



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 02:44 PM UTC

PDB ID : 9GC0 / pdb_00009gc0
EMDB ID : EMD-51226
Title : 3'-lobe of the substrate-bound U11 snRNP
Authors : Zhao, J.; Galej, W.P.
Deposited on : 2024-07-31
Resolution : 3.20 Å (reported)
Based on initial models : ., 4PJO

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

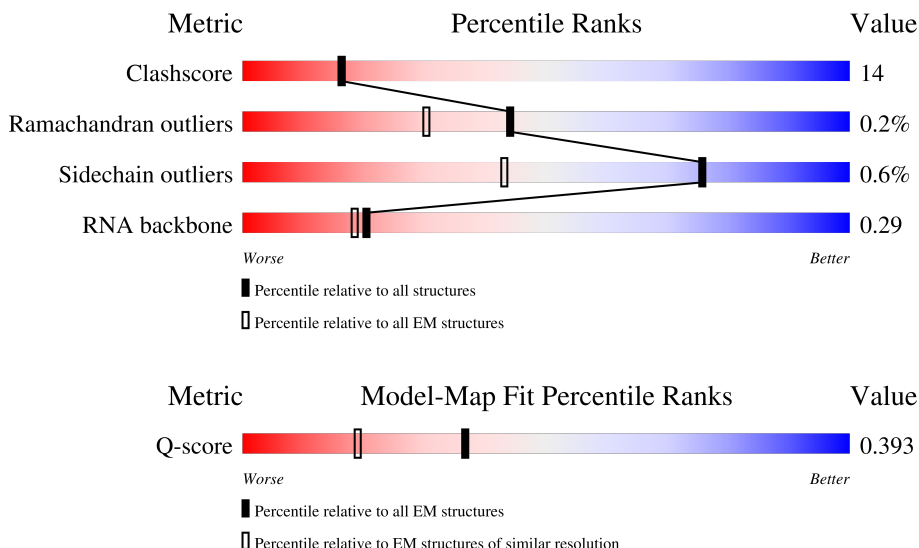
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



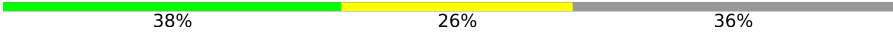
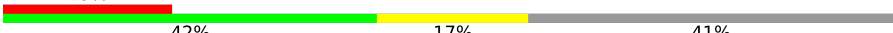
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	E	170	8% 19% 76%
2	D	485	15% 15% 9% 76%
3	h	119	44% 24% 32%

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Mol	Chain	Length	Quality of chain
4	j	126	
5	k	240	
6	l	92	
7	m	86	
8	n	76	
9	Q	135	
10	F	339	
11	i	118	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 8297 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 Zinc finger matrin-type protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	40	Total	C	N	O	S	0	0
			358	227	69	59	3		

- Molecule 2 is a protein called Programmed cell death protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	116	Total	C	N	O	S	0	0
			965	587	209	168	1		

- Molecule 3 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	h	81	Total	C	N	O	S	0	0
			641	408	112	118	3		

- Molecule 4 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	j	81	Total	C	N	O	S	0	0
			637	400	112	119	6		

- Molecule 5 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	k	86	Total	C	N	O	S	0	0
			692	435	126	124	7		

- Molecule 6 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	l	77	Total	C	N	O	S	0	0
			638	405	113	115	5		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	m	74	Total	C	N	O	S	0	0
			576	373	95	103	5		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	n	73	Total	C	N	O	S	0	0
			568	358	102	102	6		

- Molecule 9 is a RNA chain called U11 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	39	Total	C	N	O	P	0	0
			823	367	135	282	39		

- Molecule 10 is a protein called U11/U12 small nuclear ribonucleoprotein 48 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	200	Total	C	N	O	S	0	0
			1635	1016	278	330	11		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	i	94	Total	C	N	O	S	0	0
			764	478	139	141	6		

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

• Molecule 3: Small nuclear ribonucleoprotein Sm D1

Chain h: 44% 24% 32%

MET F2 L3 V4 R5 F6 L7 M8 R9 L10 L11 I17 K20 R21 R22 L23 V25 T29 V32 V33 T38 H39 L40 R41 A42 V43 K44 M45 K48 E51 Q54 L55 E56 T57 L58 R61 G62 N63 N64 I65 F68 I69 D77 T78 L79 D82 VAL GLU PRO LYS

• Molecule 4: Small nuclear ribonucleoprotein Sm D3

Chain j: 38% 26% 36%

MET SER T3 G4 V5 F6 V9 L10 H11 I17 Y18 T19 E20 E21 T22 R23 T24 G30 K31 L32 I33 D37 F38 M39 N40 C41 Q42 M45 Y50 R51 Q57 L58 E59 Q60 R64 G65 S66 I72 D75 M76 N79 A80 P81 M82 L83 LYS SER MET LYS

• Molecule 5: Small nuclear ribonucleoprotein-associated proteins B and B'

Chain k: 8% 25% 11% 64%

MET THR VAL GLY LYS S6 S7 K8 M9 L10 H11 Q12 I13 D14 Y15 R16 M17 Q22 R25 Q29 D35 M38 I41 E47 K52 P53 K54 K55 S56 K57 Q58 A59 E60 R61 E62 E63 R64 R65 R73 L77 V78 S79 T80 M80 T81 G84 P85 P86 P87 K88

• Molecule 6: Small nuclear ribonucleoprotein E

Chain l: 53% 29% 16%

MET ALA TYR ARG PRO GLN GLY GLN VAL VAL M14 P17 I18 F22 R23 Y24 R28 S29 R30 I31 Q38 I47 I48 D51 L56 V57 D60 K69 L74 I77 M78 L79 K80 G81 D82 N83 L86 L87 Q88 S89 V90 SER ASN

• Molecule 7: Small nuclear ribonucleoprotein F

Chain m: 67% 19% 14%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52290	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	41.73	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	165000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.171	Depositor
Minimum map value	-0.105	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.024	Depositor
Map size ($\text{\AA}$)	321.2, 321.2, 321.2	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.73, 0.73, 0.73	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	E	0.14	0/368	0.43	0/490
2	D	0.16	0/972	0.45	0/1301
3	h	0.16	0/649	0.52	0/878
4	j	0.17	0/645	0.55	0/870
5	k	0.16	0/702	0.45	0/936
6	l	0.16	0/646	0.46	0/867
7	m	0.16	0/588	0.42	0/795
8	n	0.21	0/575	0.65	0/768
9	Q	0.13	0/915	0.34	0/1420
10	F	0.16	0/1667	0.46	0/2251
11	i	0.18	0/773	0.54	0/1039
All	All	0.16	0/8500	0.48	0/11615

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	h	0	1
4	j	0	1
8	n	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	h	41	LYS	Peptide

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Mol	Chain	Res	Type	Group
4	j	59	GLU	Peptide
8	n	43	ASP	Peptide

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	E	358	0	340	6	0
2	D	965	0	1007	34	0
3	h	641	0	681	26	0
4	j	637	0	652	24	0
5	k	692	0	717	22	0
6	l	638	0	657	24	0
7	m	576	0	589	15	0
8	n	568	0	590	26	0
9	Q	823	0	417	23	0
10	F	1635	0	1561	50	0
11	i	764	0	783	26	0
All	All	8297	0	7994	230	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 14.

All (230) 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)
5:k:12:HIS:HB3	5:k:17:MET:HE1	1.51	0.92
2:D:276:ARG:HH21	2:D:277:TRP:HD1	1.34	0.76
10:F:78:CYS:SG	10:F:82:LYS:NZ	2.59	0.76
6:l:21:ILE:HD11	8:n:61:VAL:HG11	1.68	0.75
3:h:69:ILE:HG12	11:i:96:ILE:HD11	1.69	0.74
6:l:38:GLN:HE21	9:Q:95:G:H1	1.36	0.74
3:h:43:VAL:HB	3:h:55:LEU:HB3	1.72	0.69
4:j:40:ASN:HD21	9:Q:90:U:H3	1.41	0.69
4:j:19:THR:HB	4:j:72:ILE:HB	1.74	0.68
8:n:65:ASN:HB2	9:Q:89:U:H1'	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:h:61:ARG:NH1	3:h:63:ASN:OD1	2.27	0.68
10:F:24:SER:O	10:F:28:THR:HG23	1.94	0.67
10:F:1:MET:HE2	10:F:3:GLY:H	1.59	0.67
9:Q:128:C:H2'	9:Q:129:G:H8	1.59	0.67
2:D:230:ALA:HB2	10:F:32:VAL:HG22	1.77	0.67
6:l:31:ILE:HD11	6:l:87:LEU:HB3	1.77	0.66
10:F:75:MET:O	10:F:79:ARG:HG2	1.95	0.66
2:D:179:LEU:HB3	2:D:183:ARG:HH21	1.59	0.66
7:m:37:ASP:OD2	7:m:38:GLY:N	2.28	0.66
6:l:81:GLY:O	8:n:63:ARG:NH2	2.29	0.66
8:n:75:ARG:O	8:n:75:ARG:NH1	2.28	0.65
2:D:175:ARG:HH12	2:D:179:LEU:HG	1.60	0.65
3:h:41:LYS:HG3	3:h:41:LYS:O	1.96	0.64
10:F:13:ARG:NH1	10:F:17:GLU:OE2	2.28	0.64
8:n:71:GLU:N	8:n:71:GLU:OE1	2.31	0.63
2:D:177:ARG:HG3	2:D:222:ARG:HD3	1.81	0.62
10:F:25:GLY:O	10:F:29:LEU:HG	1.99	0.62
9:Q:95:G:O2'	9:Q:96:G:H5''	1.99	0.62
10:F:59:PRO:HD2	10:F:75:MET:HE1	1.82	0.61
5:k:9:MET:HE2	5:k:9:MET:HA	1.82	0.61
10:F:88:GLU:OE1	10:F:88:GLU:N	2.26	0.61
8:n:7:PRO:HD3	8:n:36:PRO:HA	1.81	0.61
10:F:169:VAL:HG22	10:F:173:LYS:NZ	2.16	0.61
8:n:46:VAL:HG23	8:n:48:MET:SD	2.41	0.60
10:F:157:THR:OG1	10:F:158:GLN:OE1	2.19	0.60
10:F:167:PHE:O	10:F:171:GLU:HG2	2.01	0.60
5:k:22:GLN:HG2	9:Q:96:G:H1	1.67	0.59
10:F:41:ASP:OD2	10:F:42:SER:N	2.31	0.59
3:h:32:VAL:HG22	3:h:38:THR:HG22	1.85	0.59
6:l:80:LYS:NZ	6:l:82:ASP:OD1	2.37	0.58
10:F:101:GLU:HG2	10:F:102:ASN:OD1	2.04	0.58
6:l:28:ARG:HH12	6:l:48:ILE:HG22	1.67	0.57
10:F:107:SER:O	10:F:175:LYS:NZ	2.38	0.57
10:F:165:TYR:O	10:F:169:VAL:HG12	2.05	0.57
1:E:41:PHE:O	4:j:79:ASN:ND2	2.32	0.57
11:i:23:GLU:OE1	11:i:23:GLU:N	2.30	0.56
3:h:17:ILE:HB	3:h:25:VAL:HG12	1.87	0.56
7:m:65:ARG:NH2	9:Q:93:U:O2'	2.39	0.56
9:Q:95:G:H4'	9:Q:96:G:O5'	2.04	0.56
6:l:18:ILE:HD11	10:F:245:ILE:HD11	1.89	0.55
10:F:26:CYS:HA	10:F:29:LEU:HD12	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:F:169:VAL:HG22	10:F:173:LYS:HZ2	1.72	0.55
4:j:40:ASN:OD1	4:j:65:GLY:N	2.38	0.55
6:l:56:LEU:HD11	6:l:87:LEU:HD11	1.88	0.55
1:E:9:TYR:HB2	1:E:30:HIS:CD2	2.42	0.55
7:m:51:ILE:HG22	7:m:56:SER:HB2	1.89	0.55
10:F:28:THR:HA	10:F:31:GLU:HG3	1.89	0.55
11:i:74:TRP:NE1	11:i:76:GLU:HG3	2.22	0.55
3:h:22:GLY:HA3	3:h:48:LYS:HD3	1.89	0.55
2:D:171:LEU:HD13	2:D:233:GLY:HA3	1.87	0.55
3:h:38:THR:HG21	3:h:68:PHE:HZ	1.71	0.55
10:F:56:VAL:HG21	10:F:71:LEU:HD22	1.89	0.55
2:D:276:ARG:HH21	2:D:277:TRP:CD1	2.22	0.54
5:k:25:ARG:HD2	5:k:47:GLU:CD	2.32	0.54
10:F:239:GLU:OE2	10:F:239:GLU:N	2.28	0.54
11:i:74:TRP:HE1	11:i:76:GLU:HG3	1.73	0.53
10:F:243:ASP:O	10:F:247:VAL:HG13	2.08	0.53
5:k:15:TYR:CE2	5:k:84:GLY:HA3	2.44	0.53
6:l:17:PRO:O	6:l:21:ILE:HG12	2.09	0.53
3:h:3:LEU:HB3	11:i:100:PHE:CZ	2.44	0.52
11:i:11:MET:HB2	11:i:16:LEU:HD21	1.91	0.52
6:l:51:ASP:OD2	7:m:7:PRO:HG2	2.09	0.52
9:Q:128:C:H2'	9:Q:129:G:C8	2.43	0.52
8:n:26:HIS:CD2	8:n:48:MET:HG3	2.45	0.52
11:i:30:SER:O	11:i:34:GLN:HG3	2.10	0.52
6:l:69:LYS:HG3	10:F:98:PHE:CD1	2.45	0.52
2:D:243:ARG:NH1	9:Q:124:C:OP2	2.44	0.51
8:n:36:PRO:HD2	10:F:237:TYR:CE1	2.46	0.51
2:D:266:ARG:HD3	2:D:266:ARG:N	2.26	0.51
3:h:29:ILE:HA	3:h:40:LEU:HD23	1.93	0.51
2:D:252:ARG:HD3	2:D:256:ARG:HH12	1.76	0.51
2:D:255:GLU:OE2	2:D:256:ARG:NH1	2.44	0.51
3:h:65:ILE:O	11:i:102:ARG:HD3	2.10	0.51
9:Q:109:U:O2'	10:F:63:ASN:OD1	2.26	0.51
10:F:86:THR:OG1	10:F:88:GLU:OE2	2.26	0.51
5:k:6:SER:O	5:k:10:LEU:N	2.43	0.51
2:D:223:LEU:HD11	10:F:28:THR:HG21	1.94	0.50
4:j:50:TYR:HD2	4:j:51:ARG:HH21	1.58	0.50
11:i:13:PRO:O	11:i:15:GLU:N	2.43	0.50
3:h:4:VAL:O	3:h:8:MET:HG2	2.11	0.50
10:F:77:SER:O	10:F:81:ARG:HG2	2.11	0.50
2:D:262:ALA:HA	2:D:266:ARG:NE	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:j:75:ASP:OD1	4:j:76:MET:N	2.44	0.50
6:l:22:PHE:CZ	10:F:245:ILE:HD13	2.47	0.50
8:n:50:THR:HG21	10:F:93:MET:HB3	1.93	0.50
3:h:5:ARG:HA	3:h:8:MET:HG3	1.94	0.49
6:l:31:ILE:HG21	6:l:47:ILE:HG13	1.93	0.49
11:i:45:ASN:HB2	11:i:108:VAL:HG12	1.93	0.49
8:n:17:LEU:N	8:n:29:GLY:O	2.33	0.49
2:D:275:ASP:OD1	2:D:278:ARG:NH2	2.35	0.49
9:Q:96:G:N3	9:Q:96:G:H3'	2.27	0.49
10:F:75:MET:SD	10:F:75:MET:N	2.86	0.49
11:i:75:THR:HG22	11:i:91:ASN:HA	1.94	0.49
5:k:63:GLU:N	5:k:63:GLU:OE1	2.45	0.49
10:F:72:ALA:HB3	10:F:73:LYS:NZ	2.28	0.49
4:j:31:LYS:HZ2	4:j:33:ILE:HG22	1.78	0.48
10:F:131:ASP:OD2	10:F:134:ASN:ND2	2.42	0.48
2:D:186:ARG:NH2	10:F:48:GLU:OE1	2.46	0.48
4:j:60:GLN:NE2	8:n:76:VAL:HG11	2.28	0.48
4:j:66:SER:HB3	9:Q:90:U:O4'	2.13	0.48
3:h:3:LEU:HB3	11:i:100:PHE:HZ	1.79	0.48
6:l:24:TYR:OH	8:n:59:MET:O	2.32	0.48
8:n:42:ILE:O	8:n:60:VAL:HG22	2.14	0.48
2:D:276:ARG:HH12	2:D:280:LYS:HD2	1.78	0.47
8:n:34:PHE:HA	8:n:39:ASN:O	2.14	0.47
4:j:64:ARG:NH1	8:n:64:GLY:O	2.47	0.47
11:i:20:GLU:OE1	11:i:61:ARG:NH2	2.46	0.47
6:l:74:LEU:HD23	6:l:77:ILE:HD12	1.95	0.47
7:m:37:ASP:HB3	7:m:41:ASN:H	1.79	0.47
3:h:10:LEU:HD11	3:h:79:LEU:HD13	1.96	0.47
4:j:39:MET:HE1	5:k:73:ARG:HB2	1.97	0.47
2:D:178:LEU:O	2:D:182:LEU:HG	2.14	0.47
7:m:55:LEU:HD12	7:m:56:SER:H	1.80	0.47
11:i:16:LEU:HB2	11:i:19:ARG:HD3	1.96	0.47
10:F:82:LYS:HA	10:F:82:LYS:HD3	1.76	0.46
10:F:89:GLU:O	10:F:93:MET:HG3	2.14	0.46
2:D:216:ARG:HH21	10:F:18:LEU:HA	1.79	0.46
6:l:30:ARG:NH1	6:l:60:ASP:OD2	2.41	0.46
10:F:60:TYR:HD2	10:F:78:CYS:HB3	1.80	0.46
3:h:64:ASN:ND2	5:k:78:VAL:HG13	2.30	0.46
4:j:6:PRO:HD2	5:k:35:ASP:HB3	1.97	0.46
7:m:55:LEU:HD12	7:m:56:SER:N	2.31	0.46
5:k:38:MET:HE3	5:k:77:LEU:HD23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:188:LEU:HD22	2:D:212:THR:HG23	1.98	0.46
5:k:16:ARG:HB2	5:k:84:GLY:HA2	1.98	0.46
2:D:262:ALA:O	2:D:266:ARG:HG2	2.16	0.45
7:m:40:MET:HE3	9:Q:88:A:H61	1.81	0.45
6:l:89:SER:OG	8:n:57:ILE:HD11	2.17	0.45
1:E:9:TYR:HB2	1:E:30:HIS:HD2	1.82	0.45
4:j:60:GLN:O	8:n:71:GLU:HB2	2.17	0.45
6:l:86:LEU:HD23	6:l:87:LEU:N	2.32	0.45
11:i:50:LYS:HD3	11:i:74:TRP:CG	2.52	0.45
11:i:11:MET:HE3	11:i:11:MET:HB3	1.82	0.45
6:l:31:ILE:HG13	6:l:88:GLN:O	2.17	0.45
2:D:255:GLU:OE2	2:D:256:ARG:HG3	2.16	0.44
4:j:11:HIS:NE2	4:j:37:ASP:OD1	2.32	0.44
2:D:221:GLU:O	2:D:225:PRO:HD3	2.17	0.44
2:D:188:LEU:HD21	2:D:215:LEU:HB2	1.99	0.44
5:k:16:ARG:NH1	5:k:29:GLY:HA2	2.32	0.44
10:F:89:GLU:OE2	10:F:150:LYS:NZ	2.45	0.44
2:D:175:ARG:HG3	9:Q:109:U:OP1	2.18	0.44
3:h:20:LYS:N	3:h:64:ASN:O	2.48	0.44
5:k:17:MET:HE3	5:k:17:MET:HB2	1.55	0.44
3:h:41:LYS:HB2	3:h:56:GLU:O	2.17	0.44
9:Q:98:A:O2'	9:Q:100:U:OP1	2.24	0.44
2:D:242:VAL:O	2:D:245:ARG:HG2	2.18	0.44
1:E:9:TYR:HE1	4:j:81:PRO:HG3	1.82	0.43
4:j:82:MET:H	4:j:82:MET:HG3	1.57	0.43
9:Q:100:U:H5''	9:Q:101:U:C6	2.53	0.43
10:F:66:MET:HE1	10:F:74:HIS:CG	2.53	0.43
4:j:30:GLY:HA2	4:j:45:ASN:O	2.18	0.43
11:i:76:GLU:HB2	11:i:92:LYS:NZ	2.33	0.43
2:D:260:ARG:HG3	2:D:261:GLU:N	2.32	0.43
1:E:10:CYS:SG	1:E:24:HIS:NE2	2.83	0.43
10:F:71:LEU:O	10:F:75:MET:SD	2.77	0.43
2:D:175:ARG:HH22	2:D:179:LEU:HD11	1.82	0.43
7:m:36:VAL:HG22	7:m:40:MET:HA	2.00	0.43
8:n:45:CYS:O	8:n:56:ASN:HA	2.18	0.43
2:D:256:ARG:HG3	2:D:256:ARG:HH11	1.83	0.43
3:h:69:ILE:HG12	11:i:96:ILE:CD1	2.45	0.43
10:F:29:LEU:O	10:F:32:VAL:HG12	2.18	0.43
11:i:93:ASP:C	11:i:93:ASP:OD1	2.61	0.43
1:E:4:ARG:HG3	1:E:14:PHE:O	2.19	0.43
8:n:37:PHE:HB3	9:Q:89:U:N3	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:Q:130:C:H2'	9:Q:131:C:C6	2.54	0.43
10:F:66:MET:HE2	10:F:66:MET:HB3	1.95	0.43
7:m:65:ARG:HG2	7:m:67:ASN:H	1.82	0.43
7:m:70:LEU:HD23	7:m:71:TYR:HD2	1.84	0.43
10:F:237:TYR:HD2	10:F:237:TYR:O	2.02	0.42
11:i:70:VAL:HB	11:i:96:ILE:HG23	2.00	0.42
5:k:17:MET:HG3	5:k:81:THR:O	2.20	0.42
3:h:17:ILE:HD12	3:h:40:LEU:HD11	2.01	0.42
3:h:55:LEU:HD21	5:k:81:THR:HG21	2.01	0.42
8:n:45:CYS:HB2	8:n:57:ILE:O	2.19	0.42
2:D:174:VAL:O	2:D:178:LEU:HG	2.17	0.42
2:D:238:ARG:N	2:D:241:ARG:HH21	2.18	0.42
4:j:17:ILE:HD12	4:j:17:ILE:HA	1.92	0.42
7:m:11:LEU:O	7:m:15:THR:HG23	2.19	0.42
10:F:131:ASP:HB3	10:F:134:ASN:HB2	2.00	0.42
3:h:45:MET:HE3	3:h:45:MET:HB2	1.88	0.42
2:D:180:ARG:HE	2:D:218:GLU:CD	2.28	0.42
5:k:85:PRO:HB2	5:k:87:PRO:HD2	2.01	0.42
10:F:29:LEU:HB2	10:F:40:LEU:HD22	2.01	0.42
2:D:267:ALA:O	2:D:270:ARG:HG3	2.20	0.42
4:j:57:GLN:C	4:j:58:LEU:HD12	2.45	0.42
5:k:47:GLU:HB3	5:k:65:ARG:HG3	2.01	0.42
6:l:57:VAL:HG23	7:m:7:PRO:HG3	2.02	0.42
8:n:28:GLN:O	8:n:45:CYS:HA	2.20	0.42
11:i:61:ARG:HG3	11:i:62:HIS:ND1	2.35	0.41
11:i:62:HIS:O	11:i:103:GLY:HA3	2.19	0.41
9:Q:130:C:H2'	9:Q:131:C:H6	1.84	0.41
11:i:14:GLU:H	11:i:17:GLN:HG3	1.85	0.41
3:h:3:LEU:O	3:h:6:PHE:HB3	2.20	0.41
3:h:56:GLU:N	3:h:56:GLU:OE2	2.52	0.41
4:j:22:THR:HG22	4:j:24:THR:H	1.85	0.41
6:l:87:LEU:HB2	8:n:61:VAL:HG12	2.02	0.41
8:n:50:THR:HG21	10:F:94:TYR:H	1.85	0.41
2:D:195:LEU:HD22	2:D:205:TRP:CE2	2.55	0.41
5:k:8:LYS:HA	5:k:11:GLN:OE1	2.21	0.41
6:l:30:ARG:O	6:l:90:VAL:HA	2.21	0.41
9:Q:107:G:H2'	9:Q:108:C:H6	1.85	0.41
4:j:20:CYS:SG	4:j:21:GLU:N	2.94	0.41
7:m:40:MET:CE	9:Q:88:A:H61	2.33	0.41
10:F:71:LEU:HG	10:F:75:MET:SD	2.61	0.41
10:F:160:ASP:O	10:F:164:LEU:HG	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:j:33:ILE:HD11	4:j:42:GLN:HG2	2.02	0.41
4:j:5:VAL:O	4:j:9:VAL:HG23	2.20	0.40
11:i:38:ASN:HB2	11:i:40:THR:HG23	2.04	0.40
2:D:242:VAL:HA	2:D:245:ARG:NE	2.37	0.40
3:h:77:ASP:OD1	3:h:77:ASP:C	2.64	0.40
6:l:18:ILE:HD12	6:l:18:ILE:HA	1.79	0.40
3:h:58:LEU:HD12	5:k:81:THR:HB	2.02	0.40
4:j:6:PRO:HA	5:k:41:ILE:HD11	2.01	0.40
5:k:10:LEU:O	5:k:13:ILE:HG12	2.21	0.40
8:n:13:MET:HE1	8:n:32:ARG:C	2.46	0.40
8:n:14:ASP:O	8:n:15:LYS:HD2	2.21	0.40
6:l:78:MET:HB2	7:m:10:PHE:CE2	2.56	0.40
11:i:50:LYS:HD3	11:i:74:TRP:CD1	2.56	0.40
11:i:99:MET:HB2	11:i:99:MET:HE2	1.85	0.40
9:Q:102:G:N2	9:Q:133:U:H1'	2.37	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	E	38/170 (22%)	38 (100%)	0	0	100	100
2	D	114/485 (24%)	107 (94%)	7 (6%)	0	100	100
3	h	79/119 (66%)	75 (95%)	4 (5%)	0	100	100
4	j	79/126 (63%)	71 (90%)	8 (10%)	0	100	100
5	k	84/240 (35%)	82 (98%)	2 (2%)	0	100	100
6	l	75/92 (82%)	72 (96%)	3 (4%)	0	100	100
7	m	72/86 (84%)	71 (99%)	1 (1%)	0	100	100
8	n	71/76 (93%)	59 (83%)	12 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	F	196/339 (58%)	186 (95%)	9 (5%)	1 (0%)	24	59
11	i	90/118 (76%)	85 (94%)	4 (4%)	1 (1%)	11	43
All	All	898/1851 (48%)	846 (94%)	50 (6%)	2 (0%)	44	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	i	14	GLU
10	F	53	ASP

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	E	38/151 (25%)	38 (100%)	0	100	100
2	D	93/401 (23%)	93 (100%)	0	100	100
3	h	76/101 (75%)	76 (100%)	0	100	100
4	j	71/101 (70%)	71 (100%)	0	100	100
5	k	78/177 (44%)	77 (99%)	1 (1%)	61	78
6	l	72/84 (86%)	70 (97%)	2 (3%)	38	68
7	m	63/74 (85%)	63 (100%)	0	100	100
8	n	63/66 (96%)	63 (100%)	0	100	100
10	F	185/313 (59%)	184 (100%)	1 (0%)	81	85
11	i	89/110 (81%)	88 (99%)	1 (1%)	65	79
All	All	828/1578 (52%)	823 (99%)	5 (1%)	76	84

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	k	80	MET
6	l	83	ASN

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Mol	Chain	Res	Type
6	l	89	SER
10	F	1	MET
11	i	31	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
5	k	22	GLN
5	k	76	ASN
6	l	32	GLN
6	l	38	GLN
8	n	53	GLN
10	F	15	GLN
10	F	121	GLN
10	F	135	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	Q	37/135 (27%)	14 (37%)	2 (5%)

All (14) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	Q	86	U
9	Q	90	U
9	Q	94	U
9	Q	96	G
9	Q	97	U
9	Q	98	A
9	Q	99	U
9	Q	100	U
9	Q	102	G
9	Q	106	A
9	Q	107	G
9	Q	109	U
9	Q	123	C
9	Q	129	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	Q	95	G
9	Q	106	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

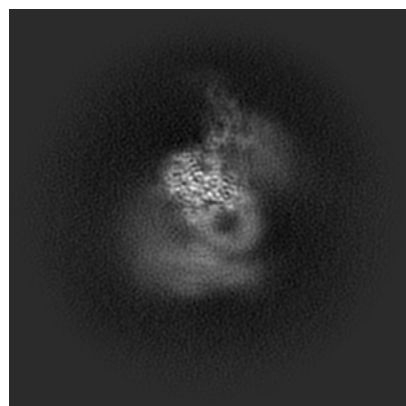
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51226. These allow visual inspection of the internal detail of the map and identification of artifacts.

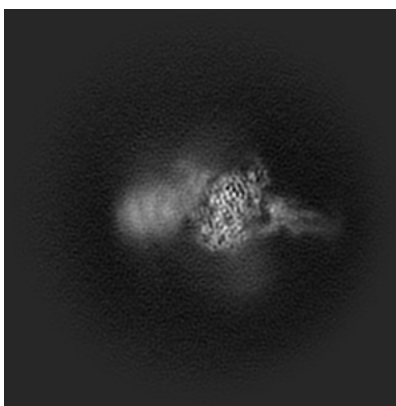
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

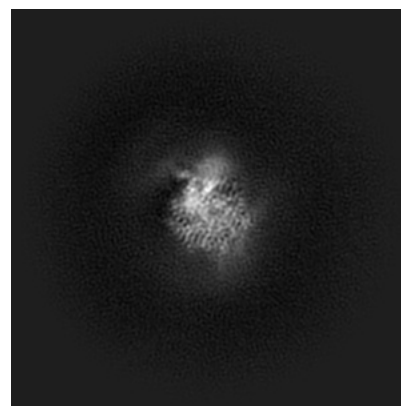
6.1.1 Primary map



X

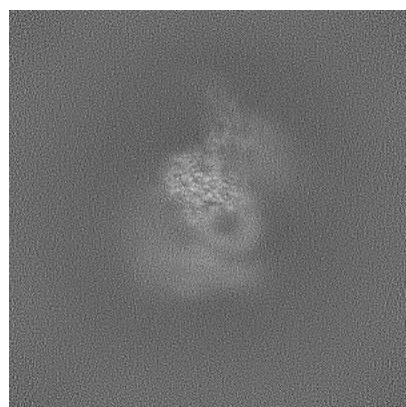


Y

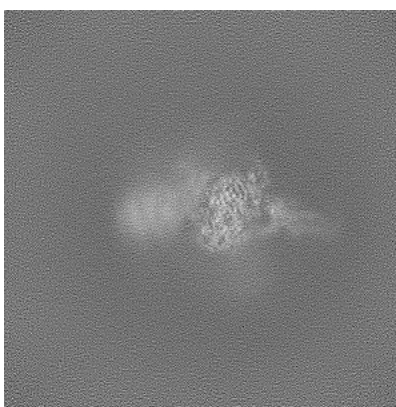


Z

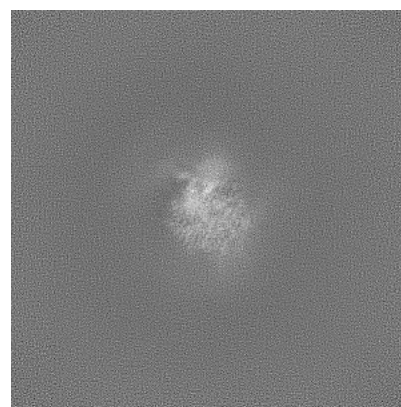
6.1.2 Raw map



X



Y

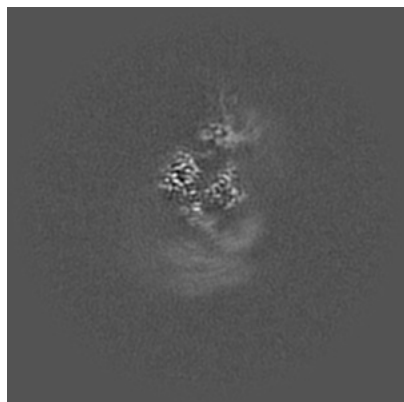


Z

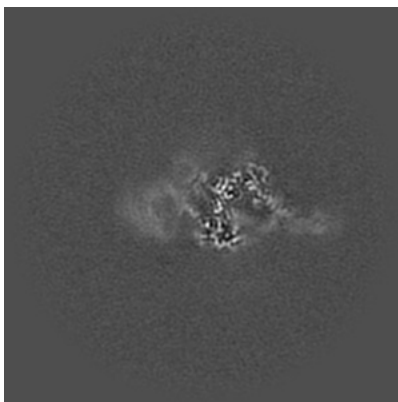
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

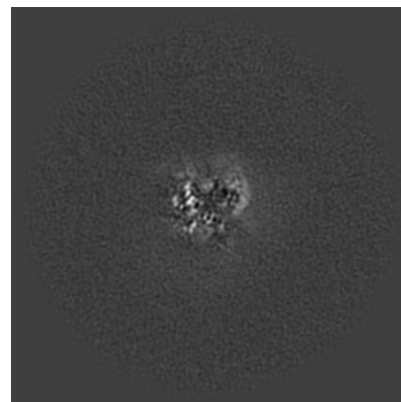
6.2.1 Primary map



X Index: 220

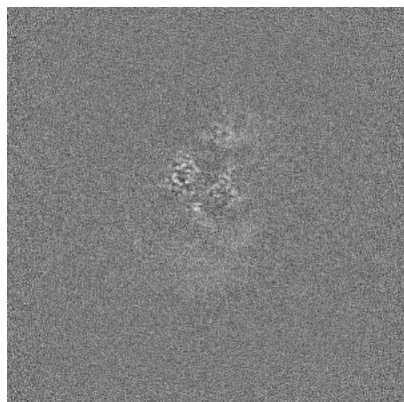


Y Index: 220

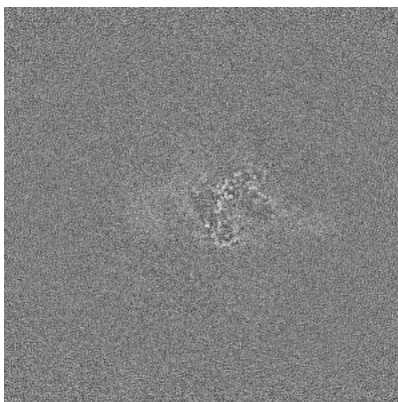


Z Index: 220

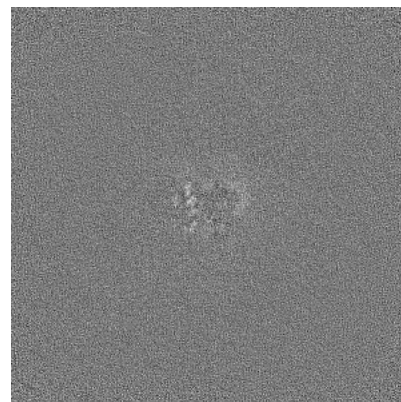
6.2.2 Raw map



X Index: 220



Y Index: 220

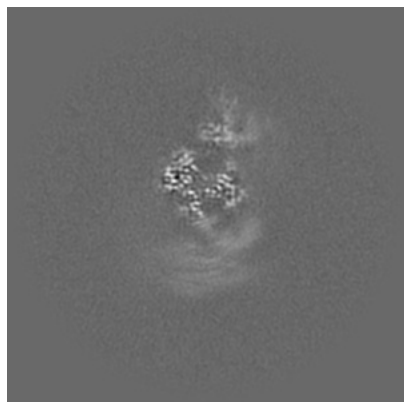


Z Index: 220

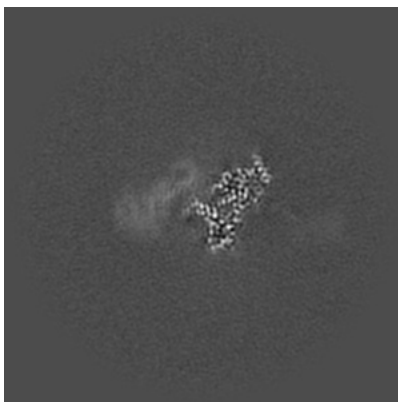
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

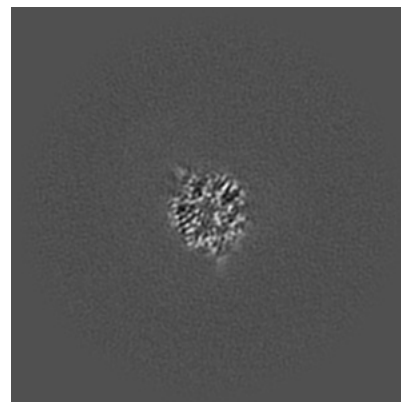
6.3.1 Primary map



X Index: 218

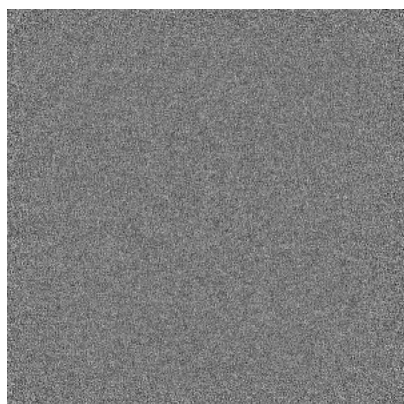


Y Index: 208

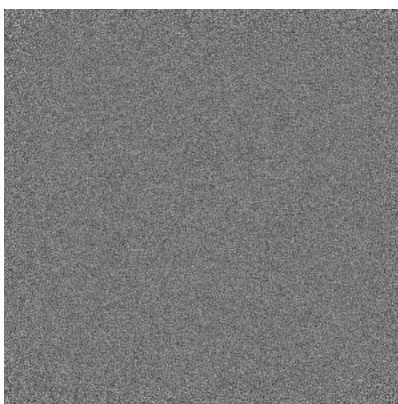


Z Index: 241

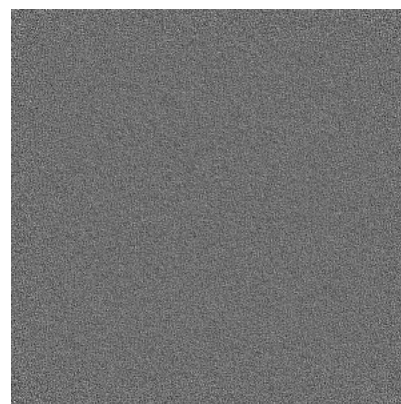
6.3.2 Raw map



X Index: 0



Y Index: 0

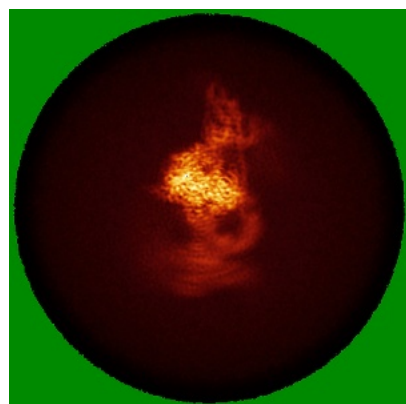


Z Index: 0

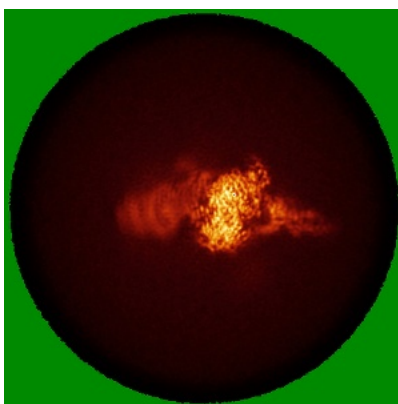
The images above show the largest variance slices of the map in three orthogonal directions.

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

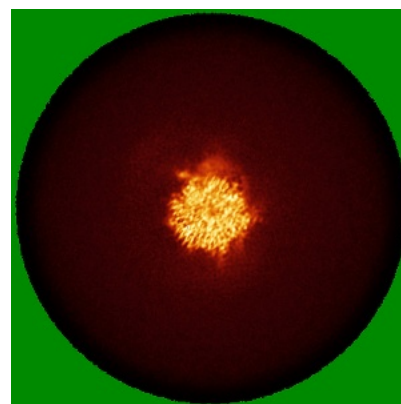
6.4.1 Primary map



X

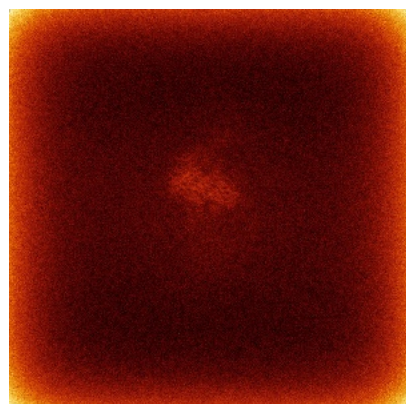


Y

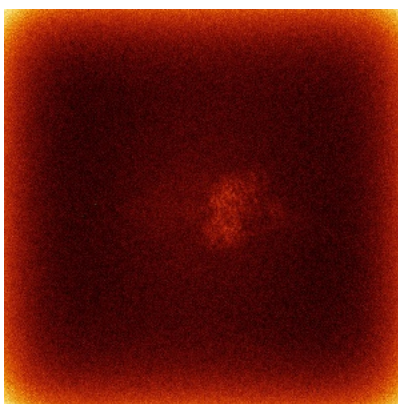


Z

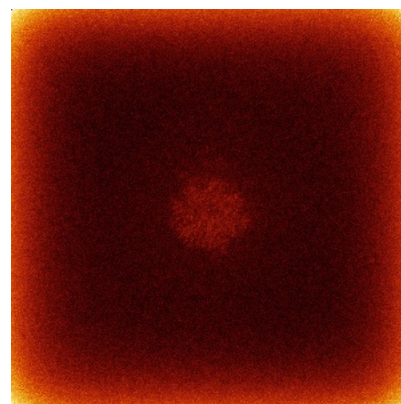
6.4.2 Raw map



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.

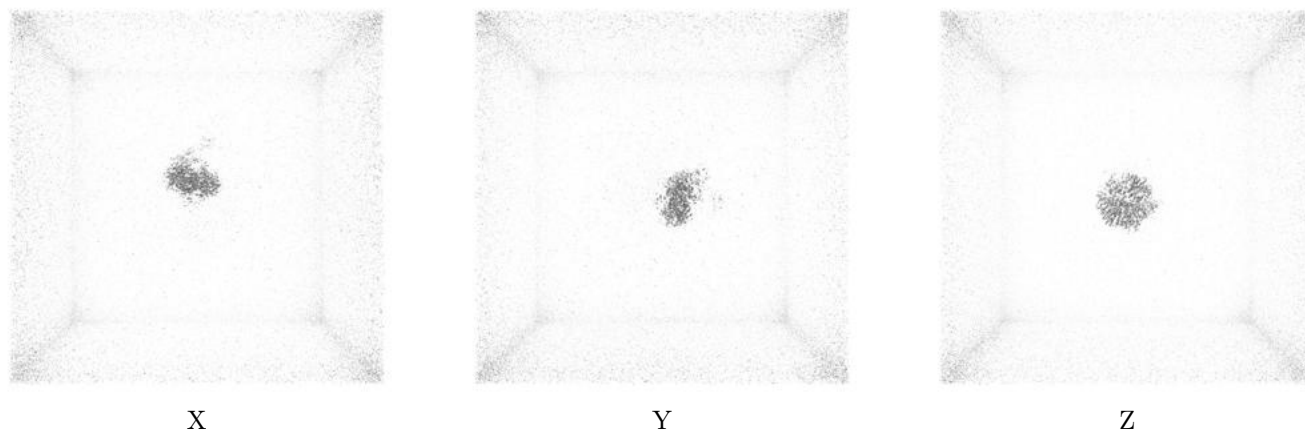
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.024. 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.

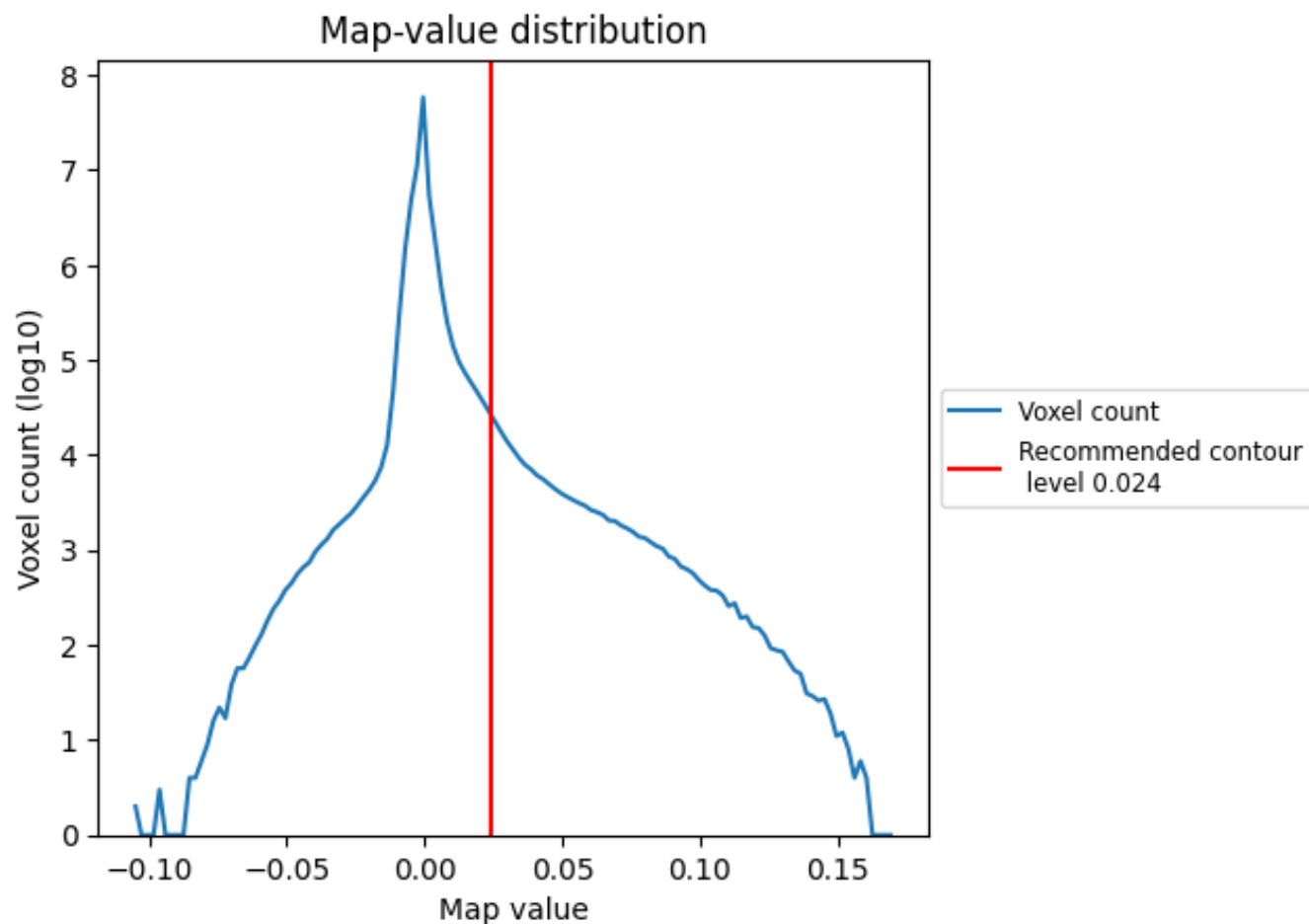
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

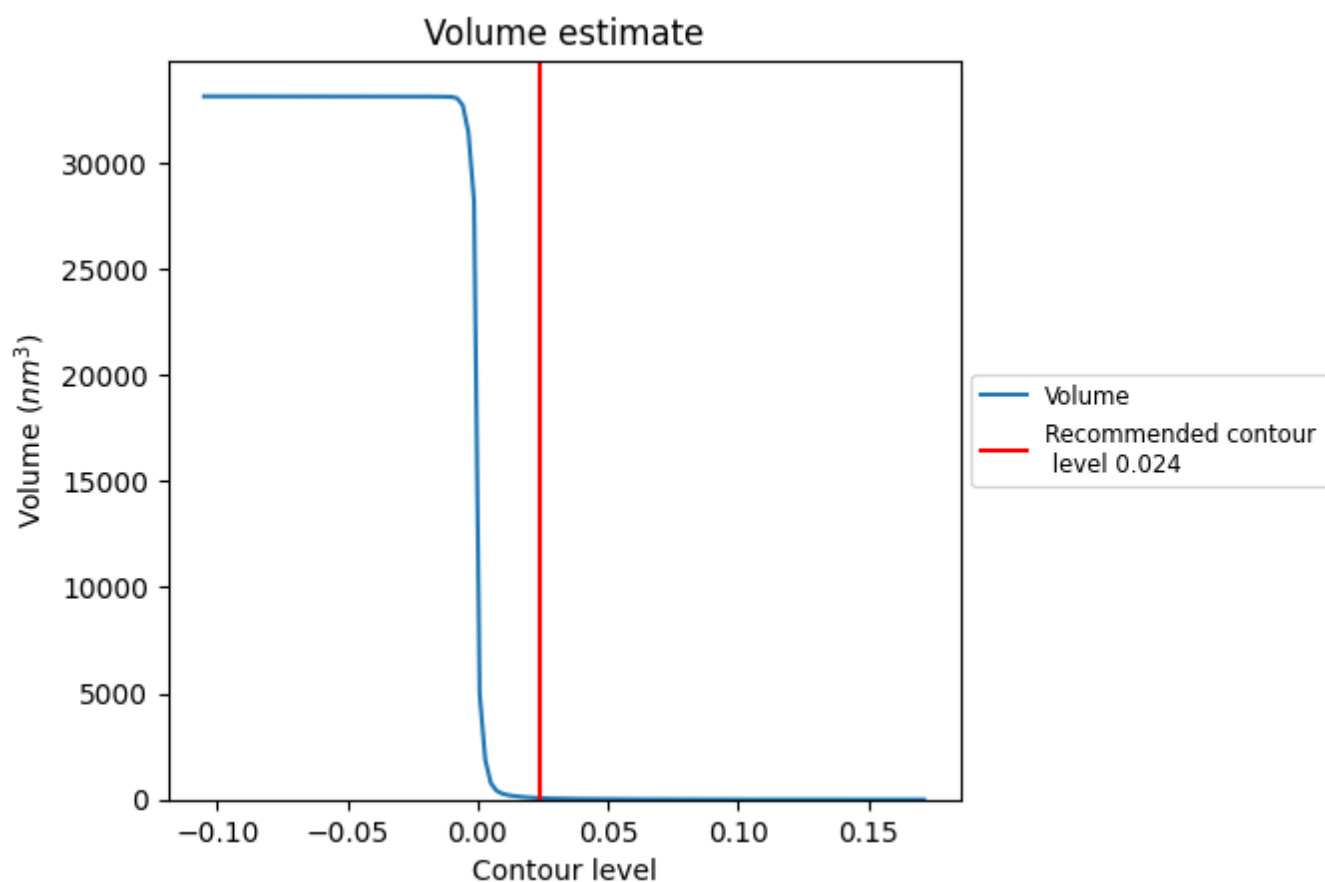
This section contains the results of statistical analysis of the map.

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.

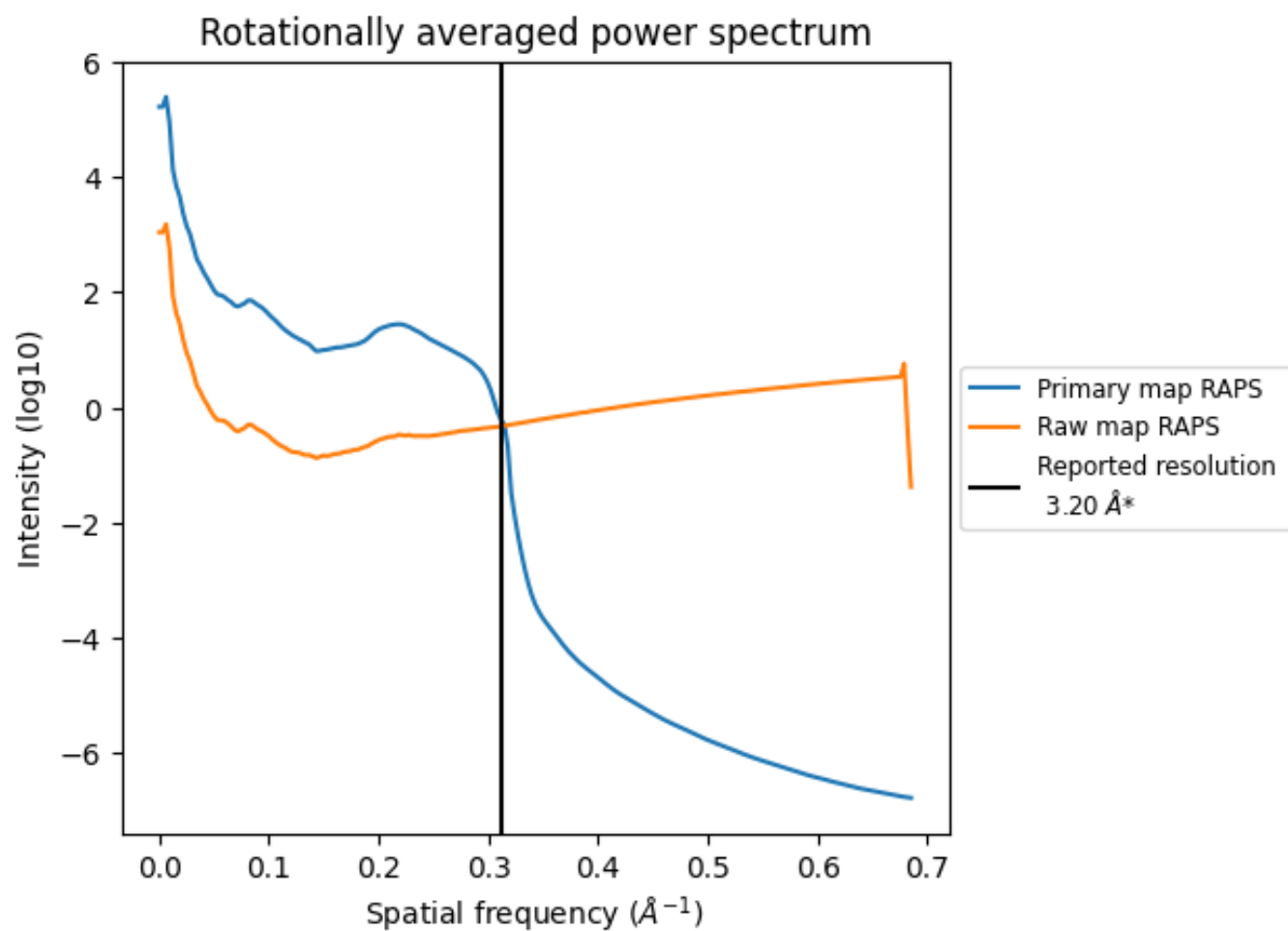
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 70 nm^3 ; this corresponds to an approximate mass of 63 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 ⓘ

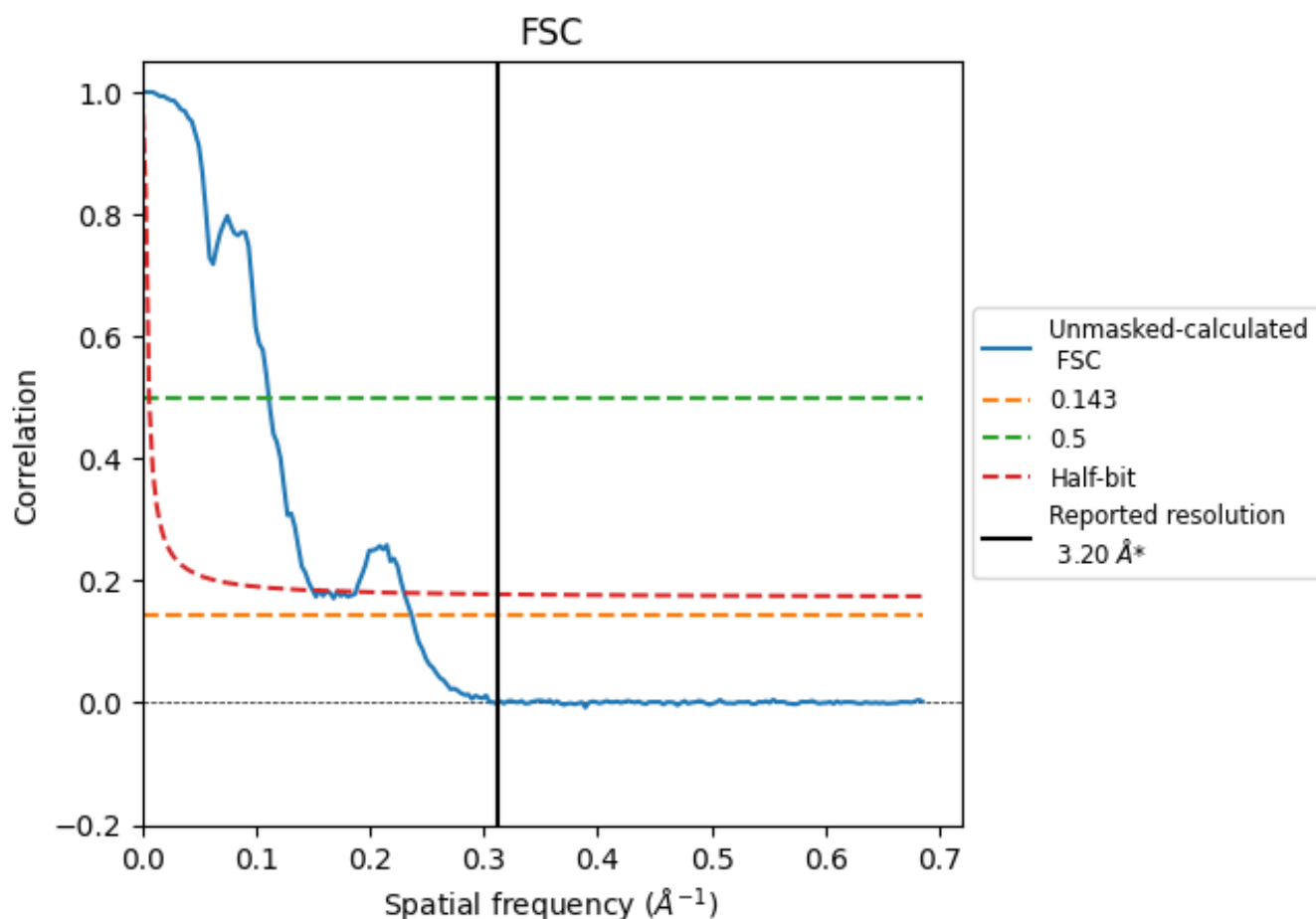


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

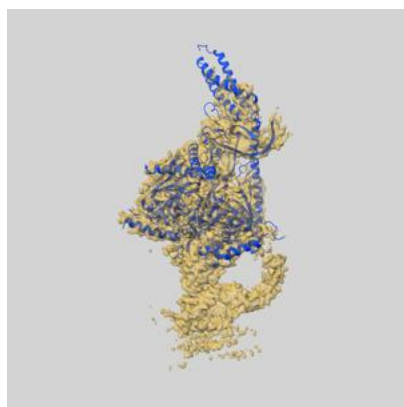
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.23	9.00	6.68

*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 4.23 differs from the reported value 3.2 by more than 10 %

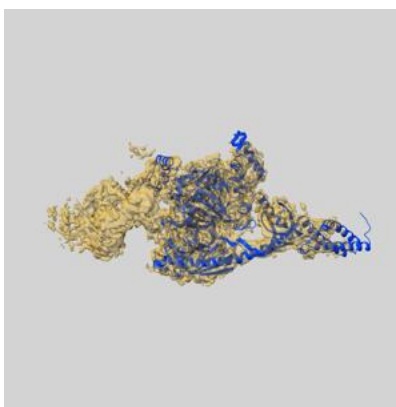
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51226 and PDB model 9GC0. Per-residue inclusion information can be found in section [3](#) on page [6](#).

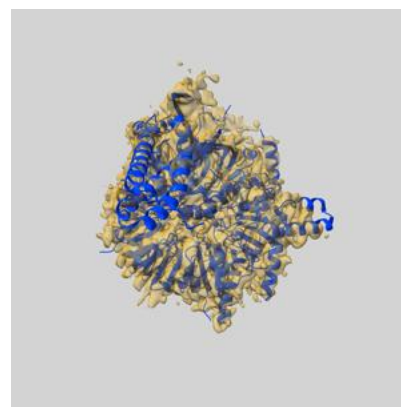
9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.024 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](#)

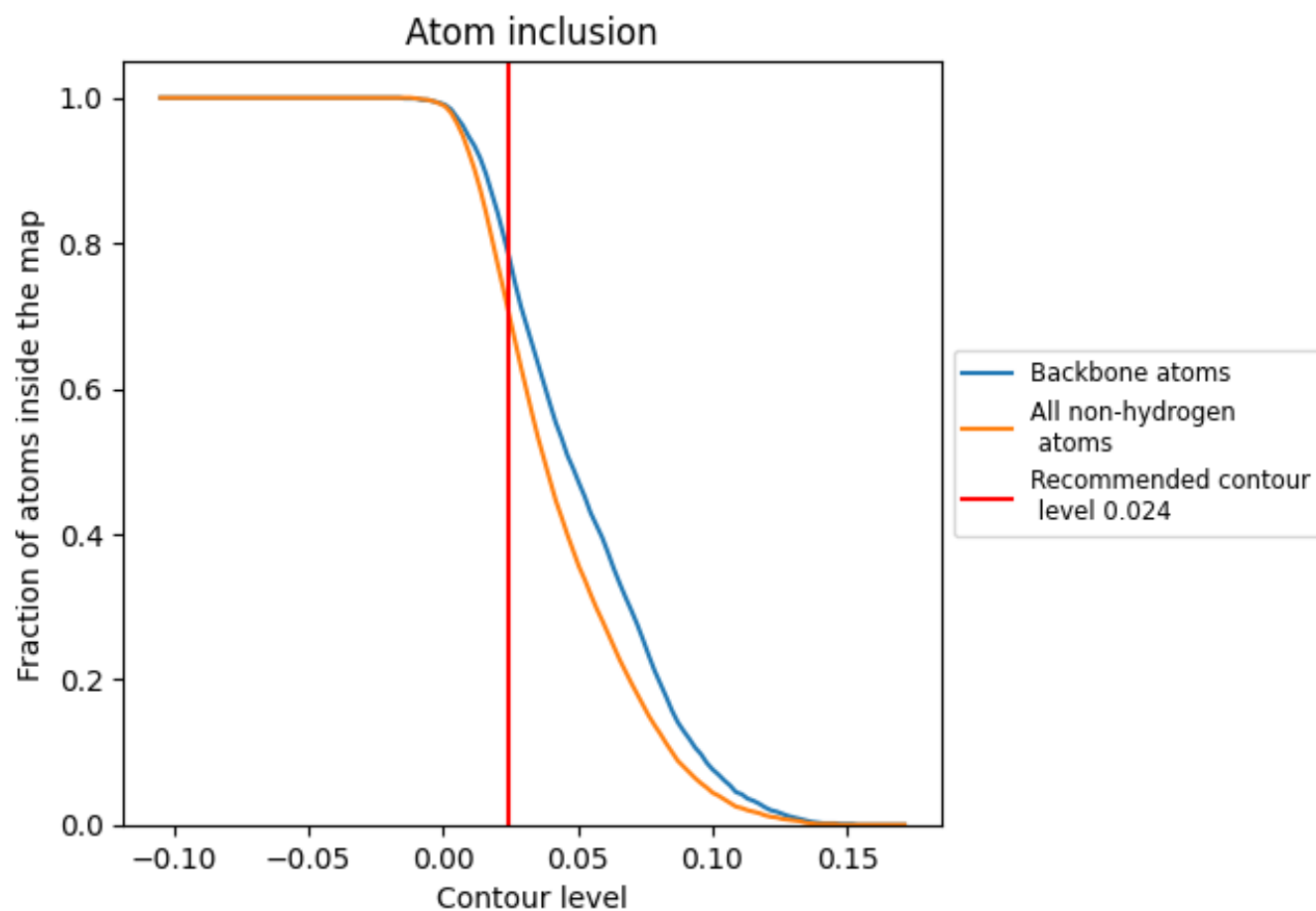


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 79% of all backbone atoms, 71% 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 (0.024) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7100	0.3930
D	0.3470	0.1760
E	0.5290	0.3260
F	0.5690	0.3300
Q	0.7490	0.3170
h	0.8450	0.4880
i	0.8260	0.4620
j	0.8690	0.4990
k	0.6840	0.4100
l	0.9160	0.5110
m	0.9010	0.5160
n	0.8860	0.5030

1.0

0.0

<0.0