



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 12:28 PM UTC

PDB ID : 8JSN / pdb_00008jsn
EMDB ID : EMD-36624
Title : The structure of EBOV L-VP35-RNA complex (conformation 2)
Authors : Qi, P.; Yi, S.
Deposited on : 2023-06-20
Resolution : 3.40 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:

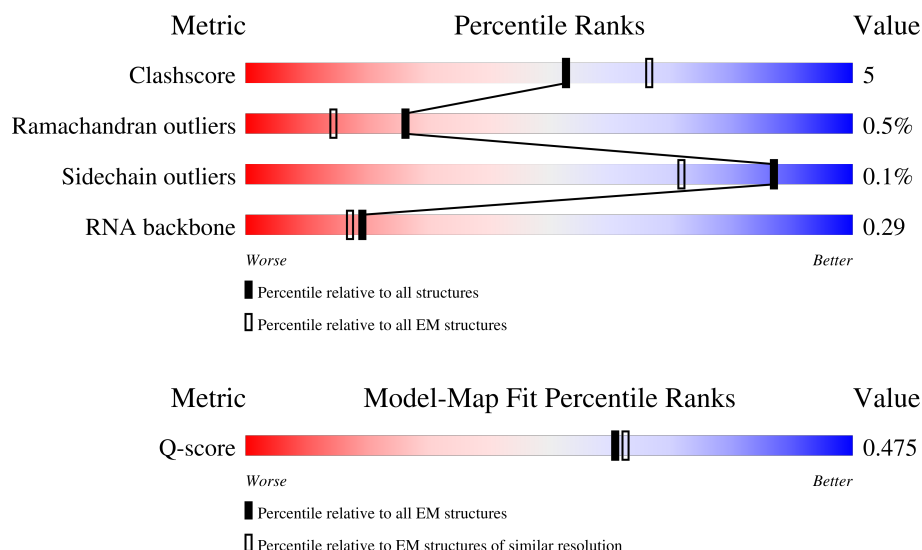
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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	-
RNA backbone	8273	3508	-
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	2212	
2	B	340	
2	C	340	

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Mol	Chain	Length	Quality of chain
2	D	340	14%6%80%
2	E	340	5%16%80%
3	G	18	39%17%44%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14856 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	1362	Total	C	N	O	S	0	0
			10897	7002	1853	1986	56		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	759	ASP	GLY	conflict	UNP A0A1C4HDB0

- Molecule 2 is a protein called Polymerase cofactor VP35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	260	Total	C	N	O	S	1	0
			1989	1247	342	391	9		
2	C	99	Total	C	N	O	S	0	0
			737	460	119	154	4		
2	D	68	Total	C	N	O	S	0	0
			511	321	80	106	4		
2	E	67	Total	C	N	O	S	0	0
			509	318	84	104	3		

- Molecule 3 is a RNA chain called The leader sequence of EBOV genome.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	10	Total	C	N	O	P	0	0
			212	94	34	74	10		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

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

- Molecule 2: Polymerase cofactor VP35



	Vt39	W324 V325	L144	Tt155	Ei165 Ht166	Ei78	Rt182	Ei186 St187	Rt188	Qt194	Ei198	K222 D223	L224	L242	L249	S253	L256	E262	S266	E269	A276 L277	I278	Q279	L280 T281	P292 P293	V294	I297	G301 D302	R312	P315	P318
GLN	THR	THR	LYS	PRO	ASN	PRO	LYS	MET	ARG	GLY	ASN	SER	THR	VAL	ALA	THR	GLN	THR	ASP	ASN	ASP	THR	GLY	ARG	GLY	PRO	GLY	THR	PRO	GLN	GLN

- Molecule 2: Polymerase cofactor VP35

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	183964	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.078	Depositor
Minimum map value	-0.038	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	298.8, 298.8, 298.8	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

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	0.11	0/11168	0.30	0/15169
2	B	0.23	0/2028	0.42	1/2759 (0.0%)
2	C	0.17	0/750	0.40	0/1027
2	D	0.17	0/514	0.39	0/698
2	E	0.11	0/513	0.30	0/697
3	G	0.08	0/235	0.14	0/364
All	All	0.14	0/15208	0.33	1/20714 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	292	PRO	N-CA-C	5.43	115.69	110.47

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	10897	0	10861	94	0
2	B	1989	0	1963	37	0
2	C	737	0	704	9	0
2	D	511	0	519	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	509	0	509	13	0
3	G	212	0	107	2	0
4	A	1	0	0	0	0
All	All	14856	0	14663	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.

All (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:1153:CYS:SG	1:A:1347:HIS:HE1	1.99	0.86
1:A:756:THR:HG23	1:A:761:GLN:HE21	1.54	0.72
1:A:905:VAL:HG23	1:A:911:GLY:HA3	1.71	0.71
2:B:128:ILE:HD11	2:E:128:ILE:HD11	1.74	0.69
2:D:93:LEU:HD12	2:E:93:LEU:HD21	1.75	0.69
2:B:330:LEU:HB2	2:B:334:LYS:HB2	1.76	0.68
2:B:124:MET:HA	2:B:127:THR:HG22	1.76	0.67
2:B:315:PRO:HD2	2:B:324:TRP:HZ2	1.60	0.67
1:A:1029:ARG:NH1	1:A:1272:ASN:OD1	2.29	0.66
1:A:1145:LYS:HD3	1:A:1146:PRO:HD2	1.78	0.65
1:A:1218:GLU:OE1	1:A:1247:ARG:NH2	2.30	0.65
2:B:276:ALA:O	2:B:280:ILE:HD12	1.97	0.65
1:A:1244:LEU:HD13	1:A:1255:ILE:HD12	1.79	0.63
2:B:94:ALA:O	2:B:98:GLN:NE2	2.31	0.63
1:A:1033:ASP:OD1	1:A:1037:ARG:NH2	2.32	0.62
2:B:121:VAL:HA	2:B:124:MET:HE3	1.81	0.62
2:D:116:ASN:HA	2:D:119:LYS:HE2	1.81	0.62
1:A:795:HIS:CD2	1:A:796:SER:H	2.19	0.61
1:A:649:ILE:HG21	1:A:663:ASN:HB3	1.83	0.61
2:B:155:THR:HG22	2:D:145:LEU:HD23	1.83	0.60
1:A:157:ILE:HD11	1:A:871:ILE:HD11	1.83	0.60
1:A:1350:LYS:HA	1:A:1350:LYS:HE3	1.83	0.60
2:D:123:ASP:OD1	2:D:124:MET:N	2.34	0.59
1:A:201:ASN:ND2	1:A:210:MET:SD	2.76	0.59
1:A:1351:CYS:O	1:A:1354:ARG:NH1	2.35	0.59
1:A:1229:VAL:HG13	1:A:1230:THR:HG23	1.84	0.58
1:A:476:SER:HA	1:A:1379:LEU:HD21	1.85	0.58
2:B:297:ILE:HD11	2:B:302:ASP:HB3	1.86	0.58
2:D:134:VAL:HG11	2:E:135:CYS:HB3	1.84	0.58
1:A:1042:LYS:HD2	1:A:1379:LEU:HD13	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1146:PRO:HG3	1:A:1342:ASN:HB2	1.85	0.57
1:A:1247:ARG:NH1	1:A:1379:LEU:O	2.38	0.57
2:C:174:SER:HB2	2:C:178:GLU:HG3	1.87	0.57
1:A:1134:CYS:HB3	1:A:1137:GLU:HG2	1.86	0.57
1:A:485:ARG:HD2	3:G:7:C:H3'	1.86	0.56
1:A:429:VAL:HG21	1:A:464:LEU:HD22	1.86	0.56
1:A:1248:VAL:HG11	1:A:1255:ILE:HD11	1.87	0.56
1:A:180:ILE:HD12	1:A:193:ILE:HG22	1.88	0.56
1:A:405:PHE:HD1	2:B:144:LEU:HD13	1.69	0.56
1:A:602:LYS:NZ	1:A:606:LEU:HB2	2.21	0.56
2:B:178:GLU:OE2	2:B:182:ARG:NH2	2.36	0.55
1:A:495:ASP:OD1	1:A:691:ARG:NH1	2.39	0.55
1:A:521:LEU:HB3	1:A:996:ALA:HA	1.88	0.55
1:A:1010:ASP:OD1	1:A:1011:PHE:N	2.40	0.55
1:A:817:LYS:HG3	1:A:818:THR:HG23	1.89	0.55
1:A:337:ILE:HD12	1:A:337:ILE:H	1.71	0.54
2:B:224:LEU:HD23	2:B:256:LEU:HD22	1.89	0.54
1:A:91:PRO:HD2	1:A:158:LEU:HD11	1.90	0.54
2:C:118:LEU:O	2:C:120:PRO:HD3	2.08	0.54
1:A:386:ILE:HD11	1:A:676:VAL:HG23	1.90	0.53
1:A:97:GLN:OE1	1:A:147:HIS:ND1	2.39	0.53
1:A:181:ASP:HB2	1:A:192:LYS:HB3	1.90	0.52
1:A:268:PRO:HB3	1:A:360:MET:HE1	1.91	0.52
1:A:1303:SER:OG	1:A:1350:LYS:NZ	2.42	0.52
2:B:194:GLN:O	2:B:198:GLU:HG2	2.09	0.52
1:A:665:MET:HE1	1:A:716:TRP:HZ2	1.74	0.52
1:A:396:LEU:HD21	2:C:148:THR:HG23	1.92	0.52
1:A:203:GLN:O	1:A:219:LYS:NZ	2.41	0.51
2:C:120:PRO:O	2:C:124:MET:HG2	2.11	0.51
1:A:967:LEU:HD21	1:A:1044:LEU:HD21	1.92	0.51
1:A:359:GLU:O	1:A:359:GLU:HG2	2.11	0.51
1:A:739:VAL:HG22	1:A:744:GLN:HB3	1.91	0.51
2:D:110:ARG:HH11	2:E:107:LEU:HD21	1.76	0.51
2:E:124:MET:O	2:E:128:ILE:HG12	2.11	0.51
2:D:82:SER:OG	2:D:83:PHE:N	2.41	0.50
2:B:262:GLU:OE2	2:B:280:ILE:HG13	2.10	0.50
2:D:124:MET:O	2:D:127:THR:OG1	2.23	0.50
2:B:242:LEU:HD13	2:B:325:VAL:HG12	1.92	0.50
1:A:1331:PHE:HZ	1:A:1341:TYR:HD2	1.59	0.50
1:A:48:LYS:HD3	3:G:0:U:H1'	1.94	0.49
1:A:1037:ARG:HH21	1:A:1225:ARG:HE	1.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:LEU:HD22	1:A:858:ARG:HD3	1.94	0.49
1:A:383:GLU:O	1:A:387:GLN:HG2	2.13	0.49
2:B:106:SER:O	2:B:109:GLN:HG3	2.13	0.49
2:D:116:ASN:O	2:D:119:LYS:HG2	2.13	0.48
2:B:182:ARG:O	2:B:186:GLU:HG2	2.12	0.48
2:B:318:PRO:HB3	2:B:324:TRP:CE2	2.48	0.48
2:B:266[B]:SER:O	2:B:269:GLU:HG3	2.14	0.48
2:E:96:VAL:O	2:E:99:GLN:HG3	2.14	0.48
2:B:266[A]:SER:O	2:B:269:GLU:HG3	2.14	0.48
2:C:117:GLY:C	2:C:119:LYS:H	2.22	0.47
1:A:870:ARG:NH1	1:A:873:GLN:OE1	2.47	0.47
2:D:110:ARG:O	2:D:113:SER:OG	2.29	0.47
1:A:678:ASP:HB3	1:A:681:ASN:OD1	2.15	0.47
1:A:883:PHE:CE1	1:A:888:LEU:HD21	2.50	0.46
2:B:178:GLU:CD	2:B:182:ARG:HH22	2.23	0.46
1:A:23:ASP:OD1	1:A:35:TYR:HB2	2.16	0.46
1:A:1241:LYS:O	1:A:1245:GLU:HG2	2.16	0.46
2:B:312:ARG:HD3	2:B:339:LYS:HB2	1.98	0.46
1:A:953:ILE:HD12	1:A:1109:LEU:HD21	1.97	0.45
1:A:1380:ILE:HG22	1:A:1381:TYR:H	1.82	0.45
1:A:330:THR:O	1:A:334:ILE:HG12	2.17	0.45
1:A:1037:ARG:NH2	1:A:1225:ARG:HH21	2.15	0.45
2:B:126:LYS:HB2	2:B:126:LYS:HE2	1.72	0.45
2:D:107:LEU:HD12	2:E:107:LEU:HD12	1.97	0.45
1:A:906:PRO:HA	1:A:913:SER:HB3	1.98	0.45
2:B:92:SER:O	2:B:96:VAL:HG23	2.17	0.45
2:B:188:ARG:HD2	2:B:188:ARG:N	2.32	0.45
1:A:963:ILE:HG13	1:A:1017:CYS:SG	2.56	0.44
1:A:1155:ASN:O	1:A:1158:GLN:NE2	2.47	0.44
2:B:277:LEU:HA	2:B:280:ILE:HD13	1.99	0.44
2:D:89:THR:HG21	2:E:86:VAL:HG22	1.99	0.44
1:A:548:PHE:HA	1:A:565:LYS:O	2.17	0.44
1:A:963:ILE:O	1:A:967:LEU:HG	2.18	0.44
1:A:553:LYS:HG2	1:A:554:GLU:H	1.83	0.44
1:A:944:GLU:C	1:A:945:MET:HE2	2.42	0.44
2:B:278:ILE:HA	2:B:281:THR:HG22	2.00	0.44
2:D:115:GLU:O	2:D:118:LEU:HB2	2.17	0.44
1:A:32:TYR:O	1:A:70:THR:OG1	2.31	0.44
1:A:290:ASP:OD2	1:A:293:LYS:NZ	2.51	0.43
1:A:82:LYS:HB3	1:A:82:LYS:HE3	1.74	0.43
2:B:118:LEU:O	2:B:121:VAL:HG12	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:831:ASP:HB3	1:A:872:LEU:HD21	1.99	0.43
1:A:1023:SER:HB2	1:A:1363:TYR:CZ	2.53	0.43
2:B:132:ASN:HA	2:E:131:LEU:HD21	1.99	0.43
1:A:405:PHE:CD1	2:B:144:LEU:HD13	2.53	0.43
1:A:453:MET:HE2	1:A:453:MET:HB3	1.84	0.43
2:D:110:ARG:HD3	2:E:107:LEU:HD21	2.01	0.43
1:A:153:TYR:OH	1:A:824:PRO:HD2	2.18	0.43
2:B:104:SER:O	2:B:107:LEU:HG	2.19	0.43
1:A:1380:ILE:HG22	1:A:1381:TYR:N	2.34	0.42
2:C:92:SER:O	2:C:96:VAL:HG23	2.19	0.42
2:B:139:VAL:HA	2:E:138:MET:HE2	2.02	0.42
1:A:299:GLU:HB2	1:A:300:PRO:HD3	2.01	0.42
1:A:1369:LEU:HD12	1:A:1369:LEU:HA	1.91	0.42
2:B:165:GLU:HG2	2:B:166:HIS:CE1	2.55	0.42
2:D:110:ARG:C	2:E:110:ARG:HH22	2.27	0.42
1:A:172:THR:HG22	1:A:185:TYR:HB2	2.01	0.41
1:A:990:ARG:HH12	1:A:994:LEU:HG	1.84	0.41
1:A:10:ASP:OD1	1:A:10:ASP:N	2.47	0.41
1:A:239:MET:O	1:A:243:LEU:HG	2.20	0.41
2:D:102:ILE:O	2:D:105:GLU:HG3	2.20	0.41
2:D:134:VAL:O	2:D:137:GLU:HG2	2.19	0.41
2:C:131:LEU:HD23	2:C:131:LEU:HA	1.89	0.41
1:A:423:GLN:HE21	1:A:1210:LYS:HG2	1.85	0.41
2:B:139:VAL:HA	2:E:138:MET:CE	2.50	0.41
1:A:299:GLU:HG3	1:A:372:GLN:OE1	2.20	0.41
1:A:780:THR:HG22	1:A:785:ILE:O	2.21	0.41
2:B:249:LEU:O	2:B:253:SER:HB3	2.20	0.41
1:A:1145:LYS:CD	1:A:1146:PRO:HD2	2.46	0.41
1:A:1163:PRO:HB3	1:A:1299:LEU:HA	2.03	0.41
2:B:222:LYS:HB3	2:B:222:LYS:HE2	1.76	0.41
1:A:93:GLU:HB3	1:A:94:PRO:HD3	2.02	0.41
1:A:507:PRO:HA	1:A:508:PRO:HD3	1.94	0.41
2:B:102:ILE:O	2:B:105:GLU:HG3	2.21	0.41
1:A:665:MET:HE3	1:A:707:GLY:HA2	2.03	0.40
2:C:81:HIS:HB2	2:D:83:PHE:HE2	1.86	0.40
1:A:391:LYS:O	1:A:392:HIS:HB2	2.21	0.40
2:D:147:MET:HE2	2:D:147:MET:HB3	1.92	0.40
1:A:671:GLN:HG2	2:C:175:LEU:HD22	2.03	0.40
1:A:757:ASP:O	1:A:761:GLN:NE2	2.54	0.40
1:A:1374:TYR:HB3	1:A:1380:ILE:CG2	2.52	0.40
1:A:454:ILE:O	1:A:454:ILE:HG23	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1316:PHE:O	1:A:1320:ILE:HG12	2.21	0.40
1:A:1253:GLN:H	1:A:1256:LEU:HD23	1.86	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	1354/2212 (61%)	1265 (93%)	82 (6%)	7 (0%)	24	54
2	B	259/340 (76%)	246 (95%)	13 (5%)	0	100	100
2	C	97/340 (28%)	91 (94%)	5 (5%)	1 (1%)	12	40
2	D	66/340 (19%)	63 (96%)	2 (3%)	1 (2%)	8	30
2	E	65/340 (19%)	63 (97%)	2 (3%)	0	100	100
All	All	1841/3572 (52%)	1728 (94%)	104 (6%)	9 (0%)	26	54

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	451	LEU
1	A	751	VAL
2	C	119	LYS
1	A	851	THR
1	A	1174	VAL
2	D	148	THR
1	A	592	ASN
1	A	593	MET
1	A	829	ILE

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	1210/1994 (61%)	1210 (100%)	0	100	100
2	B	219/294 (74%)	218 (100%)	1 (0%)	81	81
2	C	79/294 (27%)	79 (100%)	0	100	100
2	D	59/294 (20%)	59 (100%)	0	100	100
2	E	58/294 (20%)	58 (100%)	0	100	100
All	All	1625/3170 (51%)	1624 (100%)	1 (0%)	87	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	294	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	120	ASN
1	A	423	GLN
1	A	463	HIS
1	A	530	ASN
1	A	671	GLN
1	A	713	GLN
1	A	743	ASN
1	A	761	GLN
1	A	924	ASN
1	A	1269	HIS
2	B	98	GLN
2	B	166	HIS
2	B	240	HIS
2	E	88	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	G	9/18 (50%)	1 (11%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	G	8	C

There are no RNA pucker outliers to report.

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 ⓘ

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

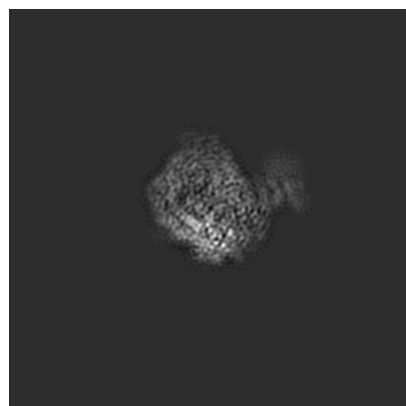
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36624. These allow visual inspection of the internal detail of the map and identification of artifacts.

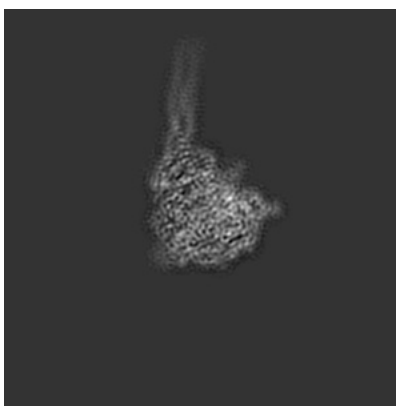
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

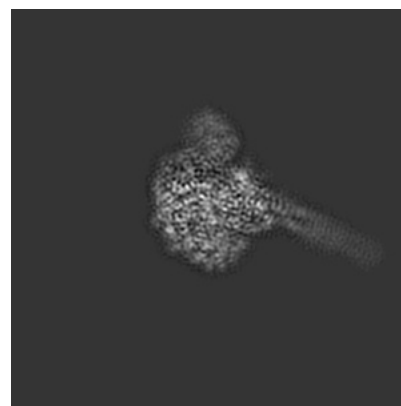
6.1.1 Primary map



X

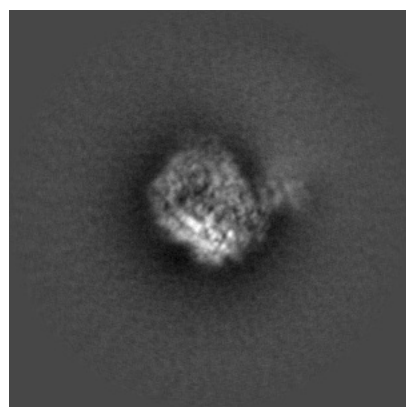


Y

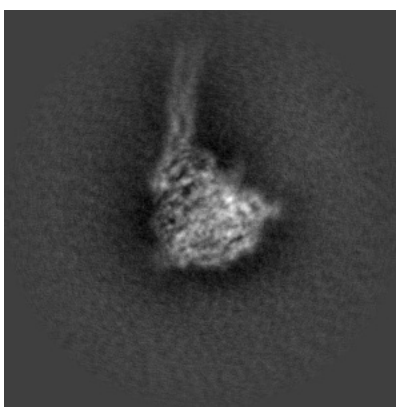


Z

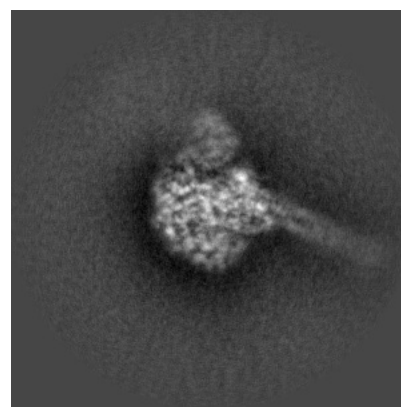
6.1.2 Raw map



X



Y

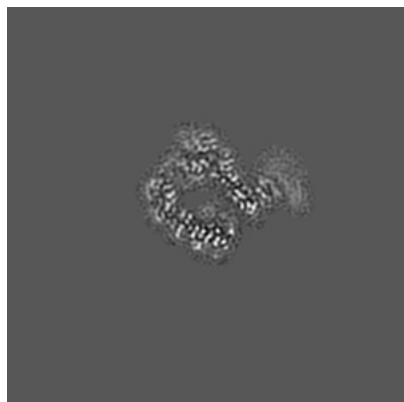


Z

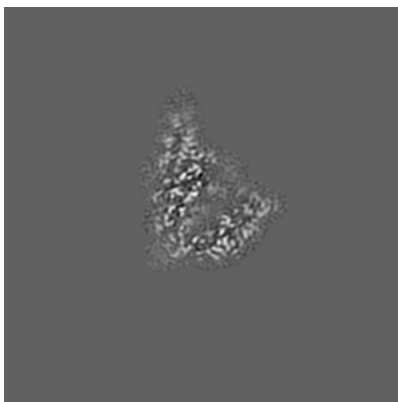
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

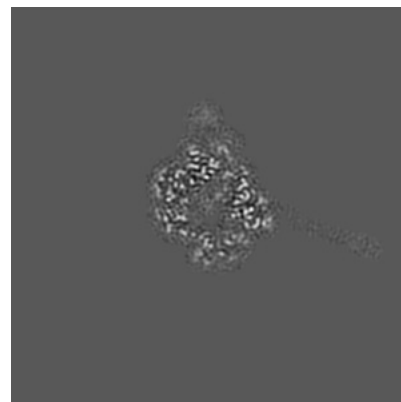
6.2.1 Primary map



X Index: 180

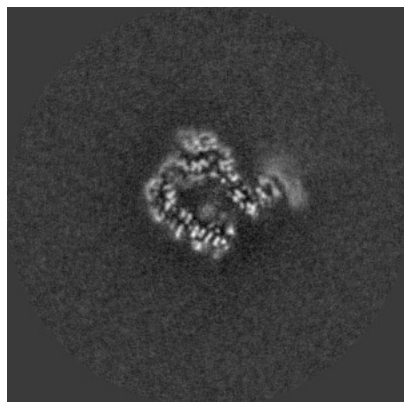


Y Index: 180

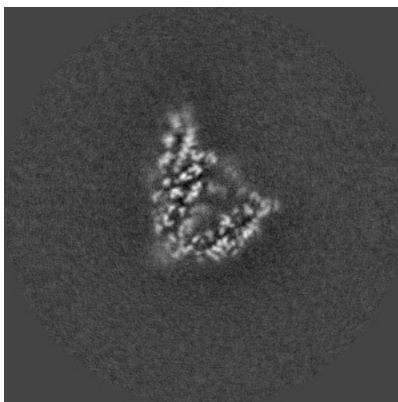


Z Index: 180

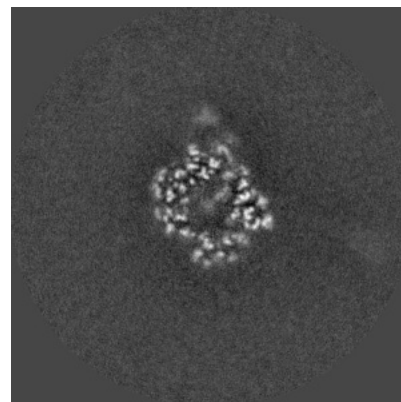
6.2.2 Raw map



X Index: 180



Y Index: 180

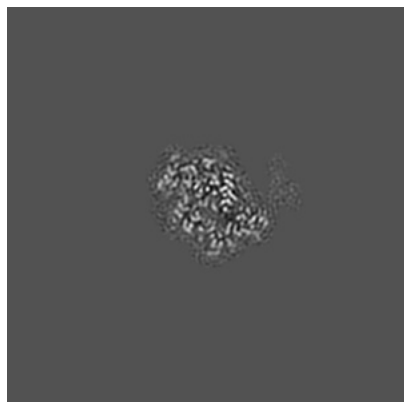


Z Index: 180

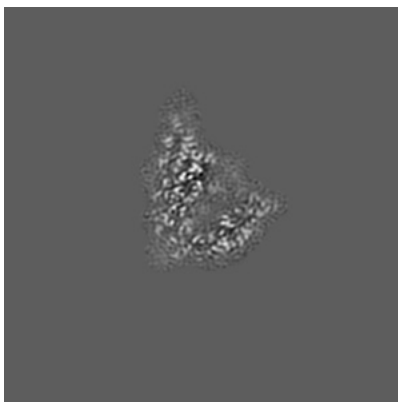
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

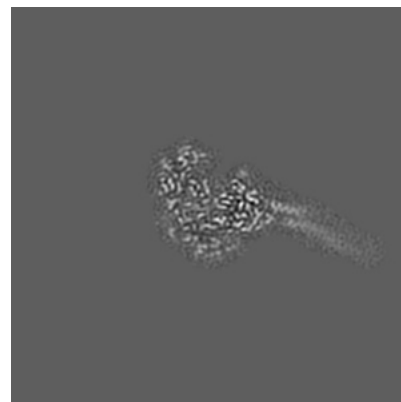
6.3.1 Primary map



X Index: 157

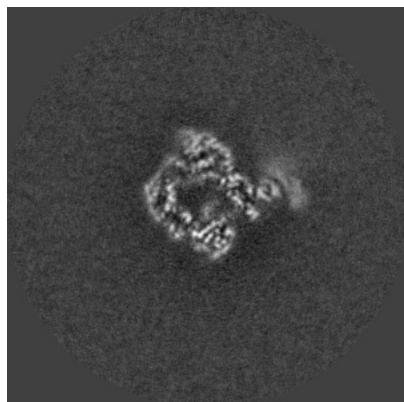


Y Index: 181

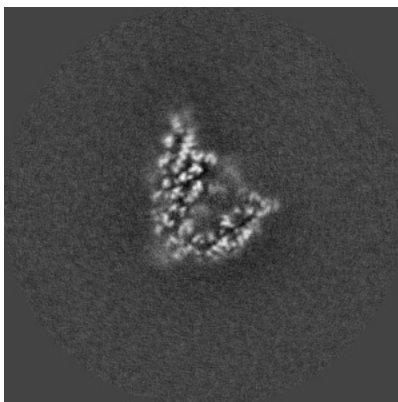


Z Index: 167

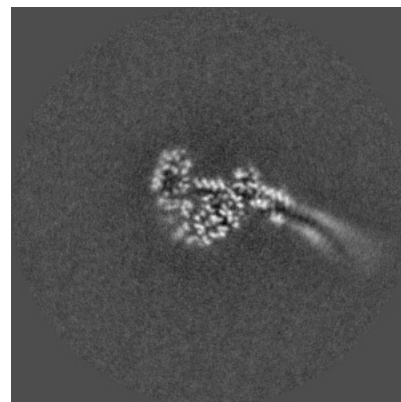
6.3.2 Raw map



X Index: 178



Y Index: 181

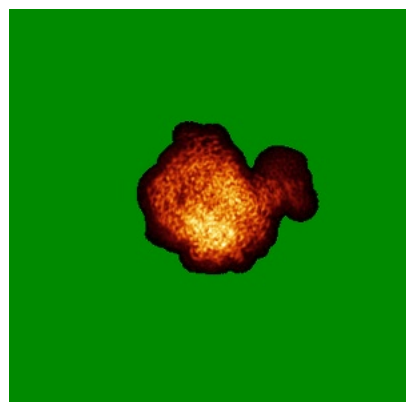


Z Index: 159

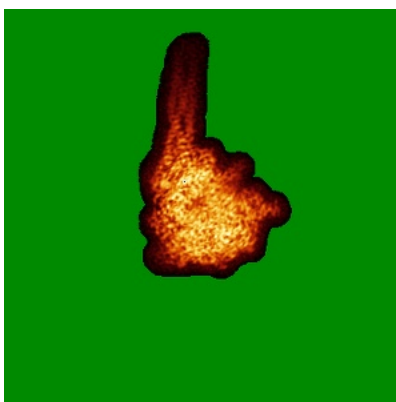
The images above show the largest variance slices of the map in three orthogonal directions.

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

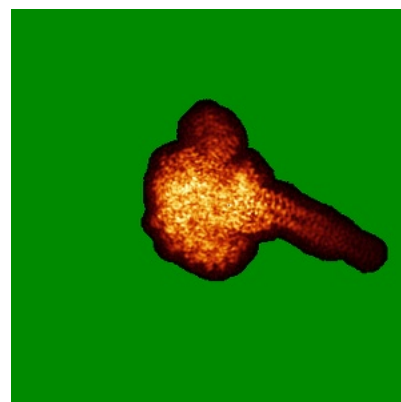
6.4.1 Primary map



X

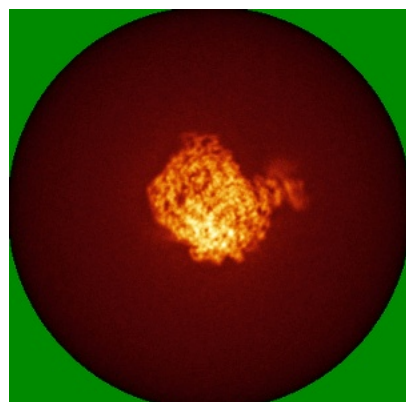


Y

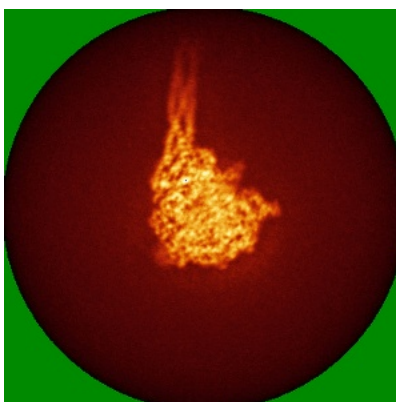


Z

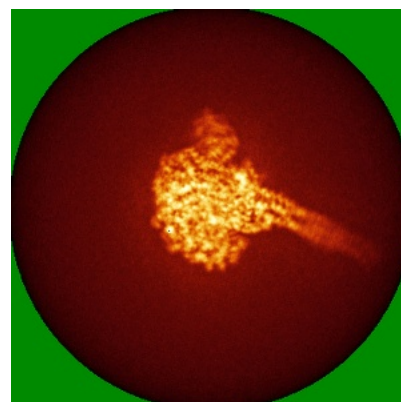
6.4.2 Raw map



X



Y

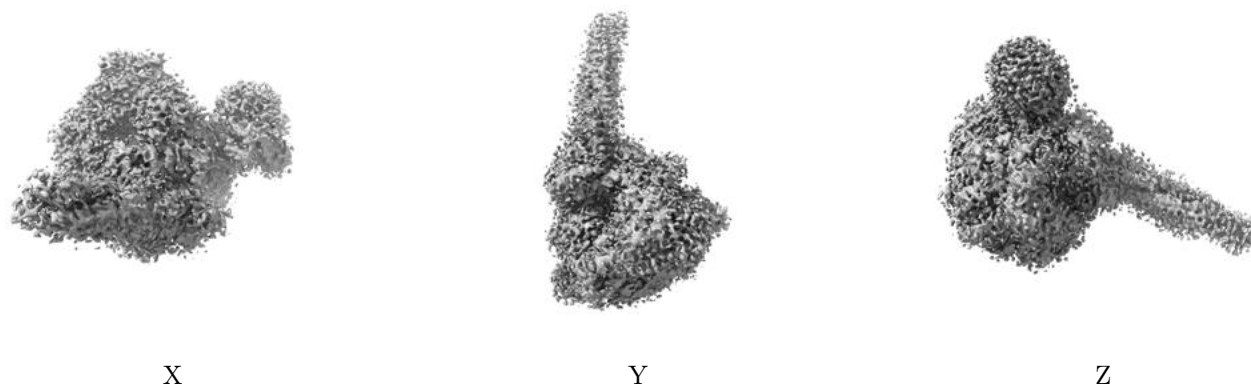


Z

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.

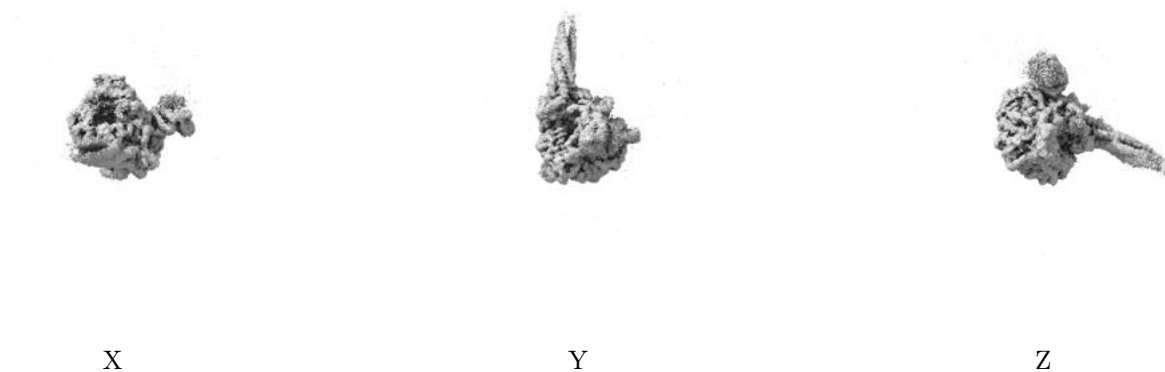
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.004. 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.

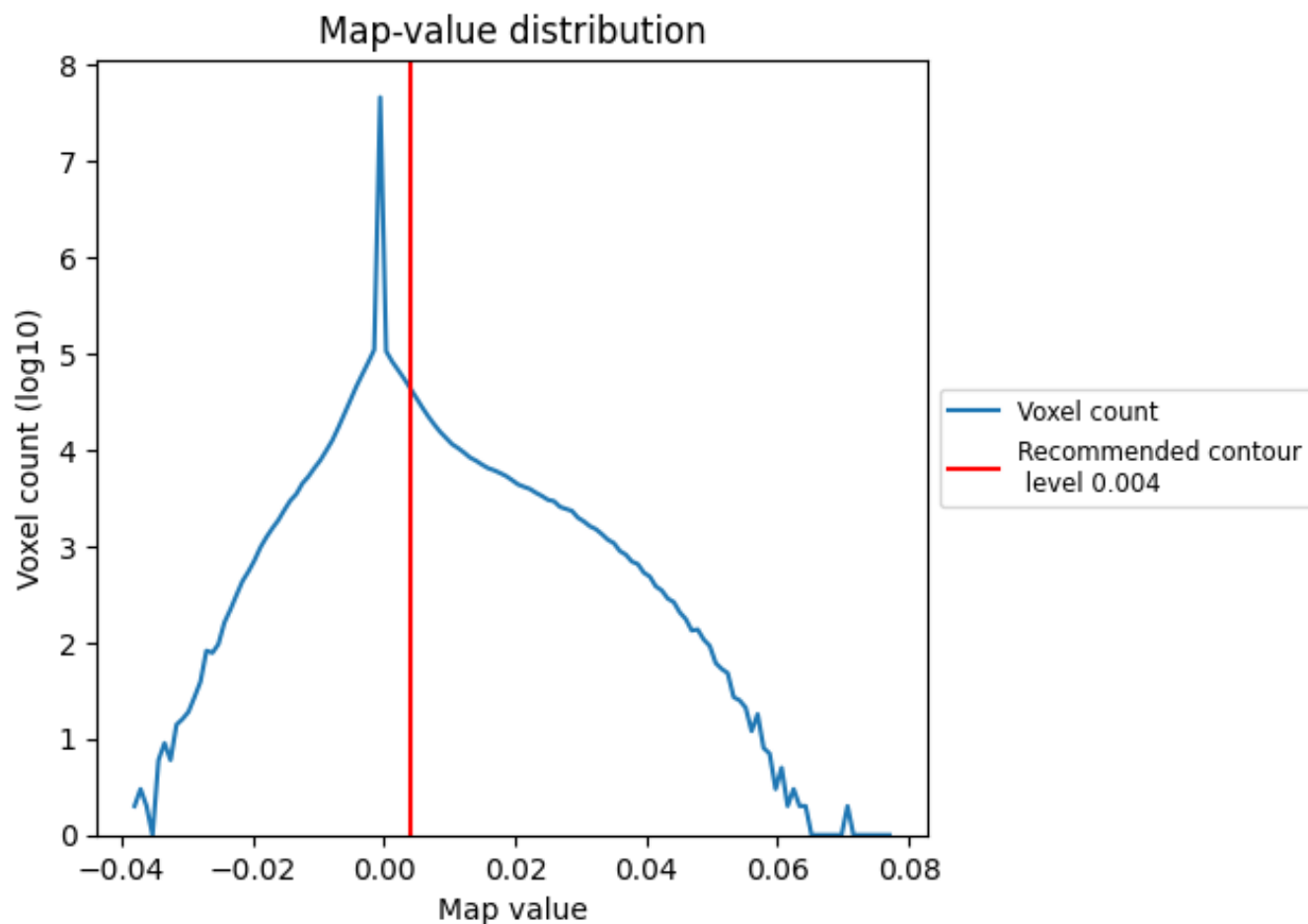
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

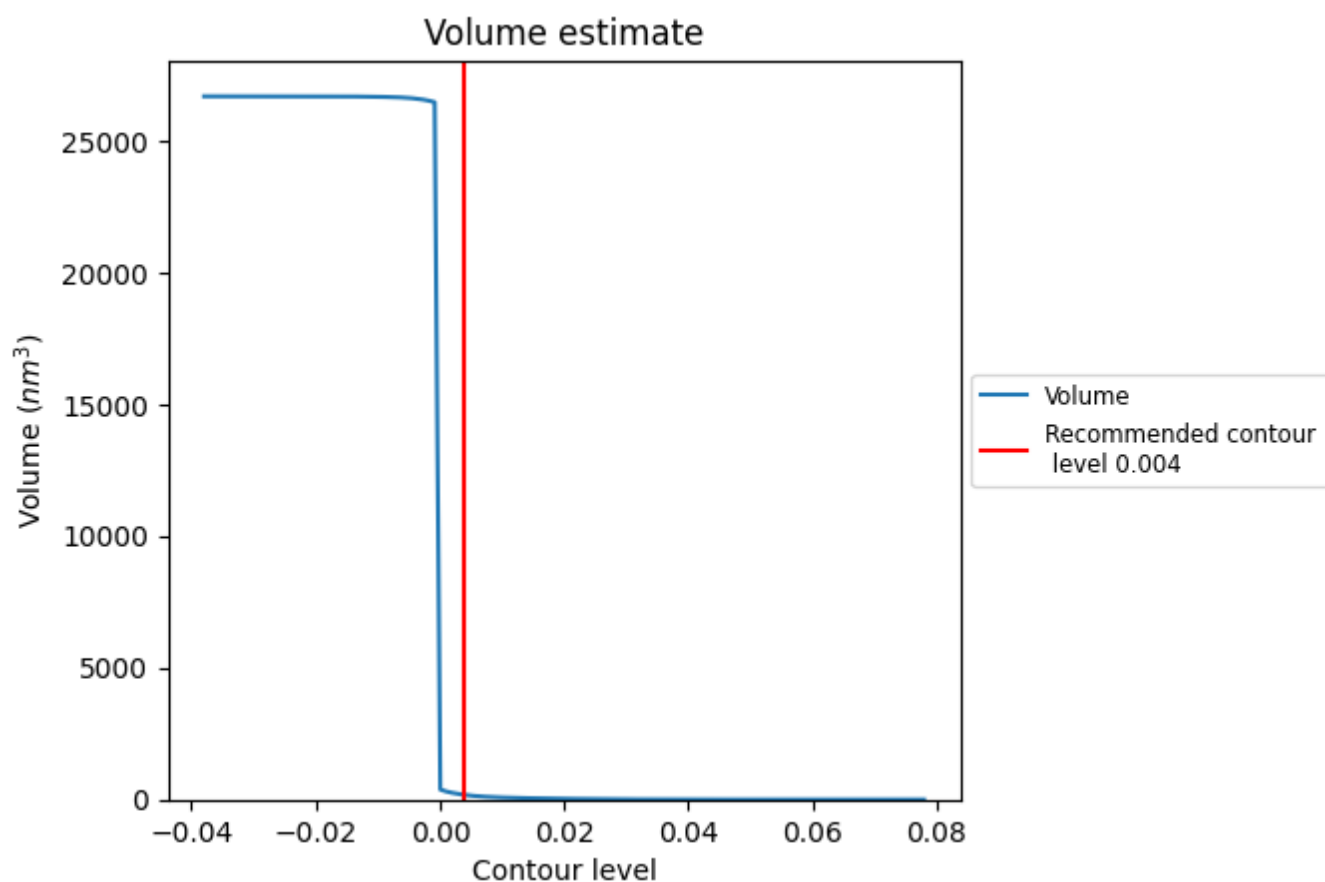
This section contains the results of statistical analysis of the map.

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.

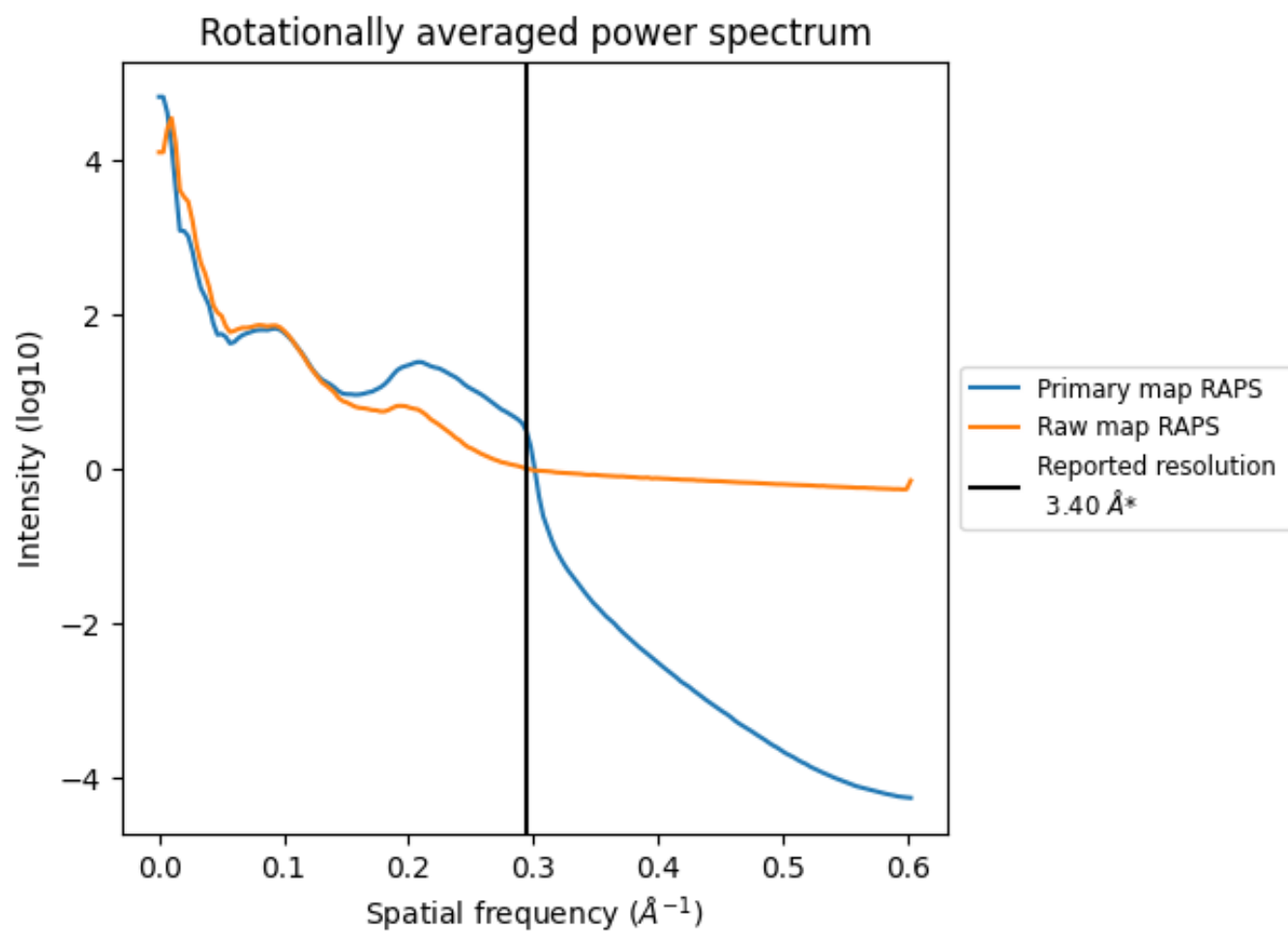
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 177 nm^3 ; this corresponds to an approximate mass of 160 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 ⓘ

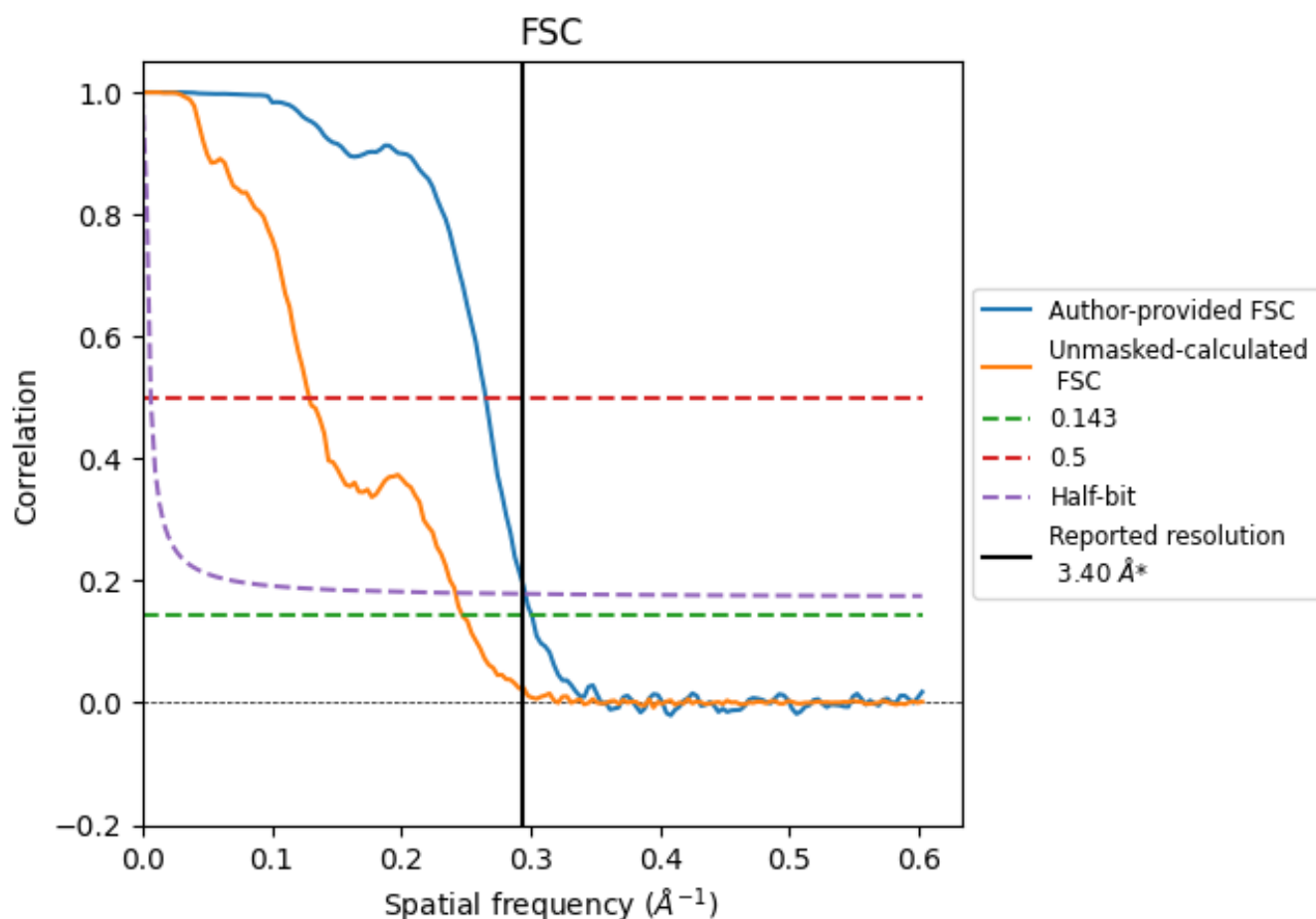


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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](#)

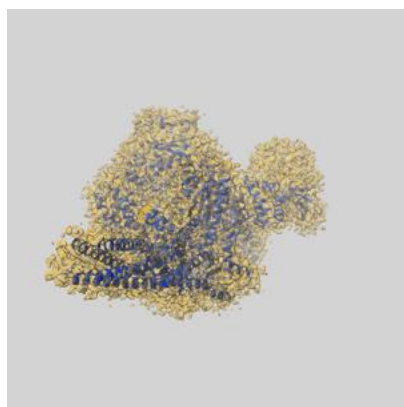
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.32	3.77	3.38
Unmasked-calculated*	4.04	7.75	4.13

*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 4.04 differs from the reported value 3.4 by more than 10 %

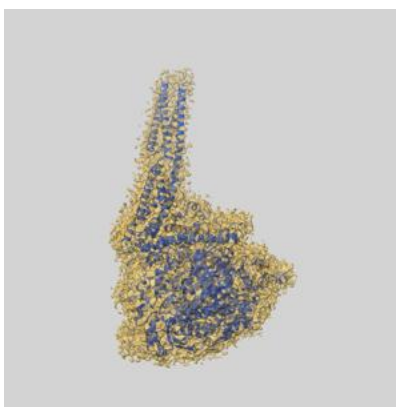
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-36624 and PDB model 8JSN. Per-residue inclusion information can be found in section [3](#) on page [5](#).

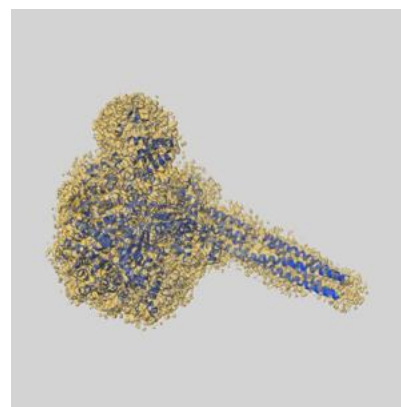
9.1 Map-model overlay [i](#)



X



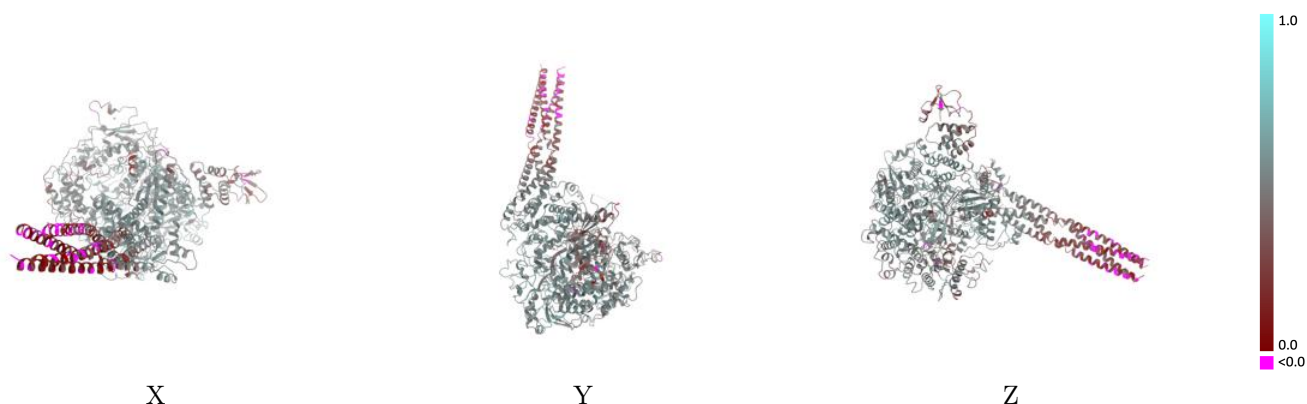
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.004 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](#)

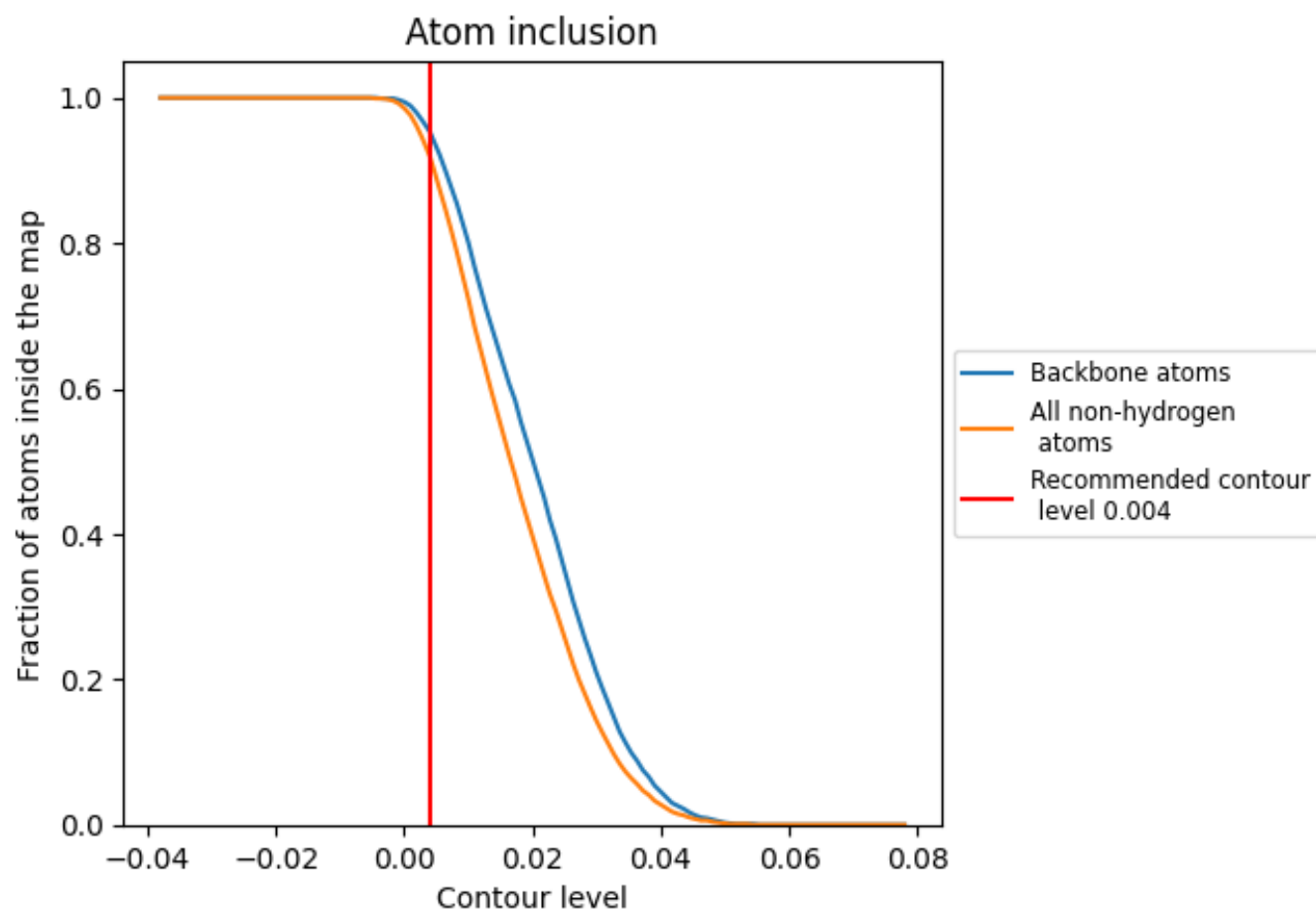


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% 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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9190	0.4750
A	0.9550	0.5210
B	0.8660	0.3880
C	0.8160	0.3450
D	0.7480	0.2480
E	0.6780	0.2320
G	0.8960	0.4720

1.0

0.0

<0.0