



Full wwPDB EM Validation Report ⓘ

Apr 24, 2025 – 11:29 AM EDT

PDB ID : 9DUS / pdb_00009dus
EMDB ID : EMD-47176
Title : Cryo-EM structure of the Measles Virus polymerase (L) protein in complex with the tetrameric phosphoprotein (P)
Authors : Liu, B.; Wang, D.; Yang, G.
Deposited on : 2024-10-04
Resolution : 3.12 Å(reported)

This is a Full wwPDB EM Validation 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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

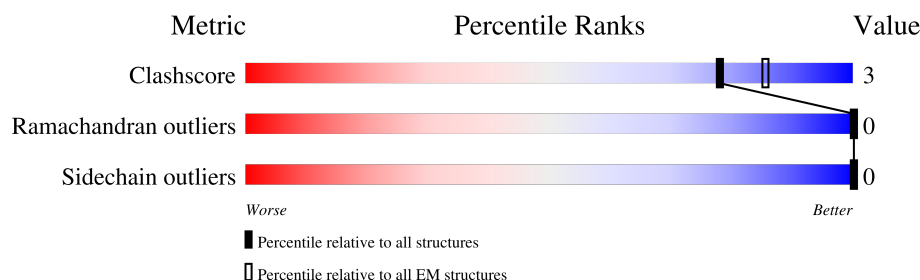
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.12 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	2183	
2	B	509	
2	C	509	
2	D	509	
2	E	509	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12702 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1253	Total	C	N	O	S	0	0
			10069	6432	1740	1844	53		

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	74	Total	C	N	O	S	1	0
			576	366	102	107	1		
2	C	132	Total	C	N	O	S	0	0
			1039	659	185	189	6		
2	D	57	Total	C	N	O	S	0	0
			442	279	77	85	1		
2	E	74	Total	C	N	O	S	1	0
			576	365	97	113	1		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	508	SER	-	expression tag	UNP Q83623
B	509	GLY	-	expression tag	UNP Q83623
C	508	SER	-	expression tag	UNP Q83623
C	509	GLY	-	expression tag	UNP Q83623
D	508	SER	-	expression tag	UNP Q83623
D	509	GLY	-	expression tag	UNP Q83623
E	508	SER	-	expression tag	UNP Q83623
E	509	GLY	-	expression tag	UNP Q83623

[illegible]

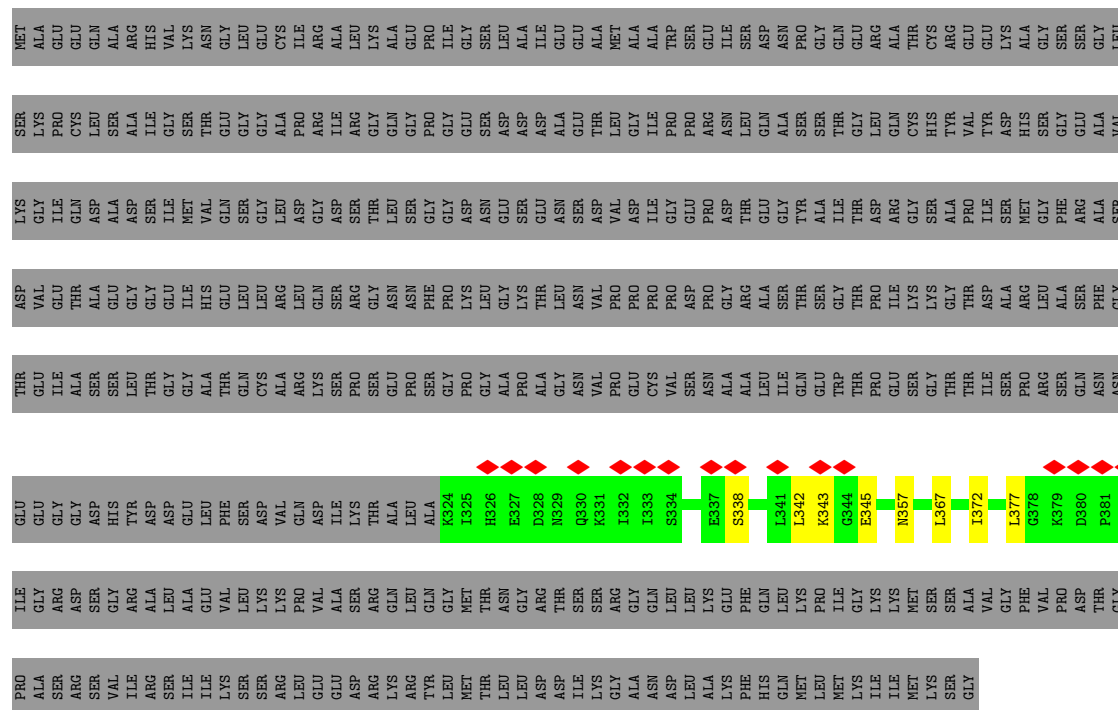
- Molecule 2: Phosphoprotein

Chain B:  13% 85%

ILE	D393	GLU	THR	ASP	LYS	SER	MET
ILE	L394	GLU	GLU	VAL	GLY	LYS	ALA
LYS		GLY	ILE	THR	ILE	PRO	GLU
SER	R400	ASP	SER	SER	GLN	CYS	GLN
ARG		HIS	SER	GLU	ALA	LEU	GLU
LEU	K412	TYR	LEU	GLY	ASP	SER	ALA
LEU	P413	ASP	THR	GLY	GLY	ASP	ARG
GLU	VAL	ASP	THR	GLY	ILE	ILE	HIS
ASP		GLU	GLY	ILE	MET	VAL	VAL
ARG		LEU	ALA	HIS	VAL	THR	ASN
LYS		PHE	THR	GLU	GLN	GLY	GLY
ARG		SER	GLN	LEU	SER	GLY	LEU
TYR		ASP	CYS	LEU	GLY	GLY	LEU
LEU		VAL	ALA	ARG	LEU	ALA	CYS
LEU		GLN	ARG	LEU	ASP	PRO	ILE
MET		GLY	LYS	GLN	GLY	GLY	ARG
MET		ASP	SER	ARG	ASP	ILE	ALA
THR		ILE	PRO	ARG	SER	ARG	LEU
LEU		LYS	PRO	GLY	SER	GLY	LYS
LEU		THR	SER	THR	THR	GLY	LEU
ASP		GLY	SER	ARG	SER	GLY	LEU
ASP		ALA	GLU	ASN	ASP	GLY	CYS
ILE		LEU	PRO	ASN	GLU	LEU	ARG
LYS		ALA	SER	PHE	SER	GLY	VAL
GLY		LYS	GLY	PRO	GLY	GLY	GLY
ALA		ARG	PRO	LYS	ASP	GLU	GLY
ASN		GLY	ALA	LEU	ASN	ASP	SER
ASN		GLN	ALA	GLY	GLU	ASP	LEU
LEU		LEU	PRO	LYS	SER	ASP	ALA
LEU		LEU	ALA	THR	GLU	ASP	MET
LYS		LYS	GLY	LEU	ASN	ASN	GLU
PHE		GLU	ASN	VAL	SER	GLU	GLU
HIS		PHE	VAL	VAL	ASP	THR	ALA
GLN		LEU	PRO	VAL	VAL	LEU	ALA
MET		LEU	GLU	PRO	ASP	GLY	MET
LEU		LYS	CYS	PRO	ILE	ILE	ALA
MET		PRO	VAL	PRO	GLY	PRO	SER
LYS		ILE	SER	ASP	GLU	PRO	THR
ILE		GLY	ASN	PRO	PRO	ASN	GLU
ILE		LYS	ALA	GLY	ASP	ASN	ILE
MET		LYS	ALA	ARG	THR	LEU	SER
LYS		MET	LEU	ALA	GLU	GLN	ASP
SER		SER	ILE	SER	GLY	ALA	ASN
GLY		SER	GLN	THR	TYR	SER	PRO
		LEU	GLU	ILE	GLY	GLY	GLY
		LYS	SER	ILE	ARG	LEU	GLY
		VAL	GLY	LYS	ILE	ARG	THR
		PRO	SER	LYS	VAL	CYS	ALA
		ASP	GLY	THR	GLY	HIS	ALA
		LYS	THR	THR	THR	TYR	ARG
		GLY	TRP	GLY	ILE	VAL	GLU
		LEU	PRO	PRO	ASP	GLY	GLU
		LYS	GLY	ILE	ARG	GLY	GLY
		GLY	SER	ALA	GLU	LEU	GLY
		ALA	ILE	SER	GLY	ALA	ASN
		GLY	GLN	THR	TYR	SER	PRO
		VAL	GLU	THR	ALA	GLY	GLY
		PHE	GLY	ILE	ARG	GLY	ALA
		VAL	SER	ALA	LEU	ASP	ALA
		PRO	GLY	ARG	ARG	MET	ALA
		ASP	THR	LEU	GLY	THR	ALA
		LYS	GLY	LYS	SER	ASP	GLY
		GLY	LEU	GLY	GLY	GLY	GLY
		LEU	TRP	THR	ILE	THR	GLY
		GLY	GLU	GLY	ALA	SER	GLY
		ILE	ASN	SER	ASN	ASP	GLY
		GLY	VAL	VAL	GLY	GLY	GLY
		GLY	ALA	GLY	ASP	GLY	GLY
		LEU	PRO	PRO	GLY	GLY	GLY
		GLY	GLN	THR	TYR	SER	ASN
		ALA	THR	THR	ALA	GLY	ALA
		GLY	ASN	VAL	ASP	ASN	GLY
		ILE	VAL	VAL	ASP	ASN	GLY
		GLY	ALA	GLY	VAL	ASP	GLY
		LYS	GLY	ARG	GLU	GLY	GLY
		ALA	LEU	ALA	LEU	ALA	ASN
		GLY	PRO	ALA	SER	ASP	GLY
		ARG	GLY	ARG	GLY	GLY	GLY
		LYS	THR	LYS	THR	ASP	GLY
		ILE	PRO	LYS	ILE	THR	GLY
		GLY	GLY	PHE	GLY	THR	GLY
		LYS	SER	ARG	ASP	SER	GLY
		ASN	PRO	ARG	SER	GLY	GLY
		THR	ASN	GLY	THR	GLY	GLY
		ALA	GLU	ASN	THR	GLY	GLY
		LEU	PRO	ASN	SER	ASP	GLY
		ALA	ASN	GLY	ASN	ASP	GLY
		GLY	ALA	GLY	GLU	ASP	LEU
		ILE	ILE	ASN	GLY	ASP	ALA
		LYS	GLY	PHE	GLY	GLU	ALA
		GLY	PRO	LYS	ASP	GLY	GLY
		ARG	PRO	GLN	ASP	GLY	GLY
		I325	PRO	LYS	ASP	GLU	GLY
		I330	ALA	GLY	ASN	ASP	SER
		K331	PRO	LYS	GLU	ASP	ALA
		I332	ALA	THR	GLU	ASP	ALA
		I333	GLY	LEU	ASN	ALA	GLU
		I337	ASN	VAL	SER	GLU	GLU
		E337	VAL	VAL	ASP	THR	ALA
		L341	CYS	PRO	ILE	ILE	ALA
		E347	VAL	PRO	GLY	GLY	MET
		R355	ALA	ARG	THR	SER	SER
		L363	LEU	ALA	GLU	GLN	ASN
		I370	GLN	THR	TYR	SER	PRO
		G376	TRP	GLY	ALA	SER	GLY
		LEU	THR	PRO	THR	GLY	GLY
		GLY	PRO	PRO	ASP	GLY	GLY
		LYS	GLY	ILE	ARG	GLY	ALA
		VAL	LEU	LYS	THR	GLY	ALA
		PRO	SER	LYS	GLY	GLY	ALA
		ASP	GLY	LYS	SER	GLY	THR
		GLY	THR	THR	THR	GLY	CYS
		LYS	GLY	LYS	ALA	GLY	ARG
		VAL	GLY	ALA	VAL	THR	GLY
		PRO	SER	ALA	ARG	ASP	GLY
		ASP	THR	PRO	SER	GLY	GLY
		GLY	ILE	ASP	GLY	THR	GLY
		LEU	SER	ALA	THR	ASP	GLY
		GLY	PRO	ALA	GLY	GLY	GLY
		ILE	ASN	PHE	GLY	GLY	GLY
		GLY	ASN	THR	THR	GLY	GLY
		ILE	GLN	THR	GLY	GLY	GLY
		GLY	THR	THR	GLY	GLY	GLY
		GLY	GLN	THR	TYR	SER	GLY
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		GLY	GLY	THR	GLY	GLY	GLY
		GLY	GLY	THR	GLY	GLY	GLY
		GLY	GLY	THR	GLY	GLY	GLY
		GLY	GLY	THR	GLY	GLY	GLY
		GLY	GLY	THR	GLY	GLY	GL

- Molecule 2: Phosphoprotein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	167313	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 ($e^-/\text{\AA}^2$)	54.3	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.748	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	339.968, 339.968, 339.968	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8853333, 0.8853333, 0.8853333	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	0.27	0/10293	0.54	0/13949
2	B	0.24	0/583	0.46	0/778
2	C	0.25	0/1048	0.53	0/1395
2	D	0.23	0/444	0.45	0/592
2	E	0.27	0/585	0.58	0/789
All	All	0.26	0/12953	0.53	0/17503

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10069	0	10078	53	0
2	B	576	0	633	6	0
2	C	1039	0	1126	11	0
2	D	442	0	479	4	0
2	E	576	0	615	8	0
All	All	12702	0	12931	69	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 3.

All (69) 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:466:ASP:HB2	1:A:497:ARG:HH11	1.37	0.88
1:A:466:ASP:HB2	1:A:497:ARG:NH1	2.04	0.73
1:A:466:ASP:HB2	1:A:497:ARG:HD2	1.80	0.63
1:A:657:SER:HA	1:A:779:VAL:O	2.01	0.60
1:A:530:LEU:HB3	1:A:705:LEU:HD22	1.86	0.58
1:A:781:LYS:HD2	1:A:799:VAL:HG11	1.86	0.58
2:B:363:LEU:HD22	2:C:367:LEU:HD23	1.87	0.57
1:A:673:TYR:O	1:A:677:SER:HB2	2.06	0.55
1:A:403:ARG:HH22	1:A:570:LYS:HB3	1.70	0.55
1:A:704:VAL:HG13	1:A:733:LYS:HA	1.88	0.54
1:A:829:PHE:HA	1:A:837:TYR:O	2.08	0.53
1:A:557:GLN:HG3	1:A:742:TYR:HD1	1.73	0.53
1:A:1066:HIS:O	1:A:1266:ARG:NH1	2.42	0.53
2:C:356:GLN:HE21	2:E:357:ASN:HB3	1.74	0.52
2:C:367:LEU:HD13	2:E:367:LEU:HD21	1.92	0.52
1:A:1239:VAL:HG13	1:A:1278:THR:HG22	1.91	0.52
1:A:885:ARG:NH1	1:A:1346:THR:OG1	2.44	0.51
2:B:370:ILE:HA	2:C:375:PRO:HD2	1.93	0.51
1:A:291:LEU:HD13	1:A:346:THR:HG21	1.93	0.51
1:A:1057:PRO:HG2	1:A:1157:LEU:HD11	1.92	0.50
1:A:1305:VAL:HA	1:A:1308:ALA:HB3	1.93	0.50
1:A:182:GLN:OE1	1:A:189:ARG:NH2	2.45	0.50
1:A:247:ILE:HG22	1:A:887:LEU:HD13	1.93	0.50
1:A:736:MET:HE1	2:B:400:ARG:HH12	1.76	0.50
1:A:965:LYS:NZ	1:A:1131:SER:O	2.41	0.50
1:A:180:LYS:HD2	1:A:908:ILE:HD12	1.94	0.49
1:A:963:ASP:OD1	1:A:966:ARG:NH2	2.43	0.48
2:D:350:LYS:NZ	2:E:345:GLU:OE1	2.47	0.48
1:A:954:GLY:HA3	1:A:1159:VAL:HG11	1.96	0.47
1:A:1307:VAL:HG11	1:A:1344:LEU:HB3	1.96	0.47
2:B:333:ILE:HG23	2:D:335:LYS:HE3	1.97	0.47
2:B:363:LEU:HD21	2:C:364:GLU:HA	1.96	0.47
2:C:329:ASN:HA	2:C:332:ILE:HD12	1.96	0.47
1:A:532:TYR:HB2	1:A:707:VAL:HA	1.97	0.47
1:A:568:ILE:O	1:A:571:TYR:HB2	2.15	0.46
1:A:705:LEU:HD12	1:A:735:PRO:HG2	1.98	0.46
1:A:466:ASP:CB	1:A:497:ARG:HH11	2.16	0.46
1:A:466:ASP:OD2	1:A:497:ARG:NH1	2.49	0.46
1:A:16:LEU:HD22	1:A:230:MET:HB2	1.98	0.46
1:A:1190:PHE:HB2	1:A:1361:LEU:HB3	1.99	0.45
1:A:128:LEU:HD13	1:A:886:TYR:HB3	1.98	0.45
1:A:568:ILE:HD11	1:A:686:ILE:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:393:ASP:OD1	2:B:394:LEU:N	2.48	0.45
1:A:116:LEU:HD22	1:A:928:ILE:HD11	1.99	0.44
1:A:522:TYR:HD2	1:A:699:ARG:HD3	1.82	0.44
1:A:454:LEU:HD11	1:A:689:LEU:HD21	2.00	0.44
1:A:1192:VAL:HB	1:A:1359:THR:HB	1.99	0.43
1:A:1304:LEU:HA	1:A:1345:GLU:HG3	2.00	0.43
2:D:343:LYS:NZ	2:E:338:SER:O	2.44	0.43
1:A:295:ASP:O	1:A:301:ARG:NH1	2.51	0.43
1:A:354:ARG:HD3	1:A:539:ILE:HD11	2.00	0.43
1:A:497:ARG:HD3	1:A:498:LEU:H	1.83	0.43
1:A:794:ARG:NH2	2:C:506:MET:SD	2.92	0.43
1:A:699:ARG:HA	1:A:699:ARG:HD2	1.78	0.43
2:C:370:ILE:HA	2:E:377:LEU:HD11	2.00	0.43
1:A:1168:GLY:HA2	1:A:1362:HIS:O	2.19	0.42
2:C:461:ARG:HH22	2:C:489:LYS:HA	1.84	0.42
1:A:509:ASP:HB3	1:A:512:ASP:HB2	2.00	0.42
2:E:372:ILE:HG23	2:E:384:PRO:HB2	2.01	0.42
1:A:1009:ILE:HB	1:A:1103:LEU:HD12	2.02	0.42
2:C:357:ASN:HA	2:C:360:ILE:HG22	2.02	0.41
1:A:128:LEU:HD22	1:A:886:TYR:HD1	1.86	0.41
1:A:266:ASP:HA	1:A:269:PHE:HD2	1.85	0.41
2:C:342:LEU:HD13	2:E:343:LYS:HG2	2.02	0.41
1:A:114:ASN:OD1	1:A:157:HIS:NE2	2.54	0.41
1:A:120:VAL:HG11	1:A:928:ILE:HG21	2.03	0.40
1:A:1386:LEU:HB3	1:A:1388:LEU:HG	2.03	0.40
1:A:748:THR:O	1:A:752:ILE:HG13	2.21	0.40
2:D:343:LYS:HE3	2:E:342:LEU:HD13	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1239/2183 (57%)	1209 (98%)	30 (2%)	0	100	100
2	B	71/509 (14%)	69 (97%)	2 (3%)	0	100	100
2	C	128/509 (25%)	124 (97%)	4 (3%)	0	100	100
2	D	55/509 (11%)	54 (98%)	1 (2%)	0	100	100
2	E	73/509 (14%)	63 (86%)	10 (14%)	0	100	100
All	All	1566/4219 (37%)	1519 (97%)	47 (3%)	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	1113/1943 (57%)	1113 (100%)	0	100	100
2	B	67/415 (16%)	67 (100%)	0	100	100
2	C	119/415 (29%)	119 (100%)	0	100	100
2	D	52/415 (12%)	52 (100%)	0	100	100
2	E	69/415 (17%)	69 (100%)	0	100	100
All	All	1420/3603 (39%)	1420 (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. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	114	ASN
2	E	356	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](#)

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.

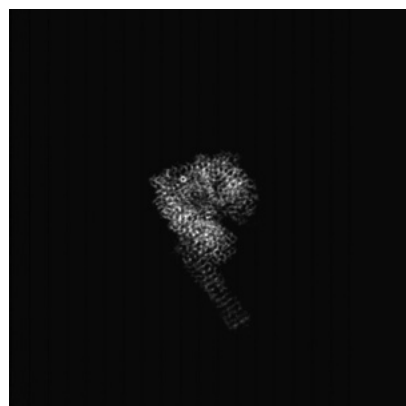
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47176. These allow visual inspection of the internal detail of the map and identification of artifacts.

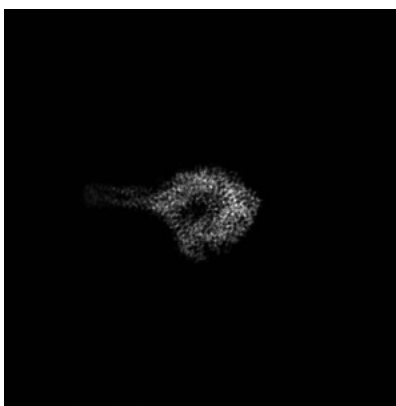
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

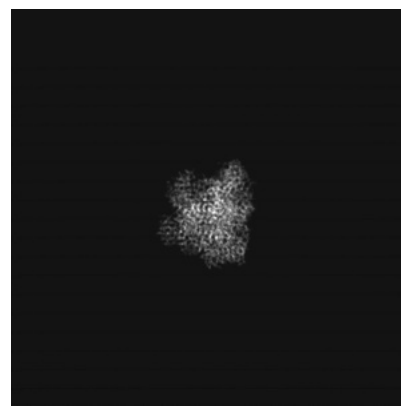
6.1.1 Primary map



X

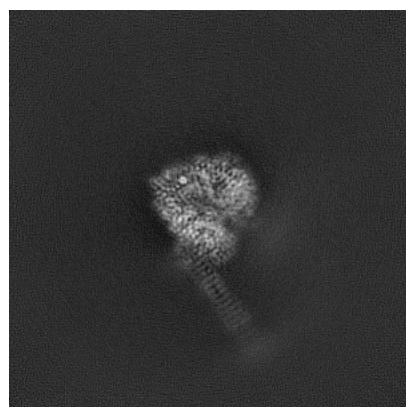


Y

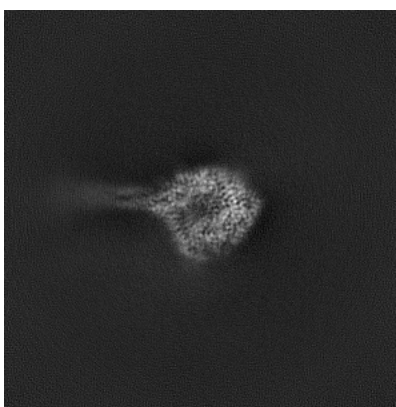


Z

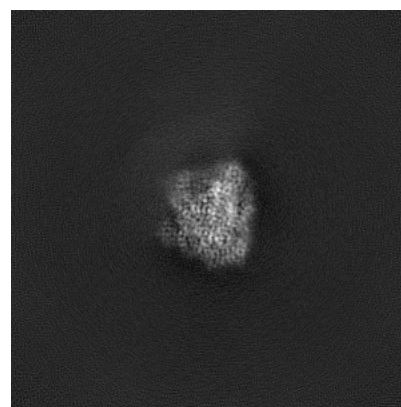
6.1.2 Raw map



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

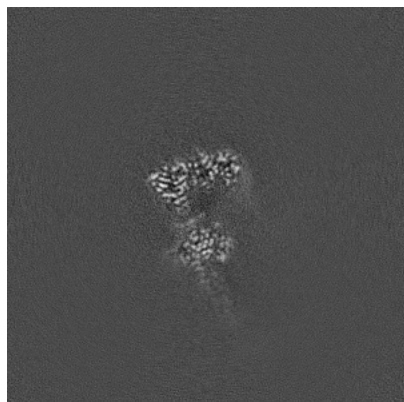


Y Index: 192

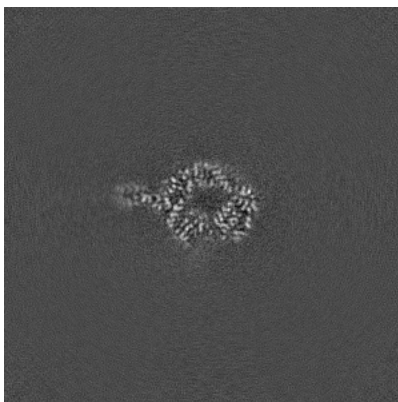


Z Index: 192

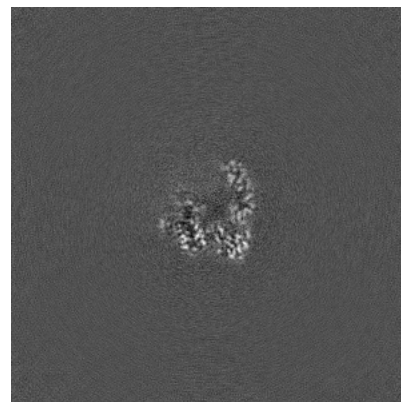
6.2.2 Raw map



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](#)

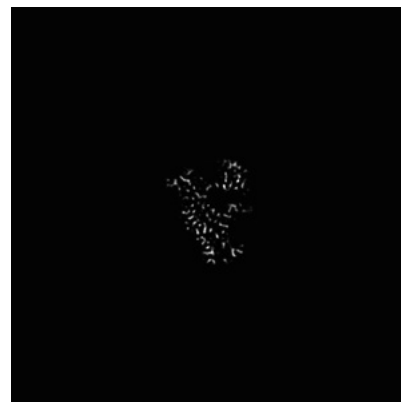
6.3.1 Primary map



X Index: 209

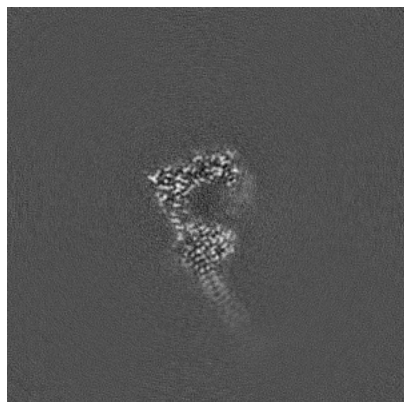


Y Index: 190

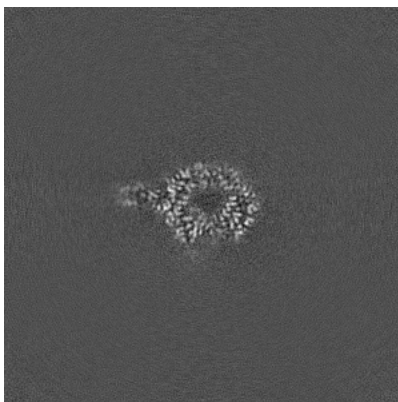


Z Index: 213

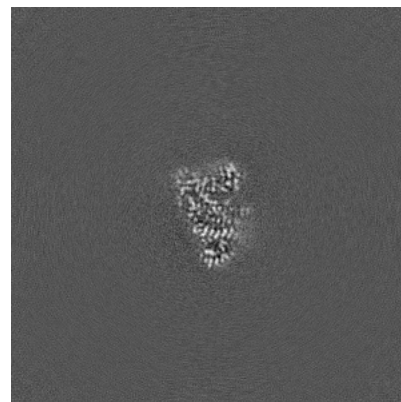
6.3.2 Raw map



X Index: 197



Y Index: 190

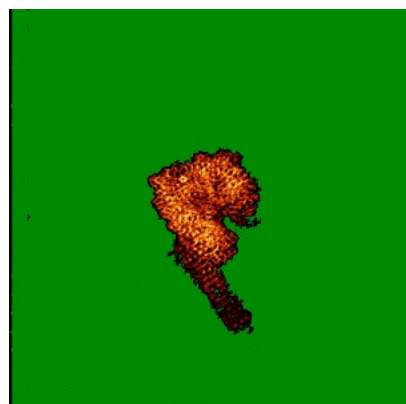


Z Index: 219

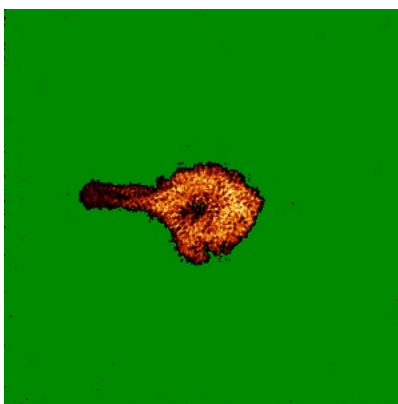
The images above show the largest variance slices of the map in three orthogonal directions.

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

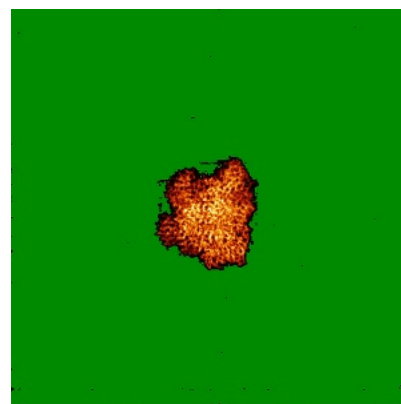
6.4.1 Primary map



X

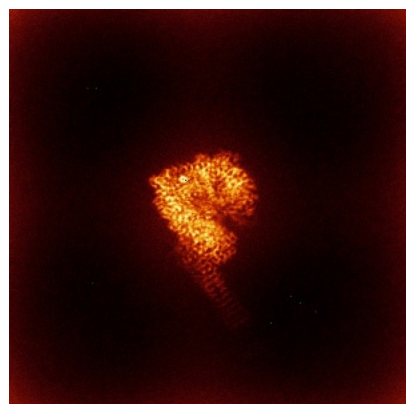


Y



Z

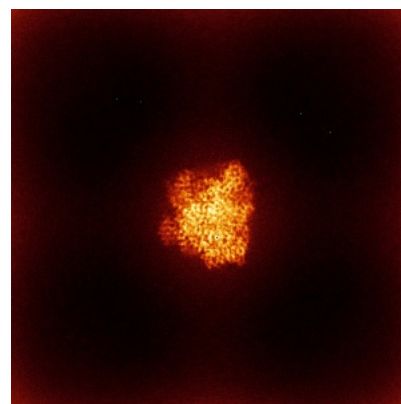
6.4.2 Raw map



X



Y

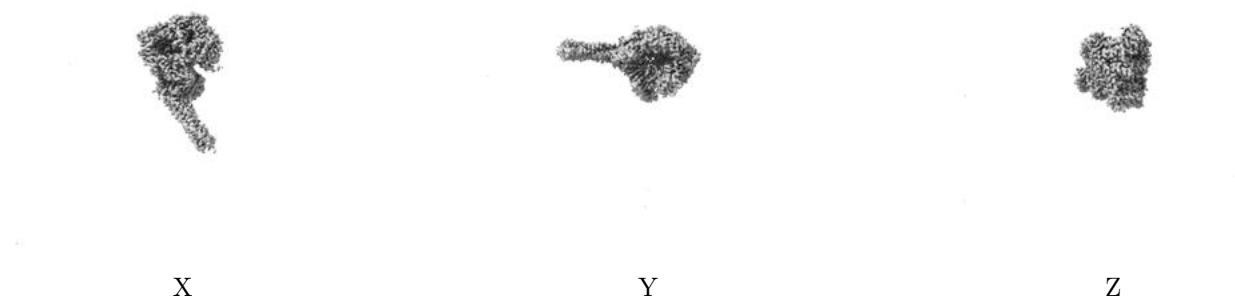


Z

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.

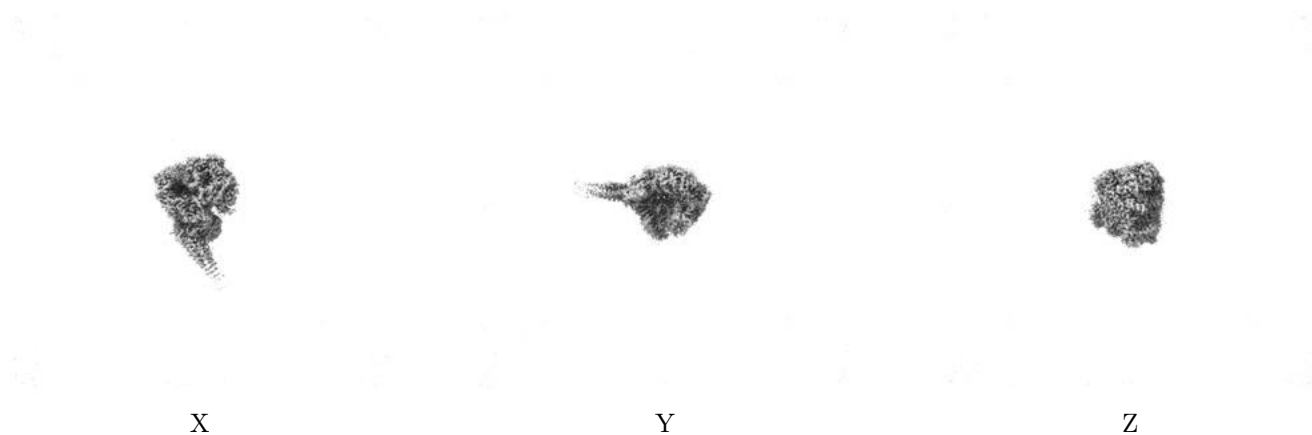
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. 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.

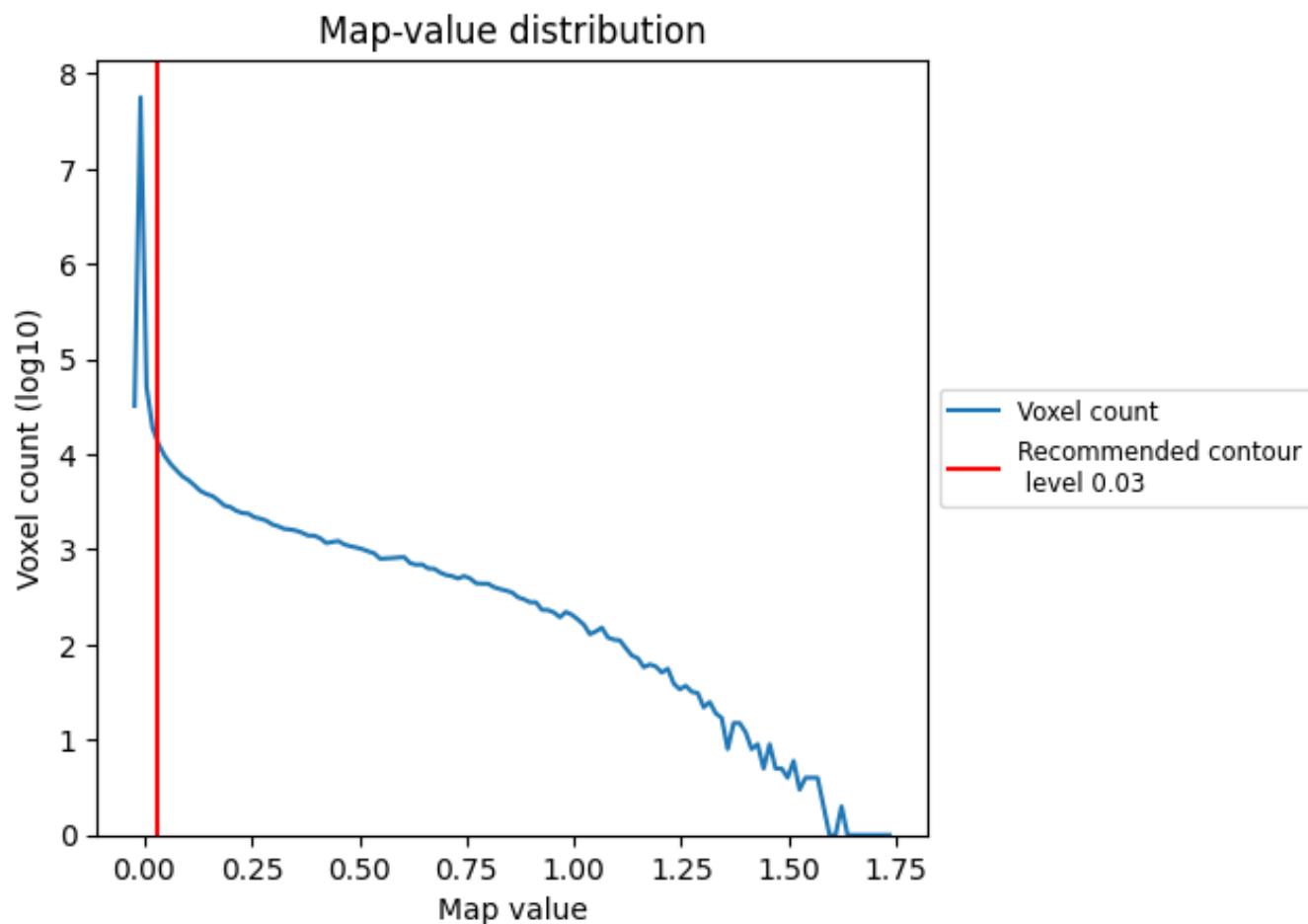
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

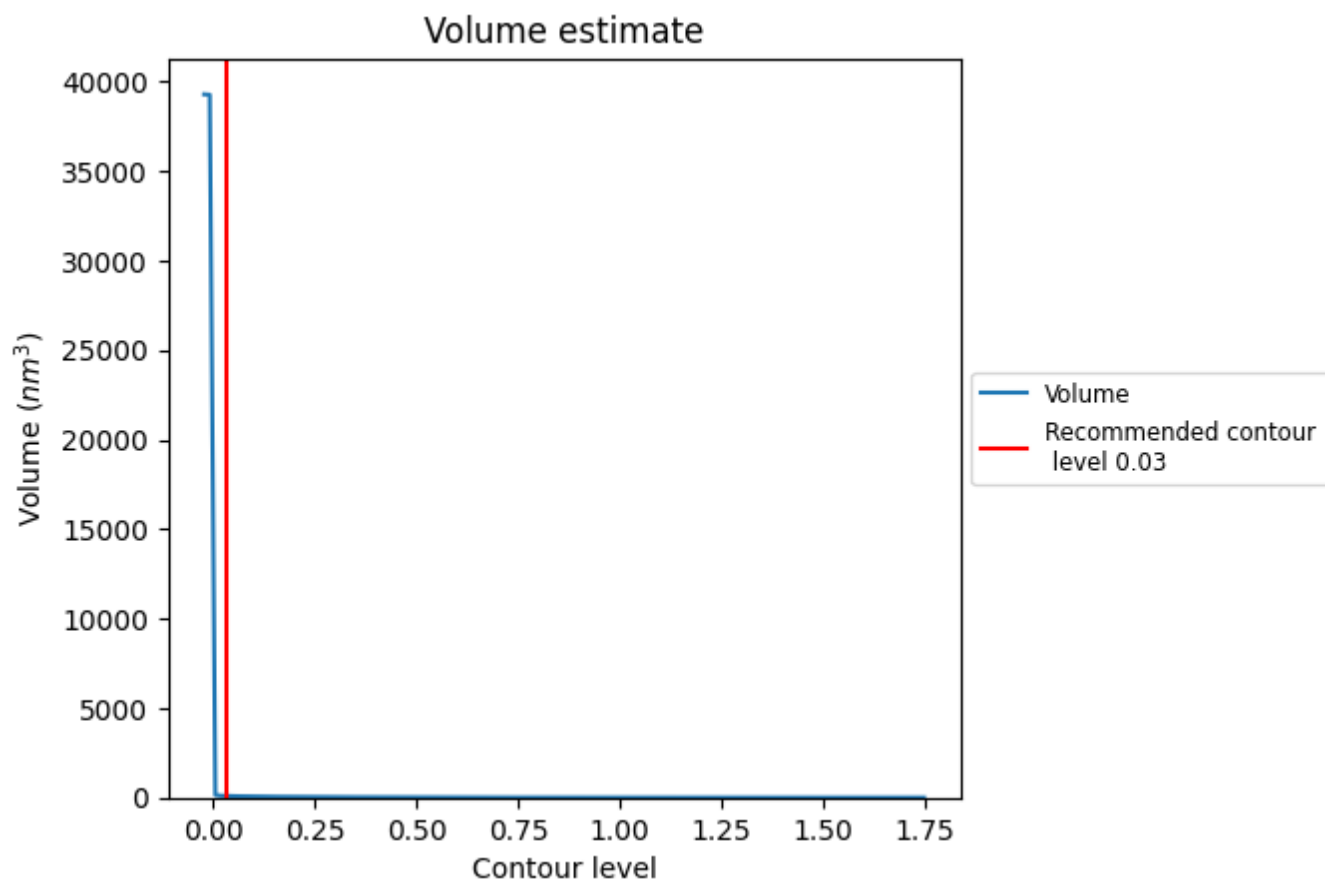
This section contains the results of statistical analysis of the map.

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.

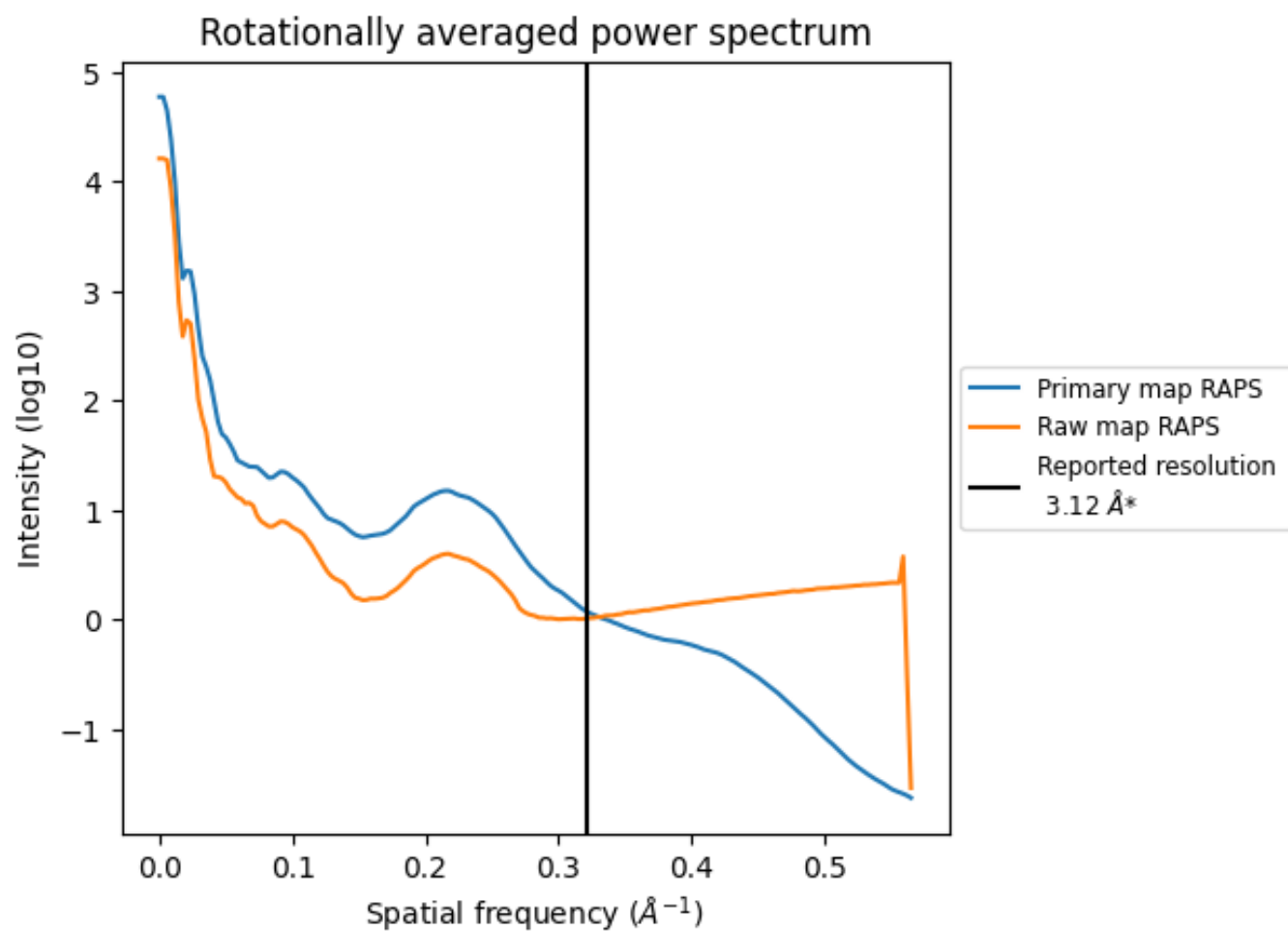
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 92 nm^3 ; this corresponds to an approximate mass of 83 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 ⓘ

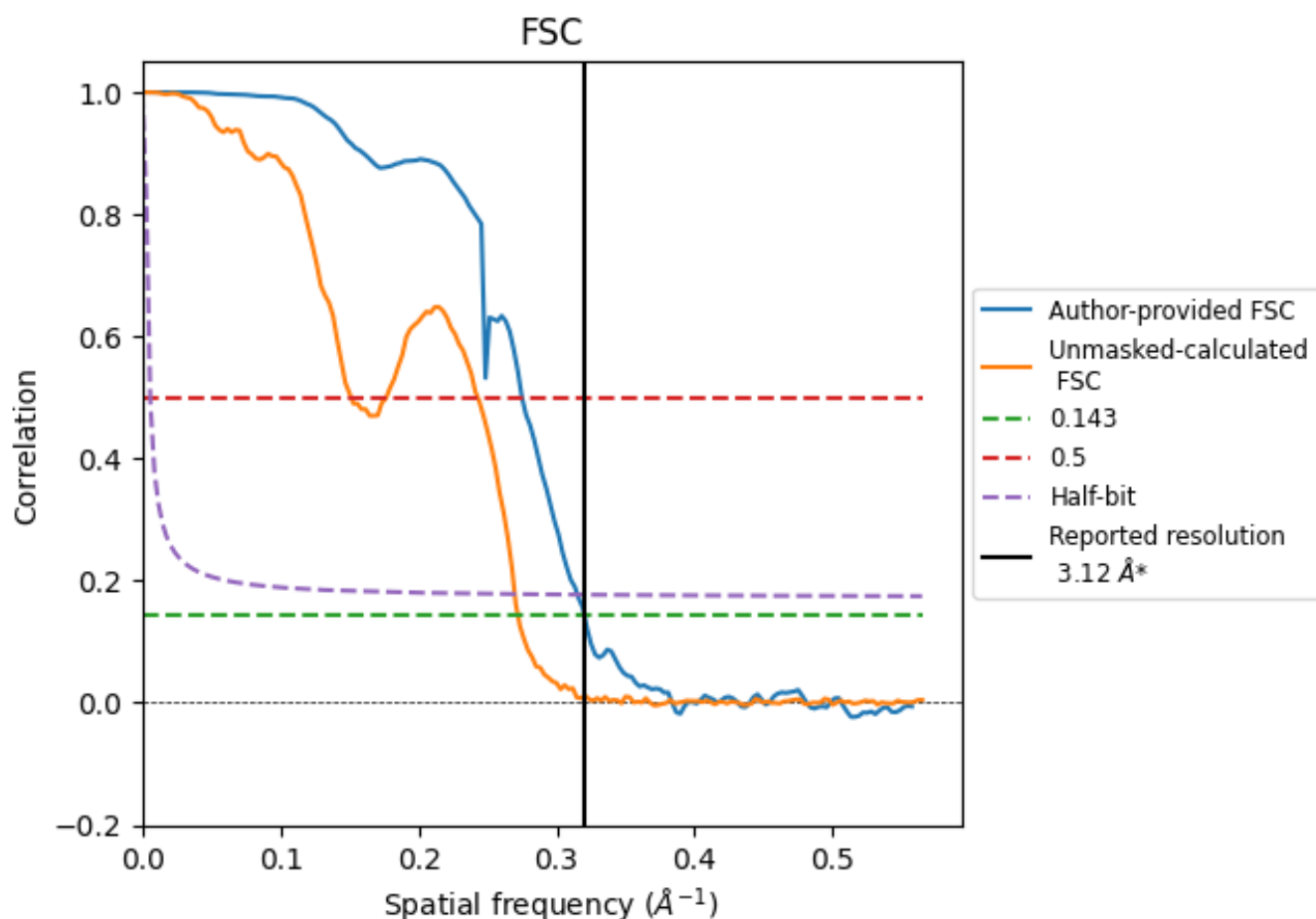


*Reported resolution corresponds to spatial frequency of 0.321 \AA^{-1}

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 0.321 \AA^{-1}

8.2 Resolution estimates [i](#)

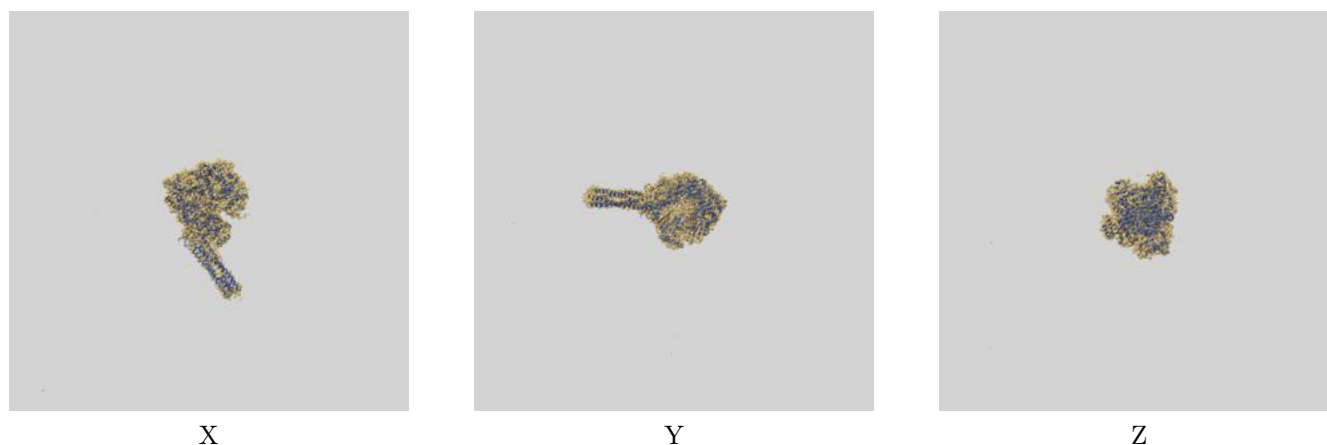
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.12	-	-
Author-provided FSC curve	3.12	3.64	3.17
Unmasked-calculated*	3.68	6.61	3.71

*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 3.68 differs from the reported value 3.12 by more than 10 %

9 Map-model fit [i](#)

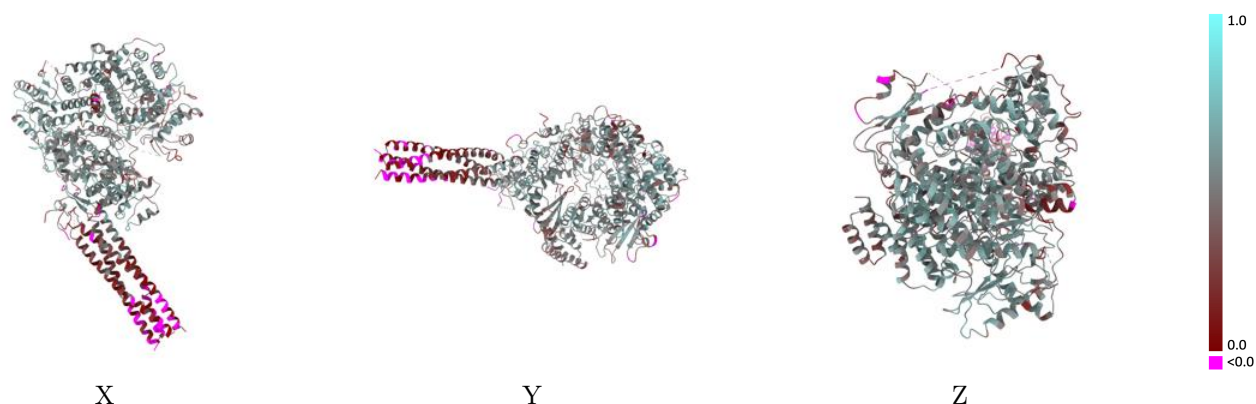
This section contains information regarding the fit between EMDB map EMD-47176 and PDB model 9DUS. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



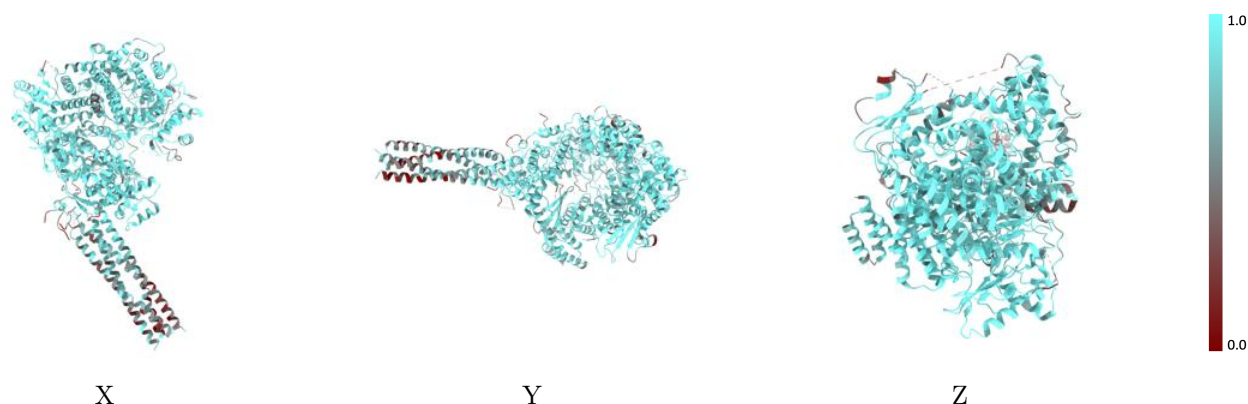
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



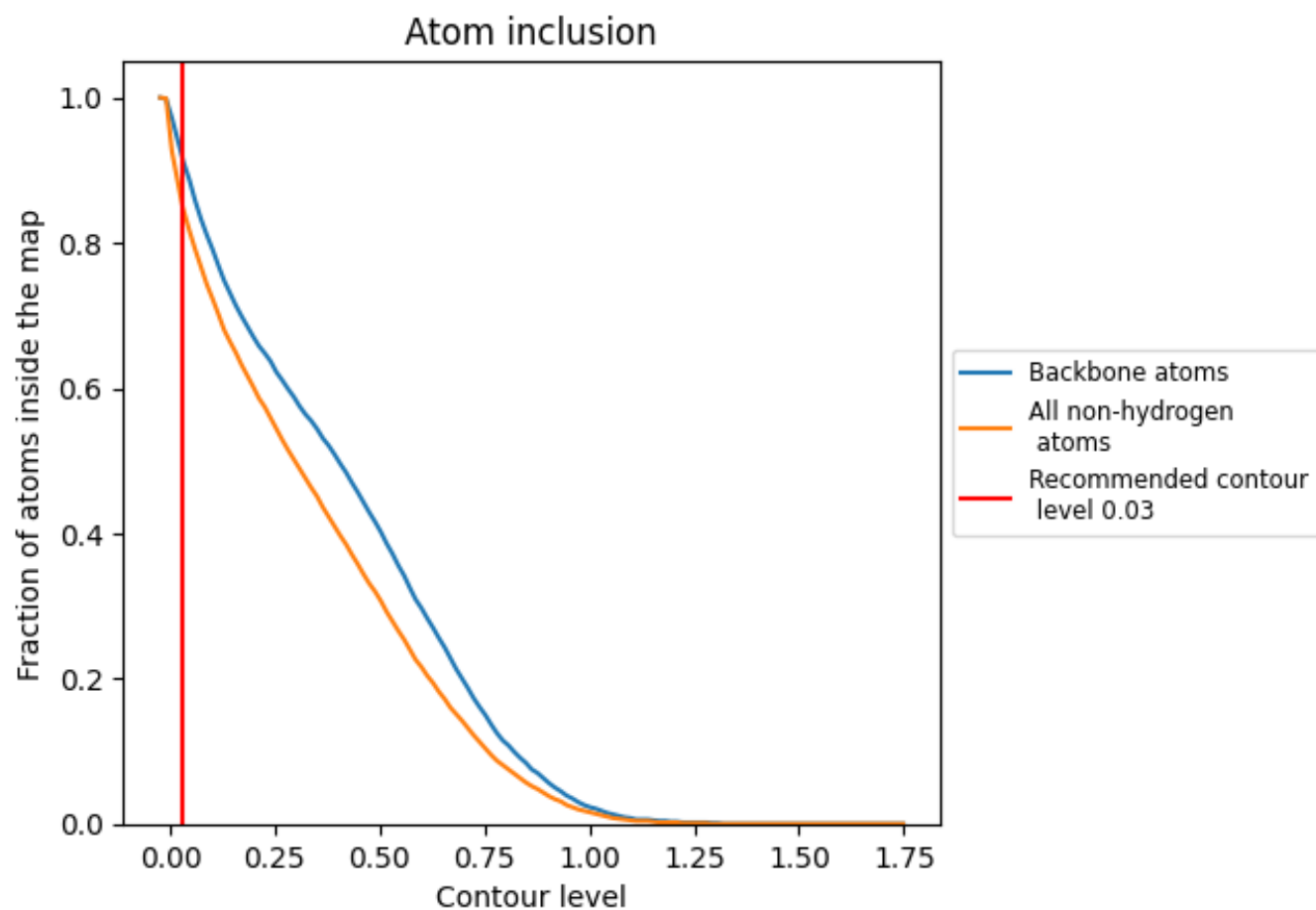
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8500	<div></div> 0.4460
A	<div></div> 0.9020	<div></div> 0.4960
B	<div></div> 0.6240	<div></div> 0.2320
C	<div></div> 0.6690	<div></div> 0.2820
D	<div></div> 0.7020	<div></div> 0.2410
E	<div></div> 0.6130	<div></div> 0.2210

