



Full wwPDB EM Validation Report ⓘ

Jul 4, 2026 – 12:49 PM JST

PDB ID : 9VXZ / pdb_00009vxz
EMDB ID : EMD-65446
Title : Cryo-EM structure of Measles Virus L Protein bound by Phosphoprotein Tetramer
Authors : Xue, L.; Gui, J.; Chang, T.; Pan, H.; Xiong, X.
Deposited on : 2025-07-20
Resolution : 2.68 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:

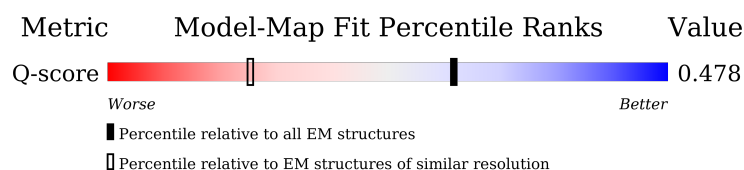
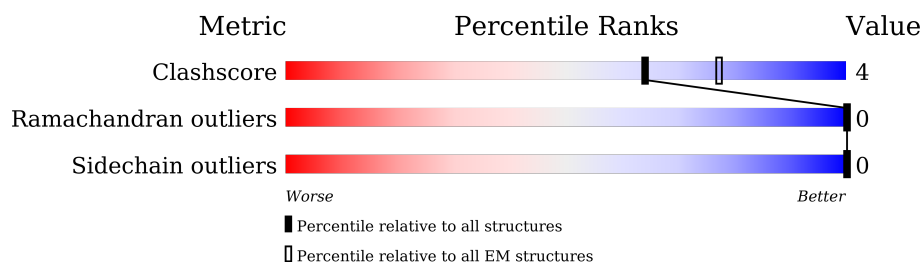
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.68 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.



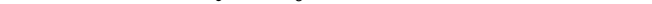
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	9255 (2.18 - 3.18)

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	507	
2	C	507	
2	D	507	

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Mol	Chain	Length	Quality of chain
2	E	507	 9% 89%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12553 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	1255	Total	C	N	O	S	0	0
			10082	6445	1743	1839	55		

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	148	Total	C	N	O	S	0	0
			1159	736	208	210	5		
2	C	47	Total	C	N	O	S	0	0
			372	233	65	73	1		
2	D	67	Total	C	N	O	S	0	0
			514	322	87	104	1		
2	E	55	Total	C	N	O	S	0	0
			425	269	74	81	1		

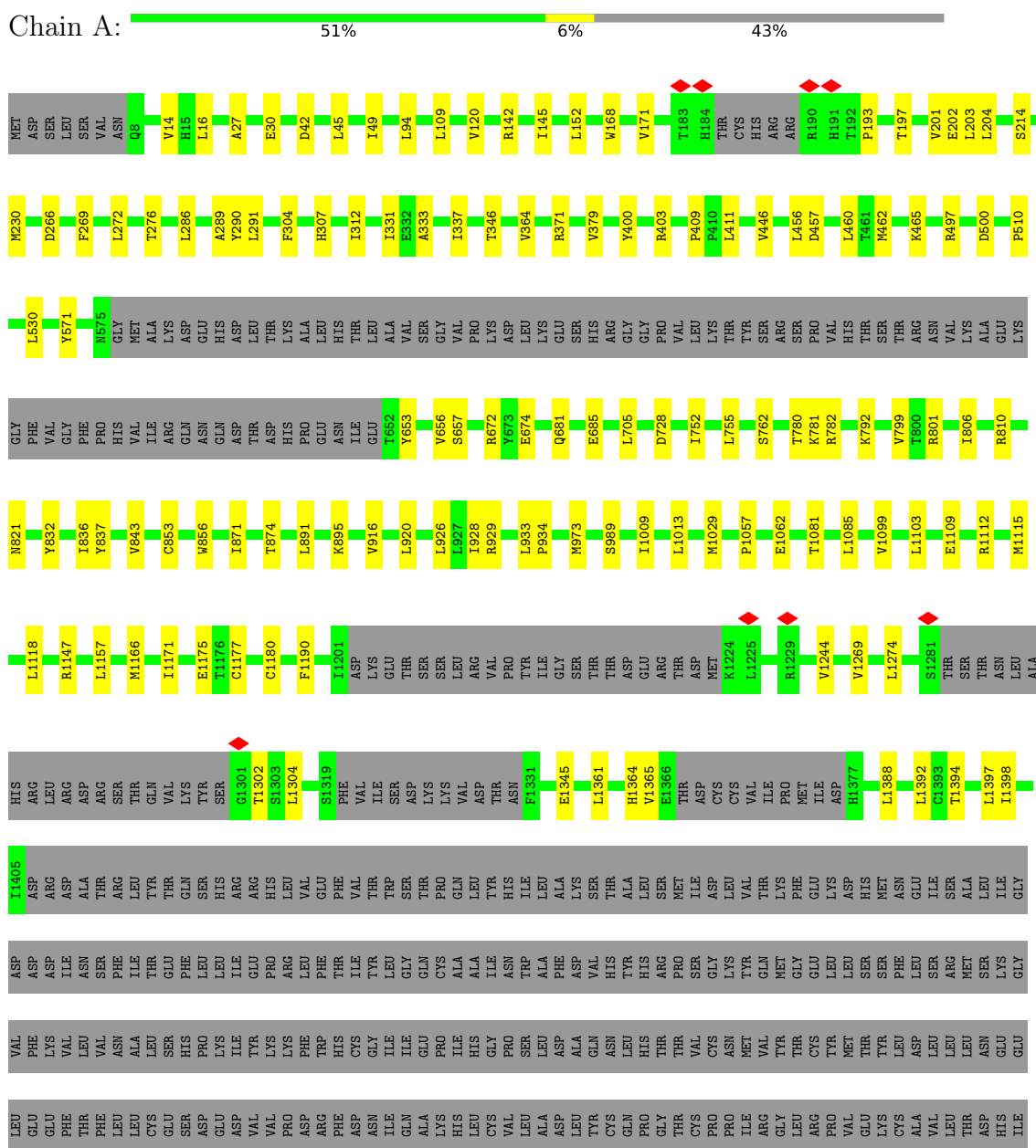
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	

3 Residue-property plots

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

• Molecule 1: RNA-directed RNA polymerase L



[illegible]

- Molecule 2: Phosphoprotein



ASP	GLU	THR	ASP	THR	ASP	LYS	SER	MET
PRO	GLU	ILE	VAL	GLU	VAL	GLY	LYS	ALA
THR	GLY	ILE	THR	ILE	GLU	ILE	PRO	GLY
ALA	GLY	ALA	THR	ALA	THR	GLN	CYS	GLN
ASP	ASP	SER	ALA	SER	ALA	ASP	LEU	GLN
VAL	TYR	LEU	GLU	LEU	GLY	ALA	SER	ALA
GLU	TYR	LEU	GLY	GLY	GLY	ASP	ALA	ARG
LEU	ASP	THR	GLY	THR	GLY	SER	ILE	HIS
ASN	ASP	GLY	ILE	GLY	ILE	MET	GLY	VAL
PRO	GLU	GLY	ILE	GLY	ILE	VAL	THR	LYS
ASP	LEU	ALA	HIS	GLU	GLY	GLN	GLY	ASN
L394	PHE	THR	GLU	GLU	LEU	SER	GLY	LEU
K395	SER	GLN	LEU	LEU	GLY	GLY	GLY	GLU
P396	ASP	CYS	LEU	LEU	GLY	SER	ASP	ASP
	VAL	ALA	LYS	LYS	ILE	GLY	ALA	ALA
G403	GLN	ARG	GLN	GLY	GLY	ARG	ARG	LEU
R404	ASP	LYS	SER	PRO	ARG	SER	ILE	ALA
A405	ILE	SER	SER	SER	ASP	SER	ARG	LYS
	LYS	PRO	GLY	GLY	GLY	ASP	GLY	LEU
K411	THR	SER	THR	THR	ARG	SER	GLY	LEU
LYS	ALA	GLU	ASN	ASN	GLY	LEU	GLN	GLY
PRO	LEU	PRO	ASN	SER	GLY	ASP	GLY	ALA
VAL	ALA	SER	PHE	GLY	PRO	GLY	SER	PRO
	LYS	GLY	PRO	LYS	LYS	ASP	GLY	GLY
SER		PRO						
ARG	L326	GLY	LEU	GLY	LEU	ASP	SER	GLY
GLN	Q330	ALA	GLY	ALA	GLY	GLY	ASP	SER
LEU	K331	PRO	PRO	PRO	LYS	GLY	ASP	LEU
GLN	I332	ALA	THR	THR	THR	GLU	ASP	ALA
GLY	I333	GLY	LEU	LEU	ASN	ASN	ALA	GLU
THR		ASN	ASN	VAL	VAL	SER	GLU	GLU
THR	L336	VAL	VAL	VAL	VAL	ASP	THR	ALA
ASN	E337	PRO	PRO	PRO	PRO	VAL	LEU	MET
GLY	S338	GLU	PRO	PRO	PRO	ASP	GLY	ALA
ARG	I339	CYS	PRO	PRO	PRO	ILE	ILE	ALA
THR		VAL	PRO	PRO	PRO	GLY	PRO	TRP
SER	L342	SER	ASN	ASN	ASN	GLY	SER	SER
		GLY	ASN	ASN	PRO	PRO	ARG	GLY
S429	E345	ALA	SER	SER	SER	ASP	ASN	ILE
R430		ALA	ARG	ALA	ALA	GLU	LEU	SER
L433	I349	LEU	ALA	LEU	ALA	GLY	GLN	ASN
L434		ILE	SER	ILE	SER	TYR	ALA	PRO
K435	Q356	GLN	THR	THR	THR	SER	SER	GLY
E436		GLU	THR	GLU	GLU	ALA	SER	GLY
F437	I360	TRP	THR	GLU	ILE	ILE	THR	GLN
Q438		PRO	THR	THR	ASP	THR	GLY	ASP
	E364	GLU	ILE	ILE	ARG	LEU	ARG	ALA
V450		SER	LYS	LYS	GLY	GLY	CYS	ALA
	L367	GLY	LYS	GLY	LYS	GLY	TYR	THR
S462		THR	GLY	THR	GLY	ALA	HIS	CYS
	K371	THR	THR	THR	THR	PRO	VAL	GLU
I488		ILE	ASP	ASP	ILE	TYR	GLY	GLU
	P375	SER	ALA	ALA	SER	SER	ASP	GLY
D493	GLY	PRO	LEU	ARG	LEU	MET	HIS	ALA
L494	GLY	SER	GLY	ALA	PHE	ARG	GLY	SER
	LYS	GLN	LYS	SER	ARG	GLY	GLY	SER
R507	ASP	ASN	PHE	THR	ALA	SER	ALA	GLY
	PRO	ASN	GLY	THR	GLY	SER	VAL	THR

- Molecule 2: Phosphoprotein







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	4035198	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	1.549	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	394.2016, 394.2016, 394.2016	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9476, 0.9476, 0.9476	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: ZN

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	0/10307	0.32	0/13966
2	B	0.13	0/1168	0.34	0/1556
2	C	0.17	0/373	0.35	0/497
2	D	0.16	0/517	0.35	0/696
2	E	0.18	0/427	0.43	0/570
All	All	0.13	0/12792	0.32	0/17285

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	10082	0	10102	76	0
2	B	1159	0	1261	21	0
2	C	372	0	398	7	0
2	D	514	0	535	8	0
2	E	425	0	462	9	0
3	A	1	0	0	0	0
All	All	12553	0	12758	103	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 4.

All (103) 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:1180:CYS:SG	1:A:1364:HIS:HE1	2.11	0.71
2:B:356:GLN:HE21	2:E:356:GLN:HE22	1.37	0.69
2:B:434:LEU:HD23	2:B:436:GLU:H	1.60	0.67
2:B:342:LEU:HA	2:B:345:GLU:HG2	1.76	0.66
1:A:1397:LEU:HD12	1:A:1398:ILE:HG23	1.76	0.66
1:A:989:SER:H	1:A:1147:ARG:HH22	1.45	0.63
2:D:352:GLN:HG2	2:D:355:ARG:HH22	1.63	0.63
1:A:933:LEU:HD12	1:A:934:PRO:HD2	1.80	0.62
1:A:1081:THR:HG22	1:A:1085:LEU:HD23	1.81	0.62
1:A:1190:PHE:HB2	1:A:1361:LEU:HB3	1.83	0.60
2:C:363:LEU:HD23	2:D:363:LEU:HD22	1.86	0.58
1:A:1109:GLU:HG2	1:A:1112:ARG:HH21	1.68	0.57
1:A:530:LEU:HB3	1:A:705:LEU:HD22	1.86	0.57
1:A:457:ASP:HA	1:A:1029:MET:HE1	1.86	0.57
2:E:329:ASN:HA	2:E:332:ILE:HG12	1.86	0.57
1:A:197:THR:HA	1:A:202:GLU:HG2	1.87	0.56
1:A:1057:PRO:HG2	1:A:1157:LEU:HD11	1.88	0.56
2:B:339:LEU:HA	2:B:342:LEU:HD23	1.88	0.56
1:A:266:ASP:HA	1:A:269:PHE:HD2	1.71	0.54
1:A:1269:VAL:HG21	1:A:1274:LEU:HD13	1.88	0.53
1:A:1302:THR:HG22	1:A:1304:LEU:H	1.73	0.53
1:A:456:LEU:HD13	1:A:510:PRO:HB2	1.91	0.52
1:A:1009:ILE:HG23	1:A:1103:LEU:HD22	1.91	0.52
1:A:14:VAL:HG11	1:A:856:TRP:HB2	1.92	0.52
1:A:27:ALA:HB2	1:A:45:LEU:HD21	1.92	0.51
1:A:1392:LEU:HD23	1:A:1394:THR:H	1.75	0.51
1:A:656:VAL:HG21	1:A:792:LYS:HB3	1.93	0.51
1:A:929:ARG:HH12	1:A:1118:LEU:HB3	1.75	0.51
1:A:289:ALA:HB2	1:A:304:PHE:HD2	1.76	0.50
2:B:488:ILE:HG22	2:B:494:LEU:HD12	1.92	0.50
1:A:681:GLN:HG2	2:D:372:ILE:HD13	1.94	0.50
1:A:30:GLU:HB3	1:A:49:ILE:HG21	1.94	0.49
1:A:1166:MET:HG2	1:A:1365:VAL:HG22	1.93	0.49
1:A:16:LEU:HD22	1:A:230:MET:HB2	1.95	0.49
1:A:307:HIS:ND1	1:A:821:ASN:HB3	2.27	0.49
2:E:333:ILE:HA	2:E:336:LEU:HG	1.95	0.49
1:A:460:LEU:HD21	1:A:1029:MET:HG2	1.93	0.49
2:C:328:ASP:O	2:C:332:ILE:HG12	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:762:SER:HB3	1:A:806:ILE:HD12	1.95	0.49
1:A:853:CYS:HB2	1:A:874:THR:HG21	1.94	0.49
1:A:333:ALA:O	1:A:337:ILE:HG13	2.13	0.49
1:A:1062:GLU:HG2	1:A:1244:VAL:HG21	1.94	0.48
2:C:367:LEU:HD21	2:D:367:LEU:HD11	1.95	0.48
2:B:375:PRO:HD2	2:B:438:GLN:HE22	1.78	0.48
1:A:193:PRO:HB2	1:A:204:LEU:HD11	1.95	0.48
1:A:781:LYS:HD2	1:A:799:VAL:HG11	1.96	0.48
1:A:752:ILE:HA	1:A:755:LEU:HD12	1.95	0.47
1:A:832:TYR:HE1	1:A:837:TYR:HB2	1.80	0.47
2:B:345:GLU:O	2:B:349:ILE:HG12	2.15	0.47
1:A:371:ARG:HH12	1:A:728:ASP:HA	1.78	0.47
1:A:142:ARG:HB2	1:A:145:ILE:HG13	1.96	0.47
1:A:152:LEU:HD11	1:A:891:LEU:HD13	1.95	0.47
1:A:331:ILE:HG21	2:B:462:SER:HB3	1.96	0.47
2:B:396:PRO:HG2	2:E:370:ILE:HA	1.96	0.47
2:C:367:LEU:HG	2:D:367:LEU:HD21	1.95	0.47
2:B:333:ILE:HD13	2:B:336:LEU:HD12	1.98	0.46
1:A:1171:ILE:HG23	1:A:1175:GLU:HB3	1.97	0.46
1:A:291:LEU:HB2	1:A:346:THR:HG21	1.98	0.46
1:A:836:ILE:HB	1:A:843:VAL:HB	1.98	0.45
1:A:286:LEU:HD22	1:A:290:TYR:HE2	1.81	0.45
1:A:801:ARG:HD2	2:B:450:VAL:HG13	1.98	0.45
2:C:331:LYS:HG3	2:D:332:ILE:HD12	1.99	0.45
1:A:1099:VAL:O	1:A:1103:LEU:HG	2.17	0.45
1:A:497:ARG:HB3	1:A:500:ASP:HB2	1.99	0.45
1:A:920:LEU:HD23	1:A:926:LEU:HD23	1.99	0.45
1:A:1029:MET:HE3	1:A:1397:LEU:HD23	1.99	0.45
1:A:1013:LEU:HD12	1:A:1013:LEU:HA	1.80	0.44
1:A:916:VAL:HA	1:A:1115:MET:HE1	1.98	0.44
1:A:1171:ILE:HD11	1:A:1177:CYS:HB2	1.98	0.44
1:A:171:VAL:HG22	1:A:203:LEU:HD21	1.99	0.44
1:A:201:VAL:HG12	1:A:214:SER:HA	1.97	0.44
1:A:403:ARG:HD2	1:A:571:TYR:HE1	1.81	0.44
1:A:674:GLU:HB2	2:E:374:ILE:HD11	2.00	0.44
1:A:286:LEU:HD11	1:A:312:ILE:HD11	1.99	0.44
1:A:411:LEU:HD11	1:A:446:VAL:HG22	1.99	0.44
1:A:685:GLU:HA	2:D:388:VAL:HG13	2.00	0.44
1:A:462:MET:HA	1:A:465:LYS:HE3	1.99	0.43
1:A:400:TYR:HB3	1:A:409:PRO:HD3	1.99	0.43
1:A:94:LEU:HB3	1:A:168:TRP:HZ2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:347:GLU:HG2	2:D:351:LYS:HE3	2.00	0.43
1:A:379:VAL:HG21	2:B:433:LEU:HD11	2.01	0.43
1:A:109:LEU:HD23	1:A:109:LEU:HA	1.91	0.43
1:A:272:LEU:HB3	1:A:276:THR:OG1	2.19	0.43
2:B:332:ILE:O	2:B:336:LEU:HG	2.19	0.43
2:B:488:ILE:HG23	2:B:493:ASP:HB3	2.01	0.43
2:B:364:GLU:HA	2:E:363:LEU:HD21	2.01	0.42
1:A:810:ARG:HA	1:A:810:ARG:HD3	1.84	0.42
1:A:120:VAL:HG11	1:A:928:ILE:HG21	2.01	0.42
1:A:871:ILE:HD13	1:A:895:LYS:HB3	2.01	0.42
2:B:371:MET:HB3	2:B:394:LEU:HD12	2.03	0.41
2:B:332:ILE:HD11	2:C:332:ILE:HG23	2.02	0.41
1:A:1388:LEU:HD23	1:A:1388:LEU:HA	1.92	0.41
1:A:973:MET:HE2	1:A:973:MET:HB3	1.92	0.41
2:B:405:ALA:HB2	2:E:375:PRO:HD3	2.03	0.41
1:A:653:TYR:HD2	1:A:782:ARG:HG2	1.86	0.41
1:A:1304:LEU:HD12	1:A:1345:GLU:HG3	2.02	0.41
2:B:349:ILE:HG23	2:C:353:ILE:HD13	2.03	0.41
2:B:360:ILE:HD13	2:B:360:ILE:HA	1.94	0.41
2:B:367:LEU:HD13	2:E:363:LEU:HD22	2.03	0.41
1:A:291:LEU:HD12	1:A:346:THR:HB	2.03	0.40
1:A:657:SER:HB2	1:A:780:THR:HG22	2.03	0.40
1:A:672:ARG:HD2	2:E:374:ILE:HG21	2.03	0.40
1:A:42:ASP:HB2	1:A:364:VAL:HG21	2.03	0.40

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	1241/2183 (57%)	1199 (97%)	42 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	142/507 (28%)	136 (96%)	6 (4%)	0	100	100
2	C	45/507 (9%)	45 (100%)	0	0	100	100
2	D	63/507 (12%)	63 (100%)	0	0	100	100
2	E	53/507 (10%)	53 (100%)	0	0	100	100
All	All	1544/4211 (37%)	1496 (97%)	48 (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	1114/1945 (57%)	1114 (100%)	0	100	100
2	B	132/416 (32%)	132 (100%)	0	100	100
2	C	45/416 (11%)	45 (100%)	0	100	100
2	D	61/416 (15%)	61 (100%)	0	100	100
2	E	50/416 (12%)	50 (100%)	0	100	100
All	All	1402/3609 (39%)	1402 (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 (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	313	HIS
1	A	358	HIS
2	B	326	HIS
2	B	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - 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.

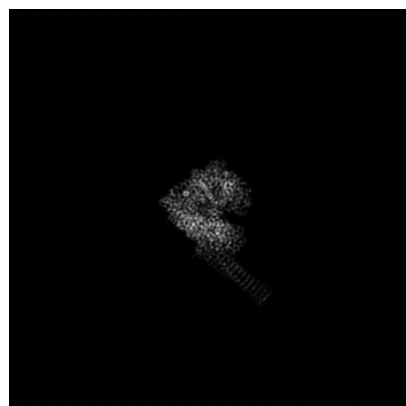
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65446. These allow visual inspection of the internal detail of the map and identification of artifacts.

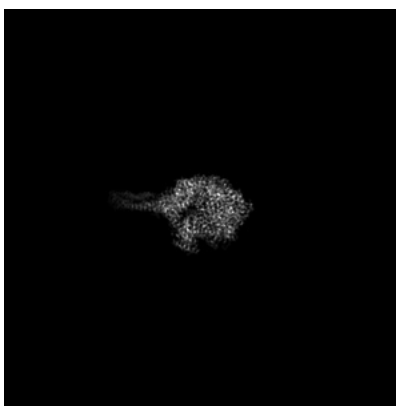
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

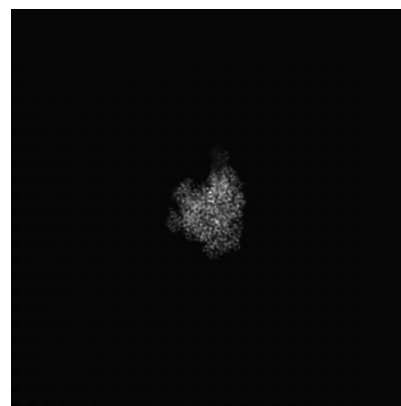
6.1.1 Primary map



X

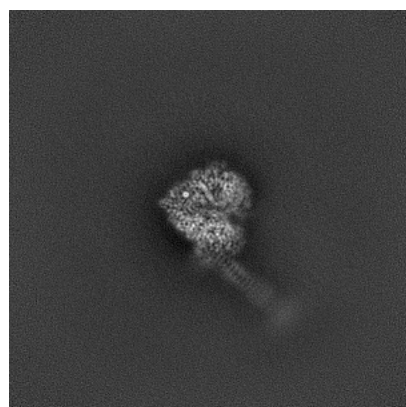


Y

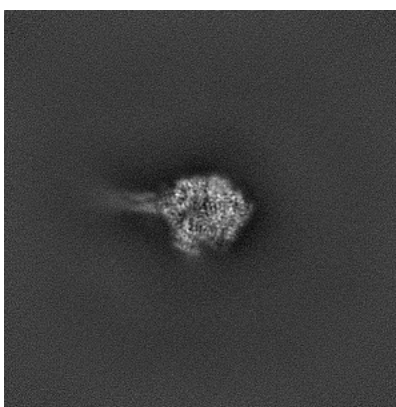


Z

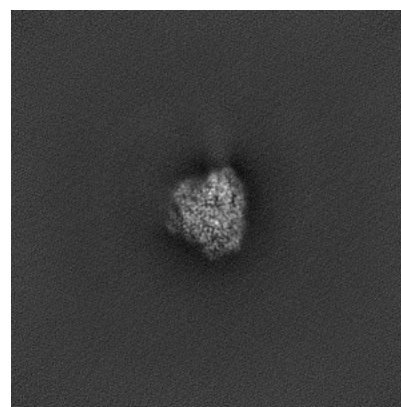
6.1.2 Raw map



X



Y

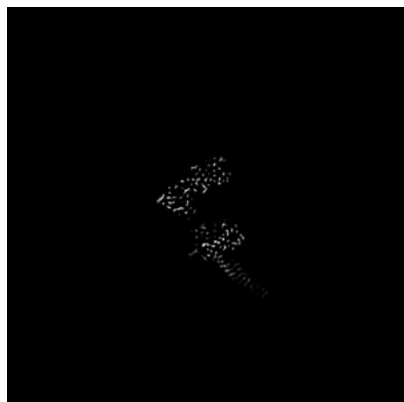


Z

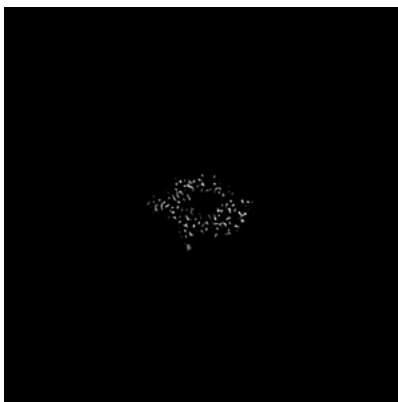
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

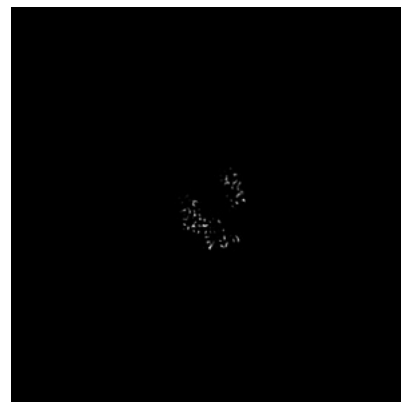
6.2.1 Primary map



X Index: 208

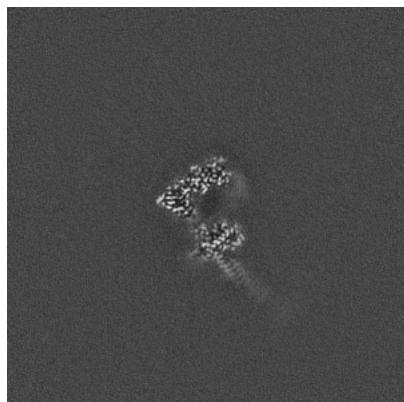


Y Index: 208

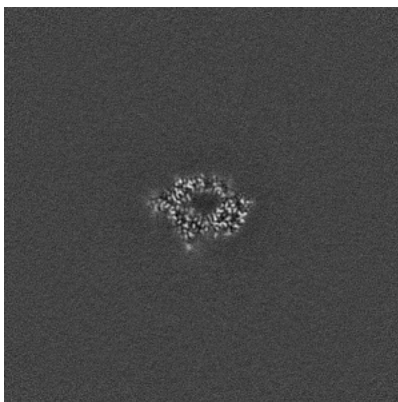


Z Index: 208

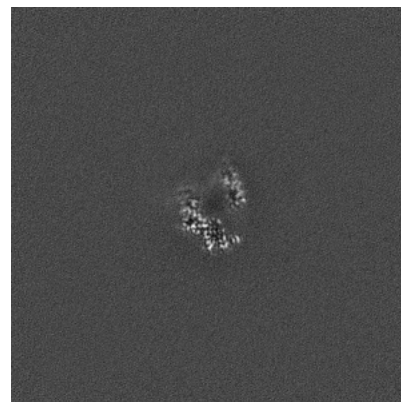
6.2.2 Raw map



X Index: 208



Y Index: 208



Z Index: 208

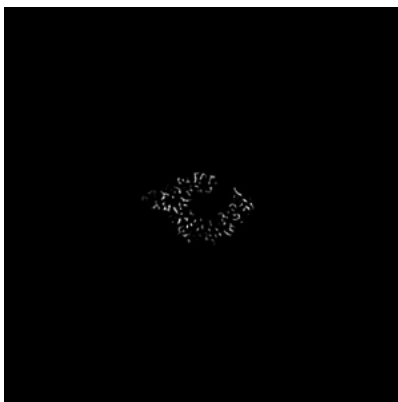
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

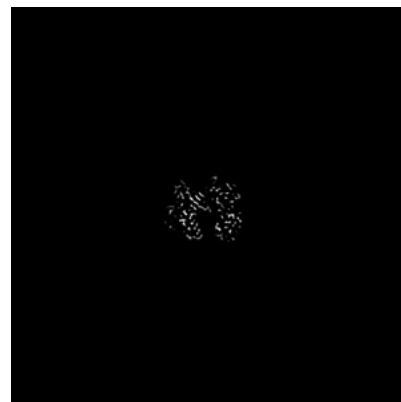
6.3.1 Primary map



X Index: 222



Y Index: 216

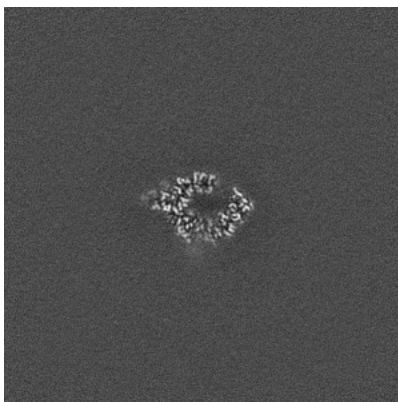


Z Index: 190

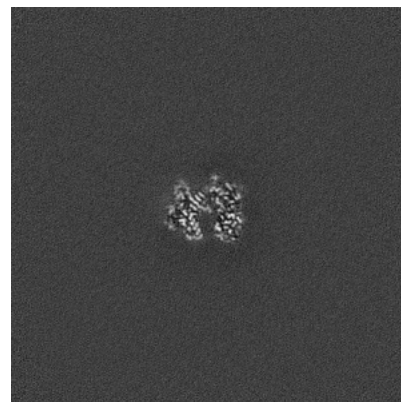
6.3.2 Raw map



X Index: 207



Y Index: 216



Z Index: 190

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

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

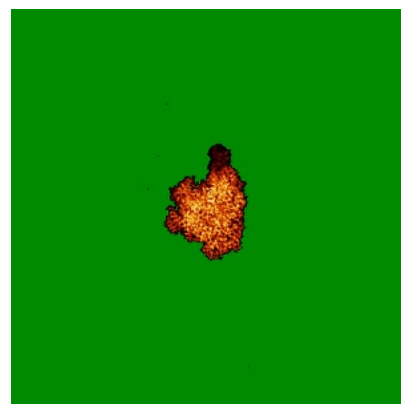
6.4.1 Primary map



X

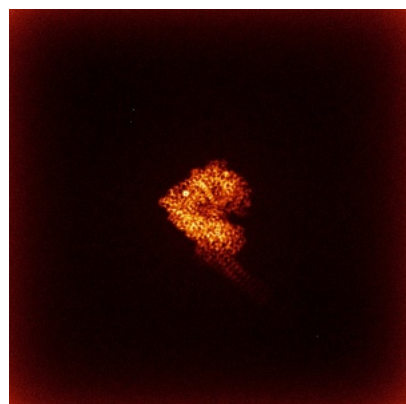


Y

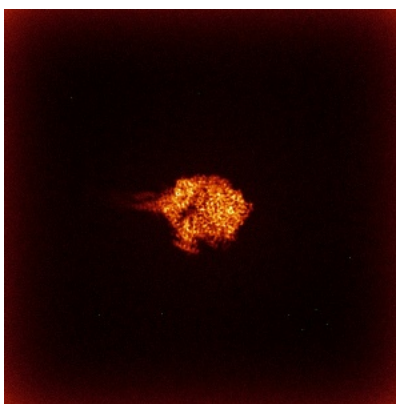


Z

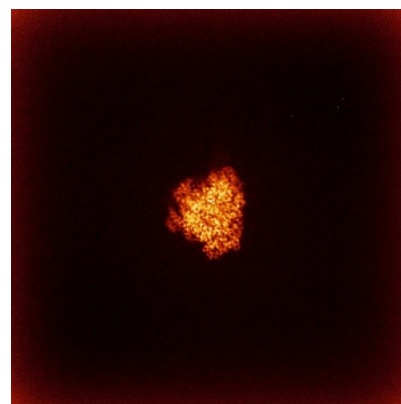
6.4.2 Raw map



X



Y

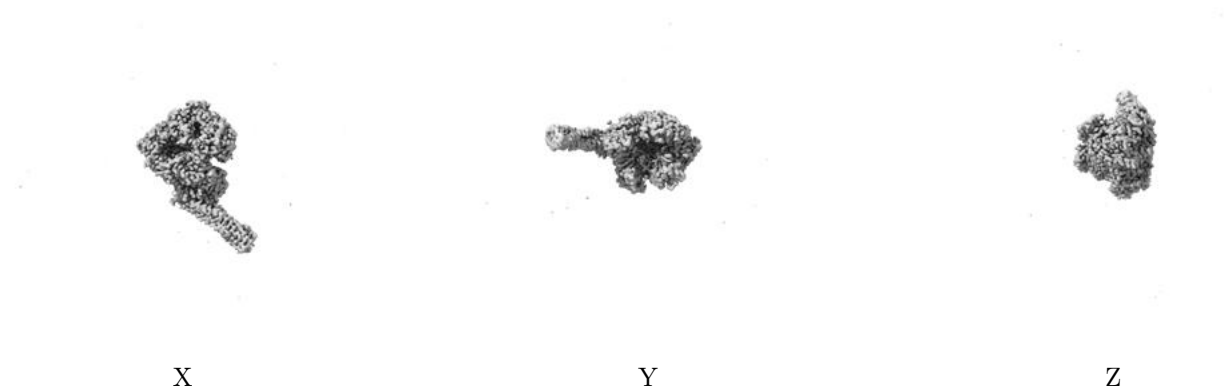


Z

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.

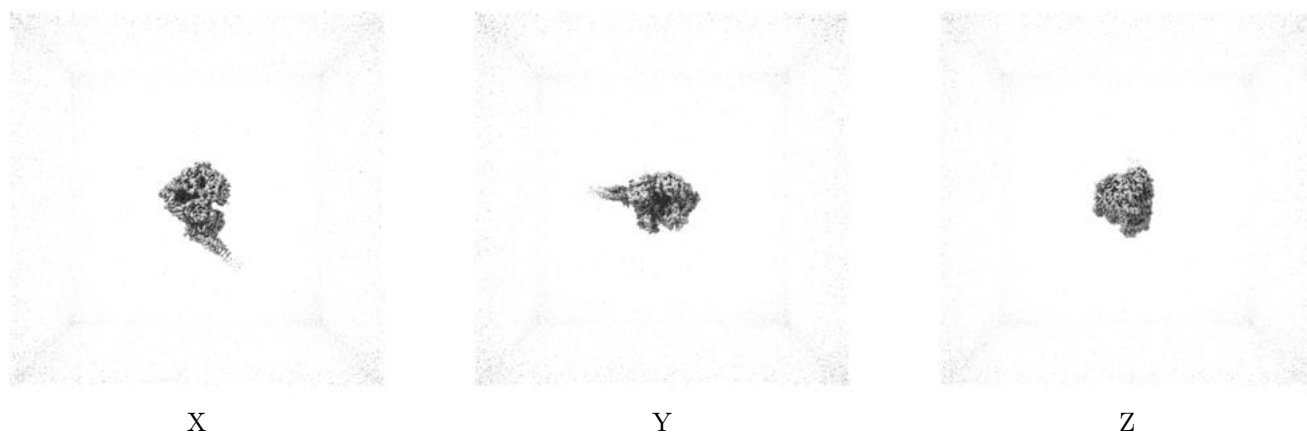
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. 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.

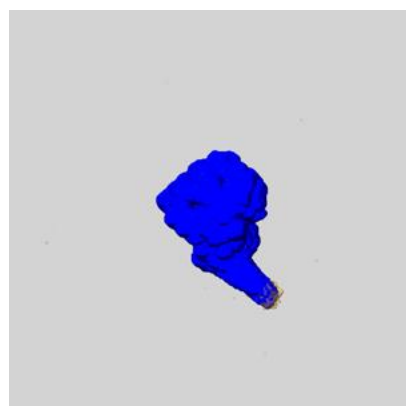
6.6 Mask visualisation [i](#)

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

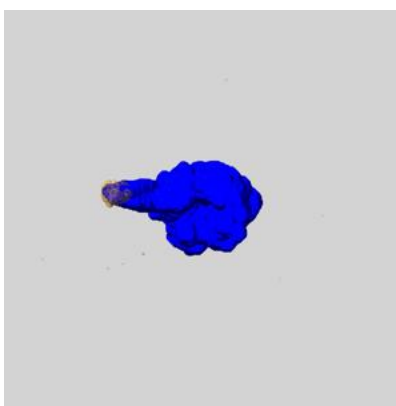
A mask typically either:

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

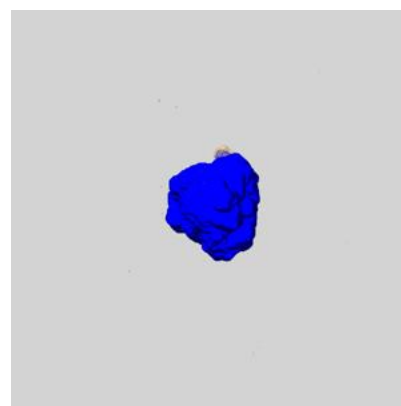
6.6.1 emd_65446_msk_1.map [i](#)



X



Y

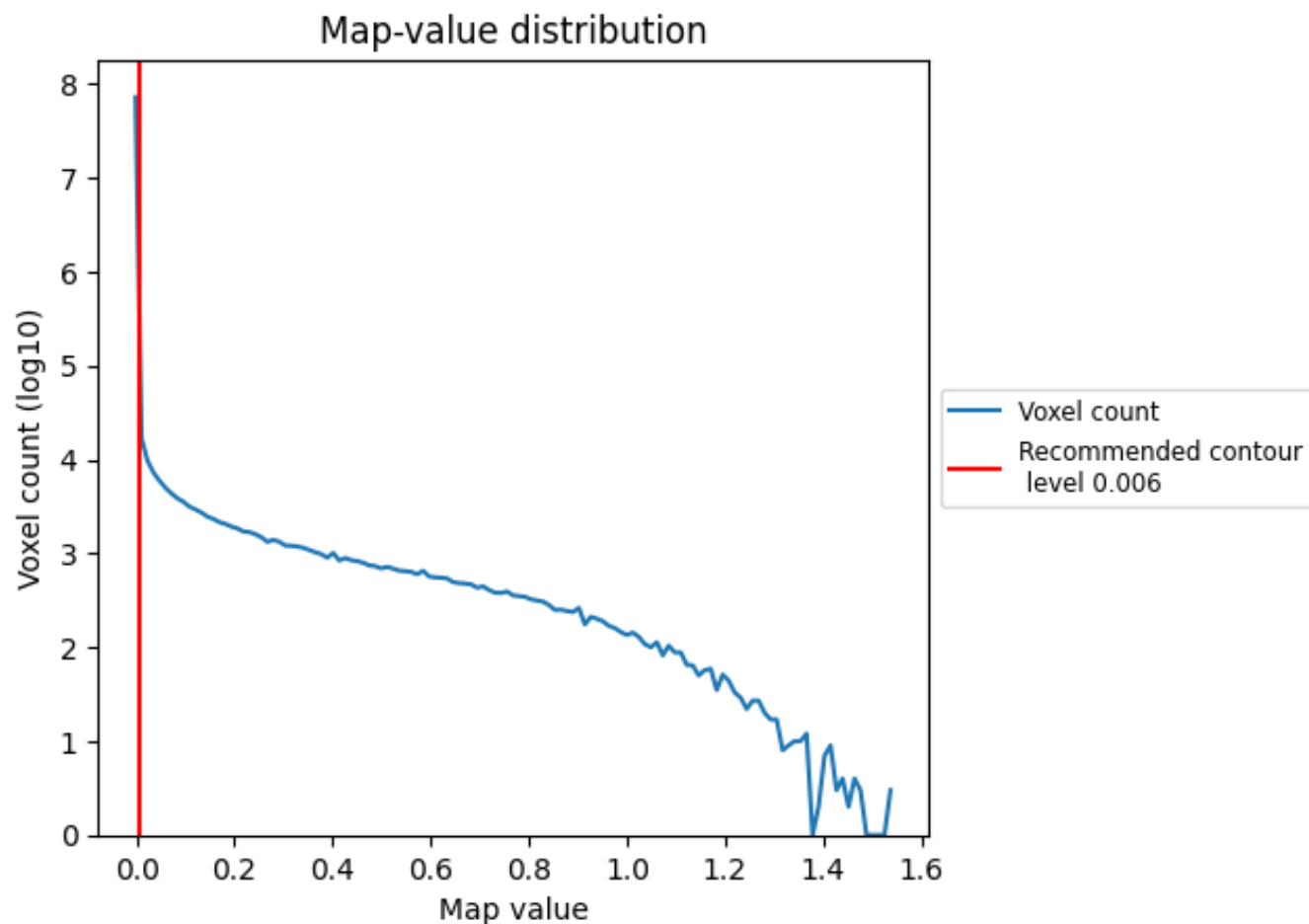


Z

7 Map analysis [i](#)

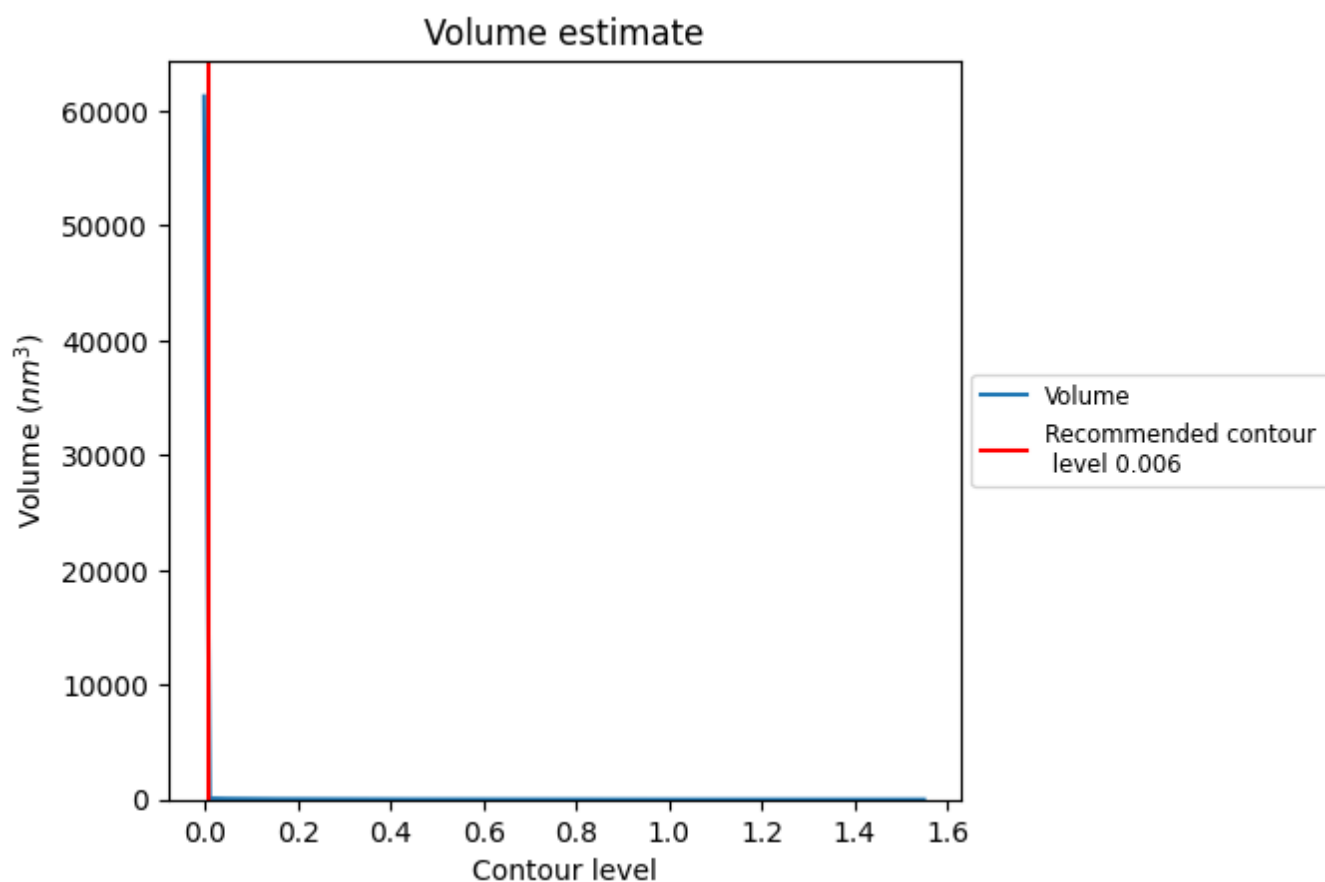
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

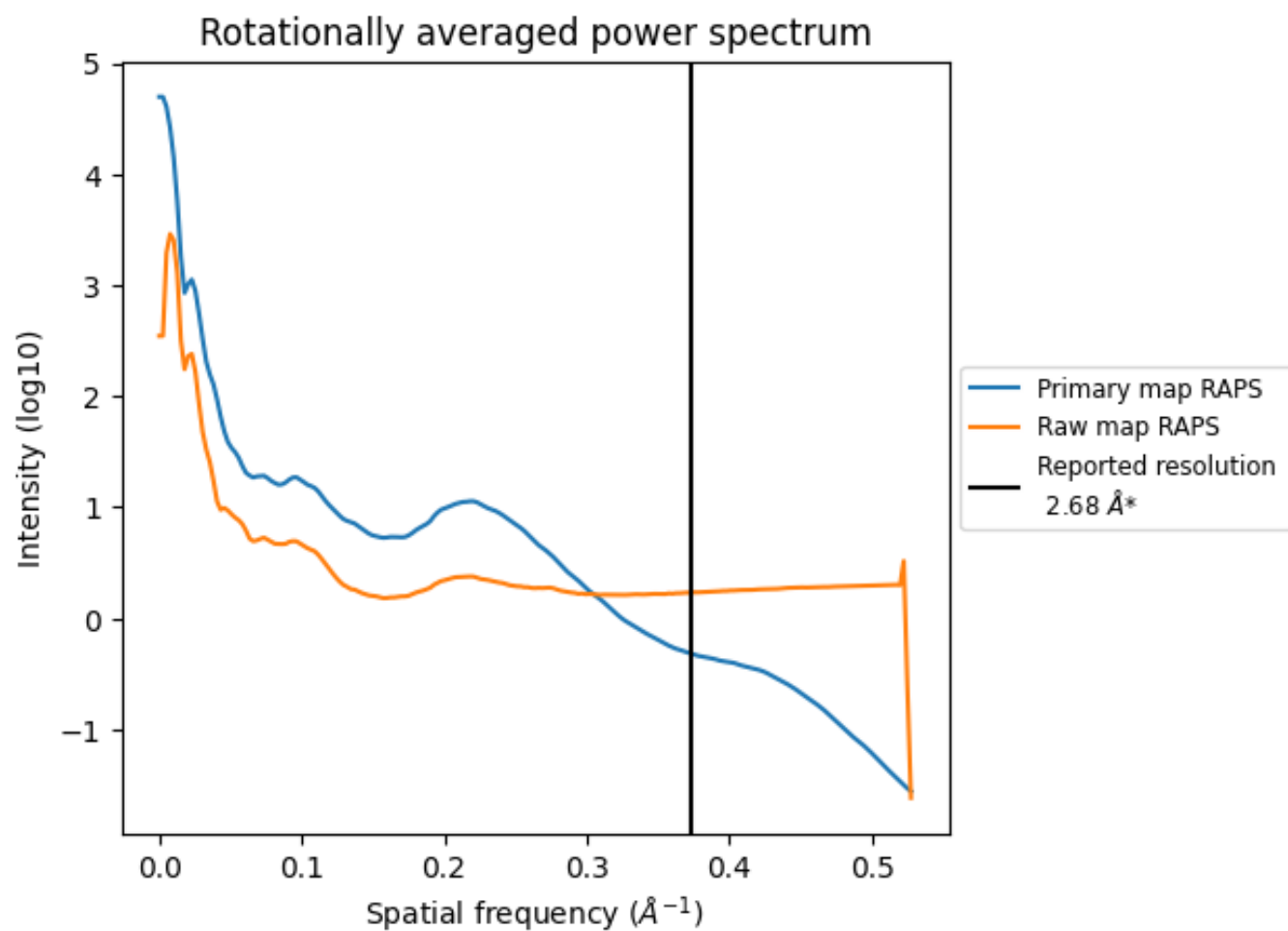
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 22068 nm^3 ; this corresponds to an approximate mass of 19935 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 [i](#)

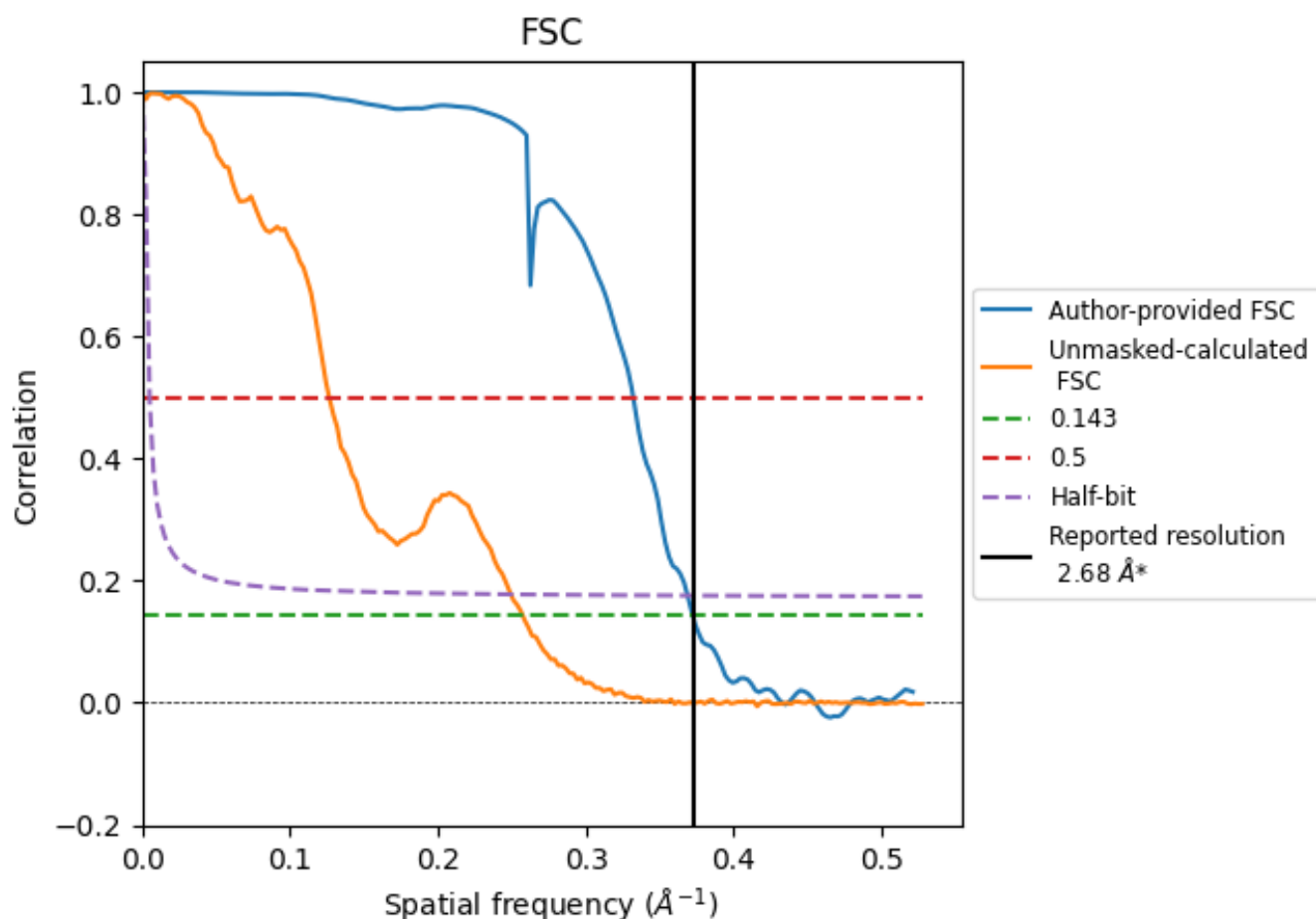


*Reported resolution corresponds to spatial frequency of 0.373 $\text{\AA}^{-1}$

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 0.373 Å⁻¹

8.2 Resolution estimates [i](#)

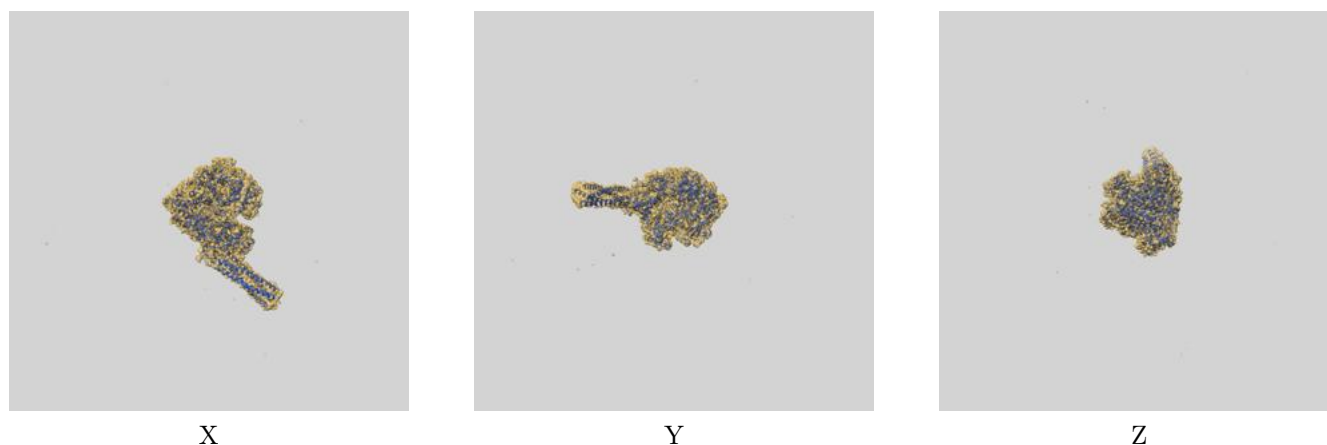
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.68	-	-
Author-provided FSC curve	2.69	3.01	2.71
Unmasked-calculated*	3.89	7.90	4.01

*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 3.89 differs from the reported value 2.68 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65446 and PDB model 9VXZ. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



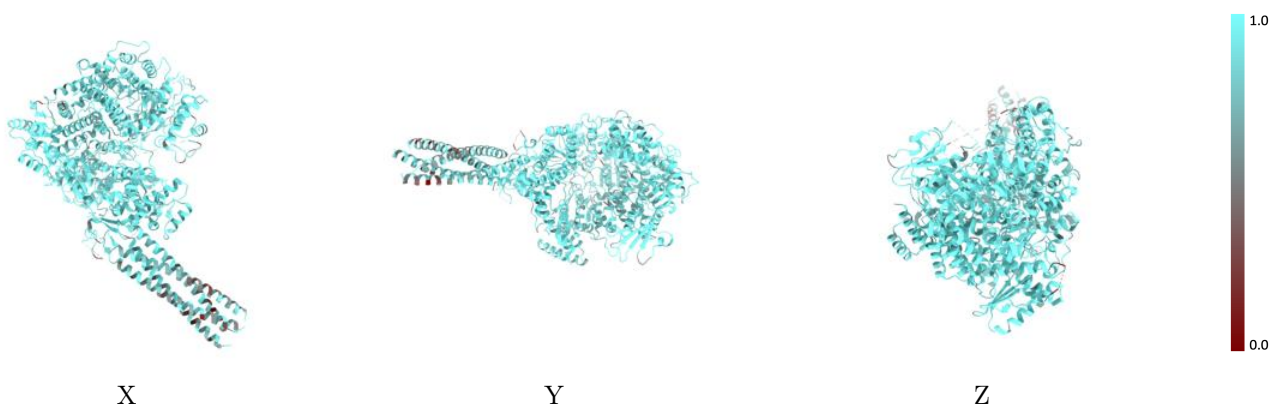
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



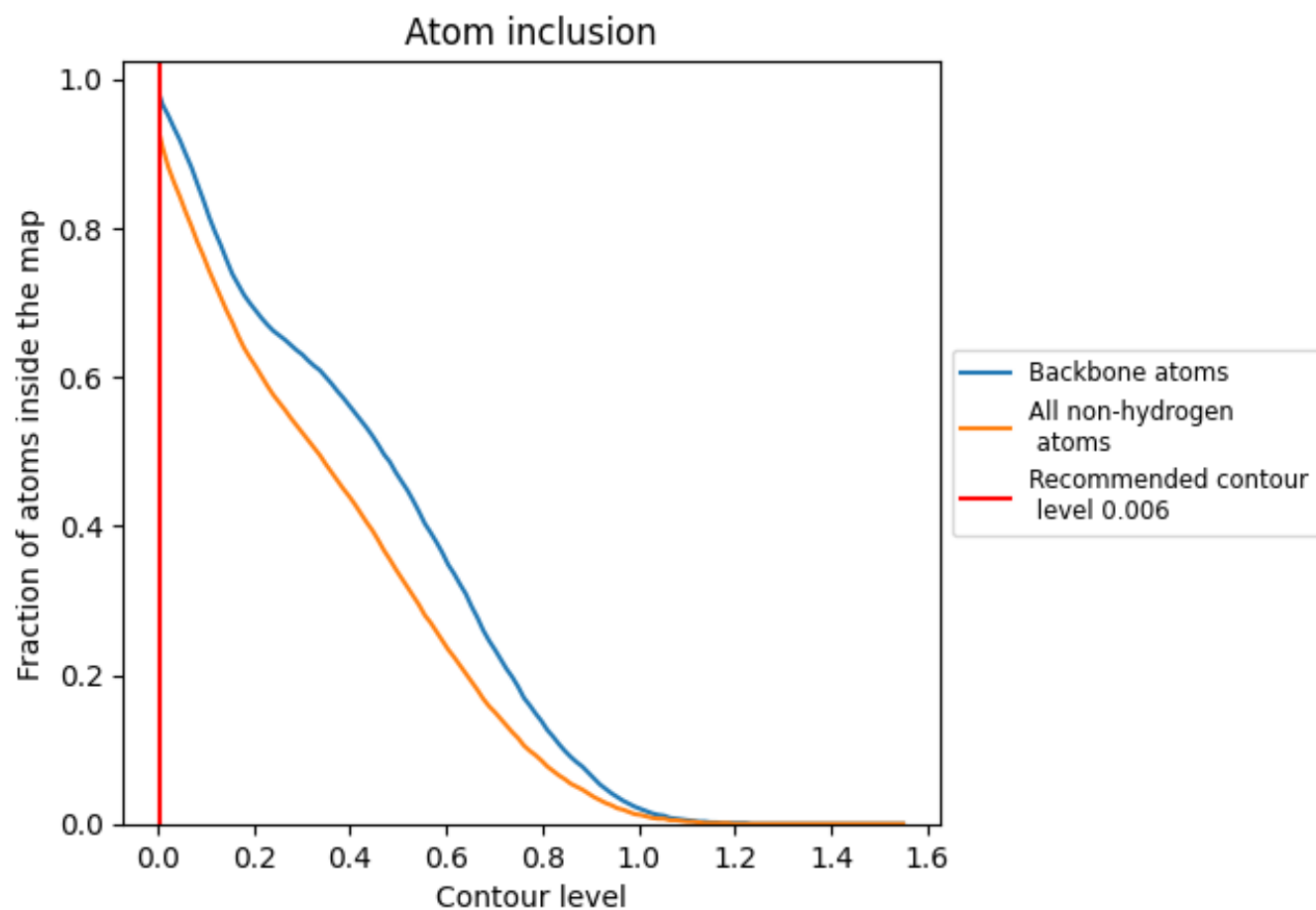
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 92% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9210	0.4780
A	0.9490	0.5230
B	0.8390	0.3530
C	0.7220	0.1470
D	0.7950	0.2940
E	0.8270	0.2580

