



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 09:53 AM UTC

PDB ID : 9NB1 / pdb_00009nb1
EMDB ID : EMD-49206
Title : CRYO-EM STRUCTURE OF human U7 SNRNP WITH MUTANT LSM11
that disrupts contacts with CPSF73
Authors : Desotell, A.; Tong, L.
Deposited on : 2025-02-13
Resolution : 3.85 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

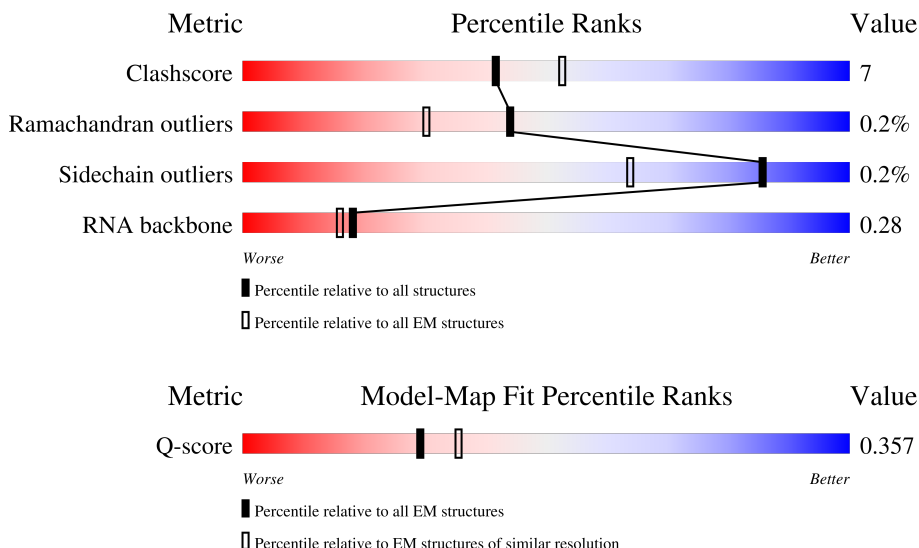
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.85 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.



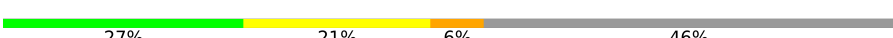
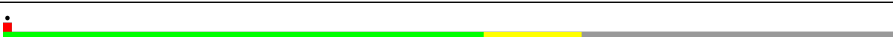
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8989 (3.35 - 4.35)

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	146	
2	C	123	
3	E	92	

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Mol	Chain	Length	Quality of chain
4	F	86	
5	G	84	
6	J	1072	
7	K	8	
8	Y	52	
9	Z	60	
10	B	95	
11	D	259	
12	H	684	
13	I	782	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 16565 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 Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	83	Total	C	N	O	S	0	0
			652	409	115	122	6		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P62318
A	-18	GLY	-	expression tag	UNP P62318
A	-17	SER	-	expression tag	UNP P62318
A	-16	SER	-	expression tag	UNP P62318
A	-15	HIS	-	expression tag	UNP P62318
A	-14	HIS	-	expression tag	UNP P62318
A	-13	HIS	-	expression tag	UNP P62318
A	-12	HIS	-	expression tag	UNP P62318
A	-11	HIS	-	expression tag	UNP P62318
A	-10	HIS	-	expression tag	UNP P62318
A	-9	SER	-	expression tag	UNP P62318
A	-8	SER	-	expression tag	UNP P62318
A	-7	GLY	-	expression tag	UNP P62318
A	-6	LEU	-	expression tag	UNP P62318
A	-5	VAL	-	expression tag	UNP P62318
A	-4	PRO	-	expression tag	UNP P62318
A	-3	ARG	-	expression tag	UNP P62318
A	-2	GLY	-	expression tag	UNP P62318
A	-1	SER	-	expression tag	UNP P62318
A	0	HIS	-	expression tag	UNP P62318

- Molecule 2 is a protein called U7 snRNA-associated Sm-like protein LSm10.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	113	Total	C	N	O	S	0	0
			903	560	174	168	1		

- Molecule 3 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	81	Total	C	N	O	S	0	0
			670	426	119	120	5		

- Molecule 4 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	74	Total	C	N	O	S	0	0
			579	375	95	104	5		

- Molecule 5 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	77	Total	C	N	O	S	0	0
			604	381	110	107	6		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	77	LEU	-	expression tag	UNP P62308
G	78	GLU	-	expression tag	UNP P62308
G	79	HIS	-	expression tag	UNP P62308
G	80	HIS	-	expression tag	UNP P62308
G	81	HIS	-	expression tag	UNP P62308
G	82	HIS	-	expression tag	UNP P62308
G	83	HIS	-	expression tag	UNP P62308
G	84	HIS	-	expression tag	UNP P62308

- Molecule 6 is a protein called Symplekin.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	306	Total	C	N	O	S	0	0
			2425	1545	416	451	13		

- Molecule 7 is a protein called CstF77.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	K	8	Total	C	N	O	0	0
			76	45	17	14		

- Molecule 8 is a RNA chain called modified H2a pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Y	28	Total	C	N	O	P	0	0
			599	269	113	189	28		

- Molecule 9 is a RNA chain called U7 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Z	30	Total	C	N	O	P	0	0
			630	282	100	218	30		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	76	Total	C	N	O	S	0	0
			612	387	111	107	7		

- Molecule 11 is a protein called U7 snRNA-associated Sm-like protein LSm11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	97	Total	C	N	O	S	0	0
			792	504	154	130	4		

- Molecule 12 is a protein called Cleavage and polyadenylation specificity factor subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	495	Total	C	N	O	S	0	0
			3951	2516	677	729	29		

- Molecule 13 is a protein called Cleavage and polyadenylation specificity factor subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	512	Total	C	N	O	S	0	0
			4070	2591	694	762	23		

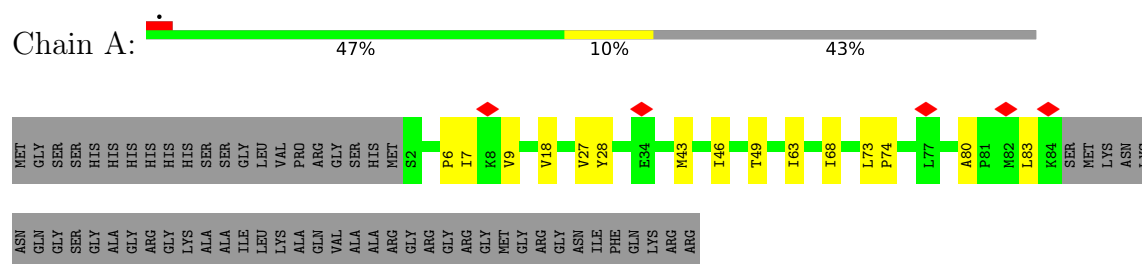
- Molecule 14 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
14	H	2	Total	Zn	0
			2	2	

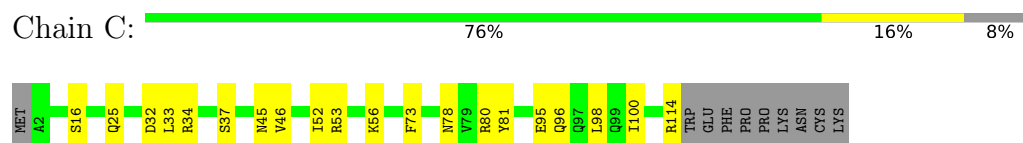
3 Residue-property plots

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

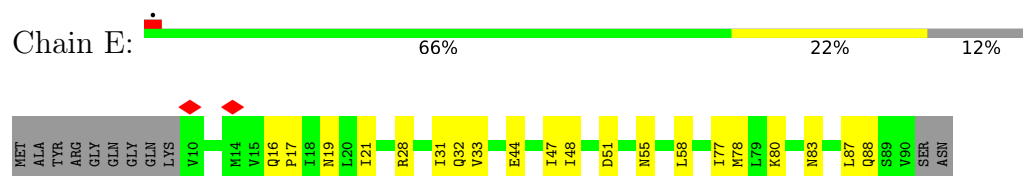
- Molecule 1: Small nuclear ribonucleoprotein Sm D3



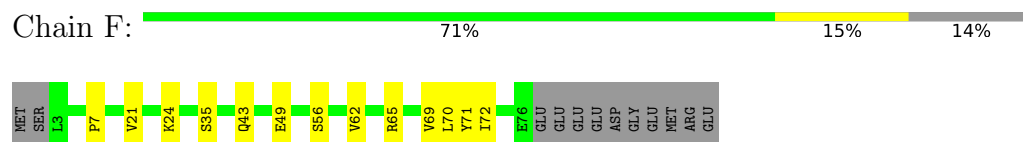
- Molecule 2: U7 snRNA-associated Sm-like protein LSm10



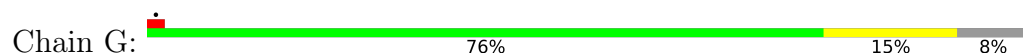
- Molecule 3: Small nuclear ribonucleoprotein E



- Molecule 4: Small nuclear ribonucleoprotein F



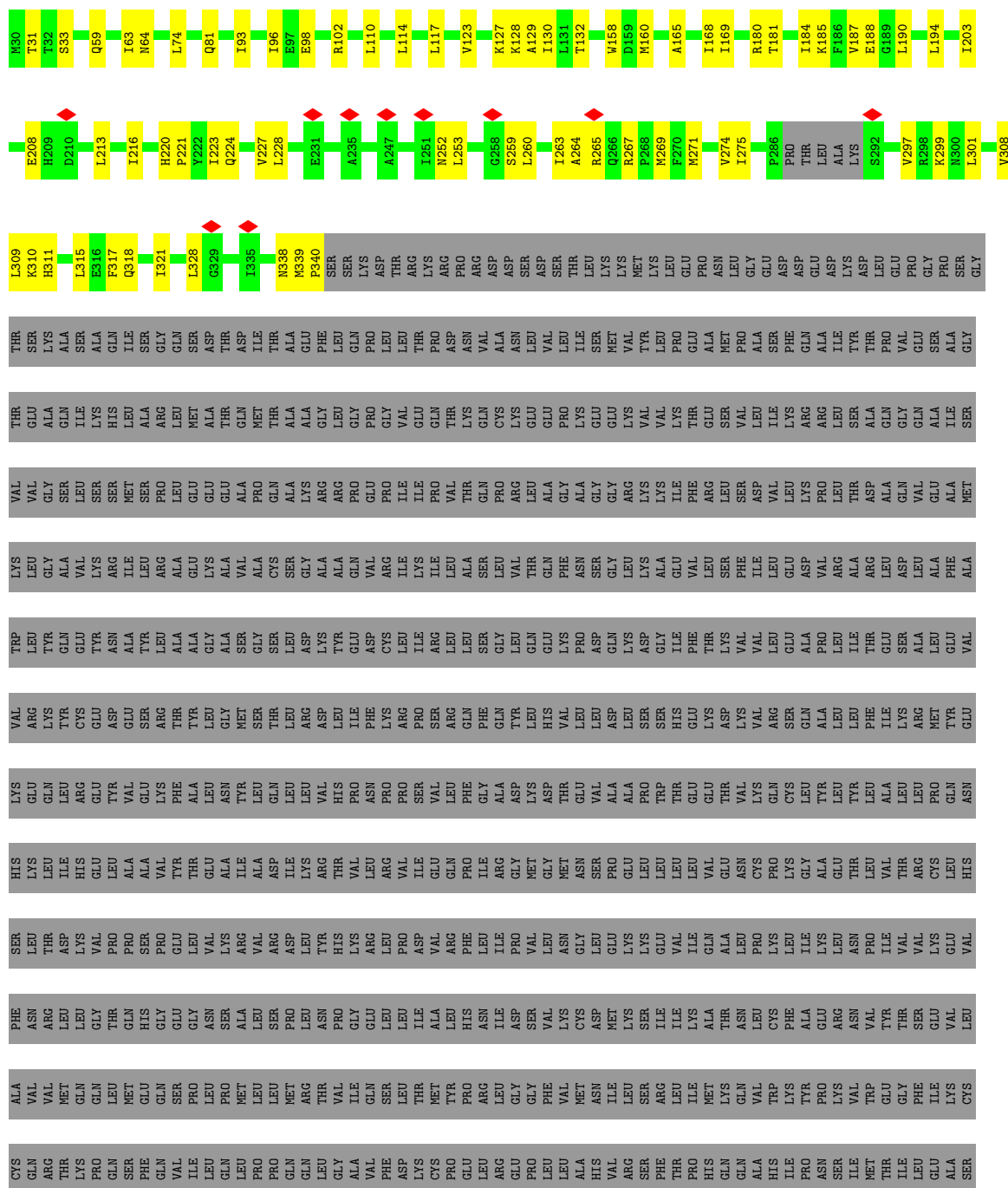
- Molecule 5: Small nuclear ribonucleoprotein G





• Molecule 6: Sympleskin

Chain J: 22% 7% 71%



• Molecule 7: CstF77

Chain K: 62% 38%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45961	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 ($e^-/\text{\AA}^2$)	56.1	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.605	Depositor
Minimum map value	-0.383	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	337.59998, 337.59998, 337.59998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.055, 1.055, 1.055	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.23	0/660	0.60	0/889
2	C	0.20	0/915	0.53	0/1236
3	E	0.15	0/678	0.45	1/910 (0.1%)
4	F	0.19	0/591	0.49	0/799
5	G	0.24	0/613	0.65	0/821
6	J	0.20	0/2459	0.50	0/3331
7	K	0.20	0/76	0.48	0/100
8	Y	0.12	0/671	0.31	0/1043
9	Z	0.11	0/701	0.29	0/1088
10	B	0.20	0/620	0.54	0/826
11	D	0.18	0/808	0.47	0/1087
12	H	0.17	0/4039	0.46	1/5459 (0.0%)
13	I	0.18	0/4151	0.47	0/5619
All	All	0.18	0/16982	0.48	2/23208 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	E	48	ILE	N-CA-C	-5.29	107.67	112.96
12	H	335	GLY	N-CA-C	5.05	121.67	112.37

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	652	0	670	9	0
2	C	903	0	911	14	0
3	E	670	0	696	14	0
4	F	579	0	590	11	0
5	G	604	0	621	11	0
6	J	2425	0	2522	43	0
7	K	76	0	71	3	0
8	Y	599	0	304	3	0
9	Z	630	0	317	3	0
10	B	612	0	634	14	0
11	D	792	0	814	10	0
12	H	3951	0	3913	53	0
13	I	4070	0	4098	58	0
14	H	2	0	0	0	0
All	All	16565	0	16161	222	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 7.

All (222) 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:G:35:ASP:OD1	5:G:36:PRO:HD2	1.75	0.86
10:B:26:ILE:HB	10:B:48:PHE:HB2	1.70	0.74
12:H:488:ARG:HA	13:I:622:LYS:HB2	1.69	0.73
6:J:130:ILE:HG12	6:J:168:ILE:HD11	1.72	0.71
13:I:211:ARG:HE	13:I:213:LYS:HE3	1.56	0.69
6:J:123:VAL:HG12	6:J:127:LYS:HE2	1.76	0.68
13:I:270:ASN:HB2	13:I:273:SER:HB3	1.77	0.67
6:J:271:MET:HA	6:J:274:VAL:HG12	1.77	0.67
12:H:409:LEU:HD22	12:H:411:PRO:HG3	1.77	0.66
5:G:35:ASP:OD1	5:G:36:PRO:CD	2.42	0.66
12:H:53:LEU:HD12	12:H:54:PRO:HD2	1.78	0.65
13:I:17:SER:HB2	13:I:360:THR:HG22	1.78	0.65
3:E:51:ASP:HB2	4:F:7:PRO:HG2	1.79	0.64
12:H:382:LEU:HD12	12:H:383:PRO:HD2	1.79	0.64
9:Z:20:G:H5'	9:Z:21:A:H5''	1.81	0.63
12:H:67:LEU:HB3	12:H:93:THR:HG22	1.80	0.63
13:I:159:ILE:HD11	13:I:189:LEU:HD21	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:721:ARG:HH22	13:I:116:LEU:HB3	1.64	0.62
12:H:485:LEU:HD21	12:H:492:TYR:HD1	1.63	0.62
6:J:310:LYS:HE2	6:J:338:ASN:HD21	1.66	0.61
13:I:31:LEU:HB2	13:I:55:ILE:HD11	1.82	0.61
5:G:48:MET:HG3	5:G:54:GLN:HG3	1.81	0.61
13:I:170:ILE:O	13:I:170:ILE:HG22	2.00	0.61
13:I:169:GLU:HB2	13:I:196:SER:H	1.66	0.60
10:B:21:LEU:HD12	10:B:25:ARG:HB3	1.84	0.60
12:H:331:MET:HE3	12:H:362:THR:HG21	1.84	0.59
13:I:97:PHE:HE1	13:I:240:ALA:HB3	1.67	0.59
2:C:73:PHE:HB3	10:B:80:MET:HB3	1.84	0.59
6:J:96:ILE:HG21	6:J:114:LEU:HD21	1.83	0.59
6:J:339:MET:HE3	6:J:340:PRO:HD2	1.83	0.59
2:C:25:GLN:HE22	2:C:45:ASN:H	1.50	0.59
12:H:269:TYR:HB3	12:H:311:LEU:HB2	1.84	0.59
13:I:291:LEU:HD11	13:I:302:PRO:HB3	1.84	0.59
1:A:27:VAL:HB	1:A:49:THR:HB	1.85	0.58
2:C:46:VAL:HG12	2:C:52:ILE:HA	1.86	0.58
3:E:17:PRO:HB3	5:G:61:VAL:HG21	1.84	0.58
7:K:716:ASP:HB2	7:K:719:ARG:HG3	1.85	0.58
12:H:275:ALA:O	12:H:279:MET:HG2	2.03	0.57
2:C:32:ASP:HB2	2:C:81:TYR:HB2	1.86	0.57
12:H:286:VAL:HG11	12:H:297:ILE:HD13	1.86	0.57
12:H:55:TYR:HB3	12:H:58:LEU:HD23	1.87	0.57
12:H:245:ARG:HD3	12:H:248:GLU:HB3	1.86	0.57
13:I:269:LEU:HD11	13:I:317:LEU:HD22	1.84	0.57
3:E:51:ASP:HB3	3:E:55:ASN:HB3	1.87	0.57
12:H:153:CYS:HB2	12:H:163:ALA:HB1	1.87	0.57
13:I:386:LYS:H	13:I:520:THR:HA	1.70	0.56
13:I:293:ARG:HA	13:I:296:GLU:HG2	1.87	0.56
12:H:24:GLY:HA2	12:H:75:ASP:HB2	1.87	0.56
1:A:28:TYR:CZ	5:G:69:MET:HE3	2.41	0.56
13:I:283:GLN:HB3	13:I:286:TRP:HB2	1.87	0.55
5:G:17:LEU:HD13	5:G:70:LEU:HD12	1.88	0.55
6:J:31:THR:HG22	6:J:33:SER:H	1.72	0.55
13:I:169:GLU:HA	13:I:169:GLU:OE1	2.06	0.55
2:C:33:LEU:HD12	2:C:37:SER:HB3	1.88	0.55
13:I:559:ARG:HH22	13:I:601:SER:HB3	1.72	0.55
2:C:56:LYS:HE3	2:C:56:LYS:HA	1.89	0.54
6:J:96:ILE:HD11	6:J:110:LEU:HB3	1.90	0.54
6:J:74:LEU:HD11	6:J:110:LEU:HD21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:I:164:LYS:HG2	13:I:168:GLU:HG3	1.89	0.54
4:F:49:GLU:HB2	4:F:56:SER:HB3	1.90	0.54
12:H:209:THR:HA	12:H:399:TYR:HB2	1.90	0.54
1:A:18:VAL:HG12	1:A:74:PRO:HD3	1.90	0.54
12:H:185:ASP:HB2	12:H:188:LEU:HB2	1.90	0.54
13:I:35:GLY:HA2	13:I:70:ALA:H	1.73	0.54
3:E:58:LEU:HD12	3:E:77:ILE:HD11	1.91	0.53
6:J:63:ILE:HG21	6:J:98:GLU:HG3	1.90	0.53
6:J:265:ARG:HH22	6:J:308:VAL:HA	1.74	0.53
12:H:352:VAL:HB	12:H:386:MET:HE2	1.91	0.53
12:H:73:HIS:HE1	12:H:158:HIS:NE2	2.05	0.53
12:H:346:THR:HG22	12:H:382:LEU:HD11	1.92	0.52
13:I:64:ASP:HA	13:I:97:PHE:CD2	2.44	0.52
3:E:16:GLN:HG3	3:E:19:ASN:H	1.74	0.52
4:F:62:VAL:HG13	11:D:355:LEU:HD13	1.91	0.52
2:C:34:ARG:HA	2:C:80:ARG:HD2	1.91	0.52
3:E:88:GLN:HA	5:G:60:VAL:HG12	1.90	0.52
13:I:151:ALA:HB2	13:I:159:ILE:HG23	1.92	0.52
8:Y:49:A:H2'	8:Y:50:C:C6	2.45	0.52
4:F:35:SER:H	4:F:43:GLN:HE21	1.58	0.51
6:J:184:ILE:HA	6:J:187:VAL:HG12	1.91	0.51
11:D:171:VAL:HG12	11:D:356:VAL:HA	1.92	0.51
6:J:318:GLN:HA	6:J:321:ILE:HG22	1.93	0.51
10:B:38:MET:HE3	10:B:40:LEU:HD11	1.93	0.51
13:I:383:LYS:HG2	13:I:520:THR:HG22	1.91	0.51
6:J:309:LEU:HD23	6:J:338:ASN:HB3	1.91	0.51
11:D:187:LEU:HD21	11:D:190:PHE:HB3	1.91	0.51
13:I:134:ILE:HA	13:I:147:THR:HG22	1.91	0.51
13:I:210:PRO:HG2	13:I:215:ARG:HE	1.76	0.51
12:H:250:LEU:HD12	12:H:308:ILE:HD13	1.94	0.50
5:G:19:LEU:HB3	5:G:70:LEU:HD13	1.93	0.50
6:J:301:LEU:HG	6:J:328:LEU:HD11	1.94	0.50
12:H:336:LEU:HD23	12:H:340:LEU:CD1	2.41	0.50
3:E:32:GLN:HG3	3:E:44:GLU:HB3	1.93	0.49
12:H:182:ARG:HG2	12:H:191:ALA:HB3	1.93	0.49
1:A:73:LEU:HB2	10:B:69:LEU:HG	1.94	0.49
6:J:315:LEU:HA	6:J:318:GLN:HG3	1.94	0.49
3:E:33:VAL:HG12	3:E:87:LEU:HD13	1.95	0.49
3:E:83:ASN:O	3:E:83:ASN:ND2	2.45	0.49
12:H:424:MET:HE1	12:H:447:ASN:HB2	1.93	0.49
5:G:57:ILE:HD12	5:G:60:VAL:HG11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:H:198:PRO:HD2	12:H:409:LEU:HD21	1.95	0.49
12:H:463:LEU:HA	13:I:609:ARG:HA	1.94	0.49
12:H:488:ARG:HH12	12:H:489:ASN:HB2	1.78	0.49
4:F:24:LYS:HA	4:F:70:LEU:HD12	1.95	0.49
13:I:60:LEU:HD23	13:I:84:ILE:HG23	1.94	0.48
2:C:16:SER:HA	11:D:191:ASP:OD1	2.14	0.48
6:J:194:LEU:HD23	6:J:228:LEU:HB2	1.95	0.48
12:H:37:ILE:HG22	12:H:66:LEU:HB2	1.95	0.48
3:E:28:ARG:O	3:E:28:ARG:HD3	2.13	0.48
4:F:70:LEU:HD22	4:F:71:TYR:HD2	1.77	0.48
6:J:129:ALA:HA	6:J:132:THR:HG22	1.96	0.48
2:C:34:ARG:HD2	9:Z:28:C:C4	2.49	0.48
6:J:160:MET:HE3	6:J:160:MET:O	2.14	0.48
12:H:291:ASP:HA	12:H:294:ARG:HG2	1.95	0.48
12:H:485:LEU:HD21	12:H:492:TYR:CD1	2.47	0.48
6:J:275:ILE:HG21	6:J:317:PHE:HD1	1.79	0.48
6:J:165:ALA:HA	6:J:168:ILE:HG22	1.97	0.47
12:H:97:HIS:CD2	13:I:285:GLU:HB2	2.48	0.47
12:H:166:MET:HE2	12:H:175:LEU:HD13	1.95	0.47
13:I:109:GLU:HG2	13:I:381:LEU:HD13	1.96	0.47
2:C:53:ARG:HD2	2:C:73:PHE:HB2	1.97	0.47
3:E:31:ILE:HD13	3:E:47:ILE:HD11	1.97	0.47
10:B:38:MET:HE3	10:B:38:MET:HB3	1.80	0.47
13:I:223:VAL:HG12	13:I:233:VAL:HG11	1.96	0.47
6:J:188:GLU:CD	6:J:259:SER:HB3	2.40	0.47
6:J:224:GLN:HB3	6:J:227:VAL:HG12	1.95	0.47
12:H:173:LYS:HG3	12:H:198:PRO:HA	1.96	0.47
12:H:207:TYR:CE2	12:H:396:HIS:HB2	2.50	0.47
2:C:78:ASN:HD22	10:B:78:VAL:HG22	1.80	0.47
6:J:64:ASN:HA	6:J:102:ARG:HH12	1.80	0.47
6:J:260:LEU:HA	6:J:263:ILE:HG12	1.96	0.46
11:D:174:ARG:HG2	11:D:354:LEU:HD12	1.96	0.46
12:H:336:LEU:HD23	12:H:340:LEU:HD12	1.97	0.46
12:H:465:LYS:HB2	12:H:493:HIS:ND1	2.30	0.46
3:E:17:PRO:O	3:E:21:ILE:HG12	2.15	0.46
10:B:32:LYS:HB2	10:B:41:ILE:HG23	1.98	0.46
13:I:238:ASP:HA	13:I:331:PRO:HD3	1.97	0.46
13:I:618:LEU:HB3	13:I:627:GLU:HB3	1.97	0.46
1:A:6:PRO:HA	1:A:9:VAL:HG12	1.97	0.46
6:J:93:ILE:HG21	6:J:128:LYS:HG2	1.97	0.46
2:C:114:ARG:HH21	12:H:366:HIS:CG	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:I:299:ARG:O	13:I:299:ARG:HG2	2.15	0.46
5:G:6:PRO:HA	5:G:36:PRO:HB3	1.98	0.46
13:I:36:TRP:CD1	13:I:70:ALA:HB2	2.51	0.46
10:B:20:ILE:HG23	10:B:78:VAL:HB	1.97	0.46
12:H:38:MET:HE3	12:H:64:ILE:HG21	1.97	0.46
13:I:620:PHE:HB3	13:I:627:GLU:H	1.81	0.46
13:I:287:MET:HE1	13:I:303:PHE:CE2	2.52	0.45
13:I:281:LYS:HB3	13:I:303:PHE:HB2	1.98	0.45
4:F:21:VAL:HG22	4:F:72:ILE:HG13	1.98	0.45
7:K:721:ARG:NH2	13:I:116:LEU:HB3	2.31	0.45
13:I:59:LEU:HD11	13:I:146:ILE:HD13	1.98	0.45
13:I:593:LEU:HD23	13:I:594:HIS:HB2	1.97	0.45
1:A:63:ILE:HG21	1:A:68:ILE:HD11	1.99	0.45
6:J:158:TRP:CZ3	6:J:223:ILE:HG12	2.52	0.44
6:J:180:ARG:O	6:J:184:ILE:HG12	2.17	0.44
6:J:81:GLN:HG3	6:J:117:LEU:HD11	1.99	0.44
3:E:78:MET:HB3	4:F:72:ILE:HG22	2.00	0.44
6:J:169:ILE:HD11	6:J:190:LEU:HD21	1.99	0.44
4:F:65:ARG:HD2	11:D:353:VAL:HG13	2.00	0.44
2:C:95:GLU:HA	2:C:98:LEU:HB2	2.00	0.44
12:H:243:LEU:HD11	12:H:278:CYS:SG	2.58	0.44
9:Z:31:G:H5'	10:B:22:GLN:HG2	2.00	0.44
12:H:497:PRO:HG3	13:I:630:TRP:HZ3	1.82	0.44
12:H:53:LEU:HD11	12:H:82:TRP:CZ3	2.52	0.43
13:I:563:ILE:HG12	13:I:574:LEU:HD23	2.00	0.43
13:I:610:LEU:HD13	13:I:614:LEU:HD21	2.00	0.43
6:J:213:LEU:O	6:J:216:ILE:HG12	2.18	0.43
6:J:203:ILE:HG12	6:J:208:GLU:HA	2.01	0.43
12:H:166:MET:HE1	12:H:194:PRO:HB3	2.00	0.43
12:H:201:LEU:HB3	12:H:414:VAL:HG12	1.99	0.43
13:I:19:LEU:HG	13:I:67:HIS:CD2	2.54	0.43
13:I:550:LYS:HD3	13:I:577:CYS:SG	2.58	0.43
12:H:285:TYR:HE1	13:I:285:GLU:HB3	1.84	0.43
12:H:85:GLN:NE2	12:H:130:GLU:HG3	2.34	0.43
12:H:207:TYR:CE2	12:H:394:SER:HB2	2.54	0.43
12:H:257:TRP:CZ3	12:H:268:ILE:HG13	2.54	0.43
1:A:80:ALA:HB3	1:A:83:LEU:HG	2.01	0.42
6:J:267:ARG:HH21	6:J:269:MET:HB2	1.84	0.42
12:H:261:PRO:HA	12:H:264:HIS:CE1	2.54	0.42
13:I:169:GLU:HB2	13:I:195:PRO:HA	2.01	0.42
12:H:182:ARG:HD2	12:H:405:PHE:HD2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:I:266:LEU:HD13	13:I:307:HIS:HB3	2.01	0.42
12:H:232:ARG:HB3	12:H:349:ARG:HH21	1.83	0.42
12:H:494:ILE:HD13	13:I:631:ILE:HD11	2.00	0.42
6:J:265:ARG:NH1	6:J:311:HIS:HB2	2.35	0.42
4:F:43:GLN:HB3	11:D:155:PRO:HG3	2.02	0.42
13:I:102:TYR:HD2	13:I:116:LEU:HG	1.84	0.42
6:J:59:GLN:HE22	6:J:98:GLU:HG2	1.84	0.42
12:H:80:LEU:HD23	12:H:103:TYR:CZ	2.54	0.42
13:I:232:ASN:H	13:I:351:ASN:HD22	1.68	0.42
6:J:252:ASN:C	6:J:252:ASN:HD22	2.28	0.41
6:J:299:LYS:HA	6:J:299:LYS:HD2	1.91	0.41
10:B:15:TYR:HD1	10:B:86:PRO:HG3	1.85	0.41
10:B:15:TYR:CD1	10:B:86:PRO:HG3	2.55	0.41
8:Y:48:A:H2'	8:Y:49:A:C8	2.55	0.41
13:I:28:PHE:HE2	13:I:30:PHE:CE1	2.38	0.41
5:G:12:PHE:HB3	5:G:17:LEU:HD11	2.02	0.41
11:D:168:LYS:HE3	11:D:184:THR:HG22	2.01	0.41
13:I:98:MET:HE3	13:I:114:PHE:CZ	2.56	0.41
13:I:353:ILE:HB	13:I:535:VAL:HG22	2.02	0.41
6:J:190:LEU:HD12	6:J:194:LEU:HD13	2.01	0.41
11:D:159:LEU:O	11:D:163:ILE:HG12	2.19	0.41
8:Y:42:A:H2'	8:Y:43:G:C8	2.56	0.41
10:B:17:MET:SD	10:B:80:MET:SD	3.18	0.41
6:J:264:ALA:HB2	6:J:274:VAL:HG21	2.02	0.41
11:D:201:VAL:HG11	11:D:346:ILE:HG12	2.02	0.41
13:I:45:ILE:HD12	13:I:45:ILE:HA	1.93	0.41
1:A:43:MET:HG2	1:A:46:ILE:HG22	2.03	0.41
13:I:64:ASP:HA	13:I:97:PHE:HD2	1.84	0.41
13:I:93:MET:HE2	13:I:155:ILE:HG21	2.02	0.41
1:A:7:ILE:HD13	1:A:7:ILE:HA	1.96	0.41
6:J:181:THR:O	6:J:185:LYS:HG2	2.21	0.41
3:E:80:LYS:HD2	4:F:69:VAL:HG23	2.02	0.40
6:J:220:HIS:HA	6:J:221:PRO:HD3	1.98	0.40
6:J:339:MET:HE3	6:J:339:MET:HA	2.02	0.40
12:H:174:LEU:HD12	12:H:200:ILE:HB	2.02	0.40
12:H:301:ASN:O	12:H:304:VAL:HG12	2.21	0.40
6:J:253:LEU:HD11	6:J:297:VAL:HG22	2.03	0.40
10:B:8:LYS:HE3	10:B:8:LYS:HB3	1.90	0.40
13:I:169:GLU:OE1	13:I:169:GLU:CA	2.70	0.40
13:I:287:MET:HE1	13:I:303:PHE:HE2	1.87	0.40
2:C:96:GLN:O	2:C:100:ILE:HG12	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	81/146 (56%)	75 (93%)	6 (7%)	0	100	100
2	C	111/123 (90%)	102 (92%)	9 (8%)	0	100	100
3	E	79/92 (86%)	76 (96%)	3 (4%)	0	100	100
4	F	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
5	G	75/84 (89%)	72 (96%)	3 (4%)	0	100	100
6	J	302/1072 (28%)	297 (98%)	5 (2%)	0	100	100
7	K	6/8 (75%)	6 (100%)	0	0	100	100
10	B	72/95 (76%)	68 (94%)	4 (6%)	0	100	100
11	D	93/259 (36%)	83 (89%)	10 (11%)	0	100	100
12	H	491/684 (72%)	459 (94%)	32 (6%)	0	100	100
13	I	506/782 (65%)	465 (92%)	38 (8%)	3 (1%)	21	55
All	All	1888/3431 (55%)	1773 (94%)	112 (6%)	3 (0%)	44	74

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	I	703	LEU
13	I	165	ASP
13	I	169	GLU

5.3.2 Protein sidechains [i](#)

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	73/118 (62%)	73 (100%)	0	100	100
2	C	100/110 (91%)	100 (100%)	0	100	100
3	E	76/84 (90%)	76 (100%)	0	100	100
4	F	63/74 (85%)	63 (100%)	0	100	100
5	G	67/74 (90%)	67 (100%)	0	100	100
6	J	274/946 (29%)	274 (100%)	0	100	100
7	K	8/8 (100%)	8 (100%)	0	100	100
10	B	69/85 (81%)	69 (100%)	0	100	100
11	D	86/203 (42%)	86 (100%)	0	100	100
12	H	431/602 (72%)	430 (100%)	1 (0%)	87	87
13	I	457/695 (66%)	454 (99%)	3 (1%)	76	78
All	All	1704/2999 (57%)	1700 (100%)	4 (0%)	85	87

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	H	336	LEU
13	I	164	LYS
13	I	167	GLU
13	I	168	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
2	C	25	GLN
2	C	40	HIS
4	F	43	GLN
6	J	113	ASN
6	J	238	GLN
6	J	252	ASN
6	J	262	ASN
6	J	300	ASN
6	J	304	HIS
12	H	73	HIS

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Mol	Chain	Res	Type
12	H	264	HIS
12	H	401	GLN
13	I	209	GLN
13	I	312	HIS
13	I	572	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	Y	27/52 (51%)	11 (40%)	1 (3%)
9	Z	29/60 (48%)	11 (37%)	1 (3%)
All	All	56/112 (50%)	22 (39%)	2 (3%)

All (22) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	Y	26	A
8	Y	27	C
8	Y	28	U
8	Y	29	G
8	Y	31	A
8	Y	35	G
8	Y	36	A
8	Y	37	U
8	Y	42	A
8	Y	47	U
8	Y	50	C
9	Z	4	U
9	Z	11	G
9	Z	20	G
9	Z	21	A
9	Z	23	U
9	Z	24	U
9	Z	26	G
9	Z	27	U
9	Z	28	C
9	Z	29	U
9	Z	32	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	Y	49	A
9	Z	26	G

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.

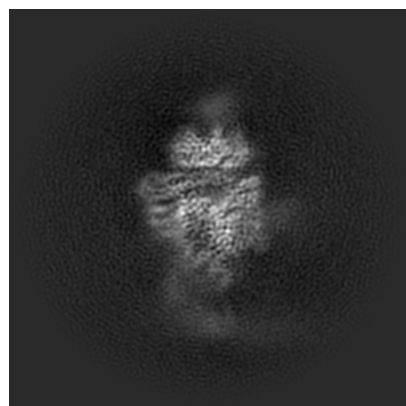
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49206. These allow visual inspection of the internal detail of the map and identification of artifacts.

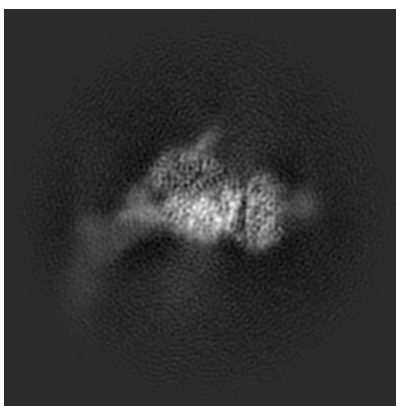
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

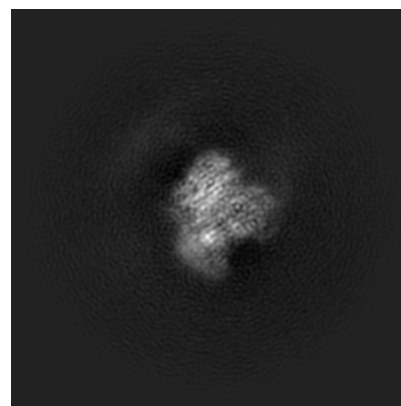
6.1.1 Primary map



X

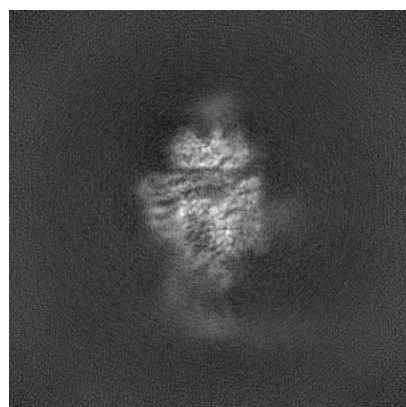


Y

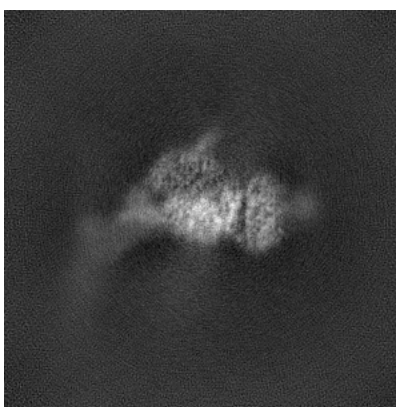


Z

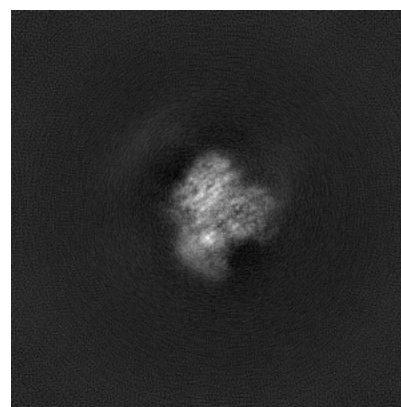
6.1.2 Raw map



X



Y

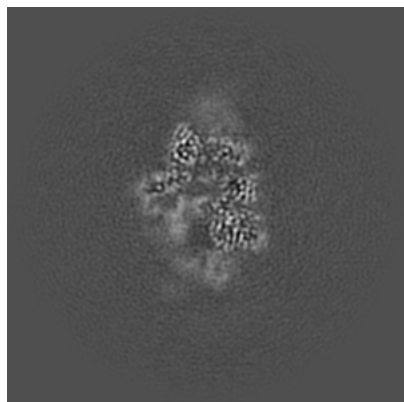


Z

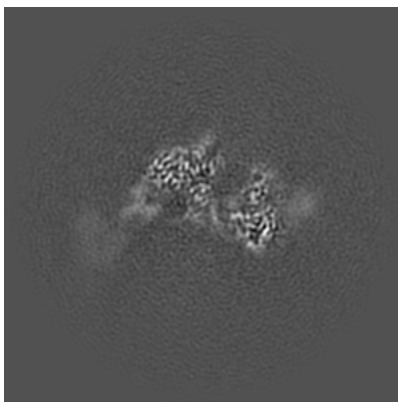
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

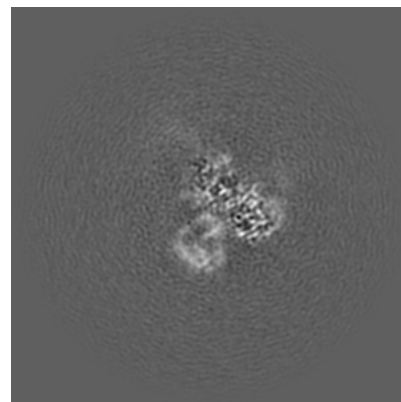
6.2.1 Primary map



X Index: 160

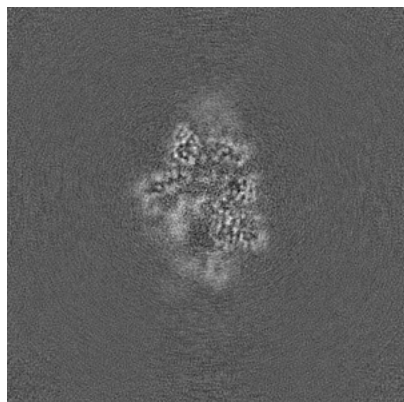


Y Index: 160

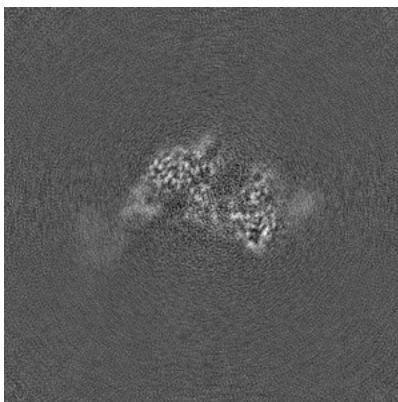


Z Index: 160

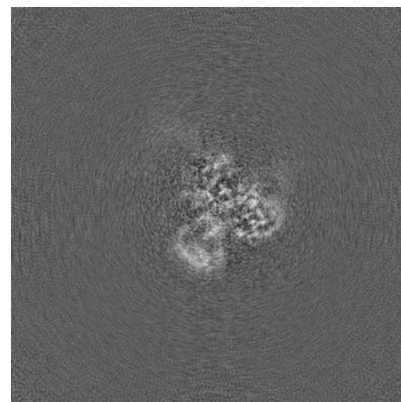
6.2.2 Raw map



X Index: 160



Y Index: 160

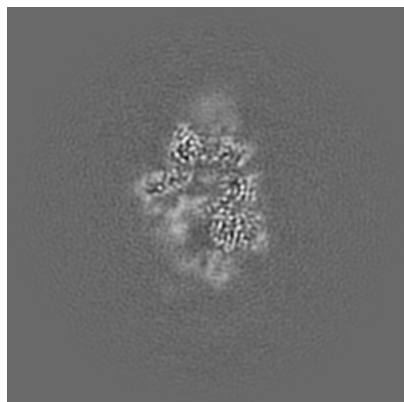


Z Index: 160

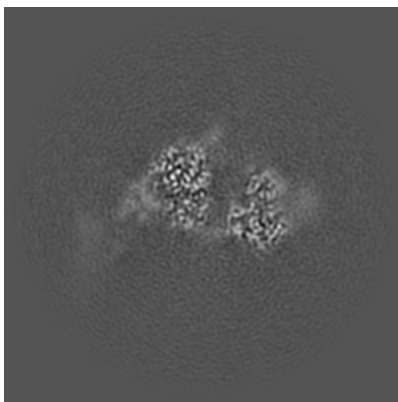
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

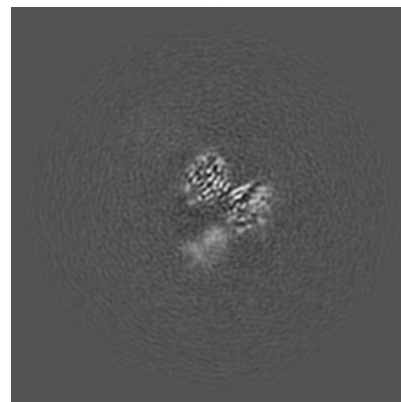
6.3.1 Primary map



X Index: 161

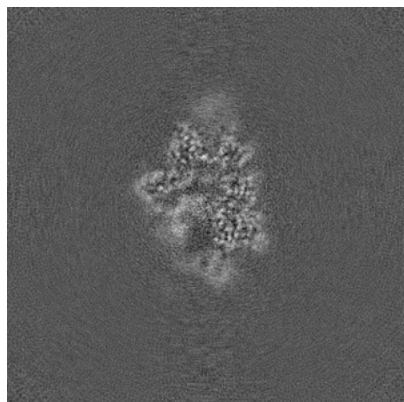


Y Index: 166

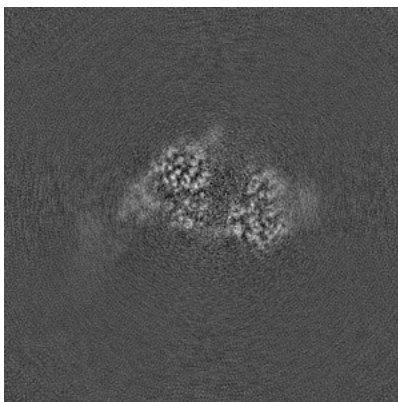


Z Index: 142

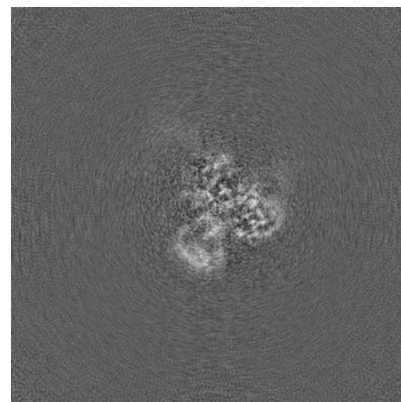
6.3.2 Raw map



X Index: 162



Y Index: 166

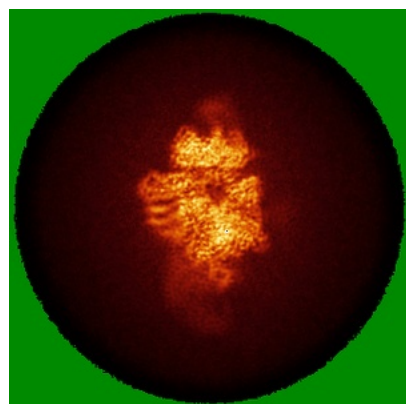


Z Index: 160

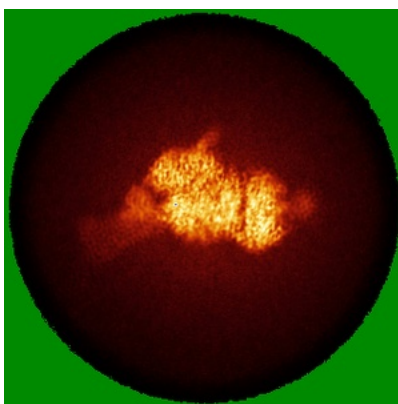
The images above show the largest variance slices of the map in three orthogonal directions.

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

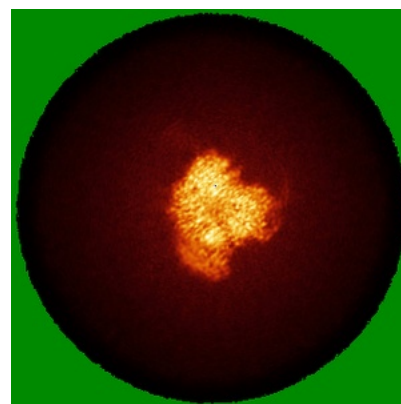
6.4.1 Primary map



X

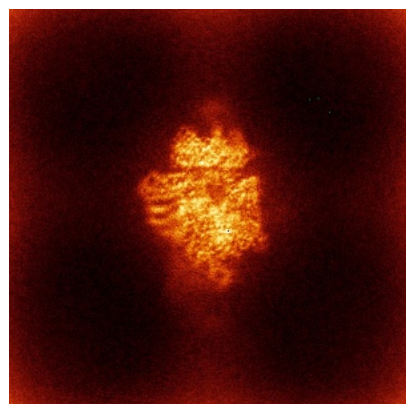


Y

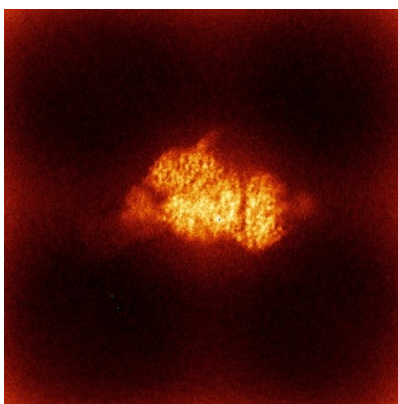


Z

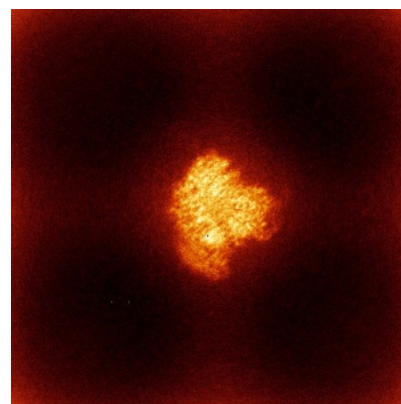
6.4.2 Raw map



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.

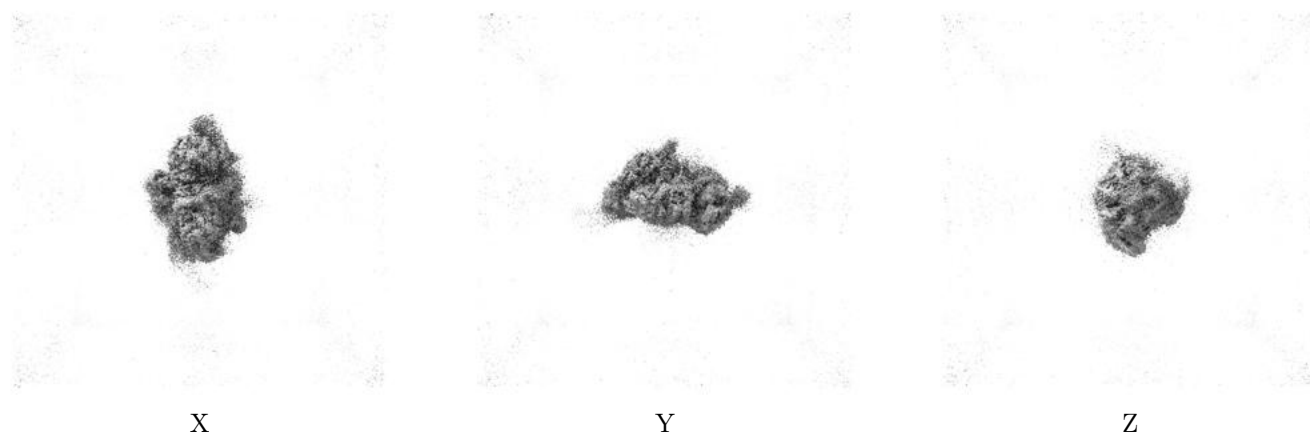
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. 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.

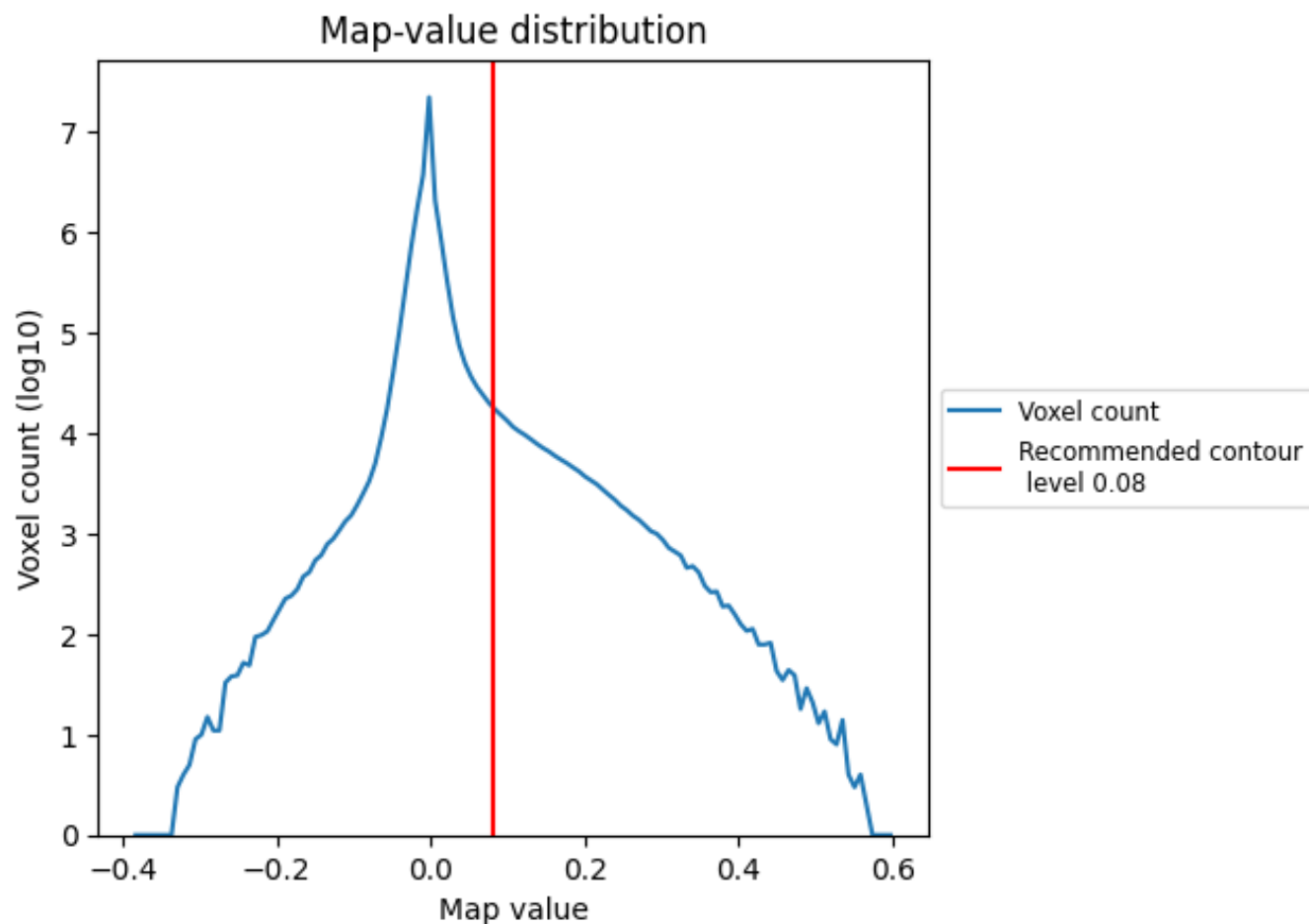
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

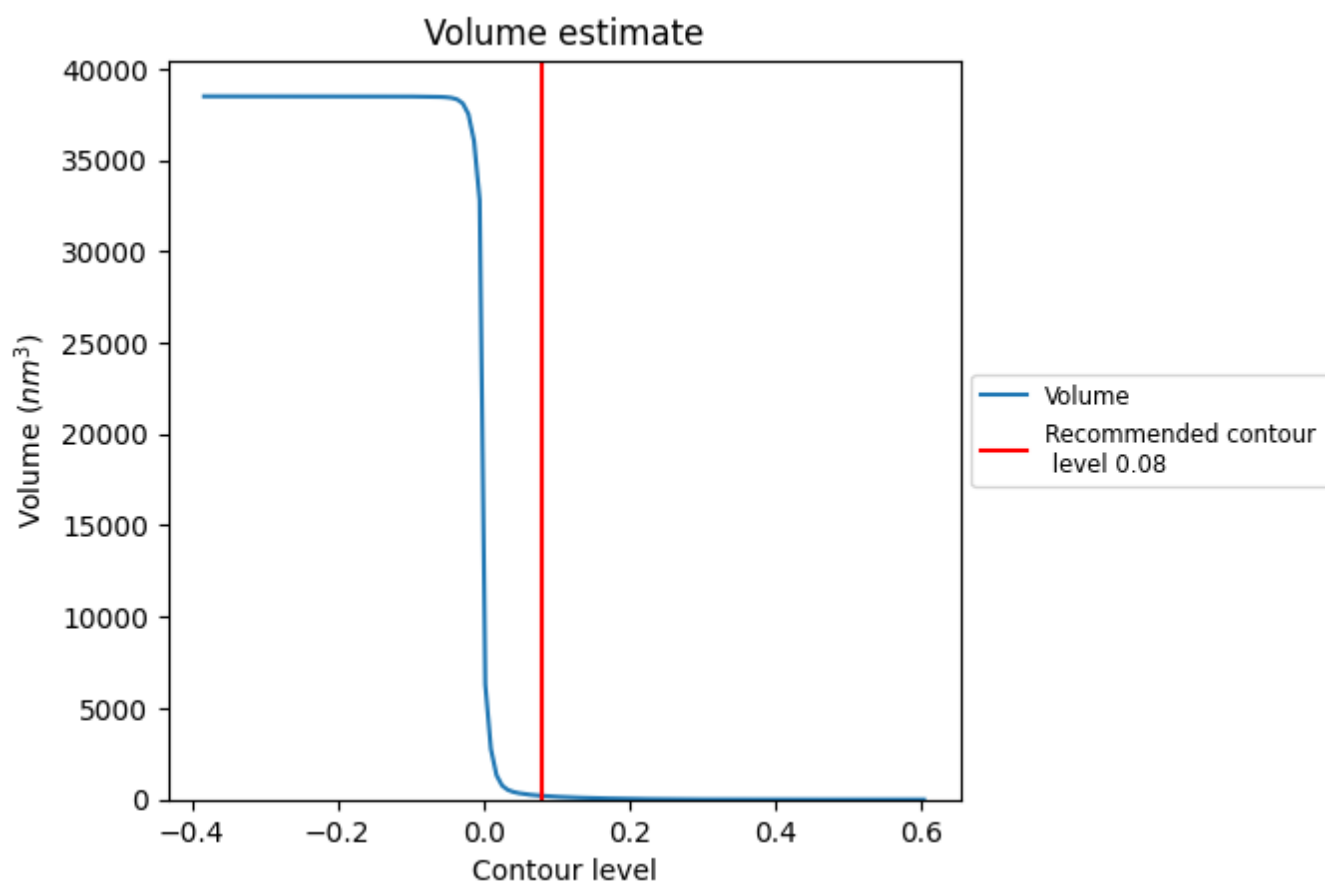
This section contains the results of statistical analysis of the map.

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.

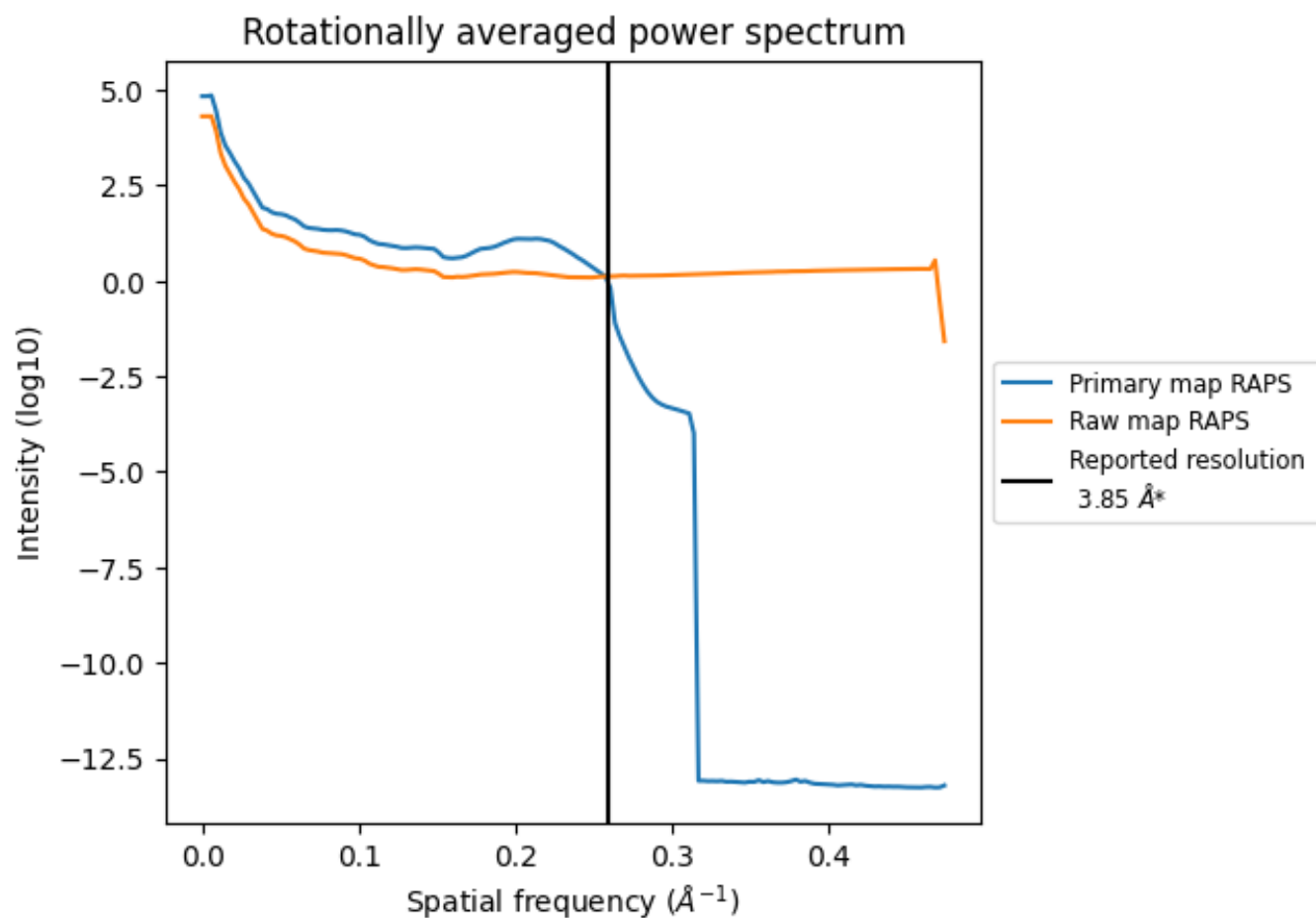
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 207 nm³; this corresponds to an approximate mass of 187 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 ⓘ

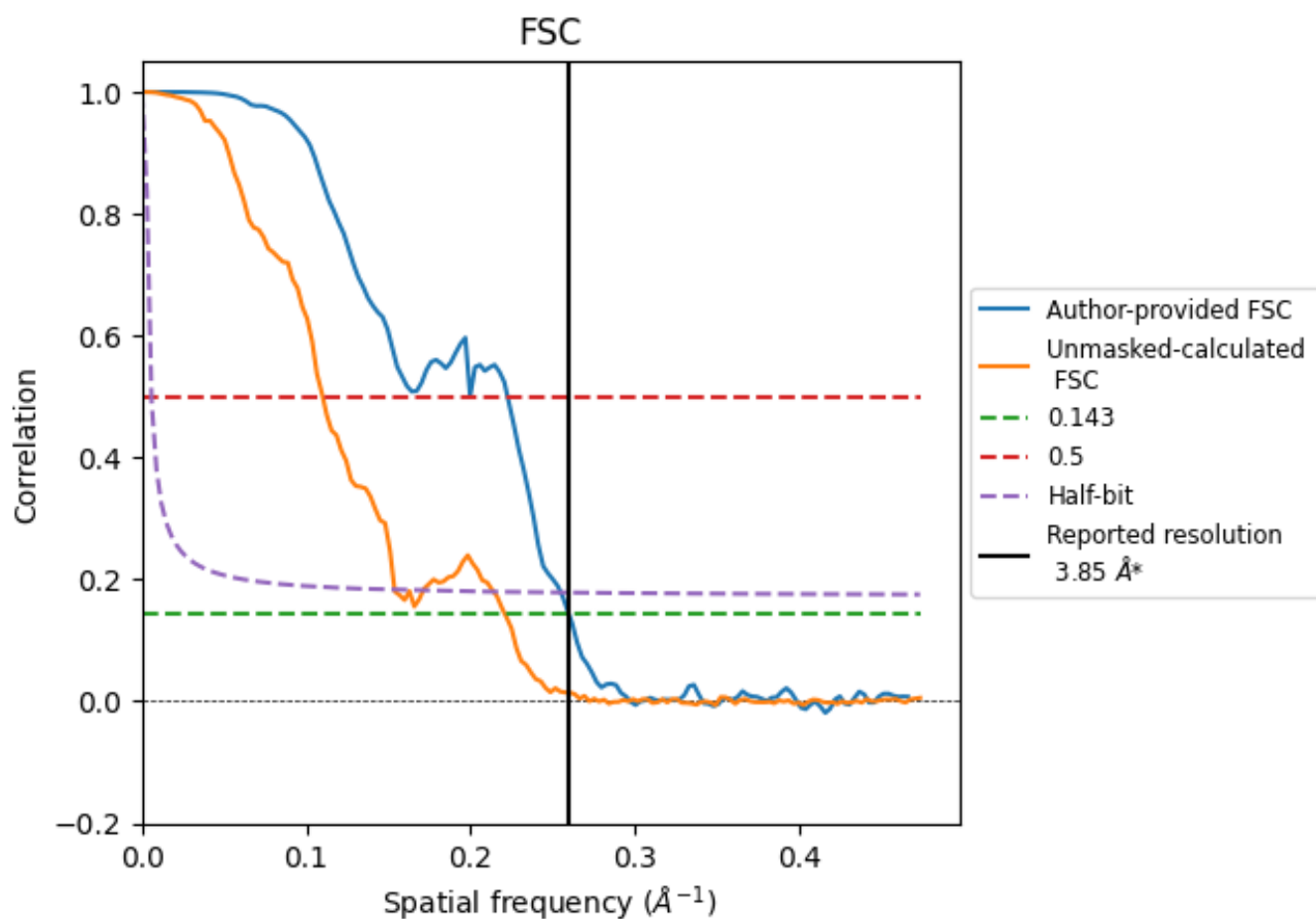


*Reported resolution corresponds to spatial frequency of 0.260 Å⁻¹

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 0.260 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.85	-	-
Author-provided FSC curve	3.85	4.49	3.92
Unmasked-calculated*	4.52	9.08	6.50

*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 4.52 differs from the reported value 3.85 by more than 10 %

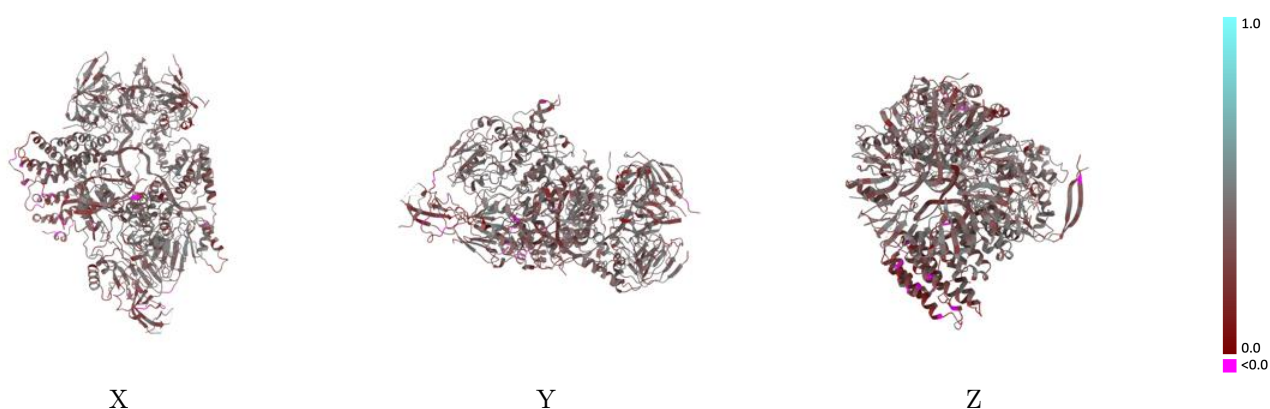
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-49206 and PDB model 9NB1. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

This section was not generated.

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

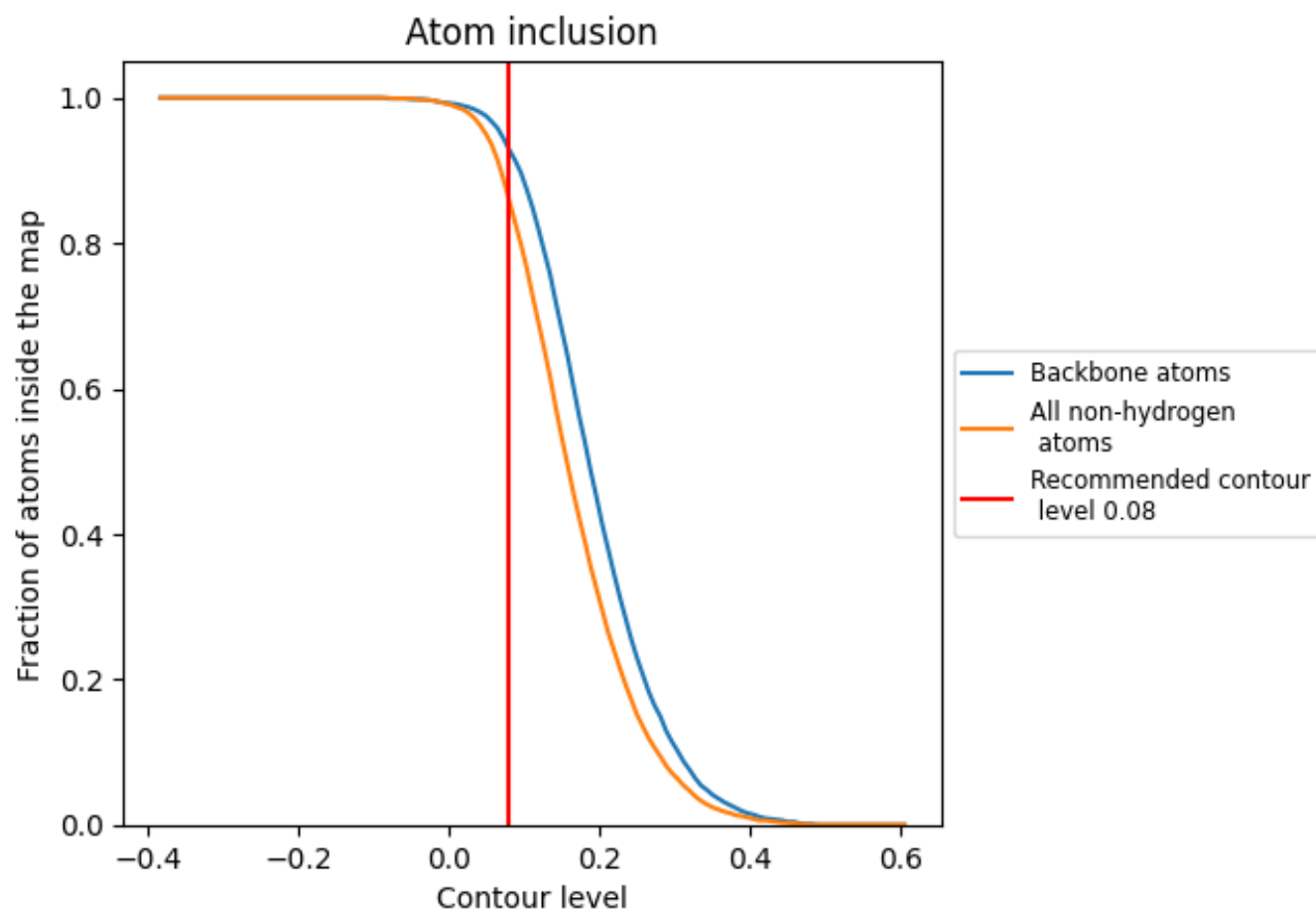


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 93% of all backbone atoms, 86% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8580	 0.3570
A	 0.7930	 0.3560
B	 0.8490	 0.3470
C	 0.8800	 0.3810
D	 0.9080	 0.3810
E	 0.8840	 0.4080
F	 0.9050	 0.3950
G	 0.8190	 0.3820
H	 0.8620	 0.3770
I	 0.8590	 0.3710
J	 0.8260	 0.2800
K	 0.8030	 0.3390
Y	 0.8660	 0.3040
Z	 0.8970	 0.3090

