



Full wwPDB EM Validation Report ⓘ

Oct 6, 2025 – 10:37 AM EDT

PDB ID : 9N0T / pdb_00009n0t
EMDB ID : EMD-48793
Title : 3.37A Bornavirus L-P complex (after incubation with RNA/NTP) (state 3)
Authors : Liu, B.; Yang, G.; Wang, D.
Deposited on : 2025-01-24
Resolution : 3.37 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:

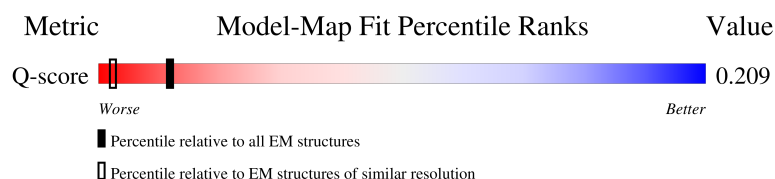
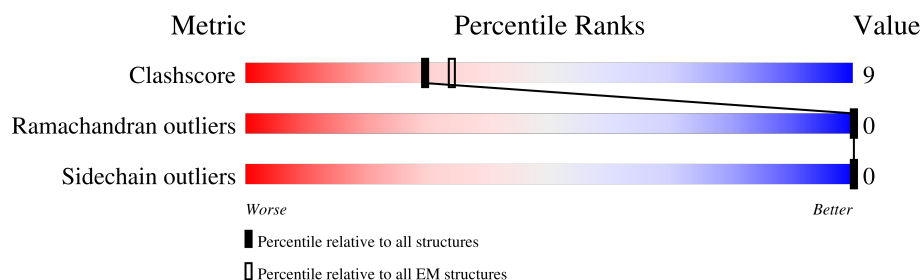
EMDB validation analysis : 0.0.1.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

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 3.37 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	14287 (2.87 - 3.87)

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	1711	
2	B	201	
2	C	201	
2	D	201	

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Mol	Chain	Length	Quality of chain
2	E	201	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14005 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1605	Total	C	N	O	S	0	0
			12665	8151	2153	2288	73		

There are 5 discrepancies between the modelled and reference sequences:

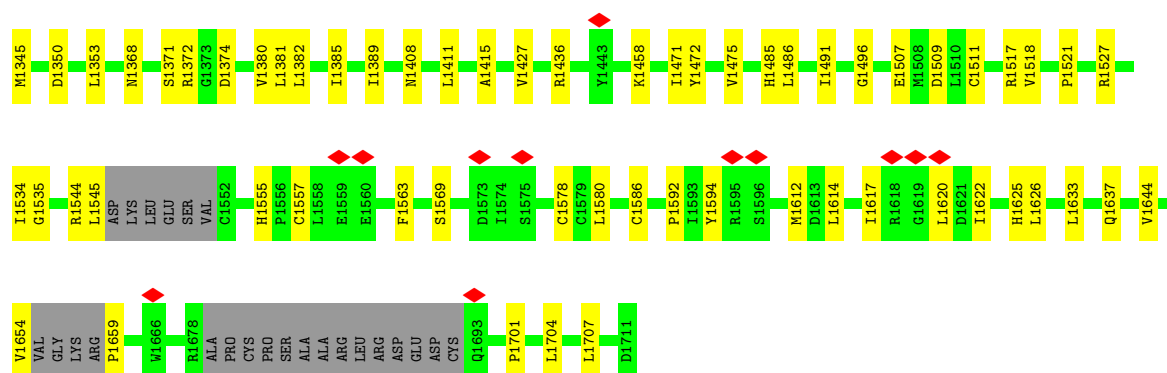
Chain	Residue	Modelled	Actual	Comment	Reference
A	6	SER	ARG	conflict	UNP A0A6C6W7Z6
A	423	PHE	TYR	conflict	UNP A0A6C6W7Z6
A	1297	ILE	VAL	conflict	UNP A0A6C6W7Z6
A	1583	ALA	SER	conflict	UNP A0A6C6W7Z6
A	1629	PHE	LEU	conflict	UNP A0A6C6W7Z6

- Molecule 2 is a protein called P protein.

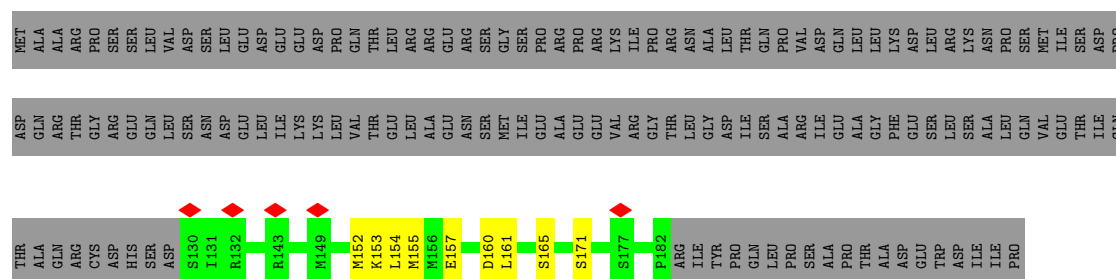
Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	53	Total	C	N	O	S	0	0
			402	255	66	74	7		
2	C	40	Total	C	N	O	S	0	0
			320	200	53	61	6		
2	D	40	Total	C	N	O	S	0	0
			320	200	53	61	6		
2	E	37	Total	C	N	O	S	0	0
			296	187	48	55	6		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

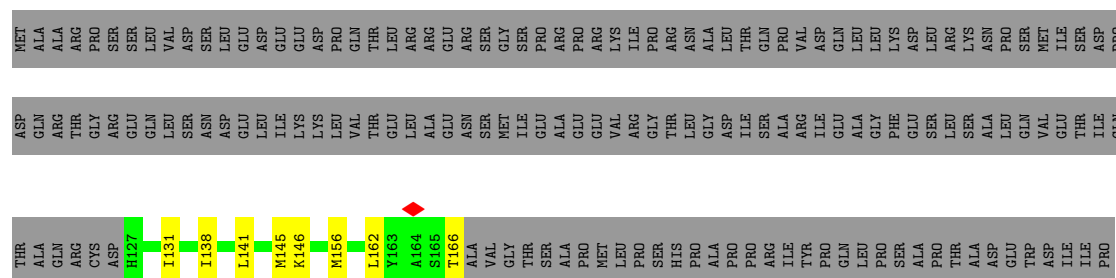
Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	



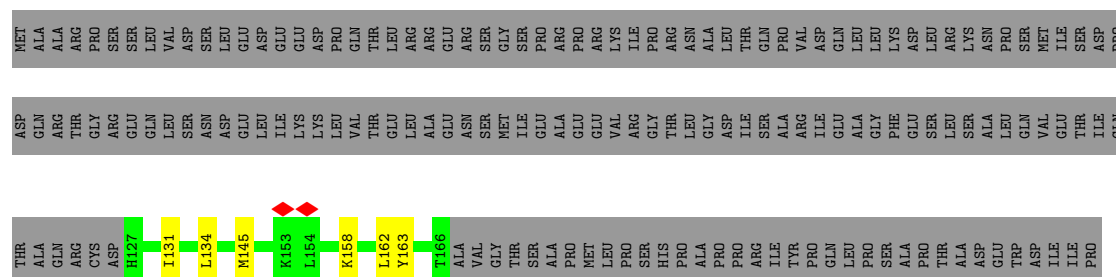
• Molecule 2: P protein



• Molecule 2: P protein



• Molecule 2: P protein



• Molecule 2: P protein



MET	ASP	GLN	ARG	THR	GLY	ARG	SER	SER	LEU	VAL	ASP	SER	SER	ASN	GLU	ASP	GLU	GLY	ASP	PRO	GLN	THR	LEU	ARG	ARG	GLU	ARG	SER	ARG	SER	GLY	SER	PRO	ARG	PRO	ARG	LYS	PRO	ILE	PRO	ARG	ASN	ALA	LEU	THR	GLN	PRO	VAL	ASP	GLN	LEU	LYS	LYS	LEU	ARG	LEU	ASP	LEU	ARG	LYS	ASN	PRO	SER	MET	ILE	SER	ASP	PRO	GLN
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ASP	GLN	ARG	THR	GLY	ARG	SER	GLU	GLN	LEU	SER	ASN	ASP	GLU	LEU	ILE	LYS	LYS	LEU	VAL	THR	GLU	LEU	ALA	ALA	GLU	ASN	SER	MET	ILE	GLU	ALA	GLU	VAL	GLY	ARG	GLY	THR	LEU	GLY	ILE	ASP	SER	ALA	ARG	ILE	GLU	ALA	PHE	GLY	SER	SER	LEU	LEU	ALA	LEU	GLN	VAL	GLU	THR	ILE	GLN
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THR	ALA	GLN	ARG	CYS	ASP	HIS	SER	ASP	S130	L134	R143	S144	M145	E150	L154	M155	Y163	T166	ALA	VAL	GLY	THR	SER	ALA	PRO	MET	LEU	PRO	SER	HIS	PRO	ALA	PRO	ALA	ARG	ILE	TYR	PRO	GLN	LEU	PRO	SER	ALA	THR	ALA	ASP	GLU	TRP	ASP	ILE	ILE	PRO
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	107976	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 ($e^-/\text{\AA}^2$)	50.5	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	0.285	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	255.01599, 255.01599, 255.01599	wwPDB
Map dimensions	254, 254, 254	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.004, 1.004, 1.004	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	0.25	0/12955	0.59	10/17602 (0.1%)
2	B	0.26	0/408	0.69	2/549 (0.4%)
2	C	0.27	0/321	0.56	0/425
2	D	0.22	0/321	0.46	0/425
2	E	0.30	0/296	0.58	0/391
All	All	0.25	0/14301	0.59	12/19392 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	563	GLN	N-CA-C	-20.23	88.08	113.97
1	A	564	ALA	CA-C-N	-6.33	113.24	119.76
1	A	564	ALA	C-N-CA	-6.33	113.24	119.76
1	A	454	ASN	CA-C-N	6.23	124.17	120.24
1	A	454	ASN	C-N-CA	6.23	124.17	120.24
2	B	171	SER	CA-C-N	5.57	128.84	122.83
2	B	171	SER	C-N-CA	5.57	128.84	122.83
1	A	572	GLN	N-CA-C	5.43	118.12	111.82
1	A	572	GLN	CA-C-N	5.14	128.13	120.31
1	A	572	GLN	C-N-CA	5.14	128.13	120.31
1	A	1594	TYR	CA-C-N	5.14	127.88	120.38
1	A	1594	TYR	C-N-CA	5.14	127.88	120.38

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	12665	0	12828	242	0
2	B	402	0	430	32	0
2	C	320	0	340	9	0
2	D	320	0	340	7	0
2	E	296	0	324	4	0
3	A	2	0	0	0	0
All	All	14005	0	14262	255	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 9.

All (255) 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:330:LEU:HD22	1:A:568:ARG:NH2	1.44	1.29
1:A:566:ILE:HG12	1:A:634:LEU:CD2	1.65	1.24
1:A:330:LEU:CD2	1:A:568:ARG:HH21	1.49	1.22
1:A:566:ILE:HG12	1:A:634:LEU:HD22	1.39	0.98
1:A:563:GLN:NE2	1:A:584:CYS:HB2	1.80	0.97
1:A:568:ARG:HD2	2:B:160:ASP:HB2	1.44	0.96
1:A:568:ARG:NH1	2:B:161:LEU:HD11	1.82	0.94
1:A:568:ARG:CD	2:B:160:ASP:HB2	2.03	0.88
1:A:568:ARG:CZ	2:B:161:LEU:HD11	2.06	0.85
1:A:322:LEU:HB3	1:A:562:LEU:HB2	1.58	0.84
1:A:568:ARG:HG2	2:B:160:ASP:HB3	1.62	0.80
1:A:566:ILE:CG1	1:A:634:LEU:CD2	2.56	0.80
1:A:568:ARG:NH1	2:B:161:LEU:CG	2.48	0.77
1:A:566:ILE:HG12	1:A:634:LEU:HD23	1.63	0.76
1:A:568:ARG:NH1	2:B:161:LEU:CD1	2.48	0.76
1:A:568:ARG:NH1	2:B:161:LEU:HD21	2.00	0.75
1:A:567:CYS:HB2	1:A:580:PHE:HB3	1.69	0.74
1:A:568:ARG:CZ	2:B:161:LEU:CD1	2.65	0.73
1:A:568:ARG:HD3	2:B:161:LEU:HG	1.70	0.73
1:A:330:LEU:HB2	1:A:568:ARG:HH22	1.53	0.73
1:A:334:ARG:HE	1:A:385:VAL:HG12	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:568:ARG:CD	2:B:160:ASP:CB	2.70	0.69
2:C:162:LEU:HD13	2:D:162:LEU:HB3	1.74	0.68
1:A:568:ARG:HD2	2:B:160:ASP:CB	2.22	0.66
1:A:793:LEU:HD13	1:A:977:LEU:HD21	1.78	0.65
1:A:1485:HIS:CE1	1:A:1509:ASP:OD1	2.49	0.65
1:A:1485:HIS:CD2	1:A:1511:CYS:SG	2.91	0.64
2:B:155:MET:HE2	2:C:156:MET:HE2	1.80	0.63
1:A:568:ARG:HD2	2:B:157:GLU:HA	1.79	0.63
1:A:330:LEU:HB2	1:A:568:ARG:NH2	2.12	0.63
1:A:568:ARG:NH1	2:B:161:LEU:CD2	2.61	0.63
1:A:1027:SER:HB2	1:A:1527:ARG:HH21	1.62	0.63
1:A:578:TYR:H	1:A:581:ARG:HH21	1.47	0.63
1:A:333:PHE:CD2	1:A:566:ILE:HG23	2.34	0.63
1:A:351:VAL:HB	1:A:365:ARG:HD2	1.80	0.63
1:A:1202:THR:HB	1:A:1527:ARG:HH22	1.63	0.63
1:A:104:MET:HG2	1:A:1192:SER:HB2	1.81	0.62
1:A:472:ARG:HD2	1:A:589:PHE:HB3	1.80	0.62
1:A:566:ILE:CG1	1:A:634:LEU:HD23	2.28	0.62
1:A:32:LEU:HB2	1:A:299:ILE:HD11	1.81	0.62
1:A:568:ARG:HA	1:A:581:ARG:HD2	1.81	0.62
1:A:396:PRO:HD3	1:A:455:ILE:HG21	1.83	0.61
1:A:568:ARG:HH11	2:B:161:LEU:HD21	1.65	0.60
2:C:162:LEU:HD22	2:D:162:LEU:HD13	1.83	0.60
1:A:563:GLN:O	1:A:634:LEU:HD13	2.01	0.60
1:A:322:LEU:O	1:A:562:LEU:HD12	2.02	0.60
1:A:45:LEU:HB2	1:A:48:HIS:HD2	1.66	0.59
1:A:330:LEU:HD22	1:A:568:ARG:HH21	0.58	0.59
1:A:556:ASN:O	1:A:559:ARG:NH2	2.36	0.59
2:D:145:MET:HG2	2:E:145:MET:HE2	1.85	0.59
1:A:1314:ARG:HA	1:A:1317:ILE:HD12	1.85	0.58
1:A:323:LEU:HD21	2:B:165:SER:HB2	1.85	0.58
1:A:85:ILE:HG12	1:A:116:LEU:HD13	1.85	0.58
1:A:1408:ASN:O	1:A:1411:LEU:HB3	2.02	0.58
1:A:553:SER:HB3	1:A:556:ASN:HB2	1.85	0.58
1:A:551:TYR:HB2	1:A:554:TRP:HB2	1.86	0.58
1:A:563:GLN:HE22	1:A:584:CYS:HB2	1.64	0.58
1:A:1036:LEU:HD13	1:A:1211:LYS:HD3	1.86	0.58
1:A:350:PRO:HG2	1:A:387:LEU:HD13	1.87	0.57
1:A:148:PRO:HA	1:A:156:LEU:O	2.04	0.57
1:A:320:GLN:NE2	2:C:166:THR:O	2.37	0.56
1:A:538:THR:HB	1:A:544:SER:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:243:LEU:HB3	1:A:277:LEU:HD22	1.87	0.56
1:A:568:ARG:NH1	2:B:161:LEU:HG	2.19	0.56
1:A:805:THR:HG22	1:A:807:ALA:H	1.70	0.56
1:A:876:ARG:HH22	1:A:962:VAL:HG11	1.69	0.56
1:A:27:LEU:HD21	1:A:31:LEU:HD11	1.88	0.56
1:A:1002:ARG:HD3	1:A:1010:LEU:HD12	1.88	0.56
1:A:316:LEU:HD13	1:A:692:ASN:H	1.70	0.56
1:A:333:PHE:CD2	1:A:566:ILE:CG2	2.90	0.55
1:A:819:ASP:HB2	1:A:1015:MET:HE3	1.89	0.55
1:A:1471:ILE:HG12	1:A:1534:ILE:HD12	1.87	0.55
1:A:1544:ARG:HE	1:A:1569:SER:HA	1.72	0.55
1:A:351:VAL:O	1:A:365:ARG:NH1	2.40	0.55
1:A:876:ARG:HB3	1:A:878:ILE:HG13	1.89	0.55
1:A:334:ARG:HG2	1:A:569:GLN:HE22	1.72	0.55
1:A:563:GLN:HE22	1:A:584:CYS:CA	2.20	0.55
1:A:388:ARG:HE	1:A:575:ASN:HB2	1.72	0.54
1:A:735:LEU:O	1:A:955:GLN:NE2	2.39	0.54
1:A:417:GLU:OE2	1:A:492:LYS:NZ	2.37	0.54
1:A:563:GLN:NE2	1:A:584:CYS:CB	2.64	0.54
1:A:568:ARG:CD	2:B:161:LEU:HG	2.36	0.54
1:A:1701:PRO:HD2	1:A:1704:LEU:HD12	1.89	0.54
1:A:798:PRO:HD3	1:A:804:PRO:HA	1.89	0.54
1:A:747:THR:HG23	1:A:806:PRO:HA	1.90	0.54
1:A:877:GLN:HB3	1:A:881:TRP:HB2	1.90	0.54
1:A:1041:TYR:OH	1:A:1183:PHE:O	2.24	0.54
1:A:1458:LYS:HG2	1:A:1486:LEU:HD11	1.89	0.54
1:A:296:PHE:HE2	1:A:480:GLU:HB2	1.73	0.54
2:C:138:ILE:HD13	2:C:141:LEU:HD12	1.90	0.53
1:A:1622:ILE:HG23	1:A:1625:HIS:HB2	1.90	0.53
1:A:146:ILE:HG22	1:A:158:PHE:HB2	1.91	0.53
1:A:1345:MET:O	1:A:1372:ARG:NH2	2.40	0.53
1:A:1371:SER:H	1:A:1374:ASP:HB3	1.74	0.52
1:A:30:PRO:HB2	1:A:299:ILE:HD13	1.92	0.52
1:A:568:ARG:NH2	2:B:161:LEU:HD11	2.24	0.52
1:A:333:PHE:CE2	1:A:566:ILE:CG2	2.92	0.52
1:A:568:ARG:CZ	2:B:161:LEU:HG	2.39	0.52
1:A:330:LEU:HD13	1:A:568:ARG:NH2	2.25	0.52
1:A:407:ILE:HD13	1:A:495:LEU:HD13	1.91	0.52
1:A:568:ARG:CG	2:B:160:ASP:HB3	2.36	0.52
1:A:292:LYS:HE2	1:A:482:GLU:H	1.74	0.51
1:A:187:LYS:O	1:A:191:HIS:ND1	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:LEU:HG	2:B:153:LYS:HE3	1.91	0.51
1:A:563:GLN:HE22	1:A:584:CYS:CB	2.24	0.51
1:A:1048:ARG:H	1:A:1051:HIS:HB2	1.75	0.51
1:A:330:LEU:CD2	1:A:568:ARG:NH2	2.32	0.50
1:A:1327:ALA:HA	1:A:1620:LEU:HD22	1.93	0.50
2:C:162:LEU:HA	2:D:163:TYR:HE1	1.76	0.50
1:A:38:PHE:O	1:A:43:SER:OG	2.23	0.50
1:A:259:VAL:HG21	1:A:696:GLU:HB3	1.94	0.50
1:A:1288:THR:N	1:A:1293:GLU:OE1	2.45	0.50
1:A:1475:VAL:HG21	1:A:1534:ILE:HG22	1.93	0.50
1:A:693:LEU:HD22	1:A:698:CYS:HB2	1.94	0.49
1:A:337:PHE:HD2	1:A:386:ILE:HG12	1.77	0.49
1:A:563:GLN:CD	1:A:584:CYS:HB2	2.37	0.49
2:C:131:ILE:HD11	2:D:131:ILE:HD12	1.94	0.49
1:A:561:GLU:HA	2:B:165:SER:HA	1.94	0.49
1:A:1288:THR:HG22	1:A:1340:THR:HA	1.94	0.49
1:A:292:LYS:HD2	1:A:481:LYS:H	1.76	0.49
1:A:459:LEU:O	1:A:463:TYR:N	2.42	0.49
1:A:481:LYS:HD2	1:A:728:VAL:H	1.77	0.49
1:A:568:ARG:HE	2:B:157:GLU:HB3	1.77	0.49
1:A:1472:TYR:HB2	1:A:1535:GLY:HA3	1.93	0.49
1:A:568:ARG:HH11	2:B:161:LEU:CD2	2.23	0.49
1:A:591:THR:HG23	1:A:617:VAL:HA	1.93	0.49
1:A:610:GLU:HG3	1:A:616:ALA:HA	1.95	0.49
1:A:187:LYS:HG2	1:A:191:HIS:CE1	2.48	0.48
1:A:565:PRO:C	1:A:567:CYS:H	2.20	0.48
1:A:568:ARG:HH12	2:B:161:LEU:HD11	1.68	0.48
1:A:864:THR:HA	1:A:1002:ARG:HH21	1.78	0.48
1:A:1052:LEU:HD23	1:A:1154:LEU:HD13	1.96	0.48
1:A:1382:LEU:HD22	1:A:1389:ILE:HG21	1.95	0.48
1:A:418:TYR:HB2	1:A:431:LEU:HD21	1.96	0.48
1:A:312:MET:HA	1:A:556:ASN:HB3	1.95	0.47
1:A:532:LEU:HD23	1:A:535:LEU:HD12	1.96	0.47
1:A:798:PRO:HD2	1:A:824:GLN:HE22	1.79	0.47
1:A:84:LEU:HD11	1:A:776:TYR:HB2	1.96	0.47
1:A:1055:ARG:HD3	1:A:1060:LEU:HD11	1.97	0.47
1:A:217:ASP:O	1:A:221:SER:HB3	2.14	0.47
1:A:914:LEU:HB3	1:A:925:MET:HG2	1.95	0.47
1:A:792:THR:HG22	1:A:831:LEU:HD21	1.96	0.47
1:A:795:LEU:HD12	1:A:831:LEU:HD13	1.96	0.47
1:A:330:LEU:CG	1:A:568:ARG:NH2	2.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:921:ARG:NH2	1:A:1218:ASP:O	2.38	0.47
1:A:354:LEU:HD13	1:A:383:LYS:HB3	1.96	0.47
1:A:566:ILE:HG12	1:A:634:LEU:HD21	1.82	0.47
1:A:187:LYS:HG2	1:A:191:HIS:HE1	1.79	0.46
1:A:1633:LEU:HD11	1:A:1707:LEU:HD22	1.97	0.46
1:A:332:ILE:HB	1:A:641:ILE:HD11	1.97	0.46
1:A:491:SER:HB3	1:A:493:GLN:HE22	1.81	0.46
1:A:568:ARG:CZ	2:B:161:LEU:CG	2.92	0.46
1:A:192:LEU:O	1:A:196:SER:HB3	2.15	0.46
1:A:314:VAL:O	1:A:559:ARG:NH1	2.49	0.46
1:A:444:VAL:HG11	1:A:943:LEU:HD23	1.96	0.46
2:B:161:LEU:HA	2:B:161:LEU:HD23	1.70	0.46
1:A:1545:LEU:HD12	1:A:1563:PHE:HB3	1.97	0.46
1:A:282:VAL:HG13	1:A:718:VAL:HG12	1.98	0.46
1:A:482:GLU:HB3	1:A:488:ARG:HH21	1.81	0.46
1:A:577:GLY:HA3	2:E:154:LEU:HD13	1.97	0.46
1:A:841:LEU:HD11	1:A:844:ARG:HH11	1.80	0.46
1:A:1368:ASN:HA	1:A:1592:PRO:HG3	1.98	0.45
1:A:920:LEU:HD12	1:A:920:LEU:HA	1.78	0.45
1:A:1622:ILE:HG22	1:A:1626:LEU:HB2	1.98	0.45
1:A:162:LEU:HD23	1:A:175:THR:HA	1.98	0.45
1:A:1329:LEU:HB3	1:A:1381:LEU:HD21	1.97	0.45
1:A:446:ALA:HA	1:A:449:ASP:HB2	1.99	0.45
1:A:58:ARG:HE	1:A:170:THR:HG22	1.81	0.45
1:A:568:ARG:HH11	1:A:568:ARG:HG3	1.81	0.45
1:A:353:LEU:HA	1:A:362:LYS:HE2	1.99	0.45
1:A:418:TYR:HE1	1:A:596:ASP:H	1.64	0.45
1:A:1496:GLY:HA2	1:A:1527:ARG:HA	1.99	0.45
1:A:1555:HIS:CE1	1:A:1557:CYS:HB3	2.52	0.45
1:A:1704:LEU:HD23	1:A:1707:LEU:HD12	1.99	0.45
1:A:354:LEU:HD22	1:A:383:LYS:HD2	1.99	0.45
1:A:385:VAL:HG13	2:B:154:LEU:HD22	1.98	0.45
1:A:65:TYR:OH	1:A:296:PHE:O	2.31	0.45
1:A:414:TRP:NE1	1:A:606:GLY:O	2.44	0.44
1:A:1039:ILE:HD12	1:A:1182:VAL:HG11	1.99	0.44
1:A:1086:LEU:HB3	1:A:1118:LYS:HE3	1.99	0.44
1:A:1301:GLN:HA	1:A:1353:LEU:HD11	2.00	0.44
1:A:189:ARG:HH21	1:A:294:TRP:HA	1.82	0.44
1:A:909:LEU:HD21	1:A:1229:GLN:HB2	1.99	0.44
1:A:361:ILE:HG21	1:A:384:VAL:HG21	2.00	0.44
1:A:805:THR:HB	1:A:808:THR:HG23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1511:CYS:HB3	1:A:1586:CYS:SG	2.58	0.44
1:A:1165:LEU:HA	1:A:1169:SER:HB3	2.00	0.44
1:A:145:ASP:HB3	1:A:159:VAL:HG12	2.00	0.44
1:A:292:LYS:NZ	1:A:297:PRO:HD2	2.33	0.44
1:A:556:ASN:HA	1:A:621:THR:HG21	1.99	0.44
1:A:1276:ILE:HD13	1:A:1329:LEU:HG	1.99	0.44
1:A:302:VAL:O	1:A:306:ARG:NH1	2.51	0.44
1:A:449:ASP:OD2	1:A:451:ARG:NH1	2.51	0.44
1:A:772:LEU:HD23	1:A:775:LEU:HD12	1.99	0.44
1:A:319:PRO:HA	1:A:322:LEU:HD12	2.00	0.43
1:A:549:LEU:HD11	1:A:682:LEU:HD13	2.00	0.43
1:A:1111:MET:HE3	1:A:1111:MET:HB3	1.83	0.43
1:A:431:LEU:HB3	1:A:434:PRO:HG3	2.00	0.43
1:A:452:LEU:HD12	1:A:495:LEU:HD23	2.00	0.43
1:A:560:PRO:HD3	1:A:620:LYS:HB3	1.99	0.43
1:A:562:LEU:HD13	1:A:689:ALA:HA	2.00	0.43
1:A:1380:VAL:HG13	1:A:1381:LEU:HD12	2.00	0.43
1:A:1654:VAL:HA	1:A:1659:PRO:HA	2.00	0.43
1:A:444:VAL:HA	1:A:447:LEU:HB3	2.00	0.43
1:A:1164:TYR:CZ	1:A:1169:SER:HB2	2.53	0.43
1:A:1262:TYR:HE1	1:A:1314:ARG:HH21	1.67	0.43
1:A:301:MET:O	1:A:305:SER:OG	2.32	0.43
1:A:45:LEU:HB2	1:A:48:HIS:CD2	2.52	0.42
1:A:354:LEU:HB3	1:A:357:CYS:HB2	2.00	0.42
1:A:228:ASP:O	1:A:232:ILE:HG13	2.20	0.42
1:A:425:LYS:HD3	1:A:425:LYS:HA	1.88	0.42
1:A:593:ILE:HG21	1:A:608:PRO:HG2	2.01	0.42
1:A:330:LEU:CB	1:A:568:ARG:NH2	2.81	0.42
1:A:475:VAL:HG22	1:A:593:ILE:HD11	2.01	0.42
2:C:145:MET:HB3	2:C:145:MET:HE3	1.81	0.42
1:A:578:TYR:N	1:A:581:ARG:HH21	2.14	0.42
1:A:1372:ARG:NH1	1:A:1507:GLU:O	2.52	0.42
1:A:1637:GLN:HB3	1:A:1644:VAL:HG22	2.02	0.42
1:A:234:LYS:HB2	1:A:485:VAL:HG13	2.02	0.41
1:A:334:ARG:HD3	1:A:384:VAL:O	2.19	0.41
1:A:813:PHE:HD2	1:A:1188:LEU:HD13	1.84	0.41
1:A:1301:GLN:NE2	1:A:1350:ASP:OD1	2.53	0.41
1:A:1612:MET:HE2	1:A:1612:MET:HB3	1.86	0.41
1:A:1382:LEU:HA	1:A:1385:ILE:HG12	2.02	0.41
1:A:329:LEU:HD22	1:A:637:CYS:HB3	2.01	0.41
1:A:568:ARG:HD3	2:B:160:ASP:HB2	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1099:VAL:HG22	1:A:1415:ALA:HB2	2.01	0.41
1:A:184:ASP:HA	1:A:187:LYS:HB3	2.02	0.41
1:A:1113:ARG:HH12	1:A:1231:ARG:HD2	1.85	0.41
1:A:1436:ARG:HA	1:A:1578:CYS:HB2	2.03	0.41
1:A:1491:ILE:HB	1:A:1518:VAL:HA	2.01	0.41
1:A:684:LYS:HE2	1:A:684:LYS:HB3	1.87	0.41
1:A:402:VAL:HG12	1:A:943:LEU:HD21	2.02	0.41
1:A:1614:LEU:HA	1:A:1617:ILE:HG12	2.03	0.41
1:A:36:VAL:HG11	1:A:62:SER:HB3	2.02	0.41
1:A:174:MET:HB2	1:A:178:HIS:HB2	2.03	0.41
1:A:1104:ASP:HB3	1:A:1107:LEU:HB3	2.03	0.41
2:B:152:MET:HE2	2:B:152:MET:HB3	1.95	0.41
2:D:158:LYS:O	2:E:163:TYR:OH	2.36	0.41
1:A:553:SER:O	1:A:557:GLY:N	2.53	0.41
2:D:134:LEU:HD11	2:E:134:LEU:HD12	2.02	0.41
1:A:235:SER:HA	1:A:238:PRO:HD2	2.02	0.40
1:A:635:THR:HA	1:A:638:TRP:CE2	2.57	0.40
1:A:308:GLN:HG2	1:A:489:PHE:CD2	2.57	0.40
1:A:334:ARG:HG2	1:A:569:GLN:NE2	2.35	0.40
1:A:351:VAL:HG11	1:A:361:ILE:HG22	2.04	0.40
1:A:841:LEU:HD12	1:A:841:LEU:HA	1.96	0.40
1:A:1027:SER:HB2	1:A:1527:ARG:NH2	2.34	0.40
1:A:1427:VAL:HG11	1:A:1517:ARG:HH22	1.87	0.40
1:A:1580:LEU:HD23	1:A:1580:LEU:HA	1.94	0.40
2:C:146:LYS:HA	2:C:146:LYS:HD3	1.86	0.40
1:A:322:LEU:HD22	1:A:562:LEU:HB3	2.02	0.40
1:A:844:ARG:HG3	1:A:980:THR:HA	2.04	0.40
1:A:1040:ILE:HG22	1:A:1206:LEU:H	1.85	0.40
1:A:1166:HIS:CD2	1:A:1521:PRO:HD3	2.56	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	1587/1711 (93%)	1504 (95%)	83 (5%)	0	100	100
2	B	51/201 (25%)	48 (94%)	3 (6%)	0	100	100
2	C	38/201 (19%)	38 (100%)	0	0	100	100
2	D	38/201 (19%)	38 (100%)	0	0	100	100
2	E	35/201 (17%)	35 (100%)	0	0	100	100
All	All	1749/2515 (70%)	1663 (95%)	86 (5%)	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	1402/1495 (94%)	1402 (100%)	0	100	100
2	B	47/179 (26%)	47 (100%)	0	100	100
2	C	38/179 (21%)	38 (100%)	0	100	100
2	D	38/179 (21%)	38 (100%)	0	100	100
2	E	35/179 (20%)	35 (100%)	0	100	100
All	All	1560/2211 (71%)	1560 (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 (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	ASN
1	A	160	GLN
1	A	248	HIS
1	A	308	GLN
1	A	363	ASN
1	A	556	ASN
1	A	563	GLN
1	A	785	GLN

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Mol	Chain	Res	Type
1	A	1023	HIS
1	A	1025	HIS
1	A	1106	HIS
1	A	1166	HIS
1	A	1178	HIS
1	A	1452	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are 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.

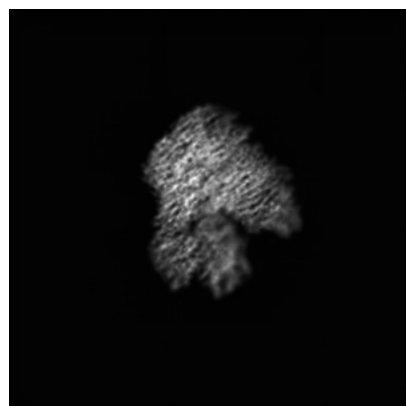
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48793. These allow visual inspection of the internal detail of the map and identification of artifacts.

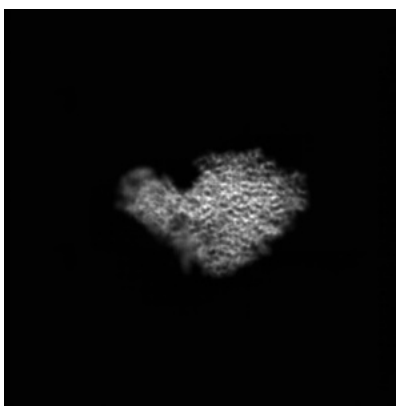
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

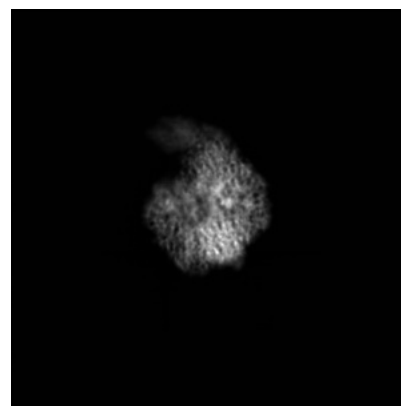
6.1.1 Primary map



X

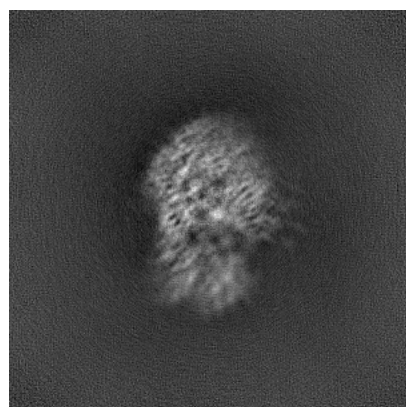


Y

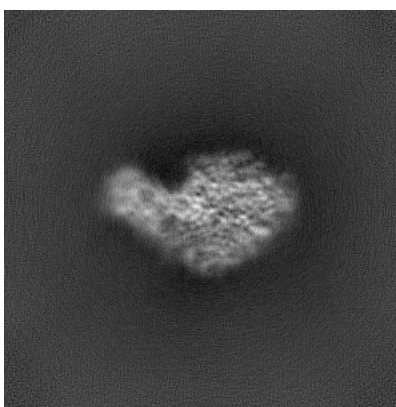


Z

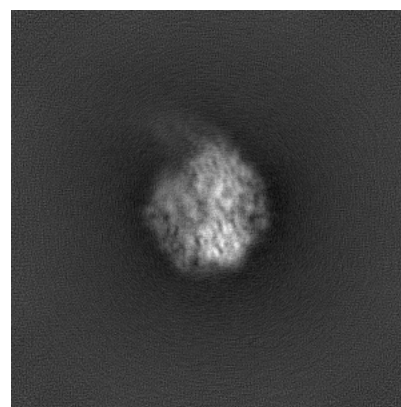
6.1.2 Raw map



X



Y



Z

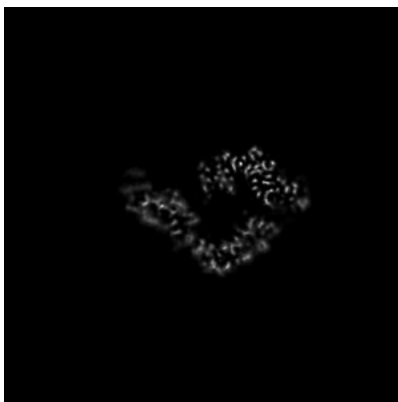
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 127

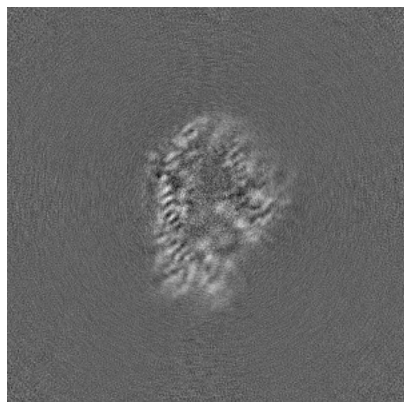


Y Index: 127

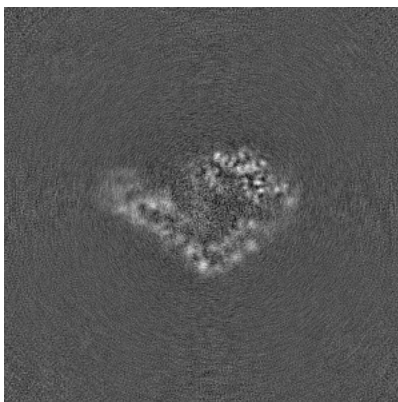


Z Index: 127

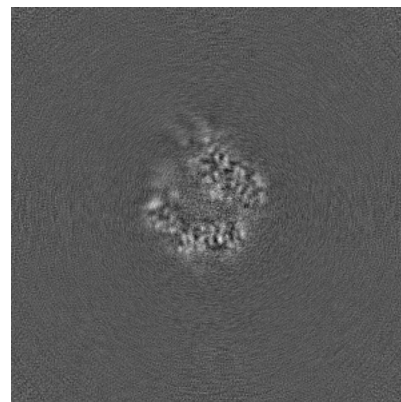
6.2.2 Raw map



X Index: 192



Y Index: 192



Z Index: 192

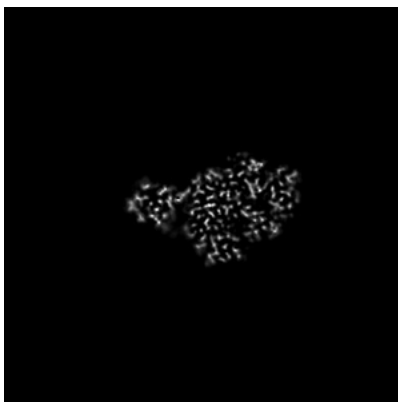
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

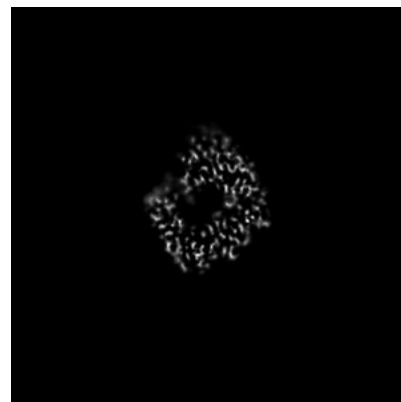
6.3.1 Primary map



X Index: 134

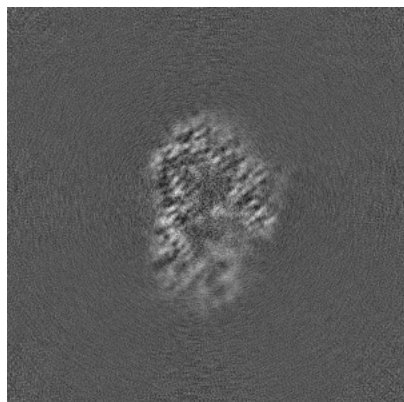


Y Index: 112

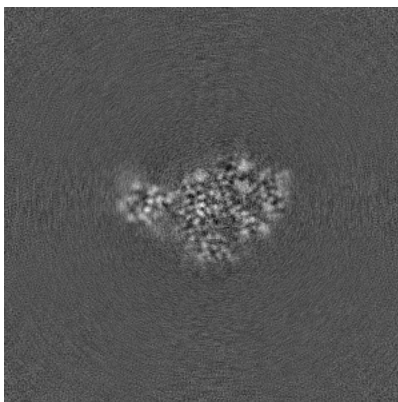


Z Index: 144

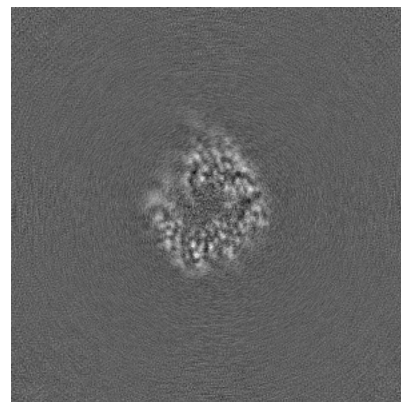
6.3.2 Raw map



X Index: 202



Y Index: 169

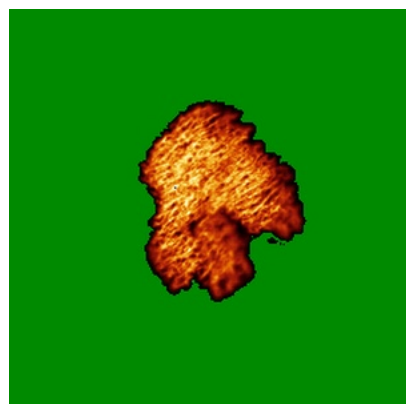


Z Index: 209

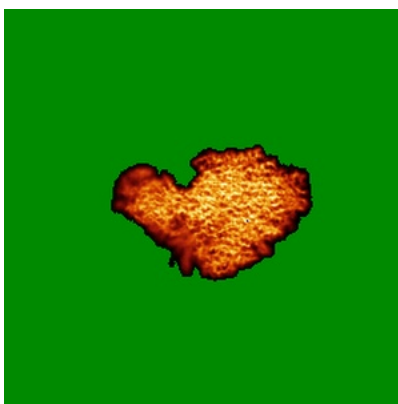
The images above show the largest variance slices of the map in three orthogonal directions.

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

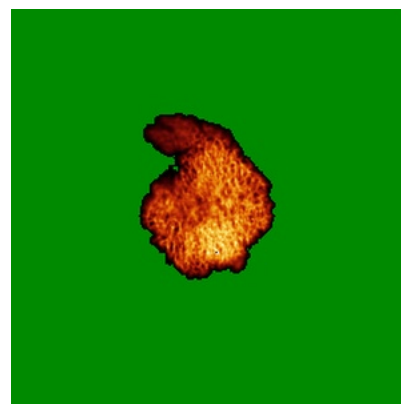
6.4.1 Primary map



X

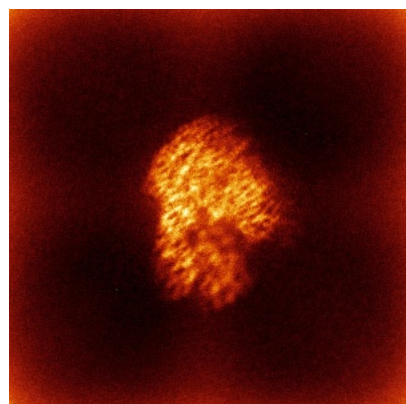


Y

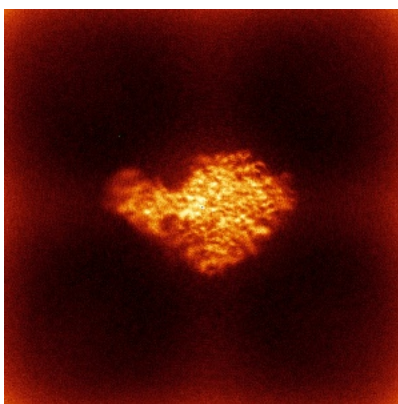


Z

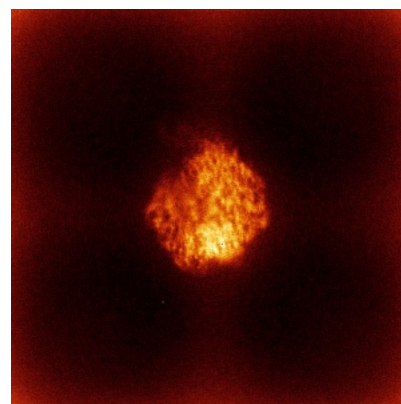
6.4.2 Raw map



X



Y

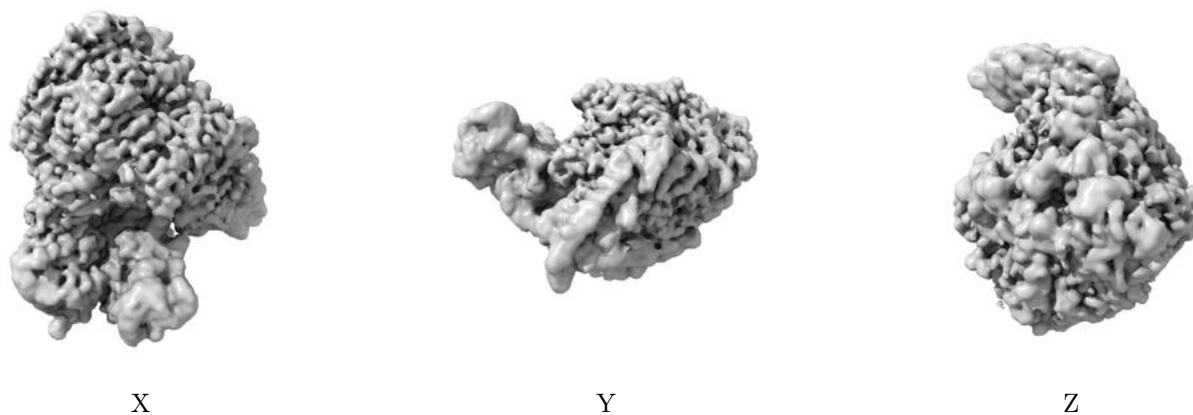


Z

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.

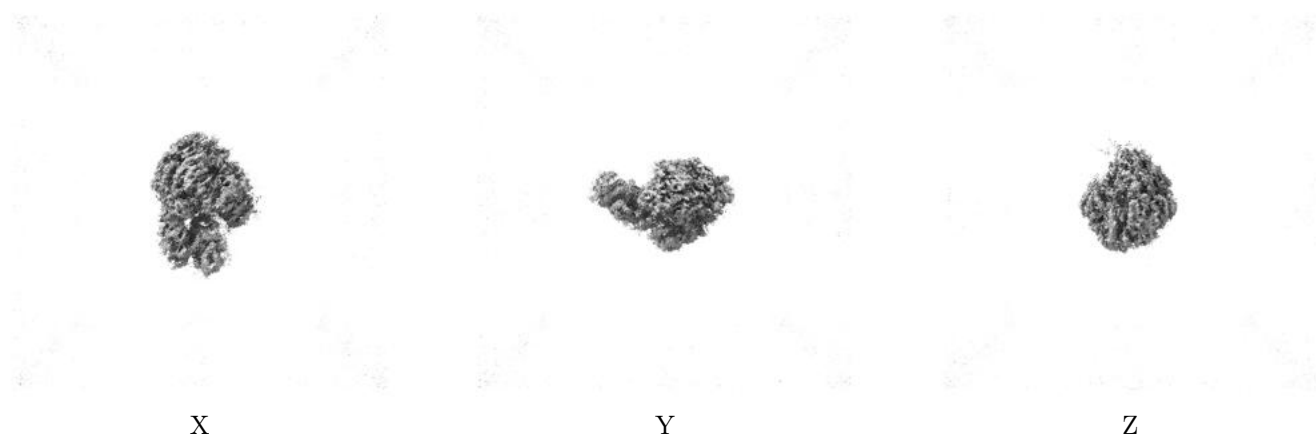
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

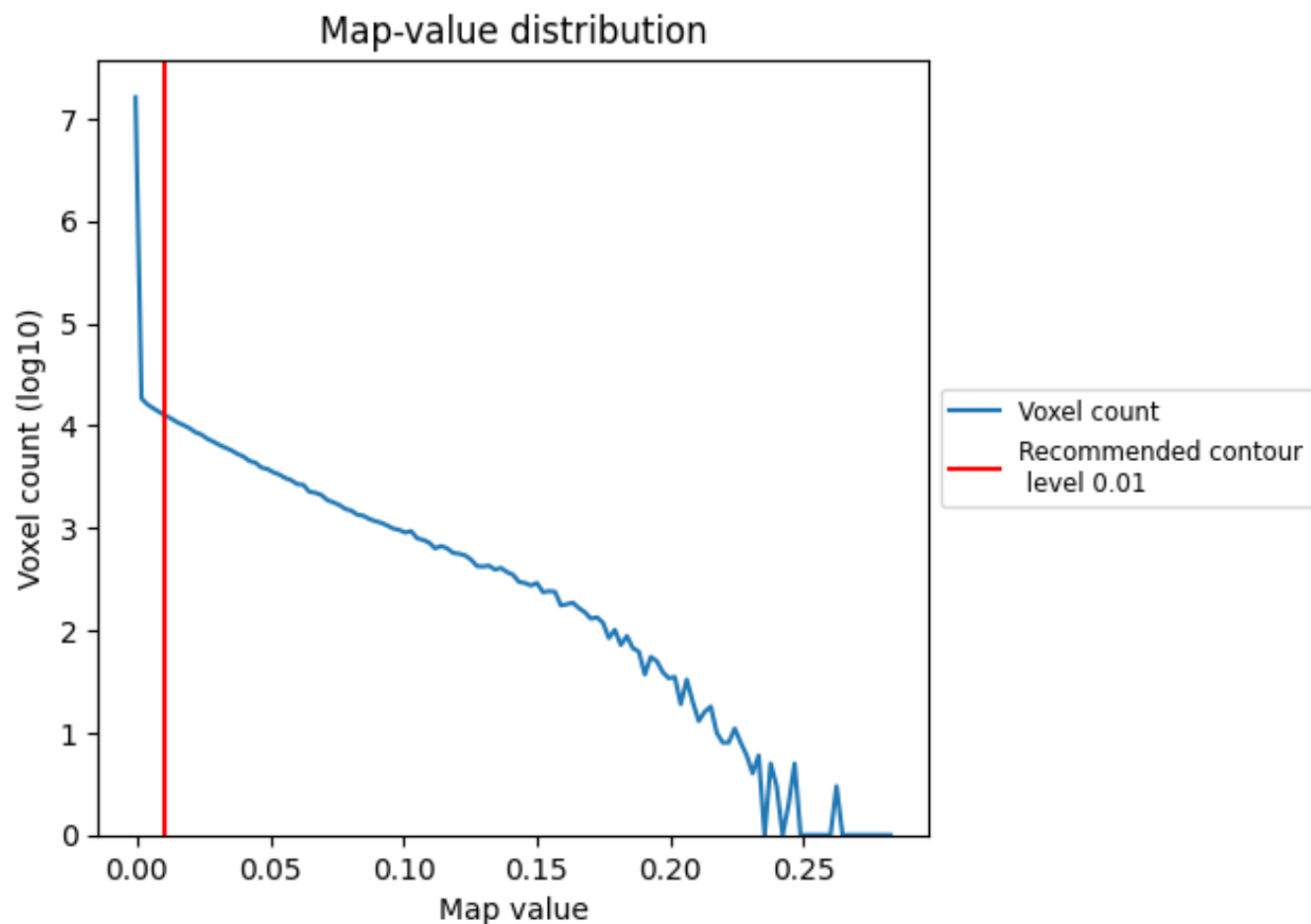
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

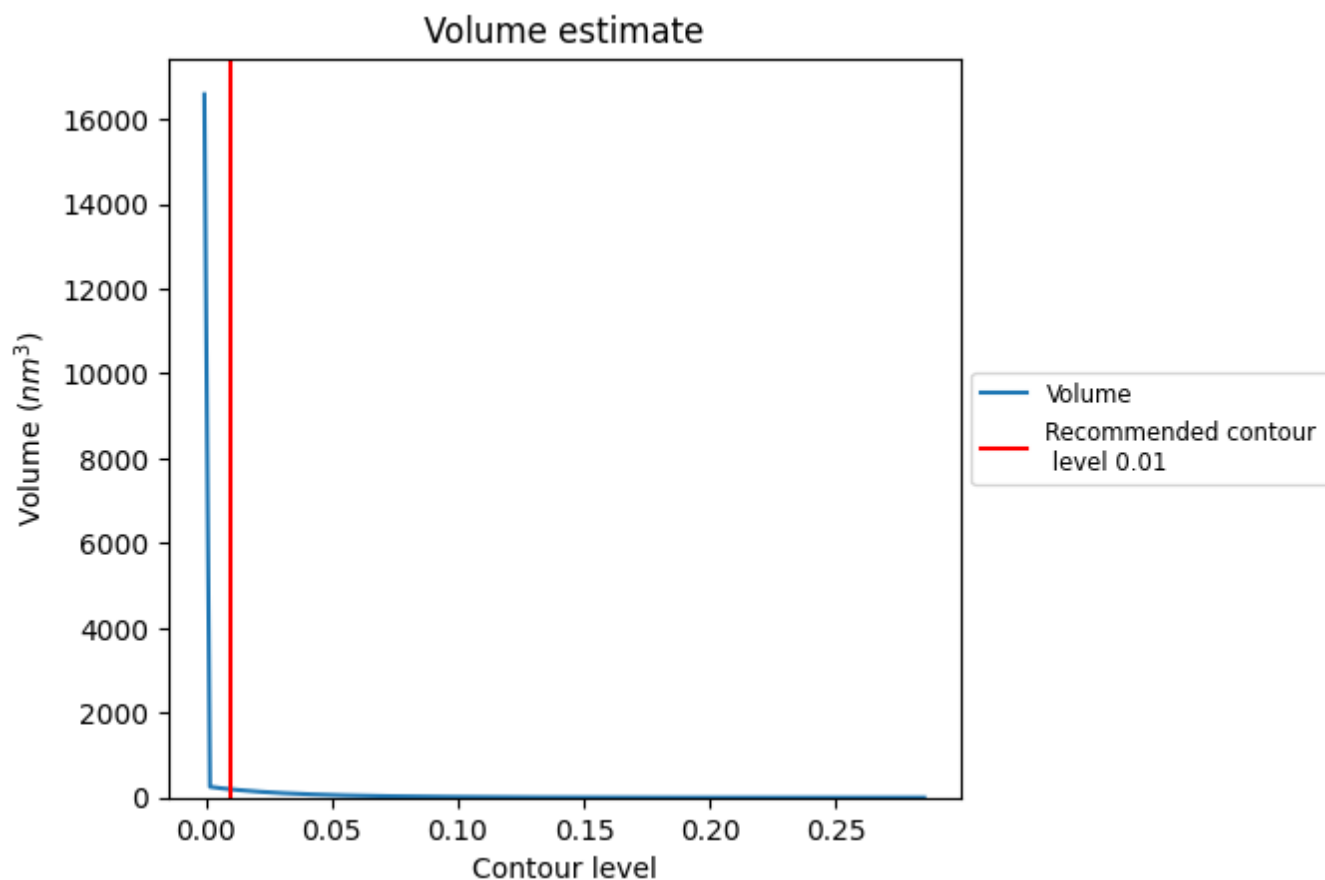
This section contains the results of statistical analysis of the map.

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.

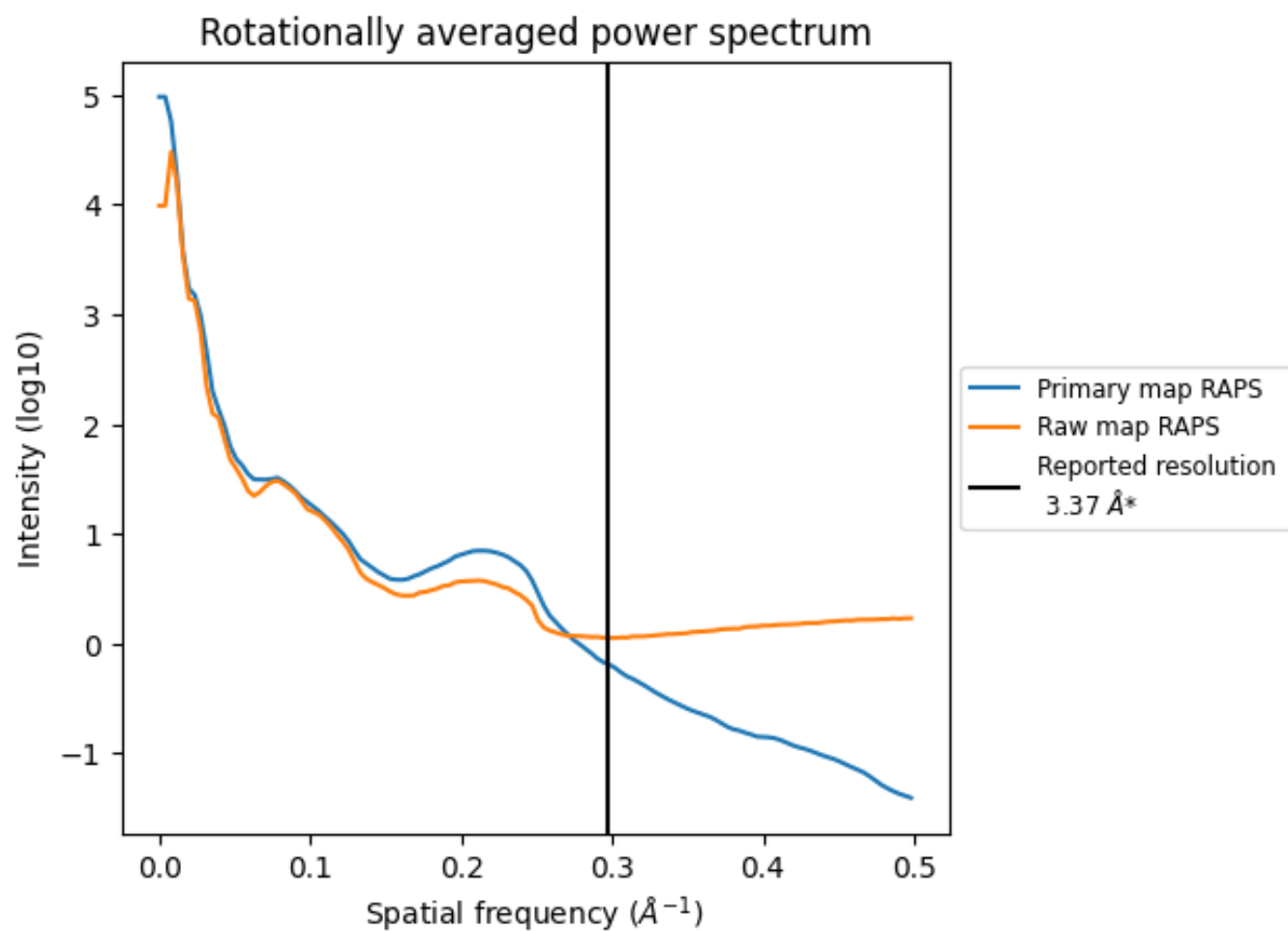
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 194 nm^3 ; this corresponds to an approximate mass of 176 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 ⓘ

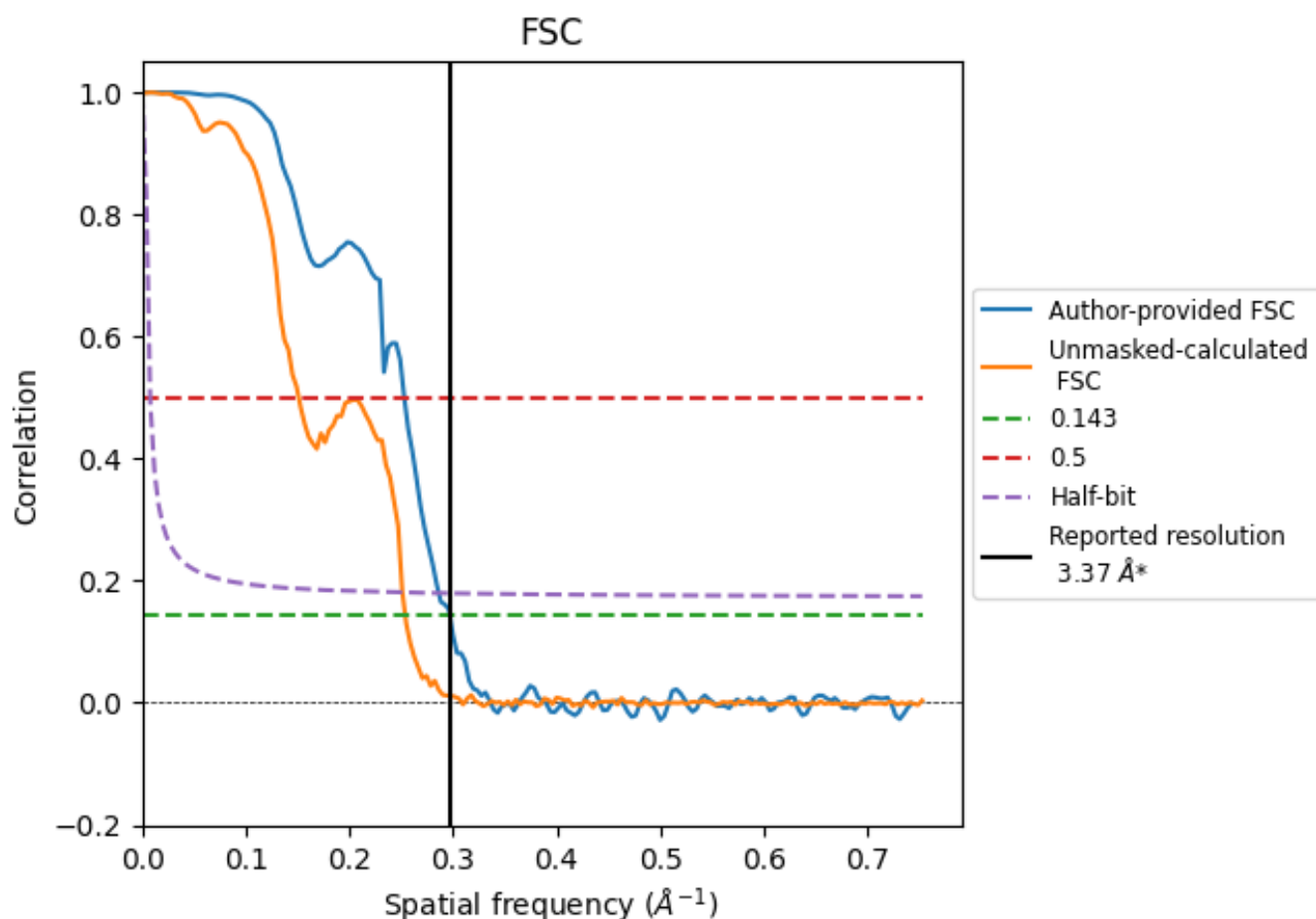


*Reported resolution corresponds to spatial frequency of 0.297 \AA^{-1}

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 0.297 \AA^{-1}

8.2 Resolution estimates [i](#)

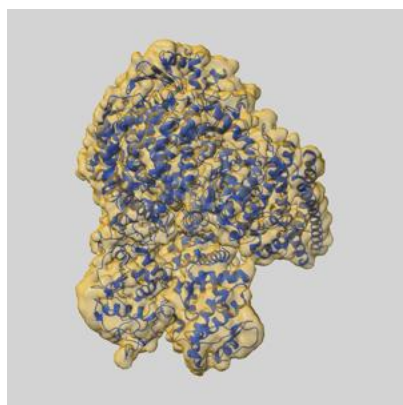
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.37	-	-
Author-provided FSC curve	3.37	3.95	3.49
Unmasked-calculated*	3.94	6.62	3.98

*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 3.94 differs from the reported value 3.37 by more than 10 %

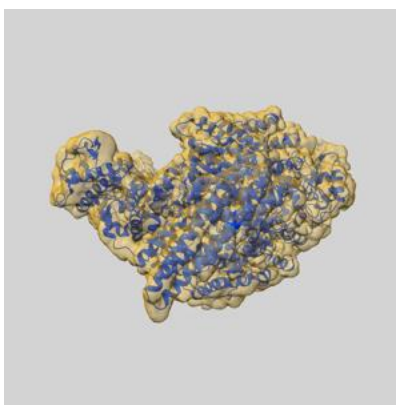
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48793 and PDB model 9N0T. Per-residue inclusion information can be found in section [3](#) on page [5](#).

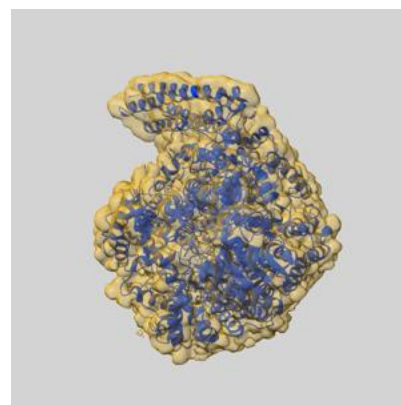
9.1 Map-model overlay [i](#)



X



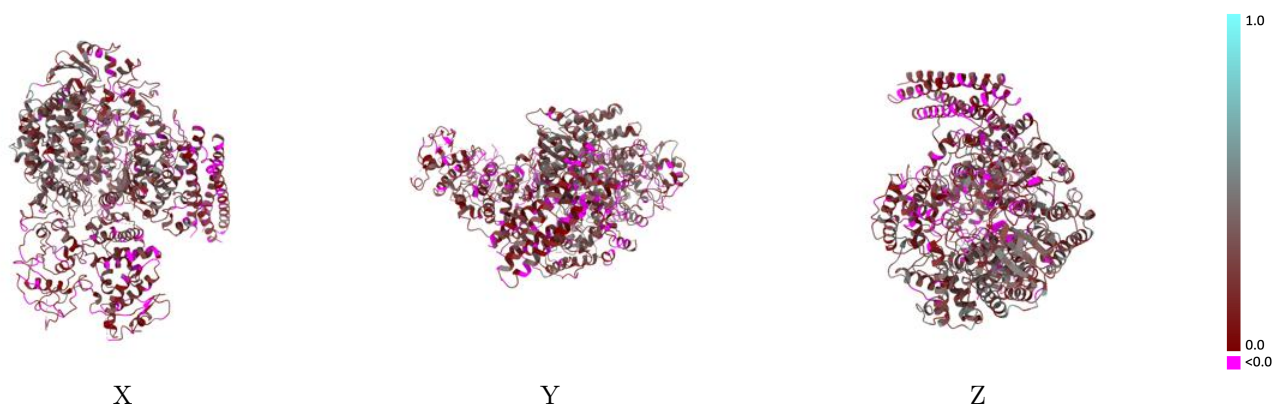
Y



Z

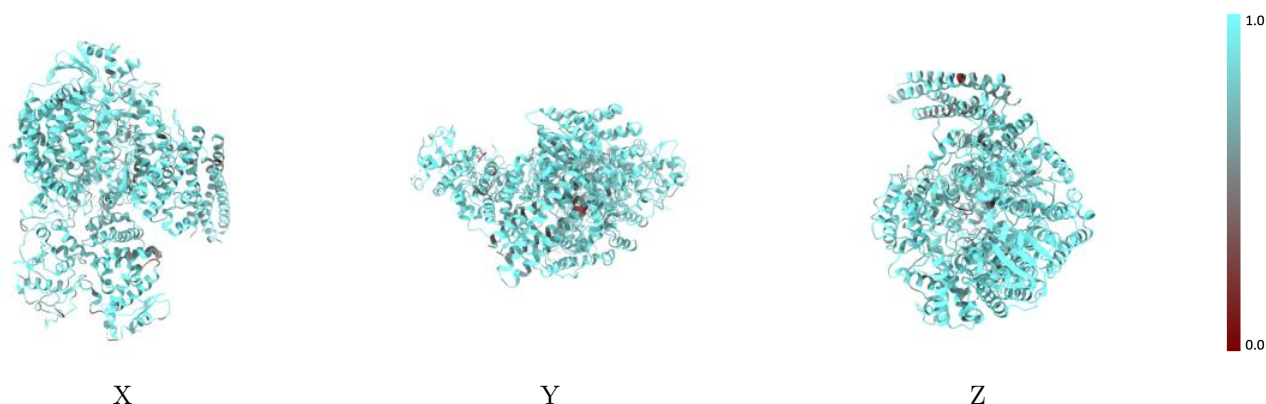
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



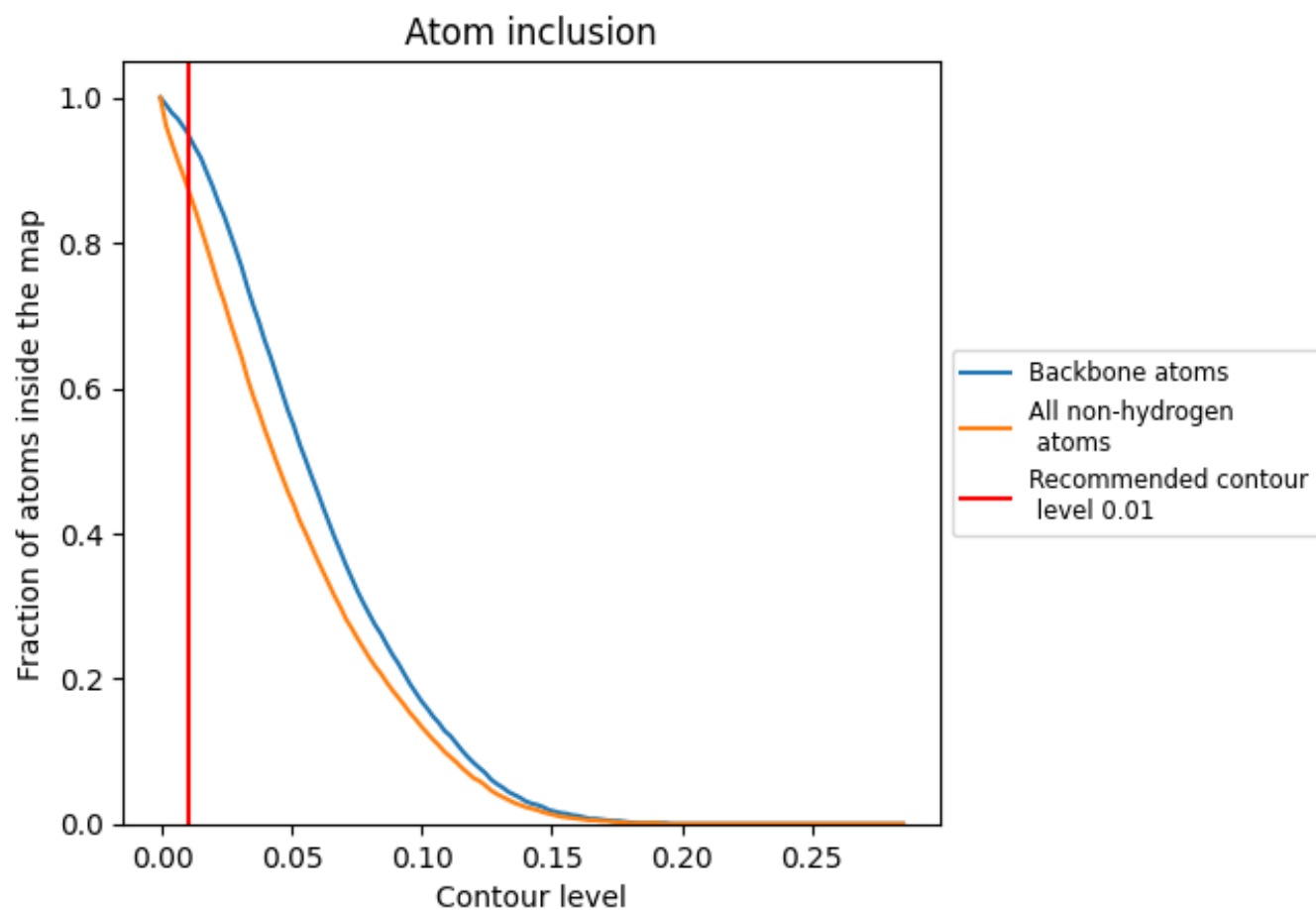
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 88% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8760	<div></div> 0.2090
A	<div></div> 0.8850	<div></div> 0.2200
B	<div></div> 0.8110	<div></div> 0.1270
C	<div></div> 0.8350	<div></div> 0.1350
D	<div></div> 0.7560	<div></div> 0.0840
E	<div></div> 0.7560	<div></div> 0.0900

