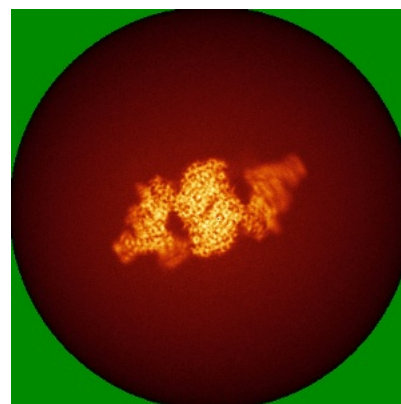
6.4.2 Raw map



X



Y

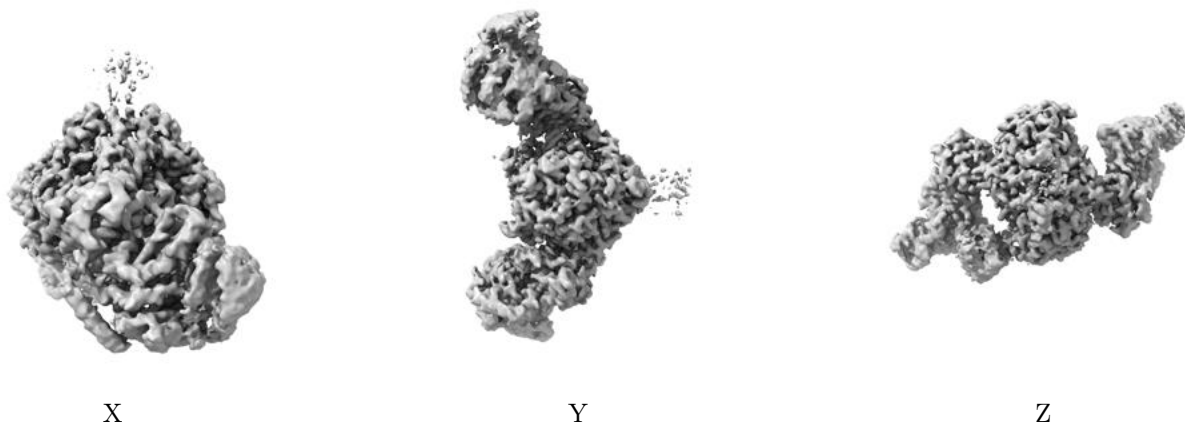


Z

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.

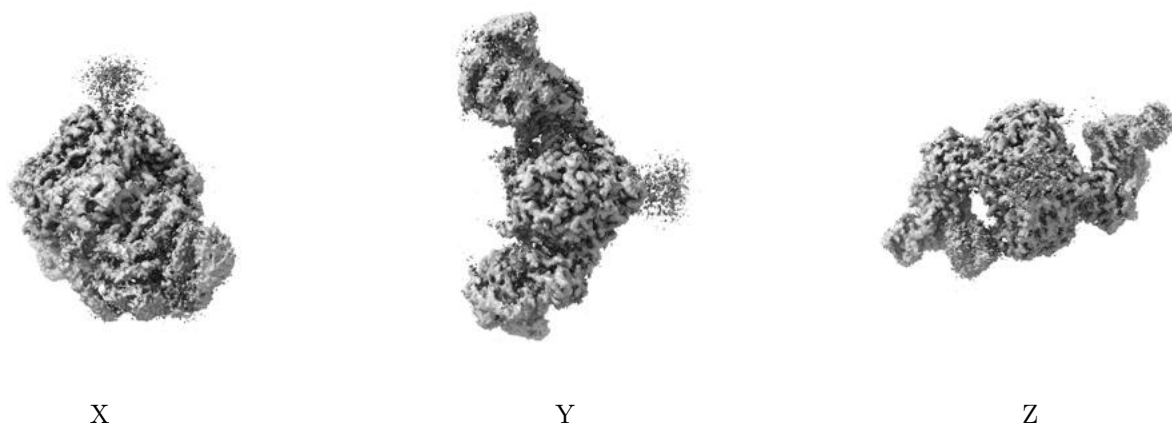
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0116. 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.

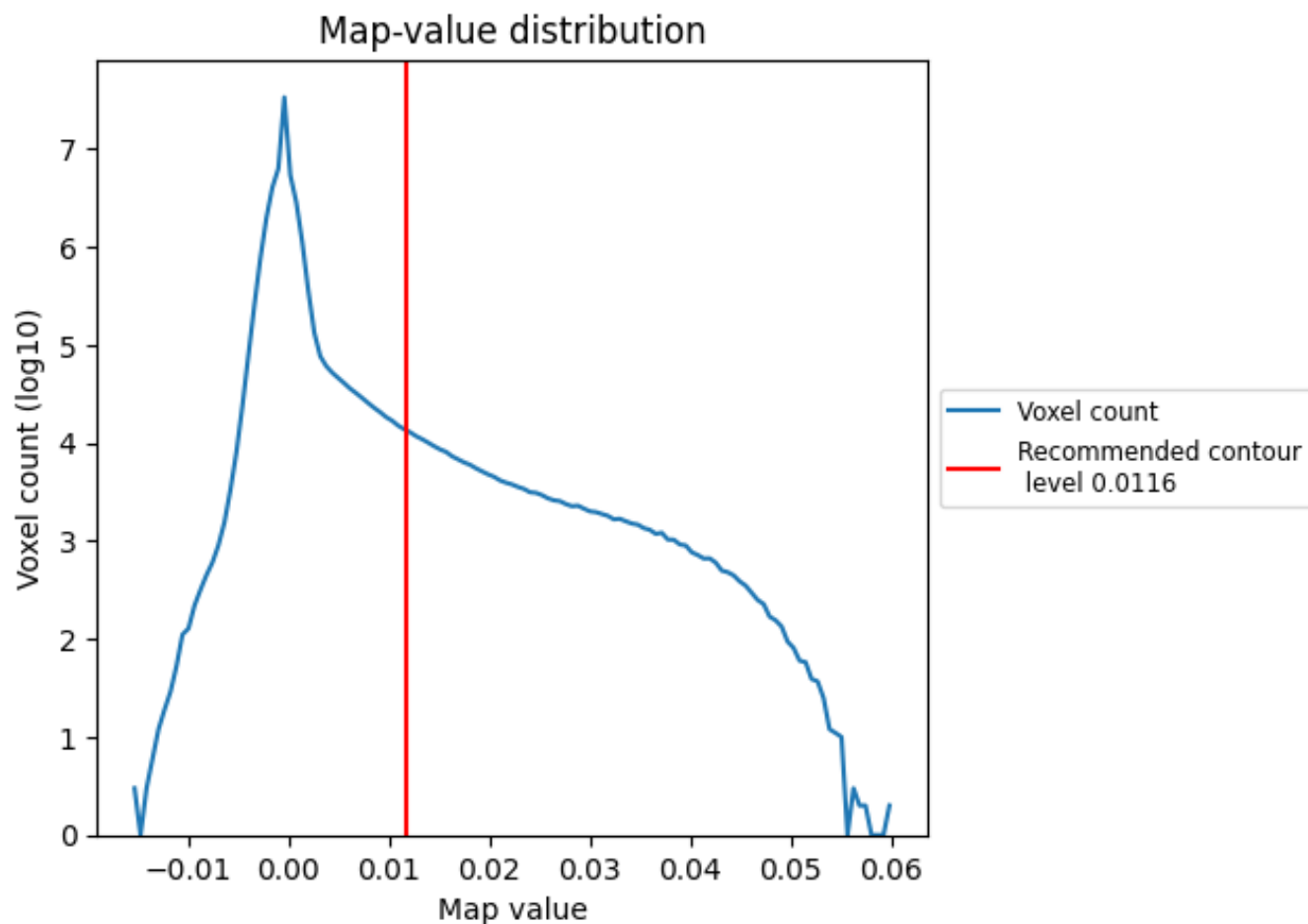
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

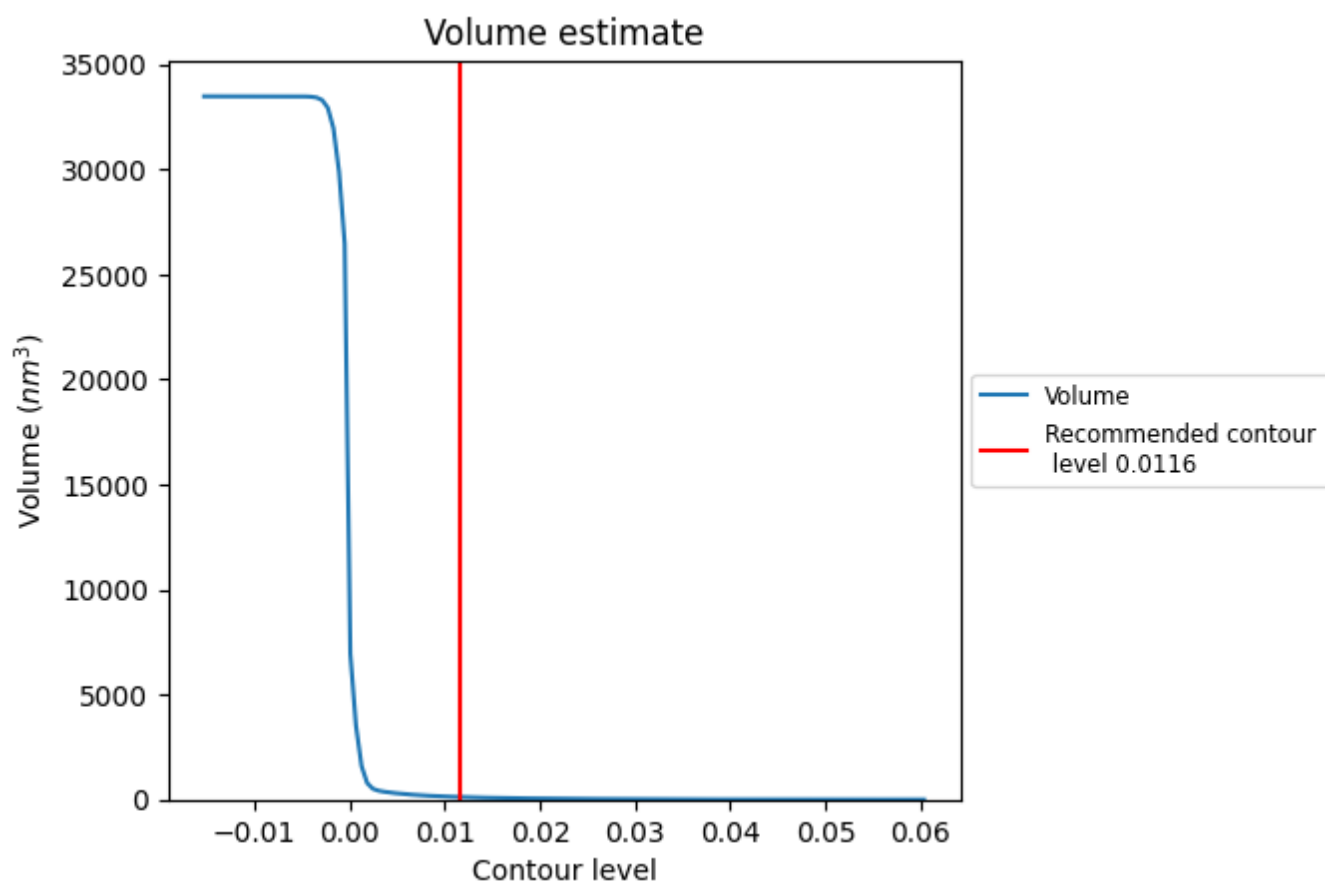
This section contains the results of statistical analysis of the map.

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.

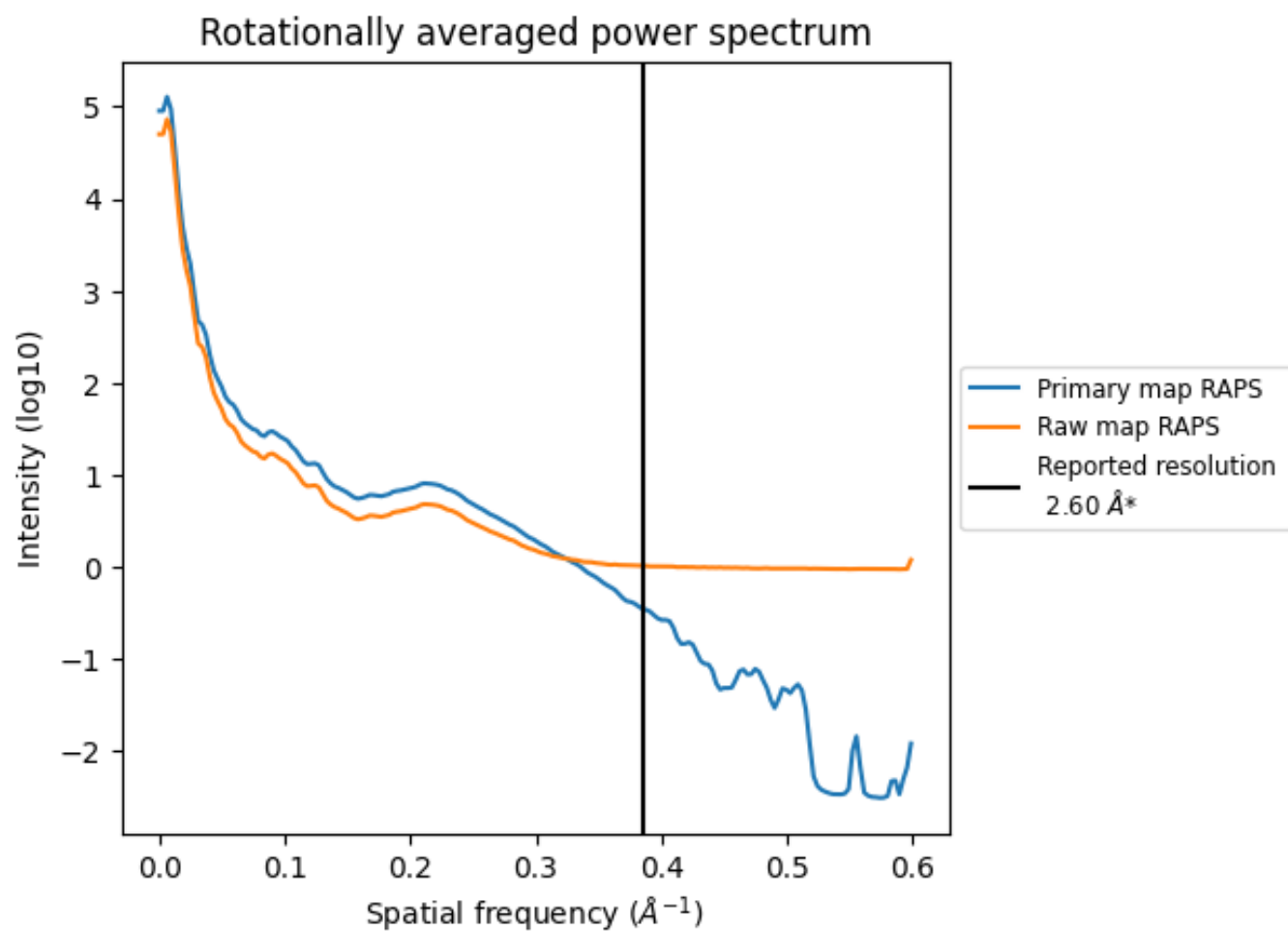
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 120 nm³; this corresponds to an approximate mass of 108 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 ⓘ

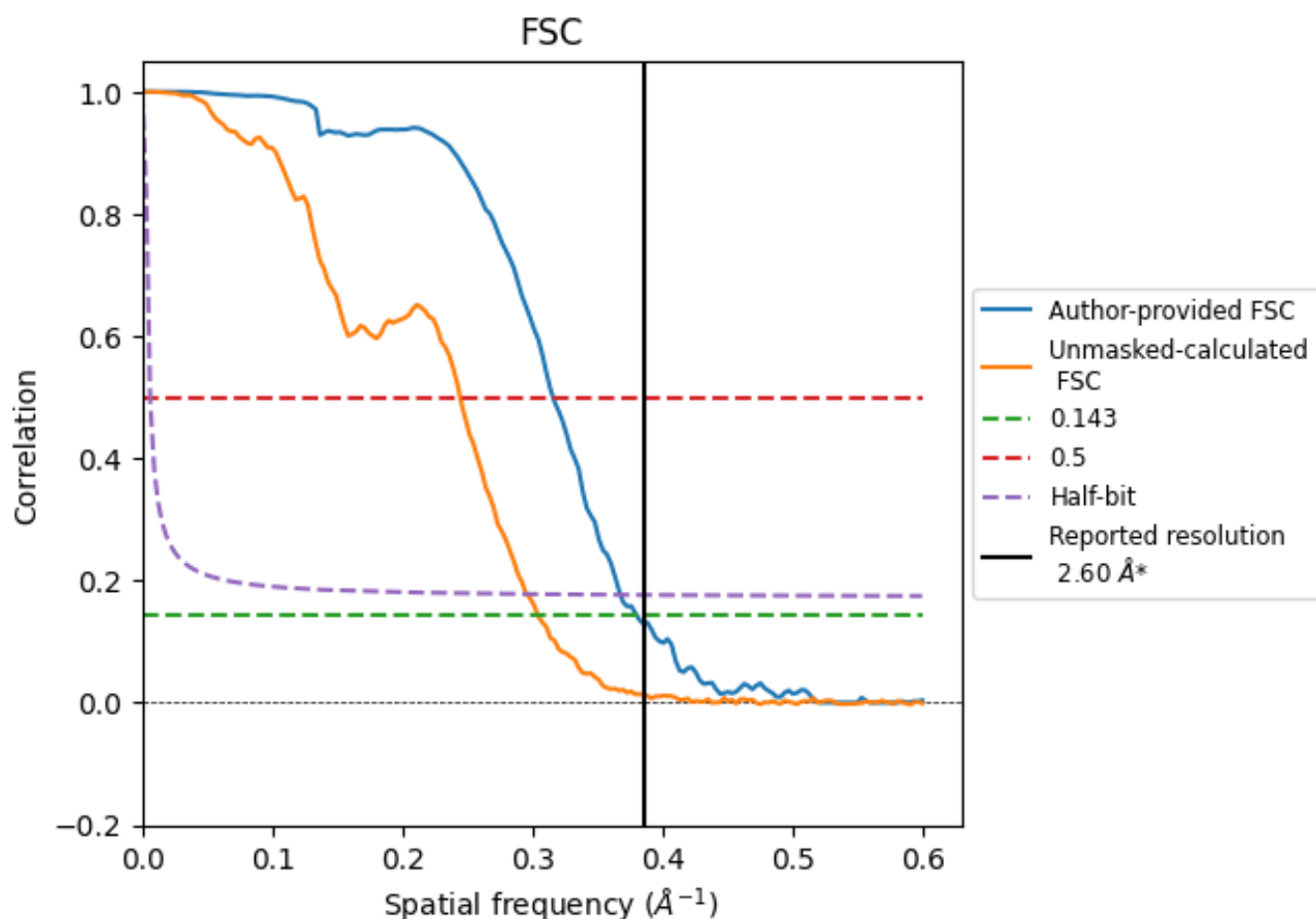


*Reported resolution corresponds to spatial frequency of $0.385 \text{ \AA}^{-1}$

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 0.385 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.63	3.17	2.72
Unmasked-calculated*	3.29	4.10	3.39

*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 3.29 differs from the reported value 2.6 by more than 10 %

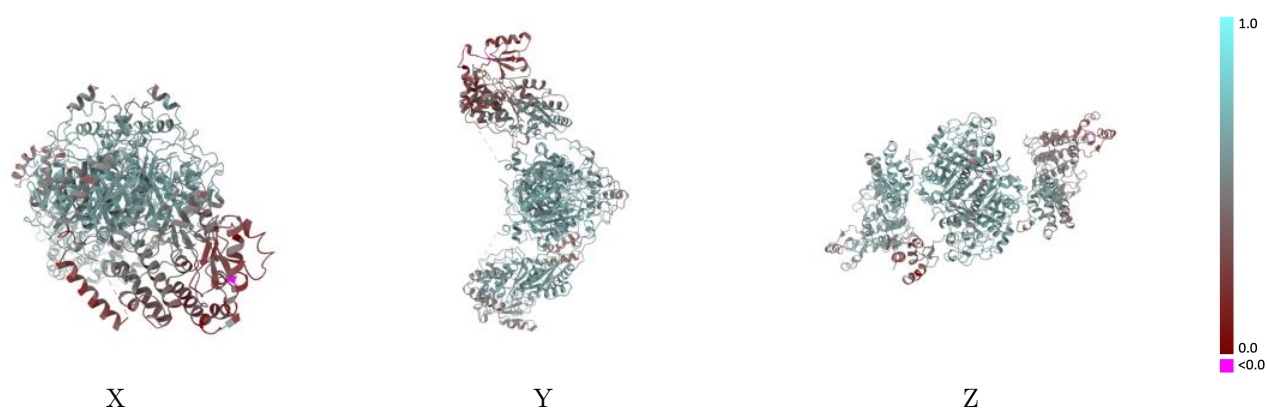
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27005 and PDB model 8CV1. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

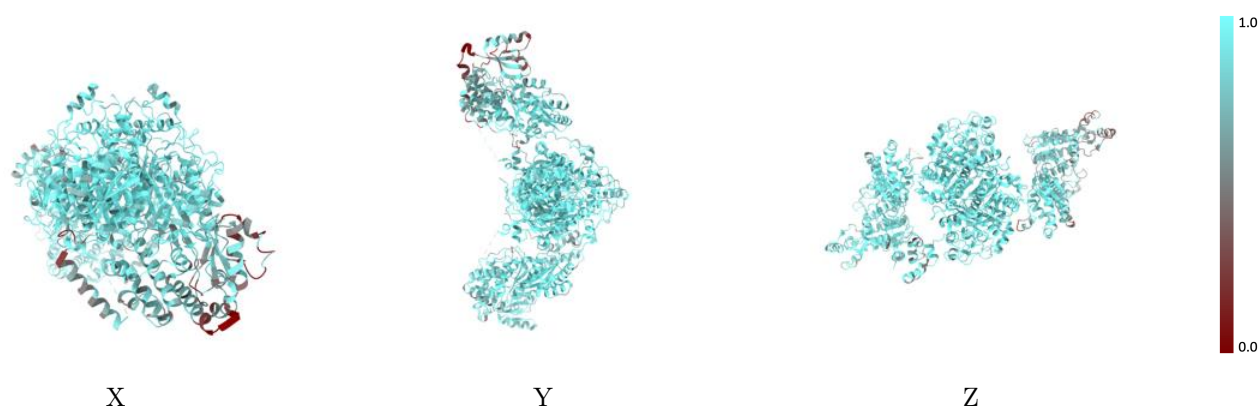
This section was not generated.

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



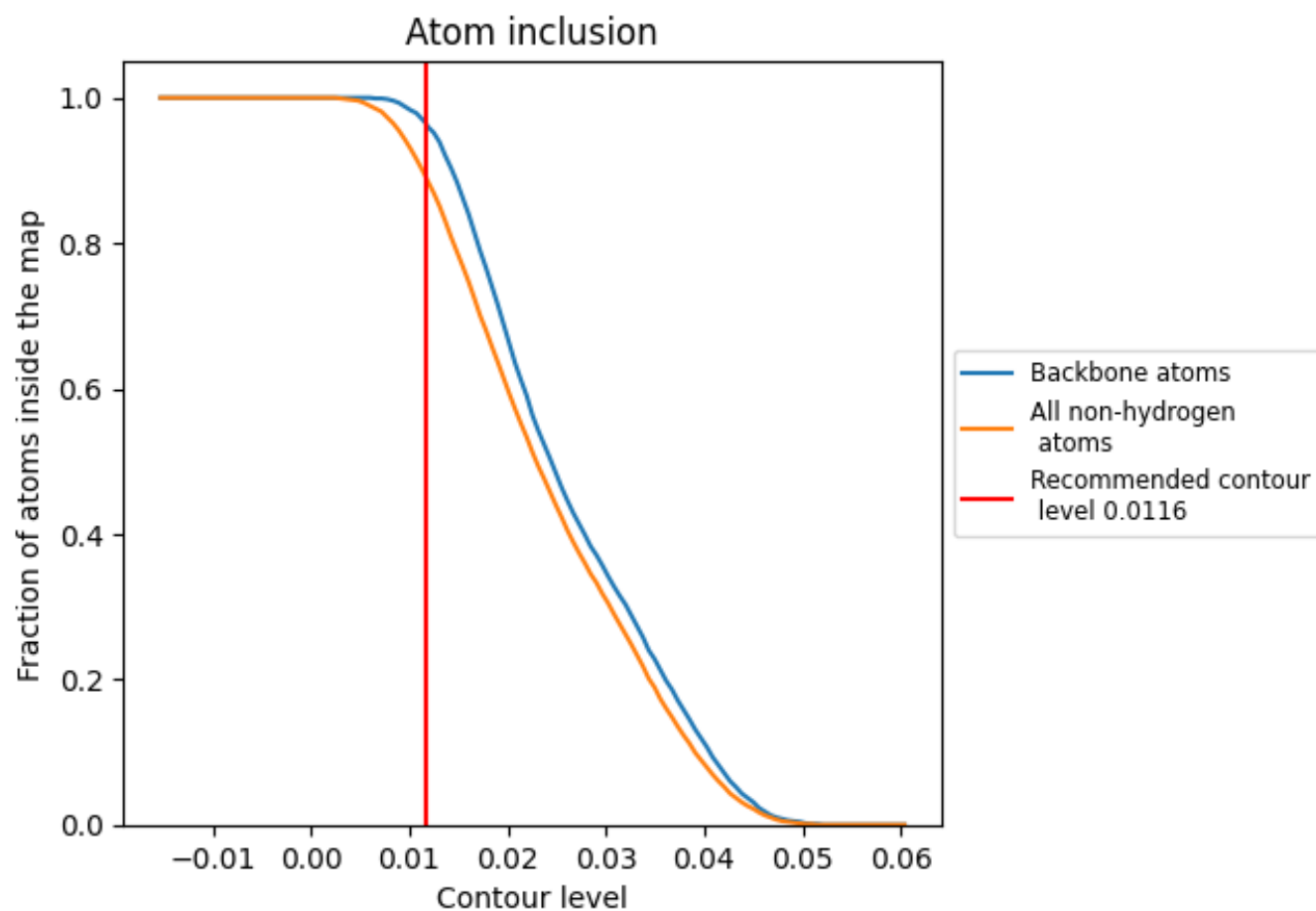
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0116).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 89% 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 (0.0116) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8930	0.5430
A	0.8510	0.4970
B	0.9440	0.5930

