



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 10:02 PM UTC

PDB ID : 8WI9 / pdb_00008wi9
EMDB ID : EMD-37561
Title : Cryo- EM structure of Mycobacterium smegmatis 30S ribosomal subunit (body 2) of 70S ribosome, bS1 and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-24
Resolution : 3.50 Å(reported)
Based on initial model : 8WHX

This is a wwPDB EM Validation Summary 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:

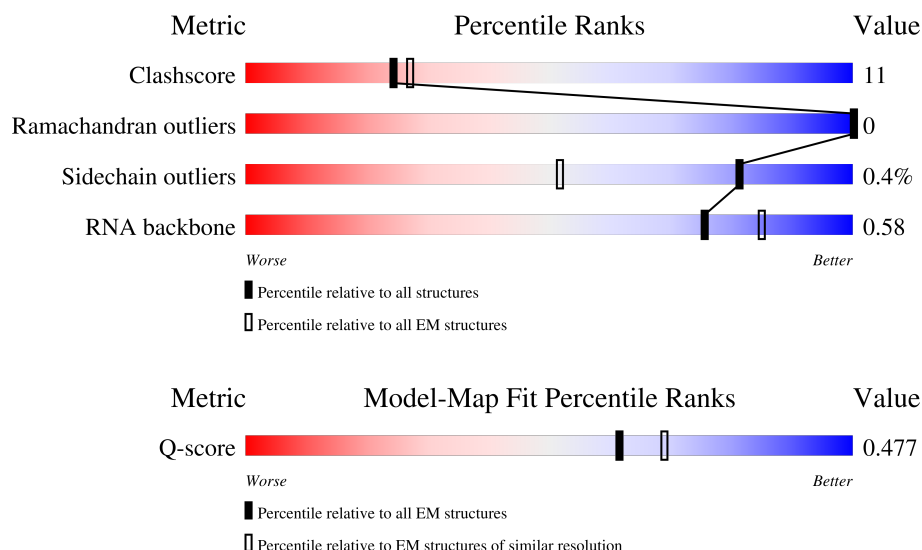
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.50 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	13950 (3.00 - 4.00)

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	1528	
2	b	479	
3	v	33	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	d	275	
5	e	201	
6	f	214	
7	g	96	
8	h	156	
9	i	132	
10	j	150	
11	k	101	
12	l	138	
13	m	124	
14	n	124	
15	o	61	
16	p	89	
17	q	156	
18	r	98	
19	s	84	
20	t	93	
21	u	86	
22	c	277	
23	x	11	
24	w	264	

2 Entry composition [i](#)

There are 24 unique types of molecules in this entry. The entry contains 54459 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 RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1515	Total	C	N	O	P	0	0
			32521	14485	5945	10576	1515		

- Molecule 2 is a protein called 30S ribosomal protein bS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	b	154	Total	C	N	O	0	0
			1193	758	198	237		

- Molecule 3 is a protein called 30S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	v	31	Total	C	N	O	S	0	0
			271	166	69	35	1		

- Molecule 4 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	207	Total	C	N	O	S	0	0
			1656	1034	321	297	4		

- Molecule 5 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 6 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	168	Total	C	N	O	S	0	0
			1223	769	230	220	4		

- Molecule 7 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 8 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	153	Total	C	N	O	S	0	0
			1207	751	235	219	2		

- Molecule 9 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 10 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	j	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 11 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	80	Total	C	N	O	S	0	0
			645	409	119	115	2		

- Molecule 12 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 13 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	121	Total	C	N	O	S	0	0
			949	588	195	164	2		

- Molecule 14 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 15 is a protein called 30S ribosomal protein S14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 16 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	88	Total	C	N	O		0	0
			720	449	147	124			

- Molecule 17 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	113	Total	C	N	O		0	0
			891	570	162	159			

- Molecule 18 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 19 is a protein called 30S ribosomal protein S18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 20 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 21 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	u	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 22 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	c	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 23 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	x	11	Total	C	N	O	0	0
			94	59	21	14		

- Molecule 24 is a protein called Ribosome hibernation promotion factor RafH.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	w	255	Total	C	N	O	S	0	0
			2030	1273	387	364	6		

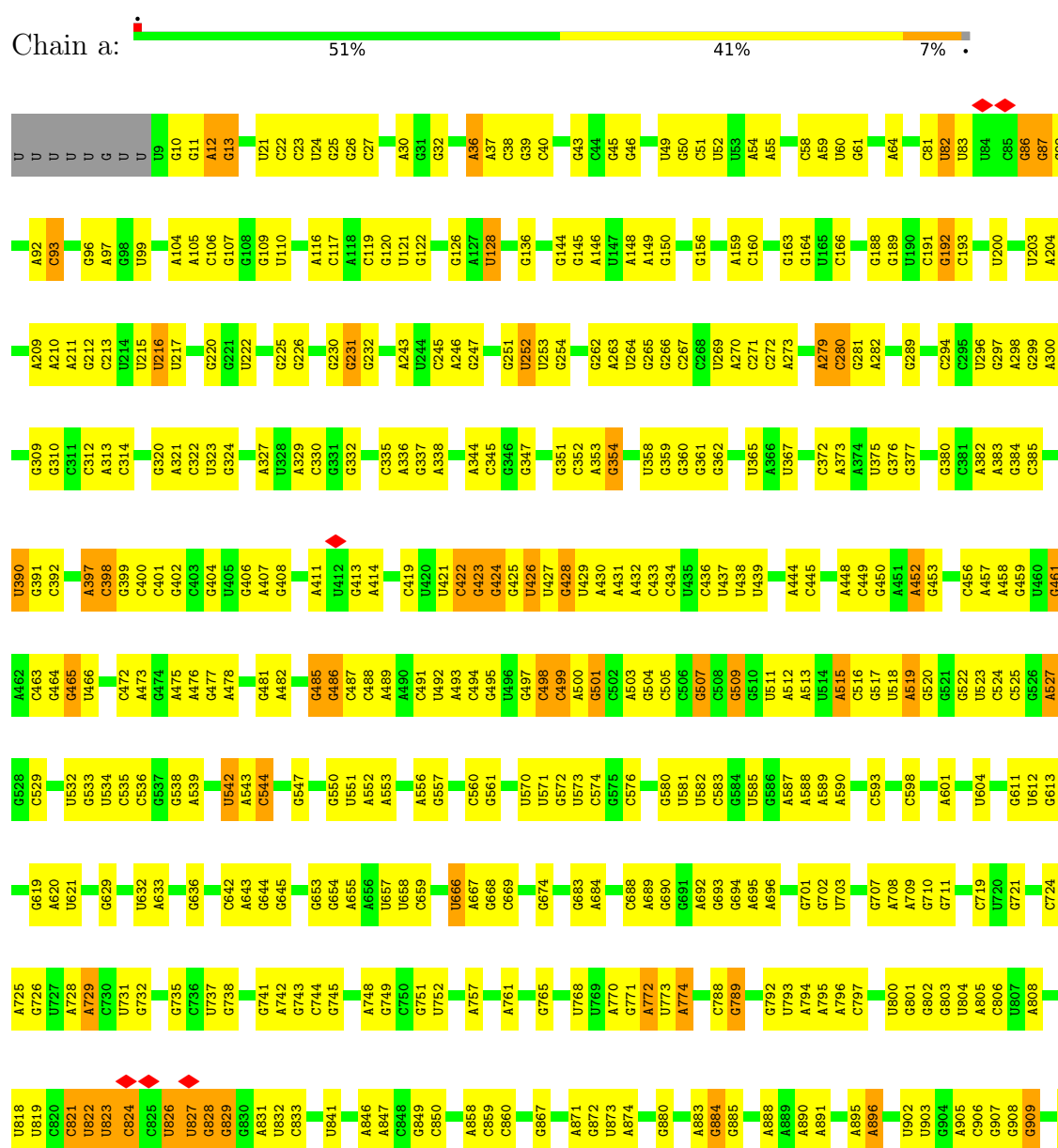
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	259	HIS	-	expression tag	UNP A0QZ86
w	260	HIS	-	expression tag	UNP A0QZ86
w	261	HIS	-	expression tag	UNP A0QZ86
w	262	HIS	-	expression tag	UNP A0QZ86
w	263	HIS	-	expression tag	UNP A0QZ86
w	264	HIS	-	expression tag	UNP A0QZ86

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: 16S rRNA





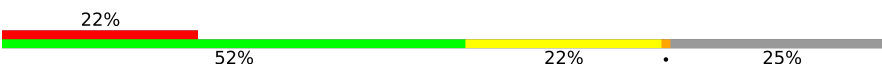
ASN GLY SER SER ARG SER SER GLU GLU SER SER GLY GLY THR LEU ALA SER ASP ALA ALA GLN LEU ALA ALA ALA LEU LEU ALA ALA GLY GLY ASN ALA

• Molecule 3: 30S ribosomal protein S22

Chain v:  79% 15% 6%

MET G2 R8 R11 R22 Q27 K30 L31 G32 LYS

• Molecule 4: 30S ribosomal protein S3

Chain d:  22% 52% 22% 25%

MET G2 N6 P7 H8 S20 R21 W22 Y23 A24 D25 K26 Q27 K33 E34 A37 I38 R39 K40 L41 L42 A43 T44 G45 L46 E47 R48 A49 G50 I51 A52 D53 V54 E55 R58 T59 R60 D61 V63 R64 V65 D66 I67 H68 T69 A70 R71 P72 G73 I74 V75 I76 G77 R78 R79 G80 T81 E82 A83 D84 R85 T86 R87 A88 D89 L90 E91 K92 L93 G95 K96 Q97 V98 Q99 L100 N101 I102 L103 E104 V105 K106 N107 P108 E109 A120 N125 R126 F129 R130 M133 R134 K135 A136 I137 Q138 S139 M141 R142 Q143 P144 V151 S163 R172 H176 T177 A180 E188 A189 K190 R195 V200 I207 V208 GLY GLY LYS ARG GLU LEU ALA ALA ALA ALA PRO SER ASP ARG PRO ARG ARG GLU ARG PRO PRO GLY THR ARG PRO ARG SER GLY SER ALA THR THR ALA THR THR THR GLU GLY ALA ARG ALA THR

SER ASP ALA PRO ALA ALA GLY THR ALA ALA ALA ALA GLU PRO ALA ALA ALA SER THR GLU SER

• Molecule 5: 30S ribosomal protein S4

Chain e:  74% 25%

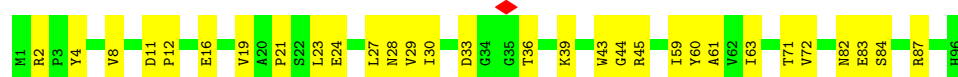
MET A2 P7 R10 R13 D23 Q24 S25 R47 Q48 Q49 L50 Q51 E52 K53 E64 K65 Q66 E73 R76 R87 E90 S91 D94 N95 Y98 R99 R104 T105 M108 A109 R110 H115 L119 G122 V132 Y135 I138 D139 L145 L148 I152 A153 R154 G158 E159 R160 P163 S164 W165 L166 T175 L176 V177 E182 Q185 D187 V188 P189 L190 E197 L198 K201

• Molecule 6: 30S ribosomal protein S5

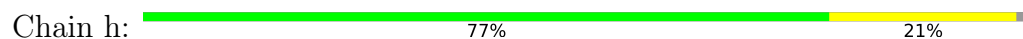
Chain f:  65% 13% 21%

MET ALA GLU GLN ALA GLY ALA GLY SER GLN ALA ALA ASP ASN ARG GLY ARG GLY ARG ARG ASP ASP ARG ARG GLY GLY ASP LYS SER N35 Y36 V50 K51 R54 I63 V64 G65 D66 G67 K68 V73 K77 A83 K87 E90 R93 R98 L101 A116 R122 V130 G133 G134 A135 A136 R137 V145 V162 V178 R181 A190 M194 E202 ALA LEU ALA ALA ALA ALA ARG GLY SER ALA

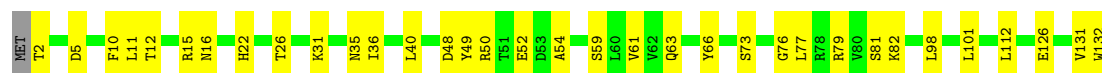
• Molecule 7: 30S ribosomal protein S6



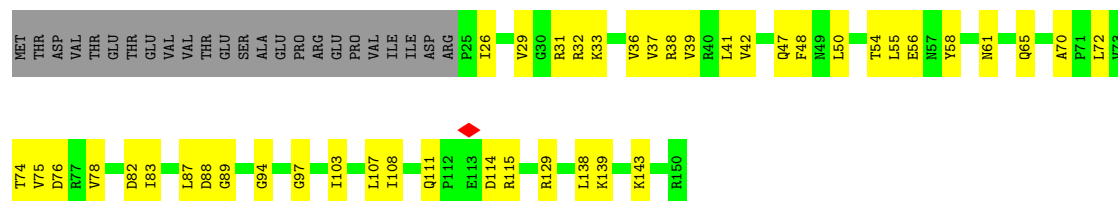
- Molecule 8: 30S ribosomal protein S7



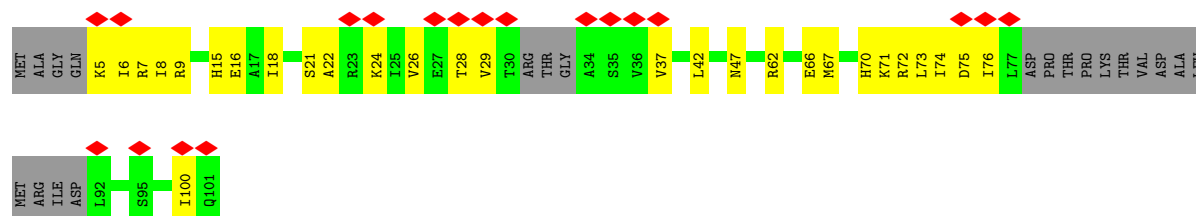
- Molecule 9: 30S ribosomal protein S8



- Molecule 10: 30S ribosomal protein S9

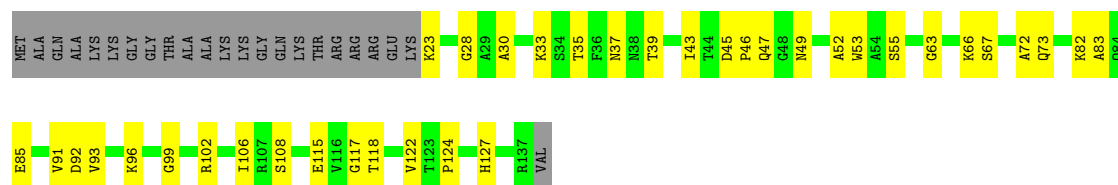


- Molecule 11: 30S ribosomal protein S10



- Molecule 12: 30S ribosomal protein S11





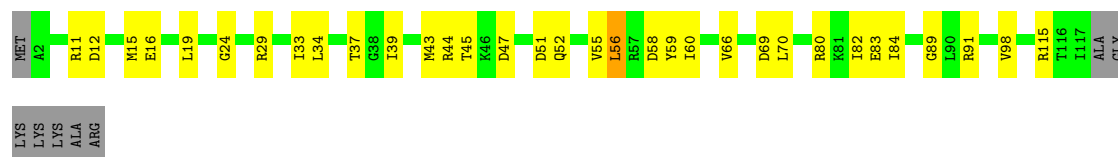
- Molecule 13: 30S ribosomal protein S12

Chain m: 79% 19% .



- Molecule 14: 30S ribosomal protein S13

Chain n: 67% 26% 6% .



- Molecule 15: 30S ribosomal protein S14A

Chain o: 67% 31% .



- Molecule 16: 30S ribosomal protein S15

Chain p: 84% 15% .

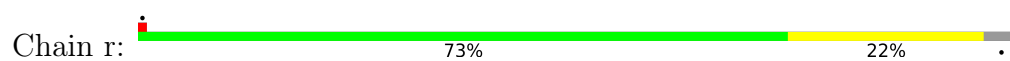


- Molecule 17: 30S ribosomal protein S16

Chain q: 53% 19% 28% .



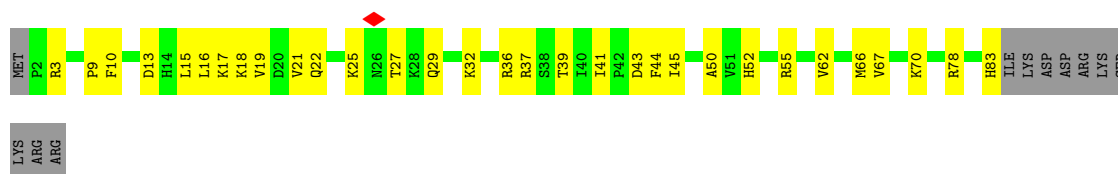
- Molecule 18: 30S ribosomal protein S17



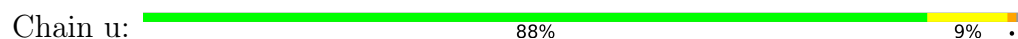
• Molecule 19: 30S ribosomal protein S18B



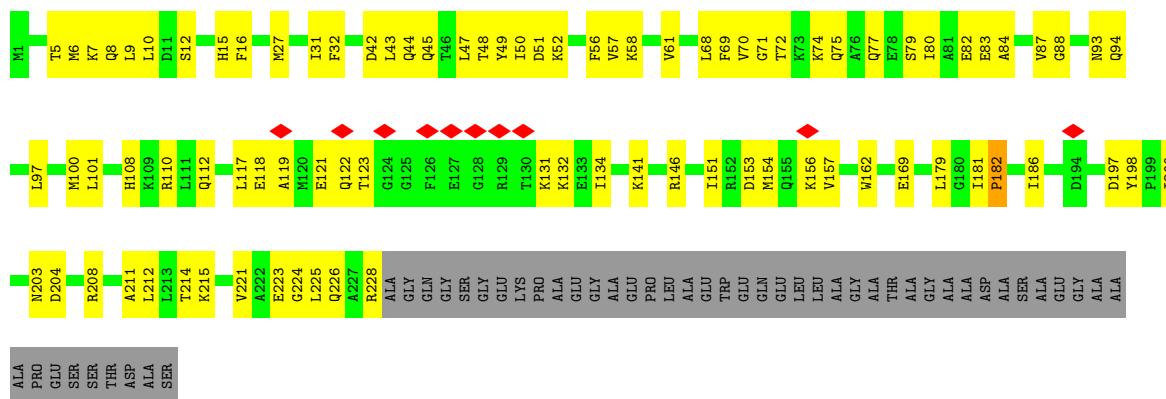
• Molecule 20: 30S ribosomal protein S19



• Molecule 21: 30S ribosomal protein S20



• Molecule 22: 30S ribosomal protein S2

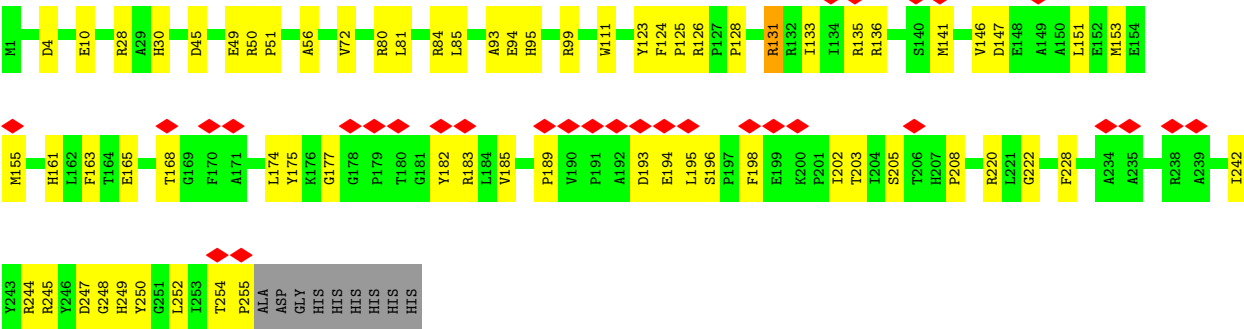


• Molecule 23: 50S ribosomal protein L31





● Molecule 24: Ribosome hibernation promotion factor RafH



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110934	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	NONE; CTF correction in RELION 3.1.4	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.196	Depositor
Minimum map value	-0.034	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	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	a	0.12	0/36400	0.26	0/56798
2	b	0.16	0/1201	0.48	0/1615
3	v	0.11	0/271	0.25	0/348
4	d	0.15	0/1680	0.37	1/2256 (0.0%)
5	e	0.12	0/1672	0.29	0/2251
6	f	0.12	0/1239	0.29	0/1673
7	g	0.14	0/782	0.36	0/1059
8	h	0.13	0/1225	0.36	1/1653 (0.1%)
9	i	0.12	0/1025	0.29	0/1385
10	j	0.16	0/1012	0.41	0/1362
11	k	0.15	0/655	0.44	0/883
12	l	0.15	0/873	0.38	0/1180
13	m	0.12	0/960	0.31	0/1283
14	n	0.14	0/942	0.40	0/1260
15	o	0.15	0/488	0.37	0/650
16	p	0.12	0/729	0.27	0/977
17	q	0.14	0/908	0.36	0/1226
18	r	0.12	0/759	0.32	0/1016
19	s	0.12	0/518	0.28	0/693
20	t	0.14	0/680	0.37	0/915
21	u	0.16	0/663	0.40	0/882
22	c	0.14	0/1822	0.40	1/2457 (0.0%)
23	x	0.16	0/95	0.44	0/123
24	w	0.14	0/2078	0.33	0/2816
All	All	0.13	0/58677	0.30	3/86761 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	c	182	PRO	CA-N-CD	-8.07	100.70	112.00
8	h	58	PRO	CA-N-CD	-8.05	100.73	112.00
4	d	108	PRO	CA-N-CD	-6.87	102.38	112.00

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	32521	0	16366	481	0
2	b	1193	0	1238	48	0
3	v	271	0	329	5	0
4	d	1656	0	1704	44	0
5	e	1641	0	1668	40	0
6	f	1223	0	1287	22	0
7	g	771	0	797	21	0
8	h	1207	0	1259	22	0
9	i	1010	0	1046	26	0
10	j	994	0	1050	35	0
11	k	645	0	672	23	0
12	l	855	0	863	26	0
13	m	949	0	1032	16	0
14	n	935	0	986	27	0
15	o	477	0	503	18	0
16	p	720	0	760	9	0
17	q	891	0	935	26	0
18	r	748	0	795	15	0
19	s	513	0	540	9	0
20	t	662	0	677	25	0
21	u	660	0	712	6	0
22	c	1793	0	1839	66	0
23	x	94	0	95	8	0
24	w	2030	0	2023	66	0
All	All	54459	0	39176	977	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 11.

The worst 5 of 977 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)
24:w:124:PHE:CD2	24:w:126:ARG:HG2	1.76	1.20
1:a:1232:A:H62	1:a:1268:C:N4	1.44	1.15
1:a:1232:A:N6	1:a:1268:C:H42	1.46	1.12
24:w:124:PHE:HD2	24:w:126:ARG:HG2	1.14	0.96
24:w:126:ARG:HG3	24:w:247:ASP:O	1.66	0.95

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	
2	b	148/479 (31%)	143 (97%)	5 (3%)	0	100	100
3	v	29/33 (88%)	29 (100%)	0	0	100	100
4	d	205/275 (74%)	195 (95%)	10 (5%)	0	100	100
5	e	198/201 (98%)	189 (96%)	9 (4%)	0	100	100
6	f	166/214 (78%)	162 (98%)	4 (2%)	0	100	100
7	g	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
8	h	151/156 (97%)	148 (98%)	3 (2%)	0	100	100
9	i	129/132 (98%)	126 (98%)	3 (2%)	0	100	100
10	j	124/150 (83%)	116 (94%)	8 (6%)	0	100	100
11	k	74/101 (73%)	71 (96%)	3 (4%)	0	100	100
12	l	113/138 (82%)	107 (95%)	6 (5%)	0	100	100
13	m	119/124 (96%)	112 (94%)	7 (6%)	0	100	100
14	n	114/124 (92%)	110 (96%)	4 (4%)	0	100	100
15	o	58/61 (95%)	52 (90%)	6 (10%)	0	100	100
16	p	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
17	q	111/156 (71%)	105 (95%)	6 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	r	92/98 (94%)	89 (97%)	3 (3%)	0	100	100
19	s	63/84 (75%)	61 (97%)	2 (3%)	0	100	100
20	t	80/93 (86%)	77 (96%)	3 (4%)	0	100	100
21	u	83/86 (96%)	83 (100%)	0	0	100	100
22	c	226/277 (82%)	211 (93%)	15 (7%)	0	100	100
23	x	9/11 (82%)	9 (100%)	0	0	100	100
24	w	253/264 (96%)	240 (95%)	13 (5%)	0	100	100
All	All	2725/3442 (79%)	2610 (96%)	115 (4%)	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	
2	b	132/407 (32%)	131 (99%)	1 (1%)	73	77
3	v	29/31 (94%)	29 (100%)	0	100	100
4	d	170/212 (80%)	167 (98%)	3 (2%)	51	69
5	e	175/176 (99%)	173 (99%)	2 (1%)	65	74
6	f	123/147 (84%)	123 (100%)	0	100	100
7	g	85/85 (100%)	85 (100%)	0	100	100
8	h	129/132 (98%)	129 (100%)	0	100	100
9	i	107/108 (99%)	107 (100%)	0	100	100
10	j	102/125 (82%)	102 (100%)	0	100	100
11	k	73/90 (81%)	73 (100%)	0	100	100
12	l	89/105 (85%)	89 (100%)	0	100	100
13	m	102/105 (97%)	102 (100%)	0	100	100
14	n	99/104 (95%)	98 (99%)	1 (1%)	68	75
15	o	49/50 (98%)	49 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	p	76/77 (99%)	76 (100%)	0	100	100
17	q	92/118 (78%)	92 (100%)	0	100	100
18	r	80/83 (96%)	79 (99%)	1 (1%)	61	72
19	s	55/72 (76%)	55 (100%)	0	100	100
20	t	73/84 (87%)	73 (100%)	0	100	100
21	u	69/70 (99%)	68 (99%)	1 (1%)	59	71
22	c	191/218 (88%)	191 (100%)	0	100	100
23	x	8/8 (100%)	8 (100%)	0	100	100
24	w	208/215 (97%)	207 (100%)	1 (0%)	81	80
All	All	2316/2822 (82%)	2306 (100%)	10 (0%)	81	81

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	r	94	LEU
21	u	45	ASP
24	w	131	ARG
4	d	142	ARG
5	e	108	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
15	o	57	GLN
17	q	107	ASN
24	w	161	HIS
22	c	19	GLN
22	c	112	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1514/1528 (99%)	266 (17%)	0

5 of 266 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	12	A
1	a	13	G
1	a	36	A
1	a	43	G
1	a	51	C

There are no RNA pucker outliers to report.

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.

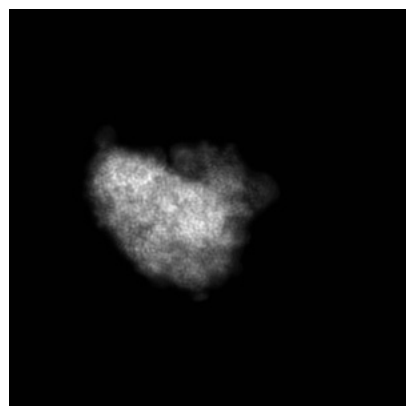
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37561. These allow visual inspection of the internal detail of the map and identification of artifacts.

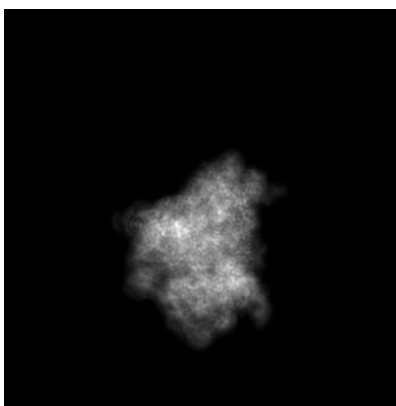
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

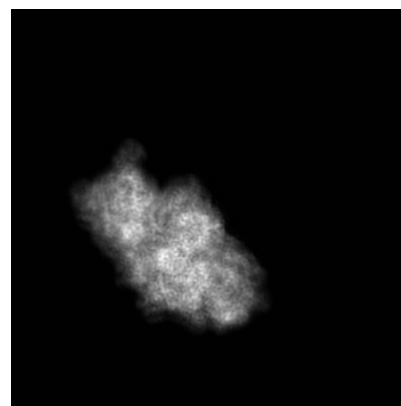
6.1.1 Primary map



X

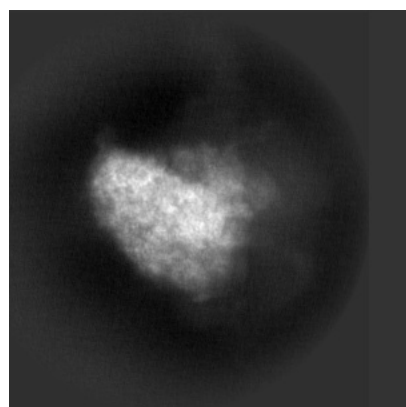


Y

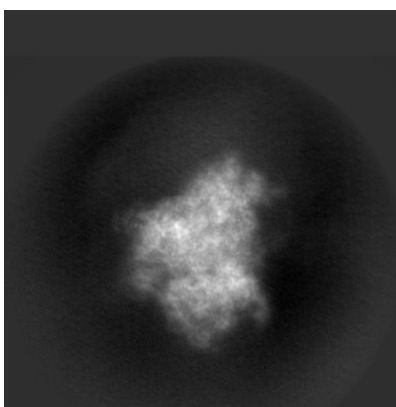


Z

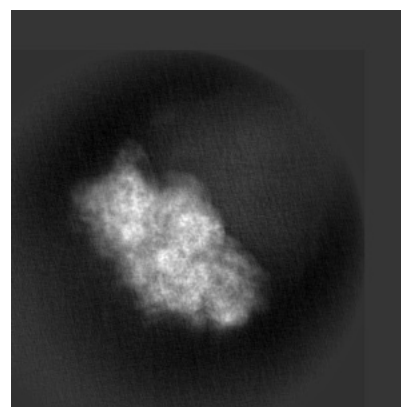
6.1.2 Raw map



X



Y

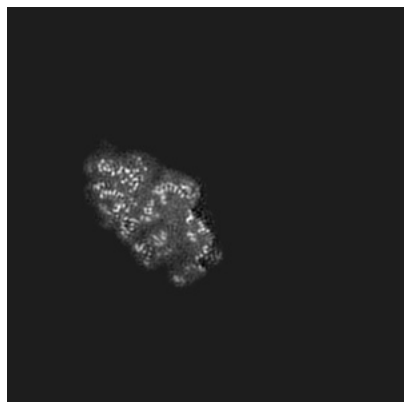


Z

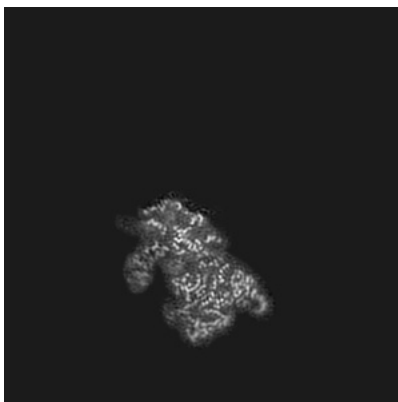
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

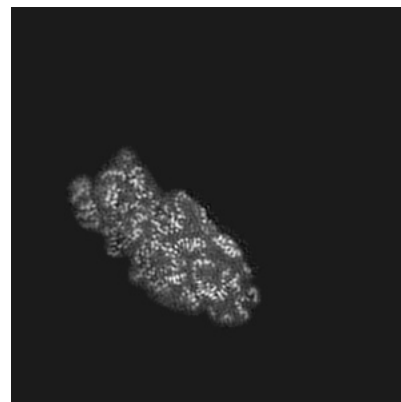
6.2.1 Primary map



X Index: 190

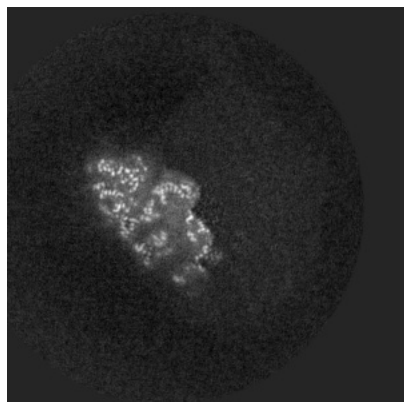


Y Index: 190

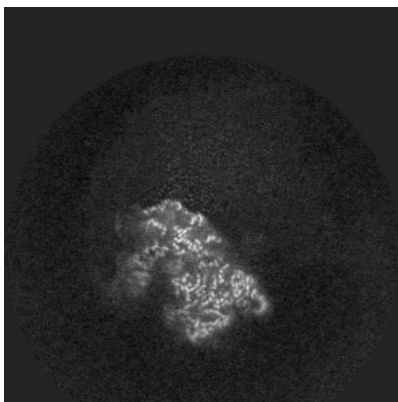


Z Index: 190

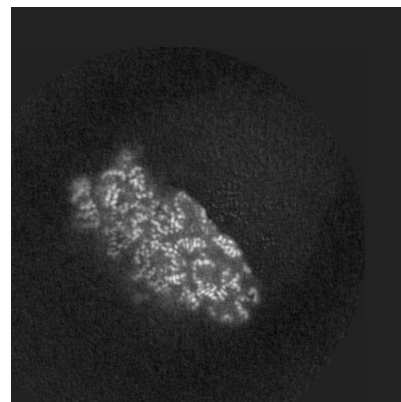
6.2.2 Raw map



X Index: 190



Y Index: 190

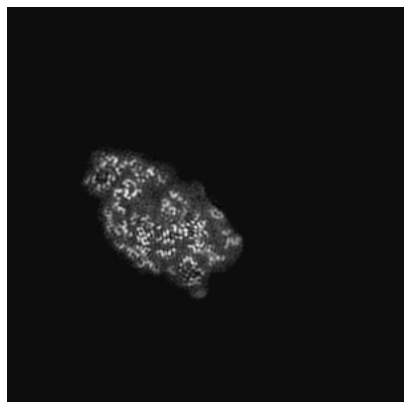


Z Index: 190

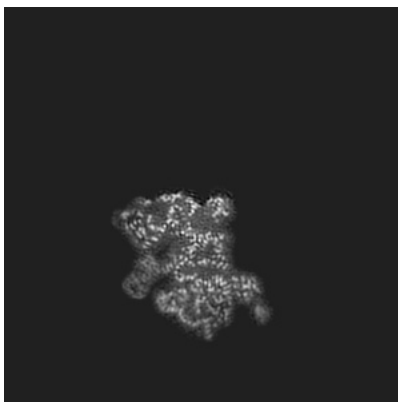
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

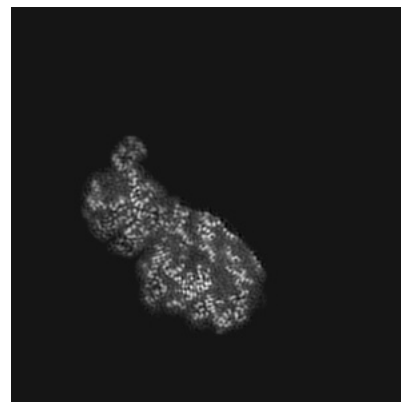
6.3.1 Primary map



X Index: 171

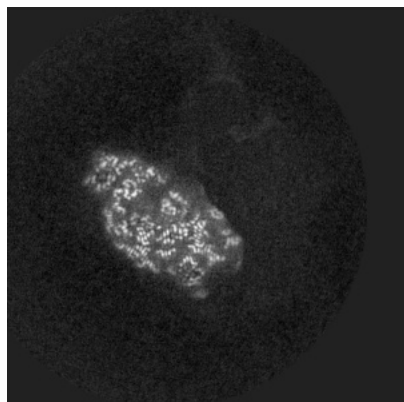


Y Index: 174

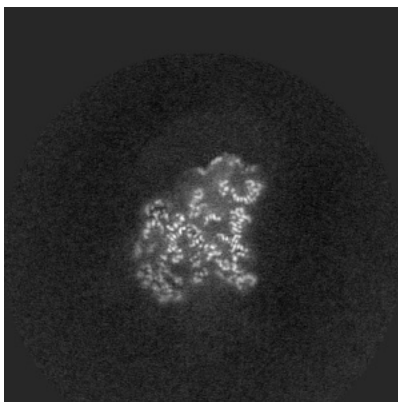


Z Index: 204

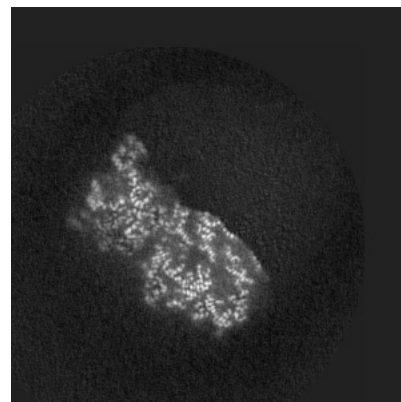
6.3.2 Raw map



X Index: 171



Y Index: 133

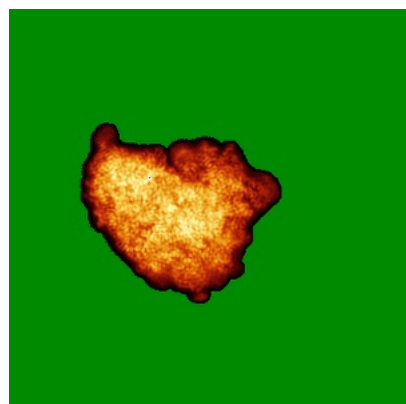


Z Index: 204

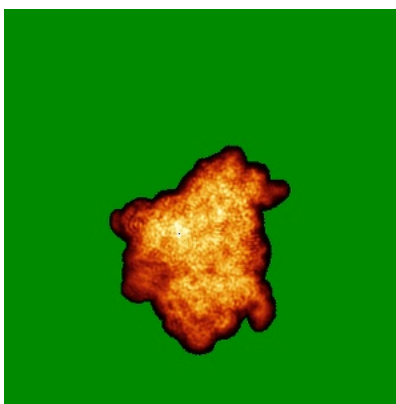
The images above show the largest variance slices of the map in three orthogonal directions.

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

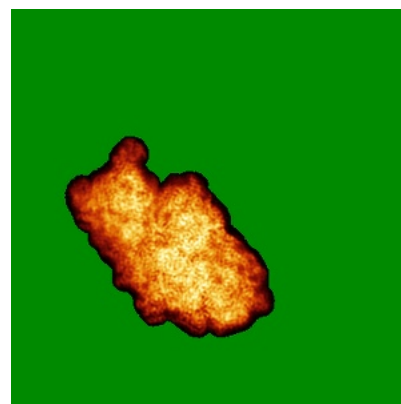
6.4.1 Primary map



X

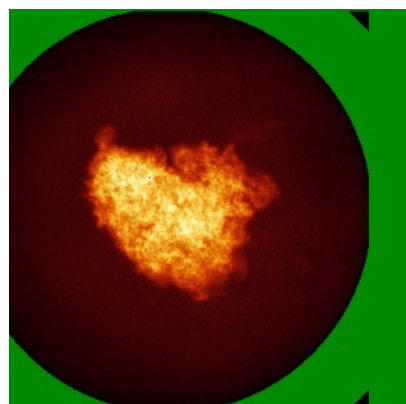


Y

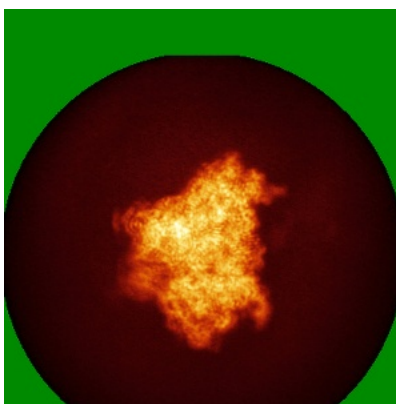


Z

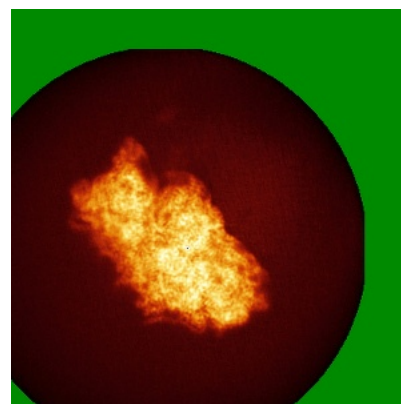
6.4.2 Raw map



X



Y

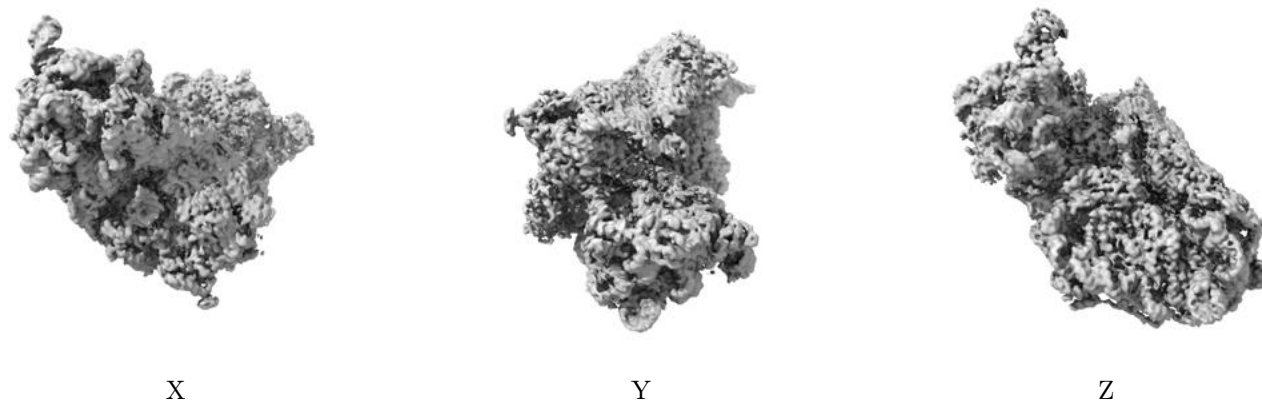


Z

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 0.04. 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.

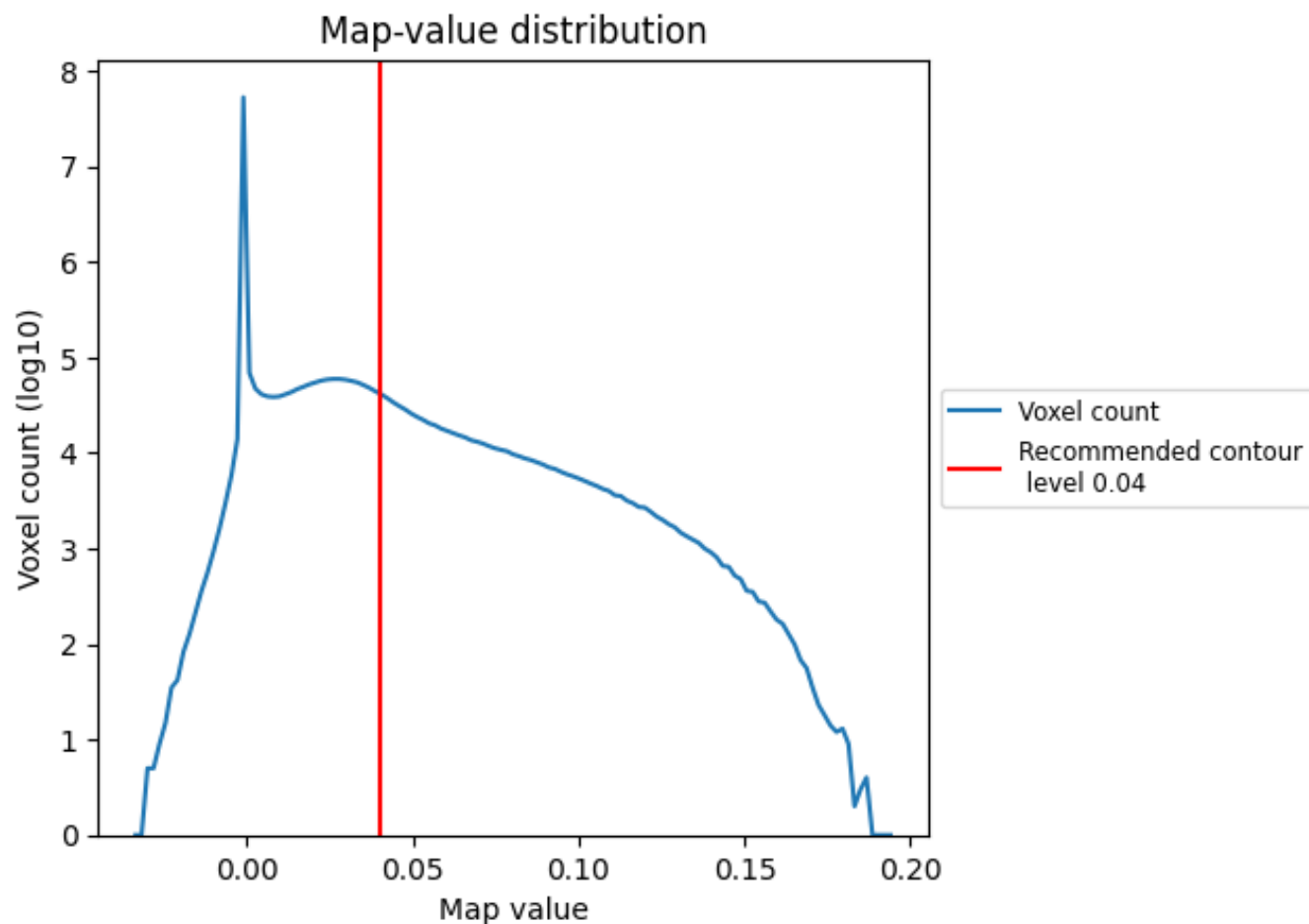
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

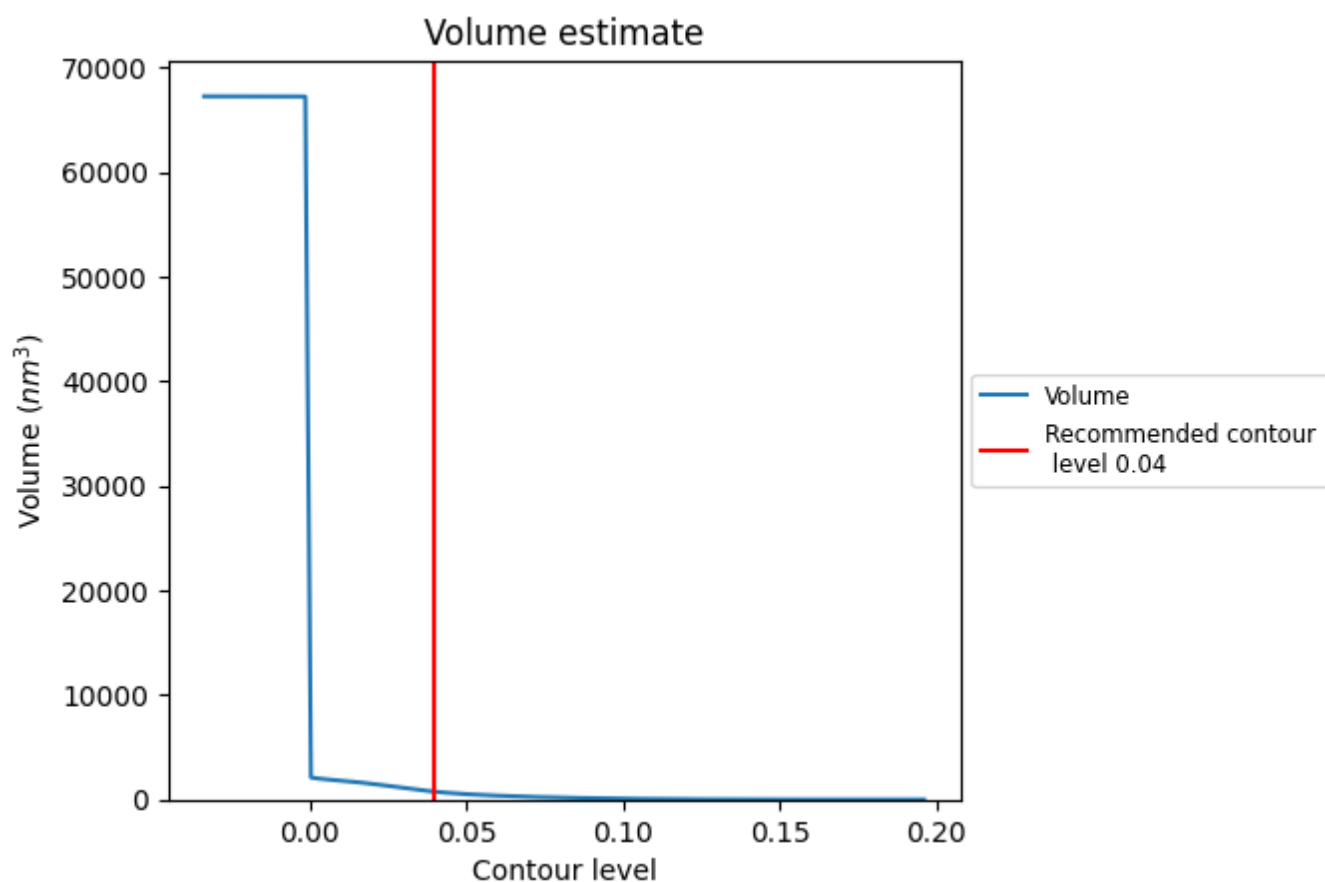
This section contains the results of statistical analysis of the map.

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.

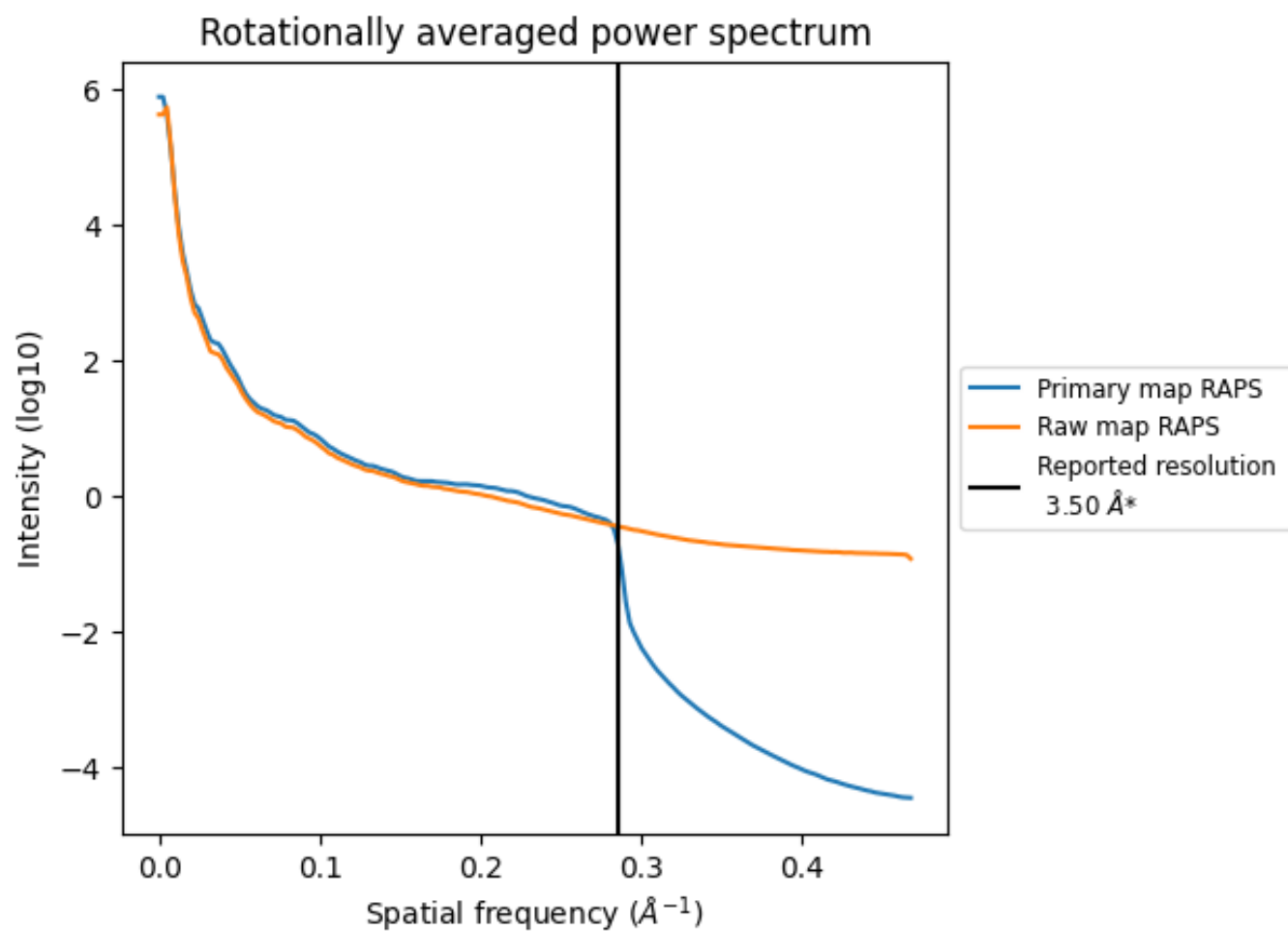
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 753 nm^3 ; this corresponds to an approximate mass of 681 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 ⓘ

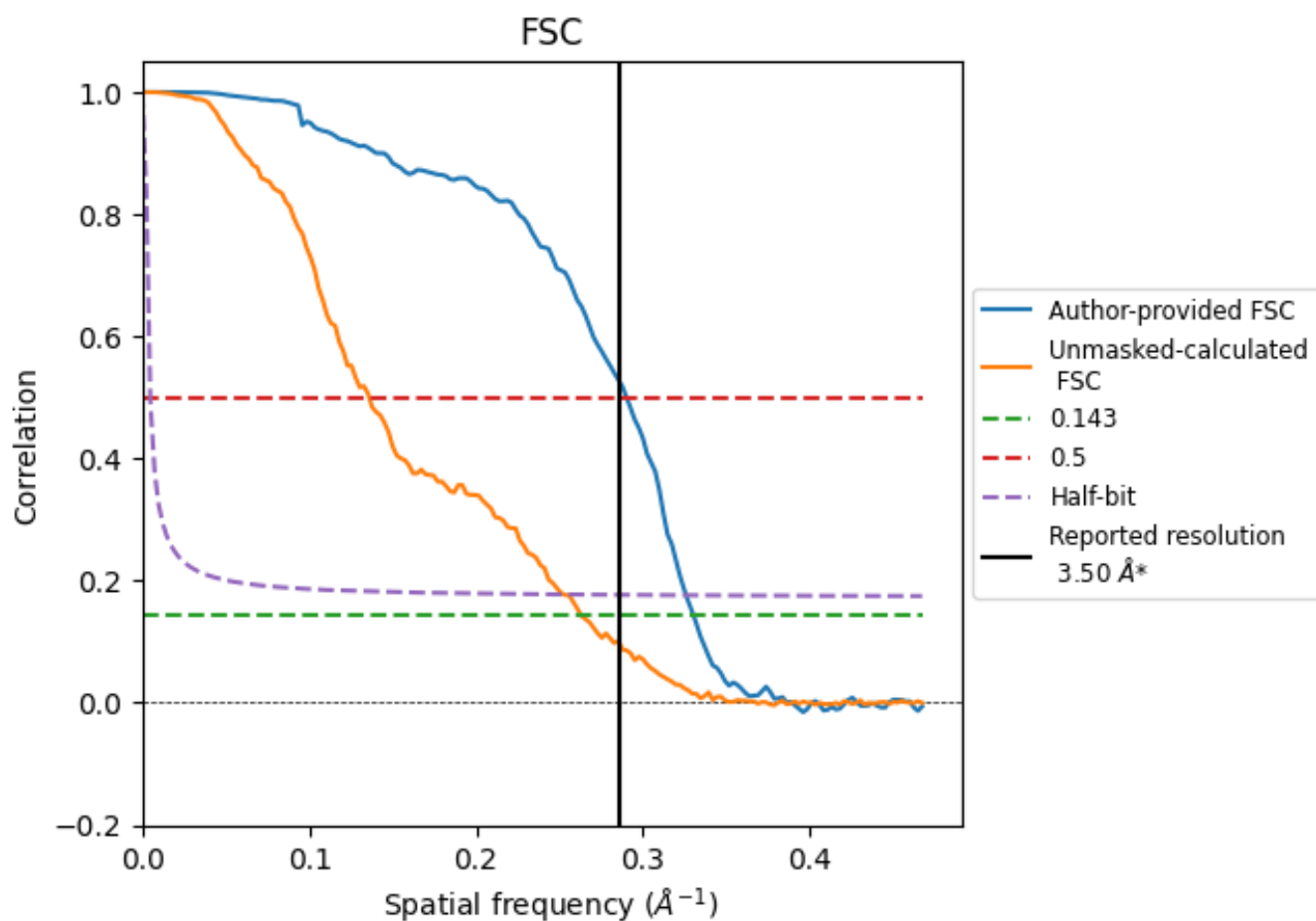


*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

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 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

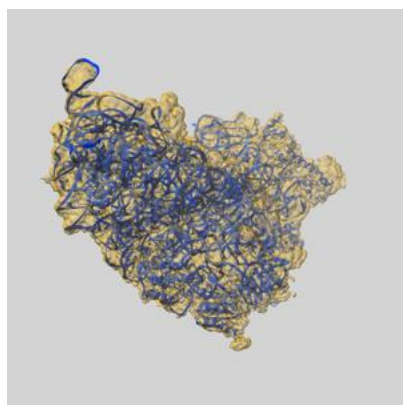
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Other
Reported by author	-	-	-	3.50
Author-provided FSC curve	3.03	3.45	3.07	-
Unmasked-calculated*	3.80	7.35	3.96	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

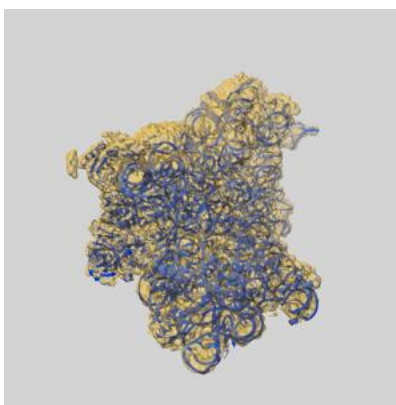
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37561 and PDB model 8WI9. Per-residue inclusion information can be found in section [3](#) on page [8](#).

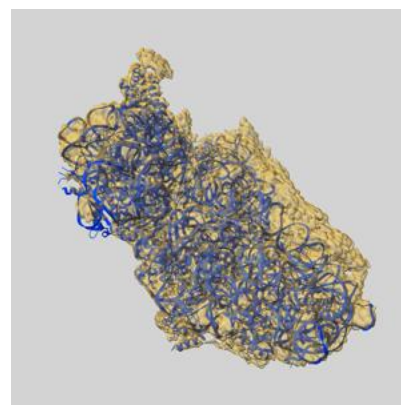
9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 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](#)



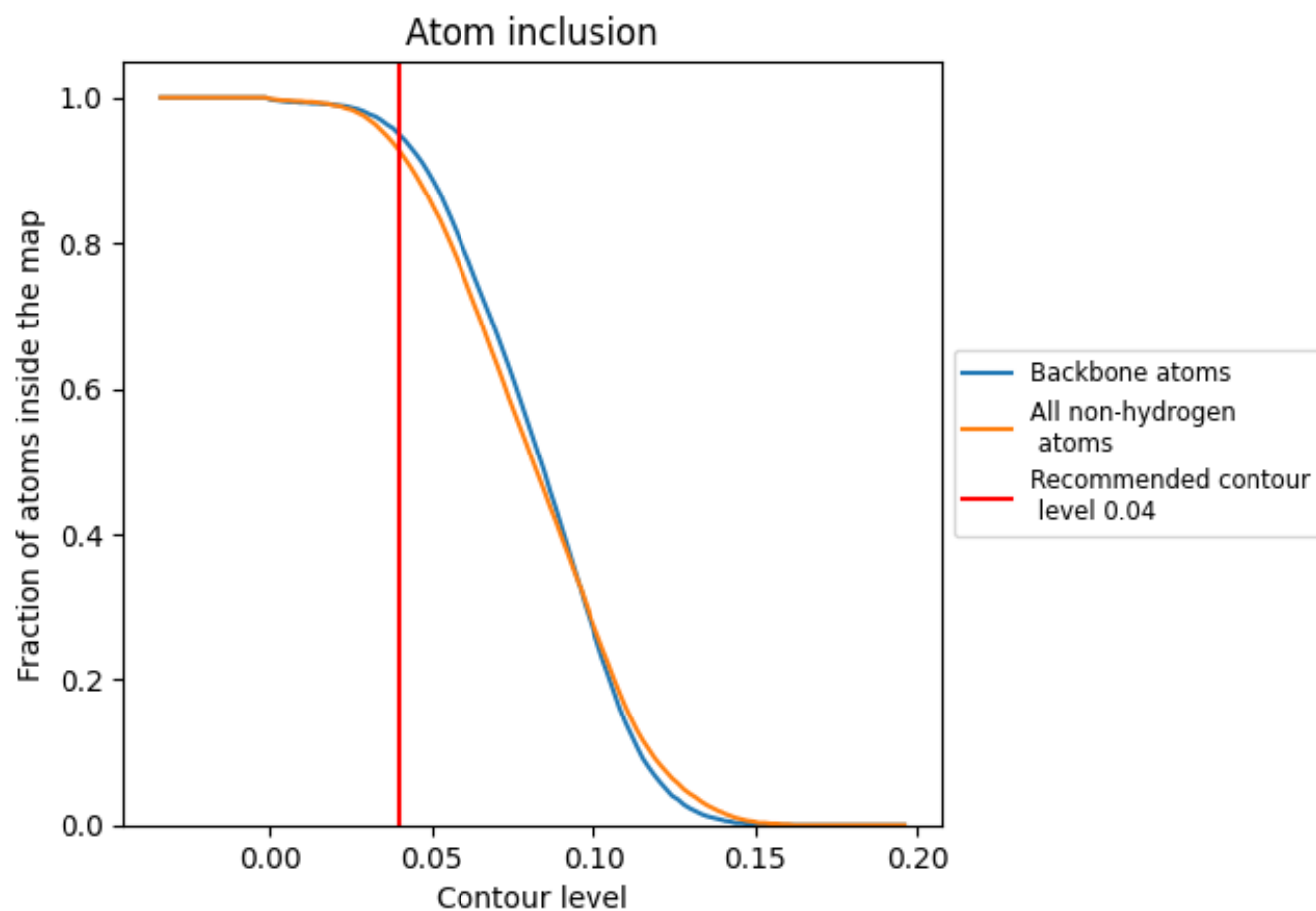
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9280	 0.4770
a	 0.9830	 0.4880
b	 0.4490	 0.2600
c	 0.8170	 0.4180
d	 0.5850	 0.3930
e	 0.9080	 0.4940
f	 0.9170	 0.5110
g	 0.9000	 0.4860
h	 0.9090	 0.4780
i	 0.9610	 0.5240
j	 0.8870	 0.4630
k	 0.6900	 0.4280
l	 0.9510	 0.5100
m	 0.9610	 0.5300
n	 0.9360	 0.4660
o	 0.8750	 0.4840
p	 0.9450	 0.5040
q	 0.9040	 0.5030
r	 0.9590	 0.5180
s	 0.9290	 0.4890
t	 0.9020	 0.4800
u	 0.9580	 0.5090
v	 0.9920	 0.5000
w	 0.7770	 0.4190
x	 0.7700	 0.3980

