



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 05:52 PM UTC

PDB ID : 9GJT / pdb_00009gjt
EMDB ID : EMD-51402
Title : Structure of Nipah Virus RNA Polymerase Complex - Apo state
Authors : Sala, F.; Ditter, K.; Dybkov, O.; Urlaub, H.; Hillen, H.S.
Deposited on : 2024-08-22
Resolution : 2.60 Å(reported)
Based on initial model : .

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

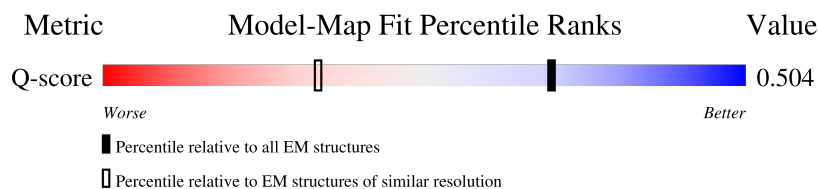
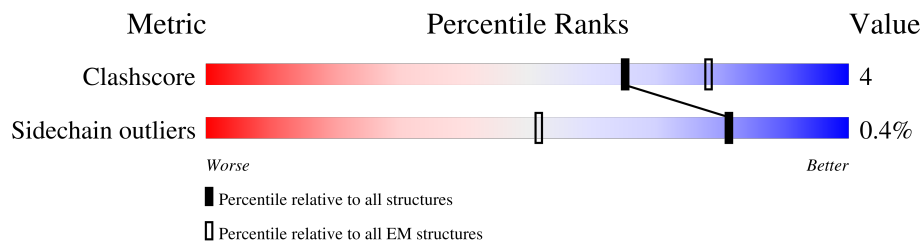
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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	-
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	B	709	
1	C	709	
1	D	709	
1	E	709	
2	A	2246	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14017 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 Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	105	Total	C	N	O	S	0	0
			839	531	138	163	7		
1	D	103	Total	C	N	O	S	0	0
			818	516	135	160	7		
1	E	104	Total	C	N	O	S	0	0
			827	522	137	161	7		
1	B	196	Total	C	N	O	S	0	0
			1572	982	264	318	8		

- Molecule 2 is a protein called RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	1233	Total	C	N	O	S	0	0
			9959	6352	1701	1840	66		

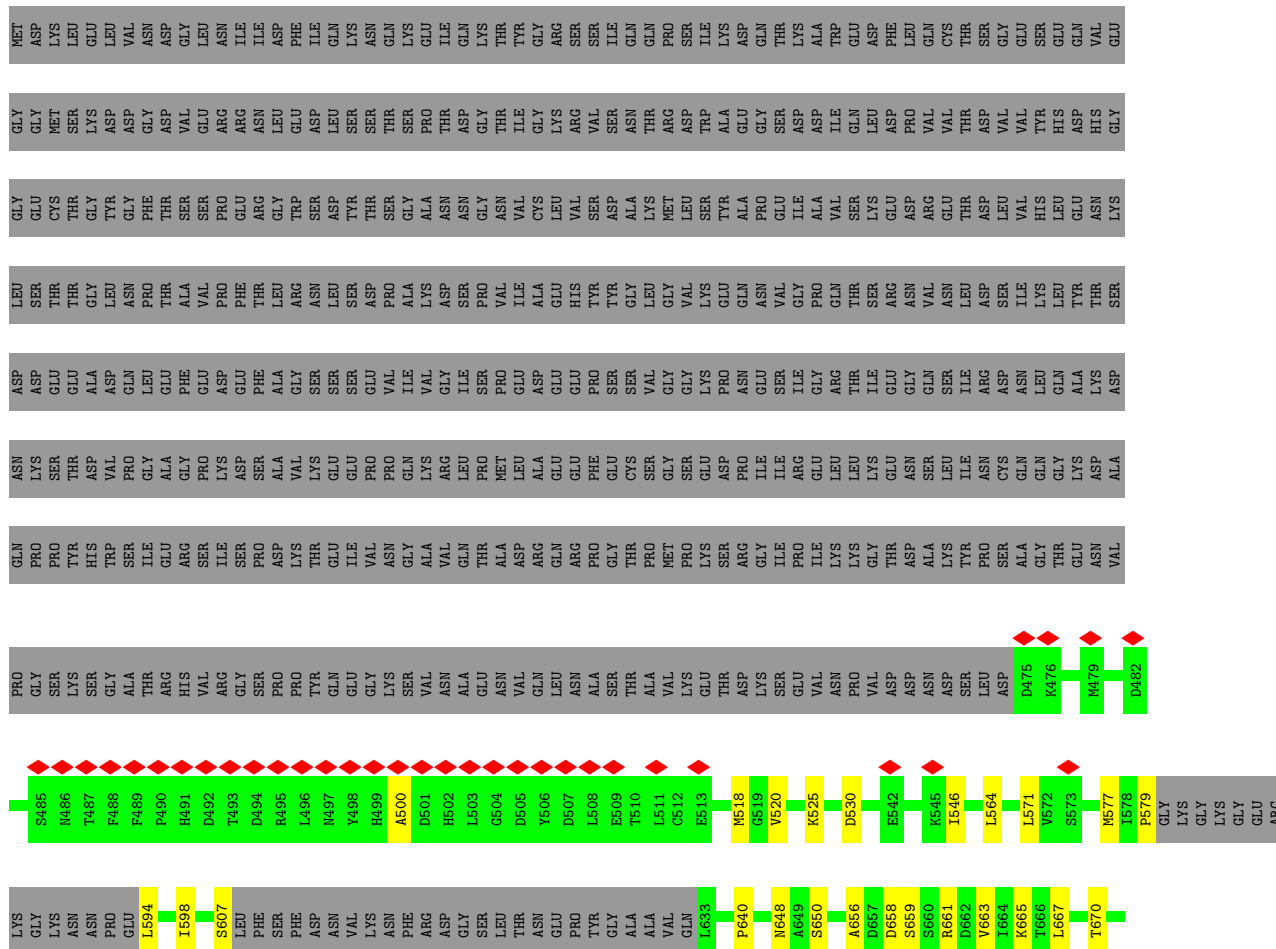
There are 3 discrepancies between the modelled and reference sequences:

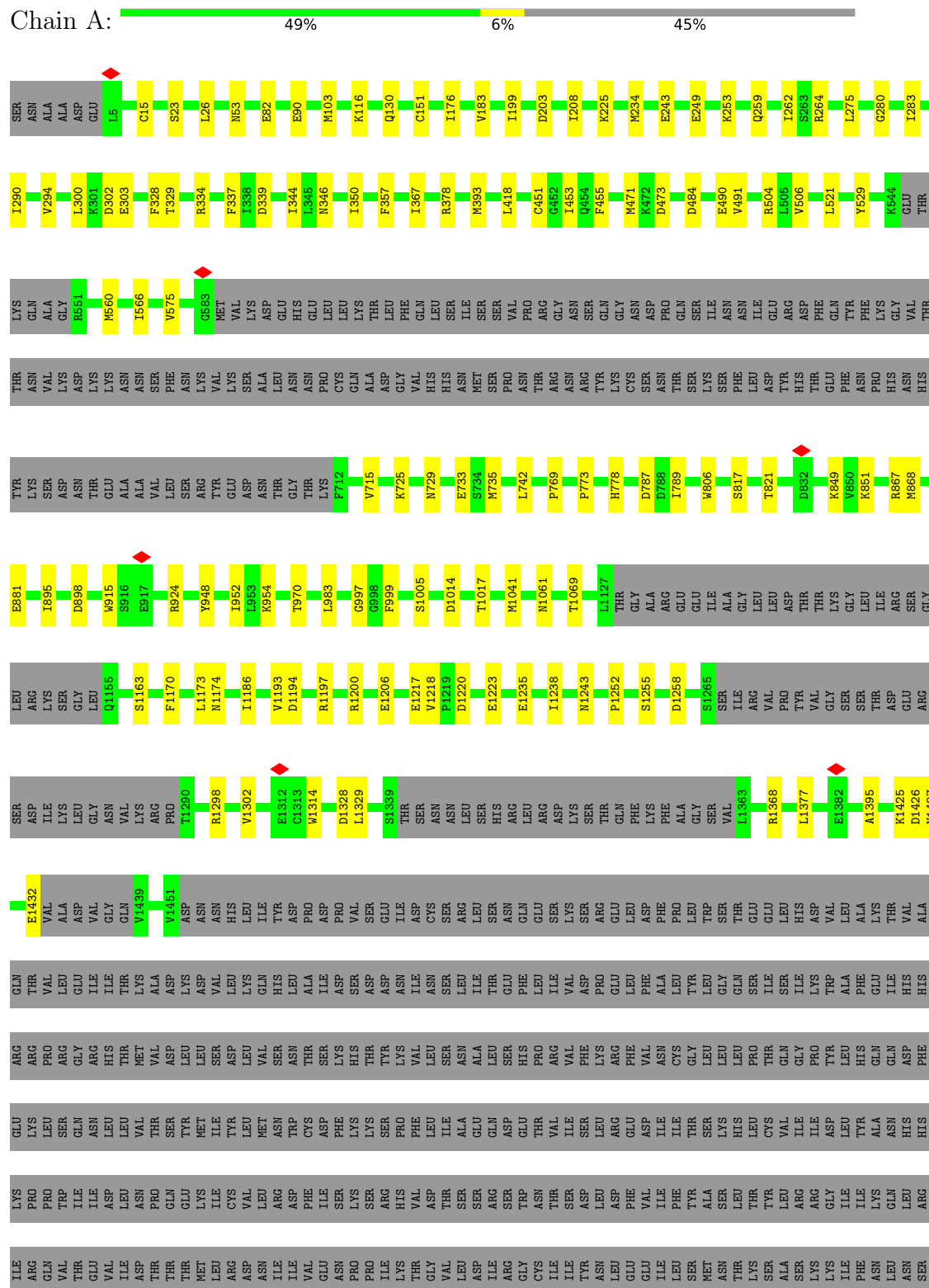
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP Q997F0
A	0	ASN	-	expression tag	UNP Q997F0
A	1	ALA	-	expression tag	UNP Q997F0

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

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	

- Molecule 1: Phosphoprotein





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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	591312	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 ($e^-/\text{\AA}^2$)	48.94	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.184	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0179	Depositor
Map size (Å)	400.32, 400.32, 400.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.834, 0.834, 0.834	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	B	0.14	0/1591	0.31	0/2147
1	C	0.16	0/853	0.34	0/1153
1	D	0.17	0/831	0.30	0/1124
1	E	0.16	0/840	0.29	0/1135
2	A	0.15	0/10165	0.30	0/13738
All	All	0.15	0/14280	0.30	0/19297

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	B	1572	0	1558	24	0
1	C	839	0	839	10	0
1	D	818	0	817	11	0
1	E	827	0	830	12	0
2	A	9959	0	9982	77	0
3	A	2	0	0	0	0
All	All	14017	0	14026	113	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 (113) 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)
2:A:26:LEU:HD22	2:A:234:MET:HE1	1.58	0.85
1:D:532:ARG:NH1	1:E:530:ASP:OD1	2.19	0.75
2:A:53:ASN:ND2	2:A:490:GLU:O	2.20	0.75
2:A:898:ASP:O	2:A:1368:ARG:NH1	2.20	0.74
2:A:881:GLU:N	2:A:881:GLU:OE1	2.24	0.71
1:D:489:PHE:O	1:D:493:THR:OG1	2.06	0.71
2:A:378:ARG:NH2	2:A:787:ASP:O	2.27	0.67
2:A:329:THR:O	2:A:334:ARG:NH2	2.28	0.66
1:B:648:ASN:OD1	1:B:650:SER:OG	2.09	0.66
2:A:1200:ARG:NH1	2:A:1217:GLU:OE2	2.28	0.66
2:A:82:GLU:OE1	2:A:225:LYS:NZ	2.30	0.64
2:A:339:ASP:OD2	1:B:665:LYS:NZ	2.23	0.64
2:A:867:ARG:NH2	1:B:640:PRO:O	2.30	0.64
1:C:543:ILE:HG23	1:B:546:ILE:HD11	1.79	0.63
2:A:90:GLU:N	2:A:90:GLU:OE1	2.32	0.61
2:A:1426:ASP:OD1	2:A:1427:ASN:N	2.34	0.61
1:C:523:SER:OG	1:B:525:LYS:NZ	2.32	0.61
2:A:418:LEU:HD22	2:A:453:ILE:HD11	1.83	0.61
2:A:999:PHE:HE1	2:A:1173:LEU:HD22	1.66	0.60
1:E:532:ARG:NH1	1:B:530:ASP:OD1	2.34	0.60
2:A:999:PHE:CE1	2:A:1173:LEU:HD22	2.38	0.59
2:A:1041:MET:HG3	2:A:1186:ILE:HG21	1.84	0.59
2:A:924:ARG:NH2	2:A:997:GLY:O	2.35	0.58
2:A:357:PHE:CE1	2:A:895:ILE:HD11	2.39	0.58
1:D:560:THR:OG1	1:E:561:ASN:OD1	2.19	0.57
2:A:275:LEU:HD11	2:A:337:PHE:CZ	2.39	0.57
2:A:357:PHE:CZ	2:A:895:ILE:HD11	2.39	0.57
2:A:183:VAL:CG2	2:A:199:ILE:HD12	2.34	0.57
2:A:471:MET:HA	2:A:506:VAL:HG12	1.86	0.56
1:B:656:ALA:N	1:B:691:ASP:OD1	2.39	0.56
2:A:1194:ASP:OD1	2:A:1197:ARG:NH2	2.38	0.56
2:A:243:GLU:OE2	2:A:954:LYS:NZ	2.39	0.56
2:A:1432:GLU:N	2:A:1432:GLU:OE1	2.38	0.56
1:C:517:LEU:HD21	1:B:500:ALA:HA	1.87	0.55
1:B:579:PRO:O	1:B:594:LEU:N	2.39	0.55
2:A:116:LYS:HE3	2:A:983:LEU:HD11	1.88	0.55
2:A:1328:ASP:OD1	2:A:1329:LEU:N	2.40	0.54
1:C:574:MET:O	1:B:598:ILE:HG22	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:659:SER:O	1:B:663:VAL:HG23	2.08	0.54
2:A:521:LEU:HD21	2:A:566:ILE:HG21	1.90	0.54
1:D:536:ILE:O	1:D:540:VAL:HG22	2.08	0.54
2:A:1223:GLU:O	2:A:1425:LYS:NZ	2.39	0.54
2:A:26:LEU:HD22	2:A:234:MET:CE	2.32	0.54
2:A:15:CYS:HG	2:A:915:TRP:CD1	2.27	0.53
2:A:1017:THR:HG21	2:A:1218:VAL:O	2.09	0.53
2:A:328:PHE:O	2:A:334:ARG:NE	2.42	0.53
1:C:516:VAL:O	1:C:520:VAL:HG23	2.09	0.53
1:C:560:THR:HG23	1:D:564:LEU:HD11	1.90	0.52
1:E:518:MET:HE1	1:B:520:VAL:HA	1.92	0.52
2:A:575:VAL:HG21	2:A:742:LEU:HD22	1.91	0.52
1:E:512:CYS:O	1:E:516:VAL:HG23	2.09	0.52
2:A:484:ASP:OD2	2:A:778:HIS:ND1	2.42	0.52
2:A:1217:GLU:N	2:A:1217:GLU:OE1	2.43	0.51
1:B:661:ARG:NH2	1:B:685:LEU:O	2.43	0.51
2:A:473:ASP:OD1	2:A:504:ARG:NE	2.40	0.50
1:E:560:THR:HG23	1:B:564:LEU:CD1	2.42	0.50
1:B:658:ASP:OD1	1:B:659:SER:N	2.44	0.50
2:A:264:ARG:NH1	2:A:344:ILE:O	2.43	0.49
2:A:1252:PRO:O	2:A:1255:SER:OG	2.30	0.49
2:A:1238:ILE:HG22	2:A:1243:ASN:HB3	1.94	0.49
2:A:733:GLU:OE1	2:A:733:GLU:N	2.42	0.49
2:A:849:LYS:NZ	1:B:706:ASP:O	2.44	0.49
1:B:704:ILE:HG13	1:B:709:ILE:HD12	1.95	0.49
2:A:715:VAL:HG11	2:A:851:LYS:HB3	1.94	0.49
1:B:690:ASN:OD1	1:B:691:ASP:N	2.45	0.49
1:E:560:THR:HG23	1:B:564:LEU:HD11	1.94	0.49
1:C:577:MET:HA	1:C:577:MET:HE2	1.95	0.48
2:A:1235:GLU:OE1	2:A:1235:GLU:N	2.43	0.48
2:A:970:THR:HG21	2:A:1163:SER:O	2.13	0.48
1:B:577:MET:HE1	1:B:607:SER:CB	2.44	0.48
1:D:488:PHE:HZ	1:E:524:ILE:HG21	1.79	0.48
2:A:1170:PHE:O	2:A:1174:ASN:ND2	2.46	0.47
2:A:1193:VAL:HG13	2:A:1217:GLU:HB3	1.97	0.47
1:D:479:MET:O	1:D:483:ASP:N	2.49	0.46
1:C:530:ASP:O	1:C:534:ASN:ND2	2.49	0.46
2:A:817:SER:O	2:A:821:THR:HG22	2.15	0.46
2:A:725:LYS:O	2:A:729:ASN:ND2	2.49	0.46
1:B:577:MET:HE1	1:B:607:SER:HB2	1.97	0.45
2:A:1061:ASN:ND2	2:A:1206:GLU:OE2	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1298:ARG:O	2:A:1302:VAL:HG23	2.16	0.45
2:A:350:ILE:HD11	2:A:1258:ASP:HA	1.99	0.45
2:A:280:GLY:O	2:A:283:ILE:HG22	2.17	0.45
2:A:529:TYR:HB2	2:A:560:MET:HE1	1.99	0.45
2:A:176:ILE:HD11	2:A:208:ILE:HD13	1.99	0.44
2:A:103:MET:HE3	2:A:203:ASP:HB2	1.99	0.44
2:A:491:VAL:HG21	2:A:769:PRO:O	2.17	0.44
2:A:948:TYR:CE2	2:A:952:ILE:HD11	2.52	0.44
2:A:249:GLU:OE2	2:A:253:LYS:NZ	2.29	0.44
2:A:575:VAL:HG21	2:A:742:LEU:CD2	2.48	0.44
2:A:130:GLN:NE2	2:A:151:CYS:SG	2.88	0.43
1:C:531:MET:HA	1:C:531:MET:HE2	2.00	0.43
1:E:552:SER:O	1:E:556:VAL:HG23	2.18	0.43
2:A:300:LEU:HD11	1:B:667:LEU:HG	2.00	0.43
2:A:868:MET:HA	2:A:868:MET:HE2	2.00	0.43
2:A:1014:ASP:HB3	2:A:1017:THR:HG22	2.01	0.43
1:D:532:ARG:NH1	1:E:530:ASP:O	2.39	0.42
2:A:346:ASN:ND2	1:B:670:THR:OG1	2.46	0.42
2:A:735:MET:HE3	2:A:806:TRP:HD1	1.84	0.41
2:A:490:GLU:OE1	2:A:490:GLU:N	2.49	0.41
2:A:23:SER:HA	2:A:367:ILE:HD11	2.02	0.41
2:A:393:MET:HE2	2:A:451:CYS:SG	2.59	0.41
1:D:556:VAL:HG11	1:E:557:LEU:HB3	2.02	0.41
2:A:302:ASP:OD1	2:A:303:GLU:N	2.54	0.41
2:A:773:PRO:HB3	2:A:789:ILE:HD11	2.03	0.41
2:A:259:GLN:HG2	2:A:262:ILE:HD12	2.03	0.41
1:C:520:VAL:HG22	1:B:518:MET:HE3	2.02	0.41
2:A:26:LEU:CD2	2:A:234:MET:HE1	2.41	0.41
2:A:418:LEU:HD21	2:A:455:PHE:CE1	2.56	0.41
2:A:1005:SER:OG	2:A:1220:ASP:OD1	2.37	0.41
1:D:491:HIS:ND1	1:D:492:ASP:OD1	2.52	0.40
2:A:290:ILE:O	2:A:294:VAL:HG23	2.21	0.40
2:A:1377:LEU:HD21	2:A:1395:ALA:HB3	2.03	0.40
1:D:532:ARG:NH2	1:E:534:ASN:OD1	2.49	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.

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	B	182/625 (29%)	181 (100%)	1 (0%)	81	92
1	C	98/625 (16%)	96 (98%)	2 (2%)	48	74
1	D	96/625 (15%)	96 (100%)	0	100	100
1	E	97/625 (16%)	95 (98%)	2 (2%)	47	73
2	A	1112/2047 (54%)	1110 (100%)	2 (0%)	87	95
All	All	1585/4547 (35%)	1578 (100%)	7 (0%)	81	93

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	531	MET
1	C	533	LEU
1	E	514	GLU
1	E	529	LEU
2	A	1069	THR
2	A	1314	TRP
1	B	571	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	522	ASN
1	D	502	HIS
1	D	539	GLN
1	D	561	ASN

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Mol	Chain	Res	Type
2	A	131	ASN
2	A	139	GLN
2	A	365	HIS
2	A	427	HIS
2	A	876	ASN
2	A	1164	HIS
1	B	502	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are 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.

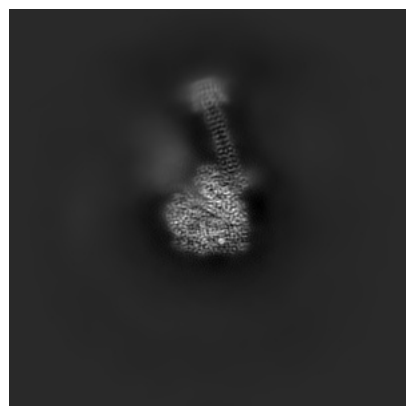
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51402. These allow visual inspection of the internal detail of the map and identification of artifacts.

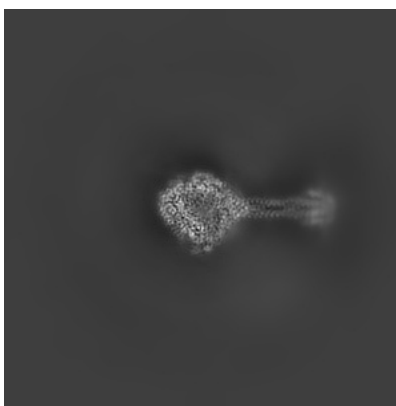
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

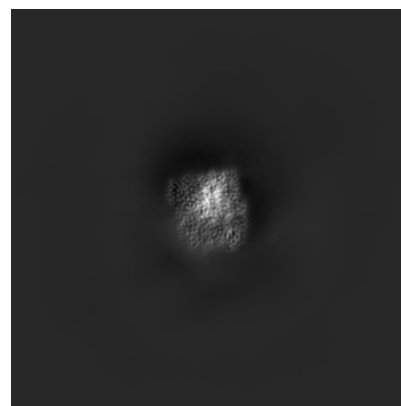
6.1.1 Primary map



X

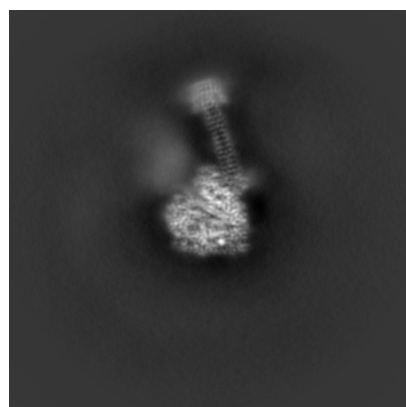


Y

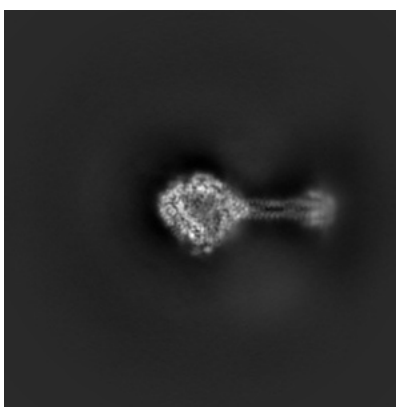


Z

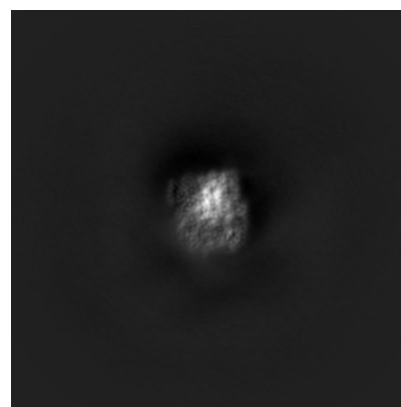
6.1.2 Raw map



X



Y

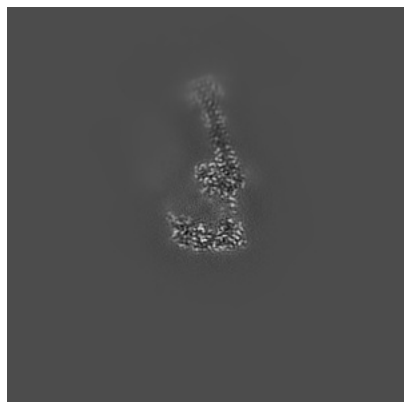


Z

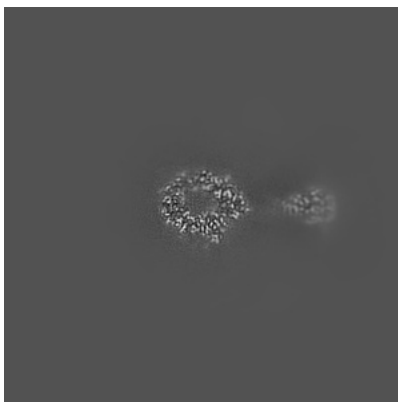
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

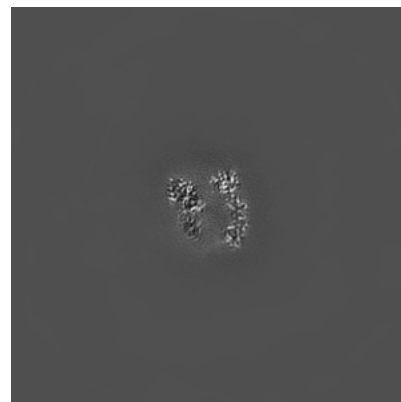
6.2.1 Primary map



X Index: 240

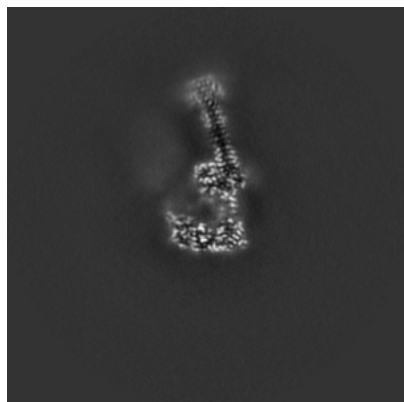


Y Index: 240

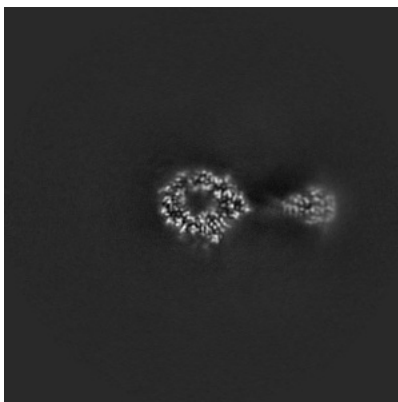


Z Index: 240

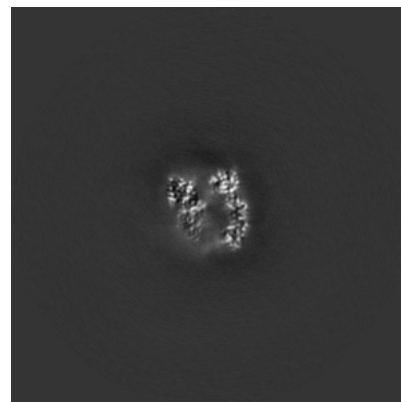
6.2.2 Raw map



X Index: 240



Y Index: 240

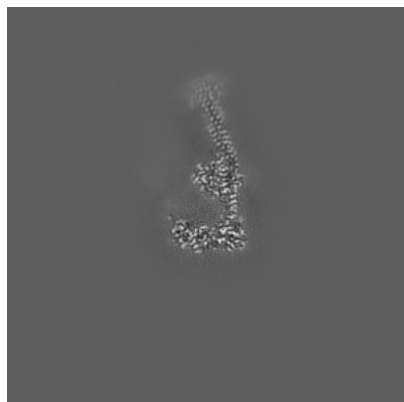


Z Index: 240

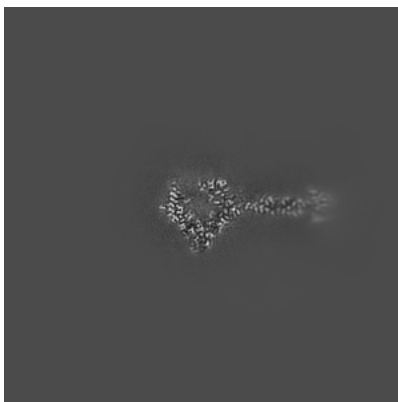
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

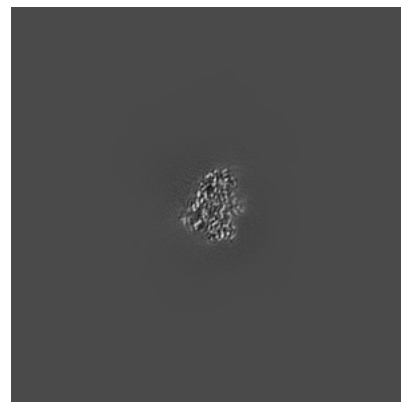
6.3.1 Primary map



X Index: 244

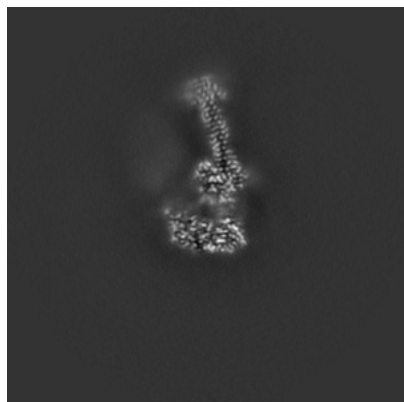


Y Index: 253

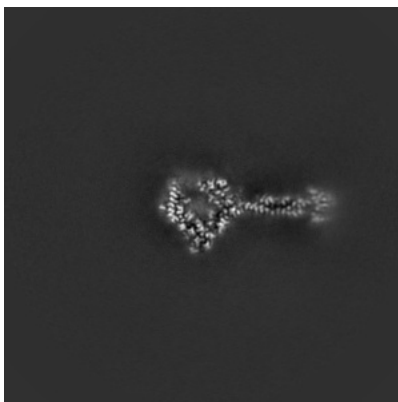


Z Index: 208

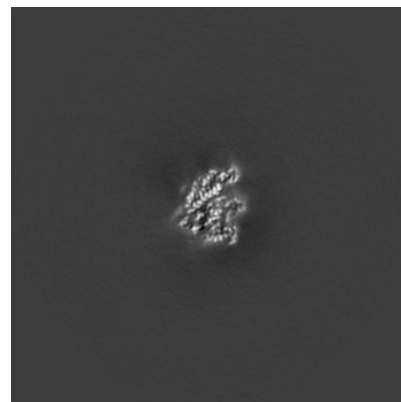
6.3.2 Raw map



X Index: 237



Y Index: 253



Z Index: 212

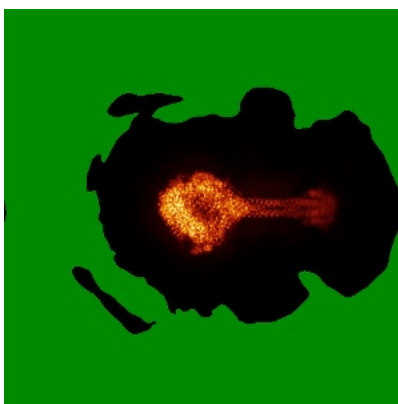
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

6.4.1 Primary map



X

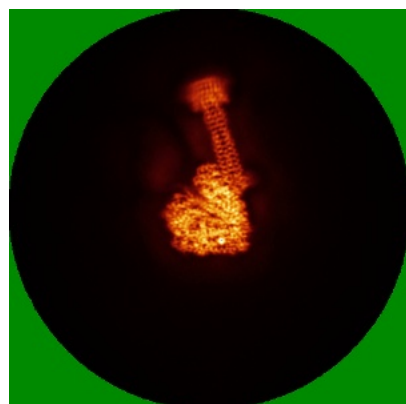


Y

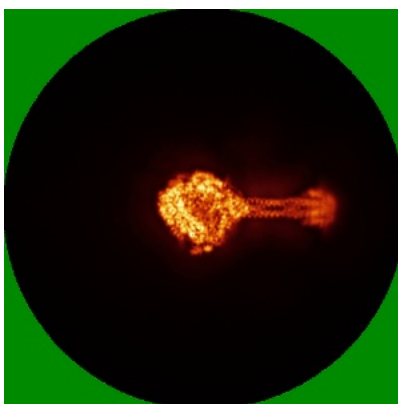


Z

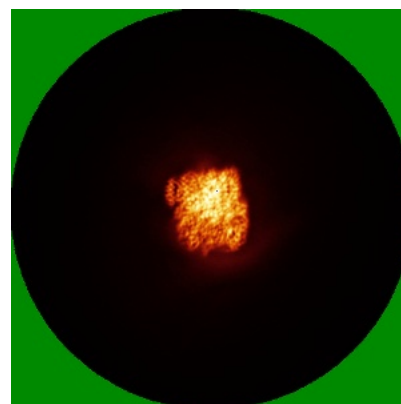
6.4.2 Raw map



X



Y

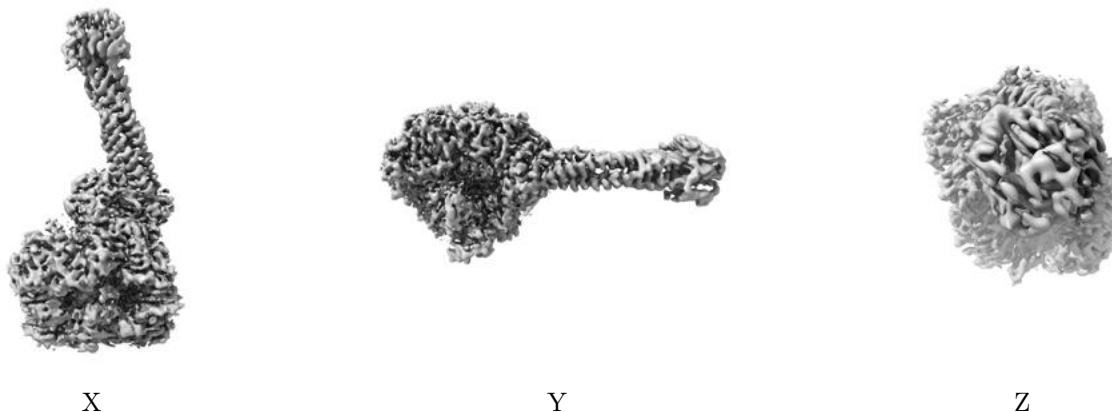


Z

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.

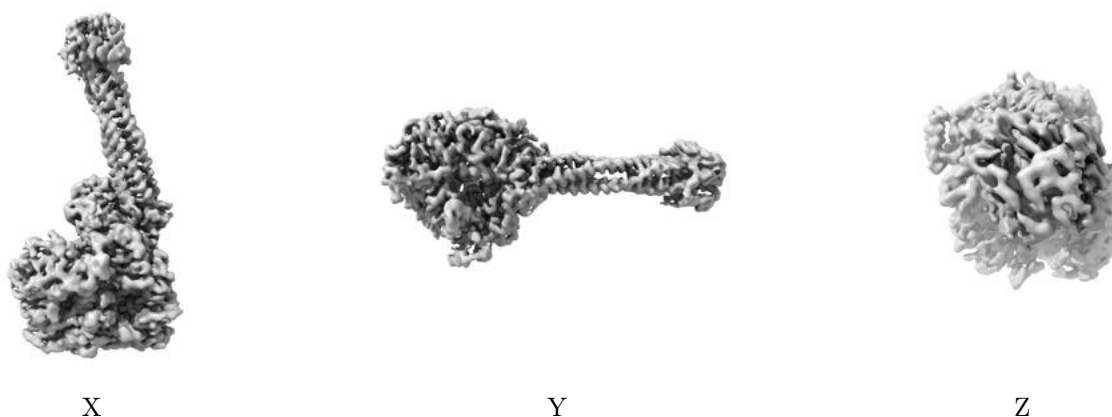
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0179. 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.

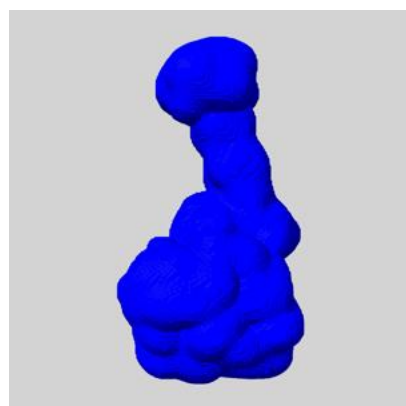
6.6 Mask visualisation [i](#)

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

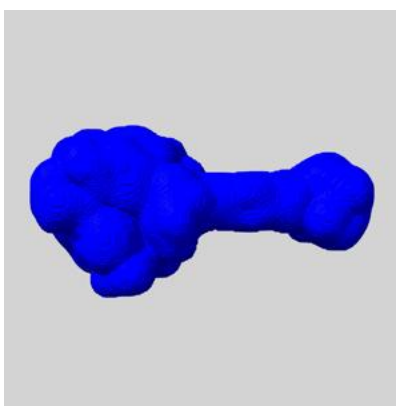
A mask typically either:

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

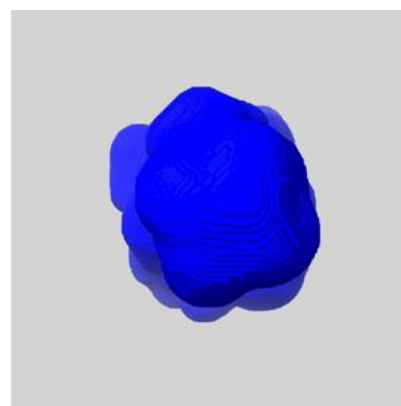
6.6.1 emd_51402_msk_1.map [i](#)



X



Y

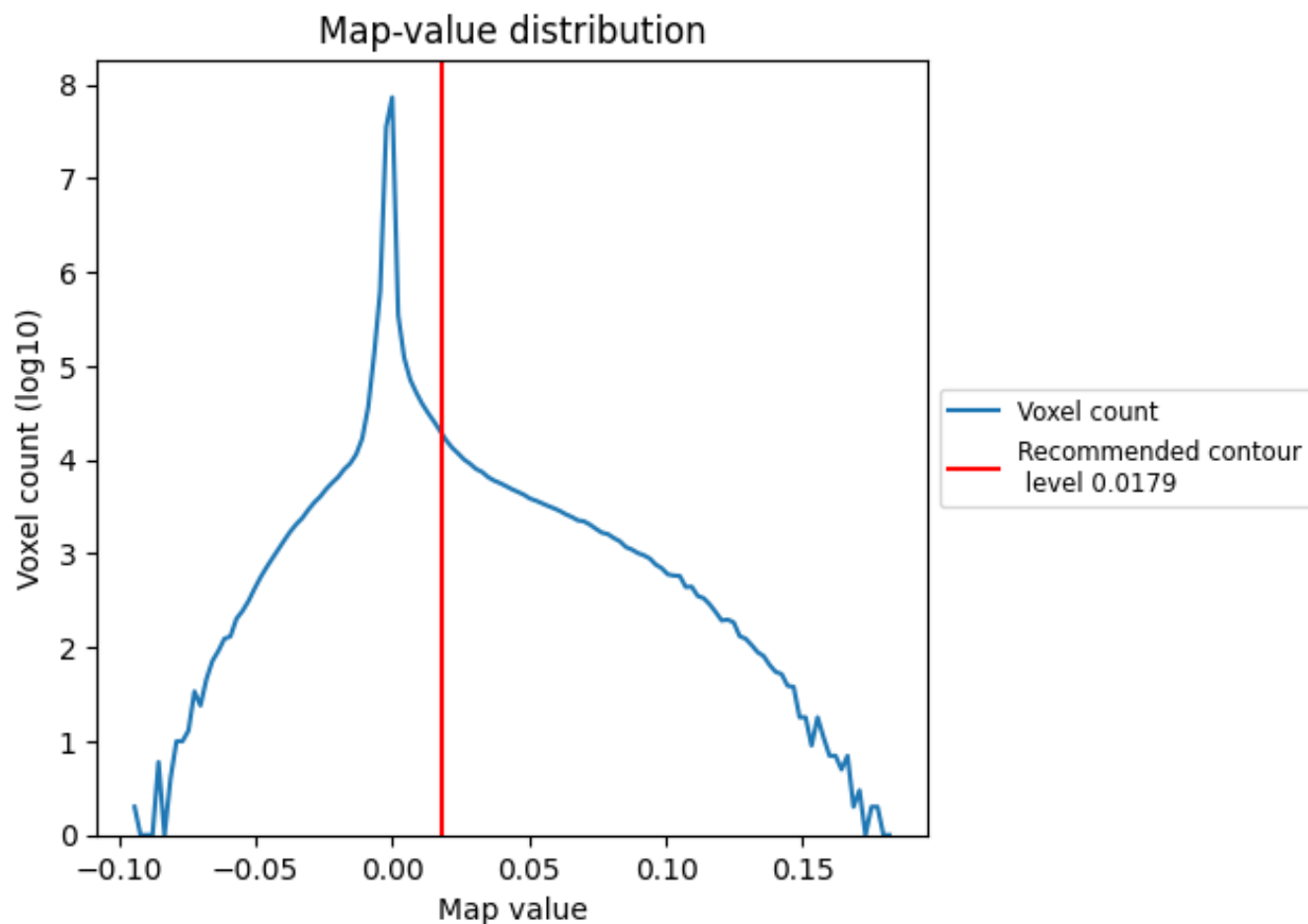


Z

7 Map analysis [i](#)

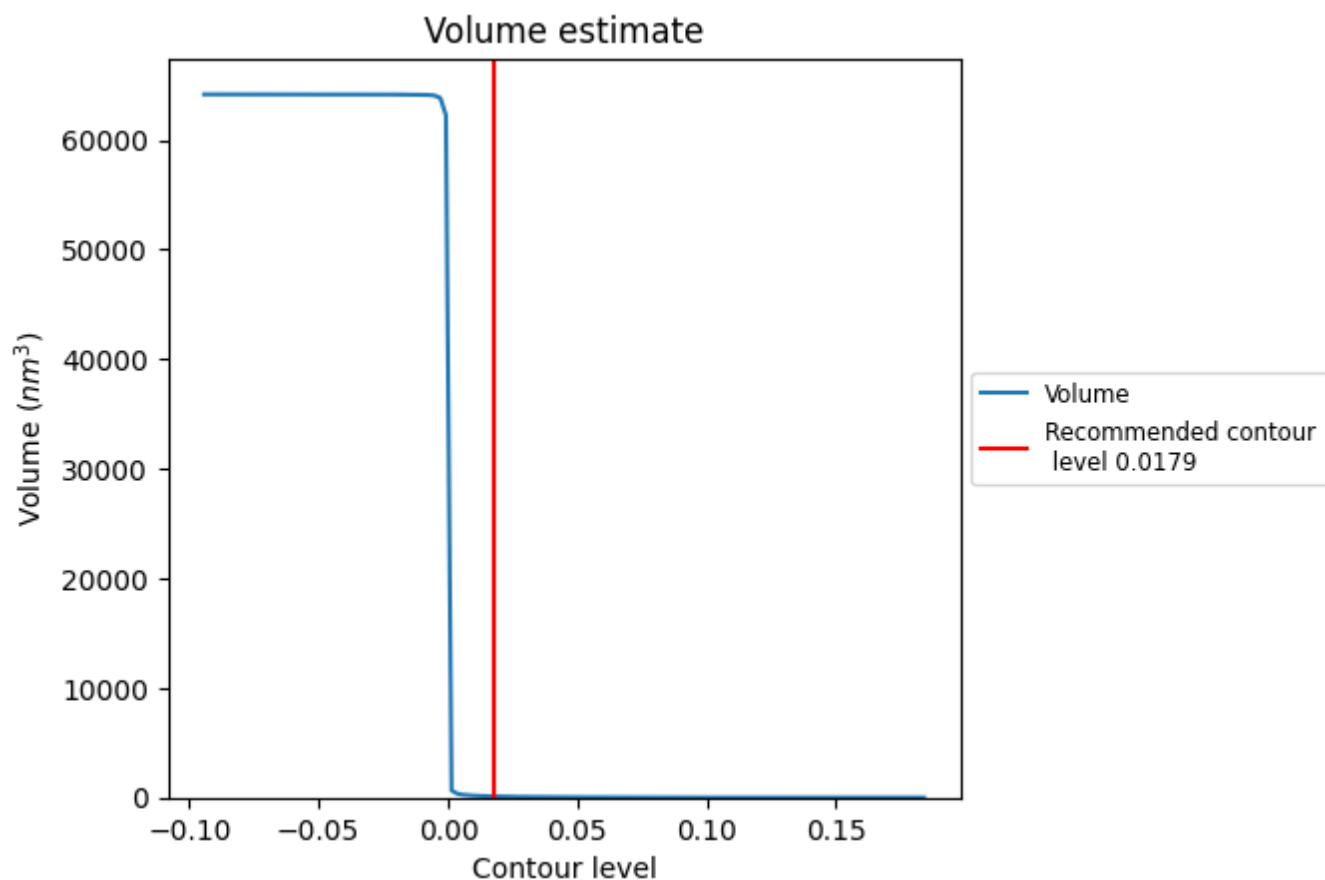
This section contains the results of statistical analysis of the map.

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.

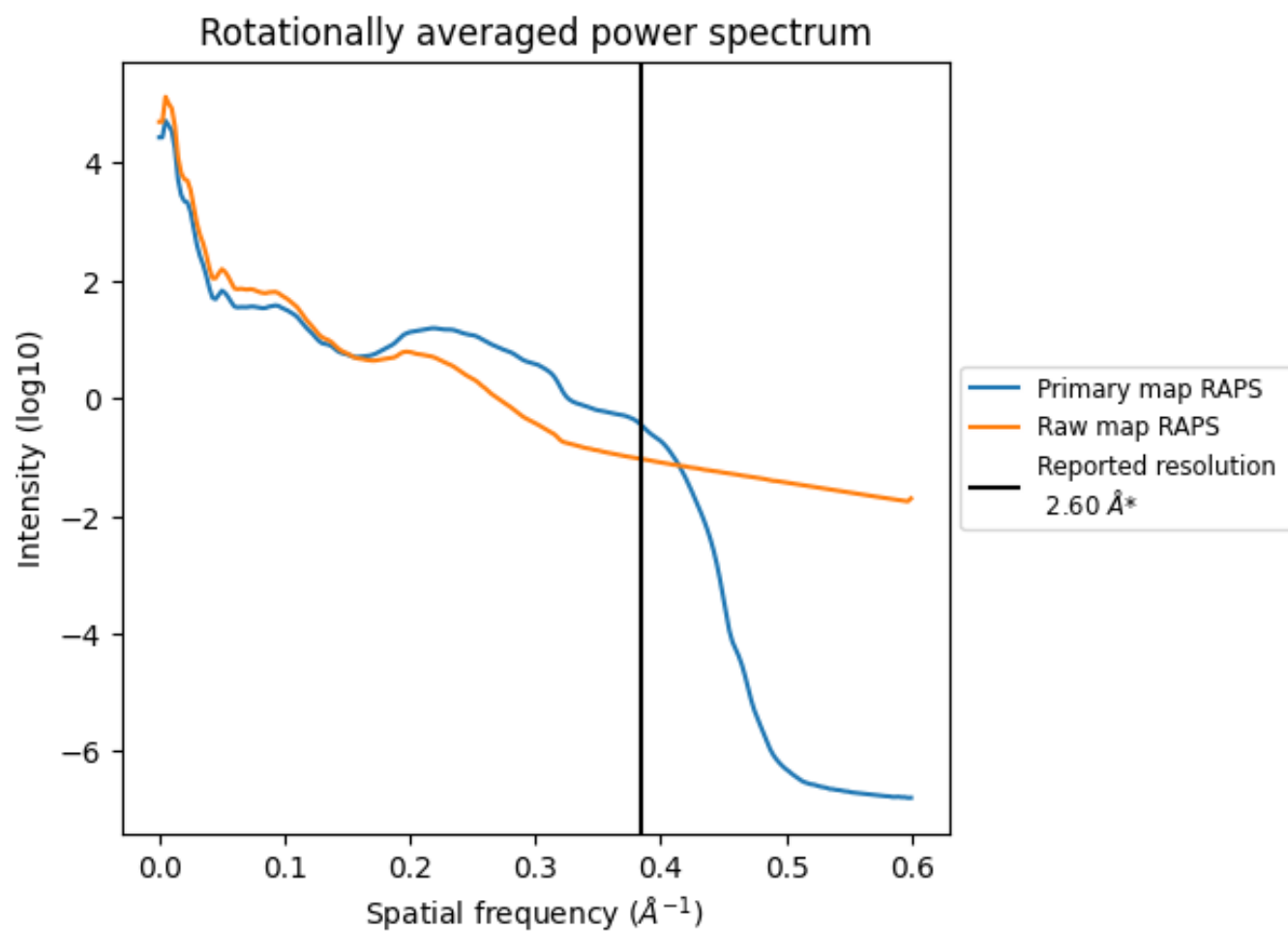
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 105 nm^3 ; this corresponds to an approximate mass of 95 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 ⓘ

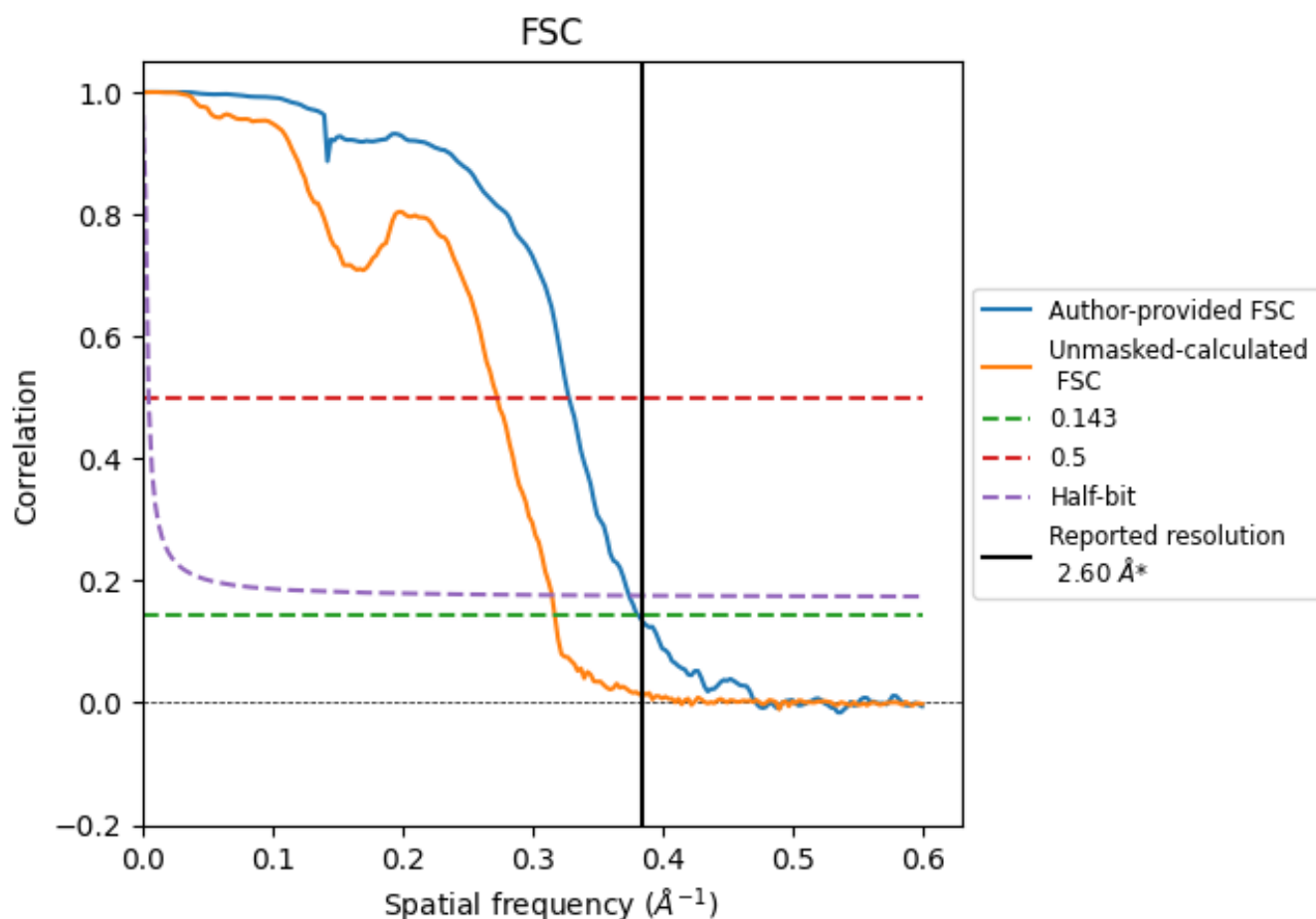


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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

8.2 Resolution estimates [i](#)

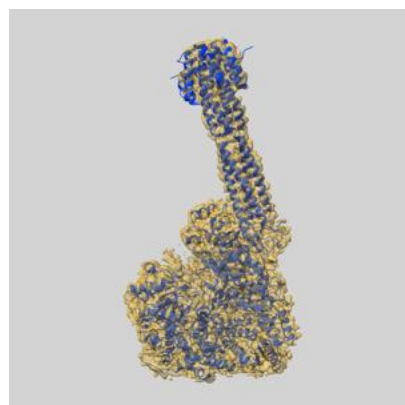
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.62	3.05	2.67
Unmasked-calculated*	3.15	3.67	3.18

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

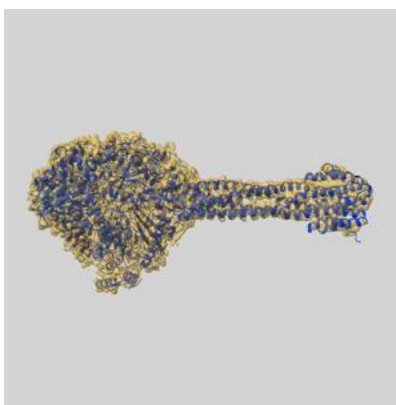
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51402 and PDB model 9GJT. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

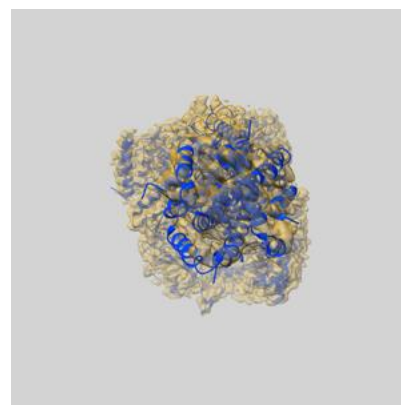
9.1 Map-model overlay [i](#)



X



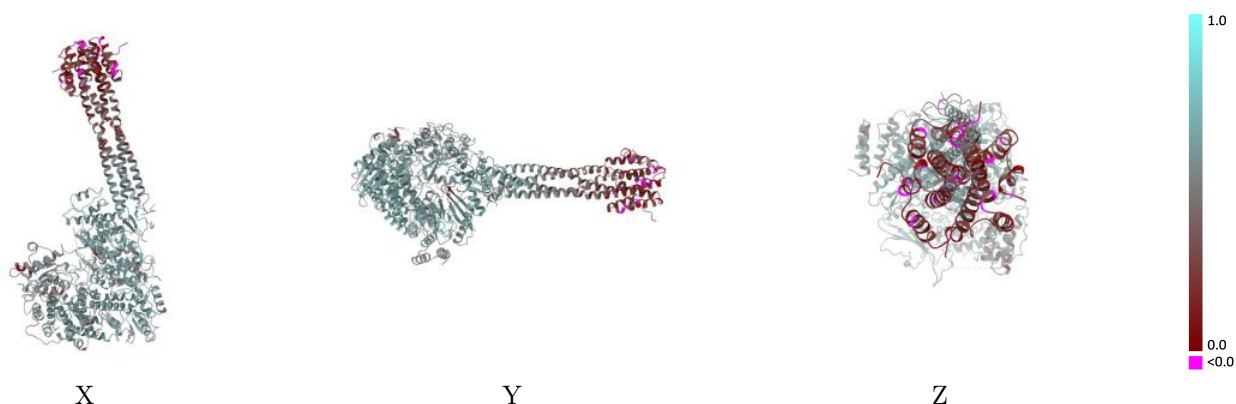
Y



Z

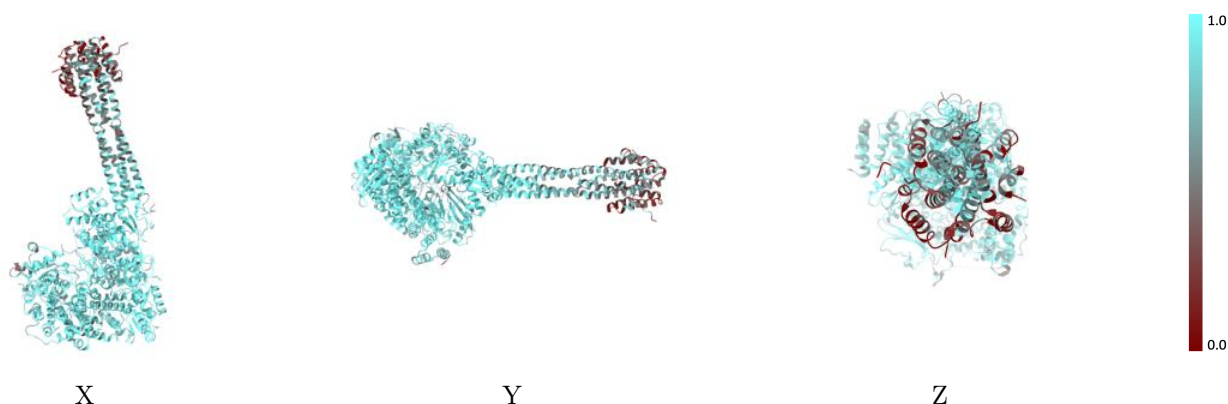
The images above show the 3D surface view of the map at the recommended contour level 0.0179 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



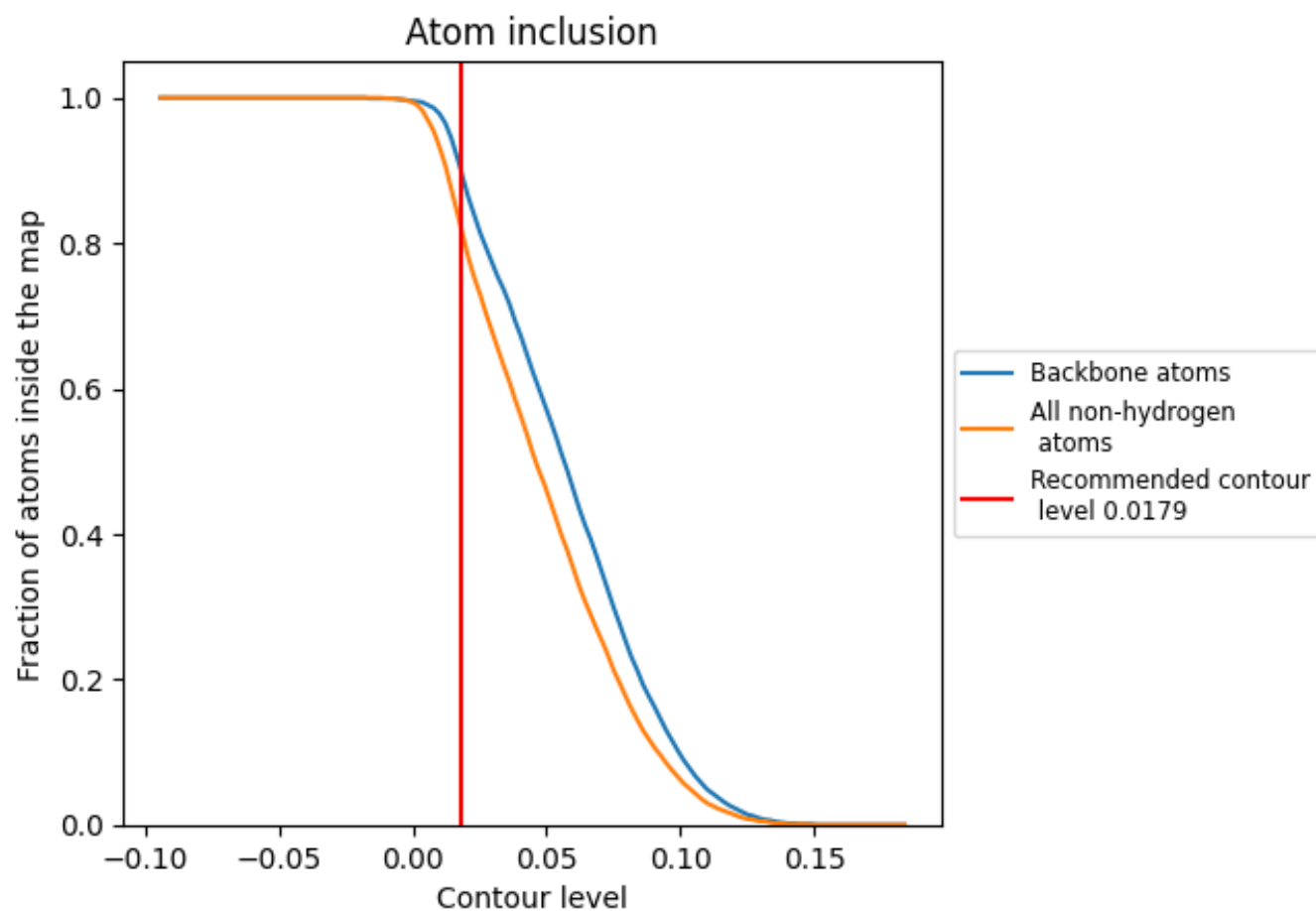
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0179).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 82% 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 (0.0179) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8230	0.5040
A	0.9110	0.5660
B	0.6600	0.4020
C	0.5450	0.3020
D	0.6220	0.3280
E	0.5710	0.3370

