



## wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:52 AM UTC

PDB ID : 6PPF / pdb\_00006ppf  
EMDB ID : EMD-20435  
Title : Bacterial 45SRbgA ribosomal particle class B  
Authors : Ortega, J.; Seffouh, A.; Jain, N.; Jahagirdar, D.; Basu, K.; Razi, A.; Ni, X.;  
Guarne, A.; Britton, R.A.  
Deposited on : 2019-07-06  
Resolution : 3.40 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

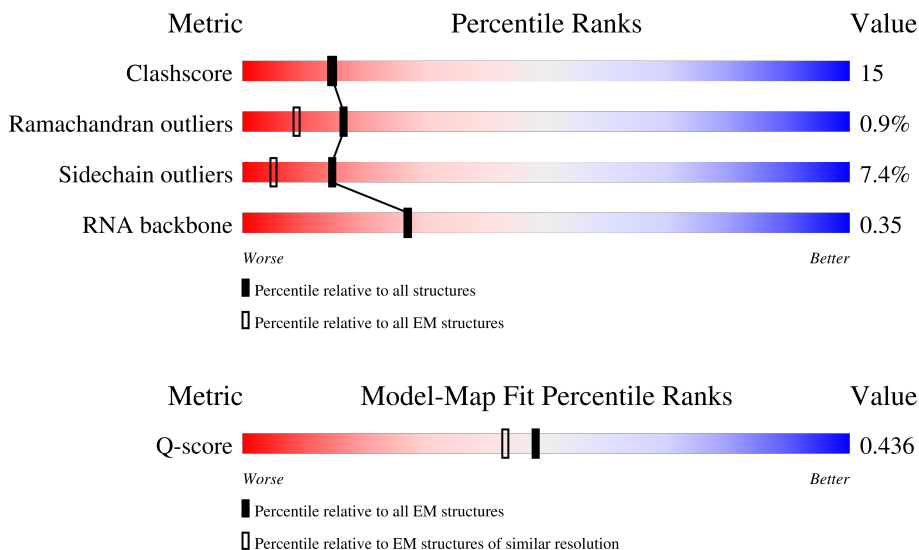
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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 3.40 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	14717 ( 2.90 - 3.90 )

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  $\geq 3$ , 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	2927	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right; margin-right: 5px;">9%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 9%, orange 46%, yellow 87%, grey 100%);"></div> </div>
2	B	119	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right; margin-right: 5px;">34%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 34%, orange 67%, yellow 91%, grey 100%);"></div> </div>
3	C	277	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right; margin-right: 5px;">6%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 6%, orange 51%, yellow 78%, grey 100%);"></div> </div>

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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	207	
6	J	145	
7	K	122	
8	L	145	
9	N	120	
10	O	120	
11	P	115	
12	Q	118	
13	R	102	
14	S	113	
15	T	95	
16	U	103	
17	V	94	
18	Z	59	
19	b	59	
20	Y	66	
21	d	44	

## 2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 71835 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	2471	53094	23688	9835	17100	2471	0	0

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	112	2395	1068	435	780	112	0	0

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	221	1684	1047	326	307	4	0	0

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	167	1265	802	220	240	3	0	0

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	194	1484	937	270	275	2	0	0

- Molecule 6 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	J	141	1119	708	205	201	5	0	0

- Molecule 7 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	K	122	920	571	173	172	4	0	0

- Molecule 8 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	L	128	952	594	179	177	2	0	0

- Molecule 9 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	N	119	953	583	186	180	4	0	0

- Molecule 10 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	O	104	791	492	157	142	0	0

- Molecule 11 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	P	103	846	540	162	144	0	0

- Molecule 12 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	Q	117	940	591	189	156	4	0	0

- Molecule 13 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	R	96	758	485	134	139	0	0

- Molecule 14 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 15 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	88	Total	C	N	O	S	0	0
			707	441	131	132	3		

- Molecule 16 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	U	98	Total	C	N	O	S	0	0
			739	464	138	134	3		

- Molecule 17 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	V	73	Total	C	N	O	0	0
			555	344	106	105		

- Molecule 18 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 19 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	b	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 20 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 21 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	d	44	367	222	89	54	2	0	0

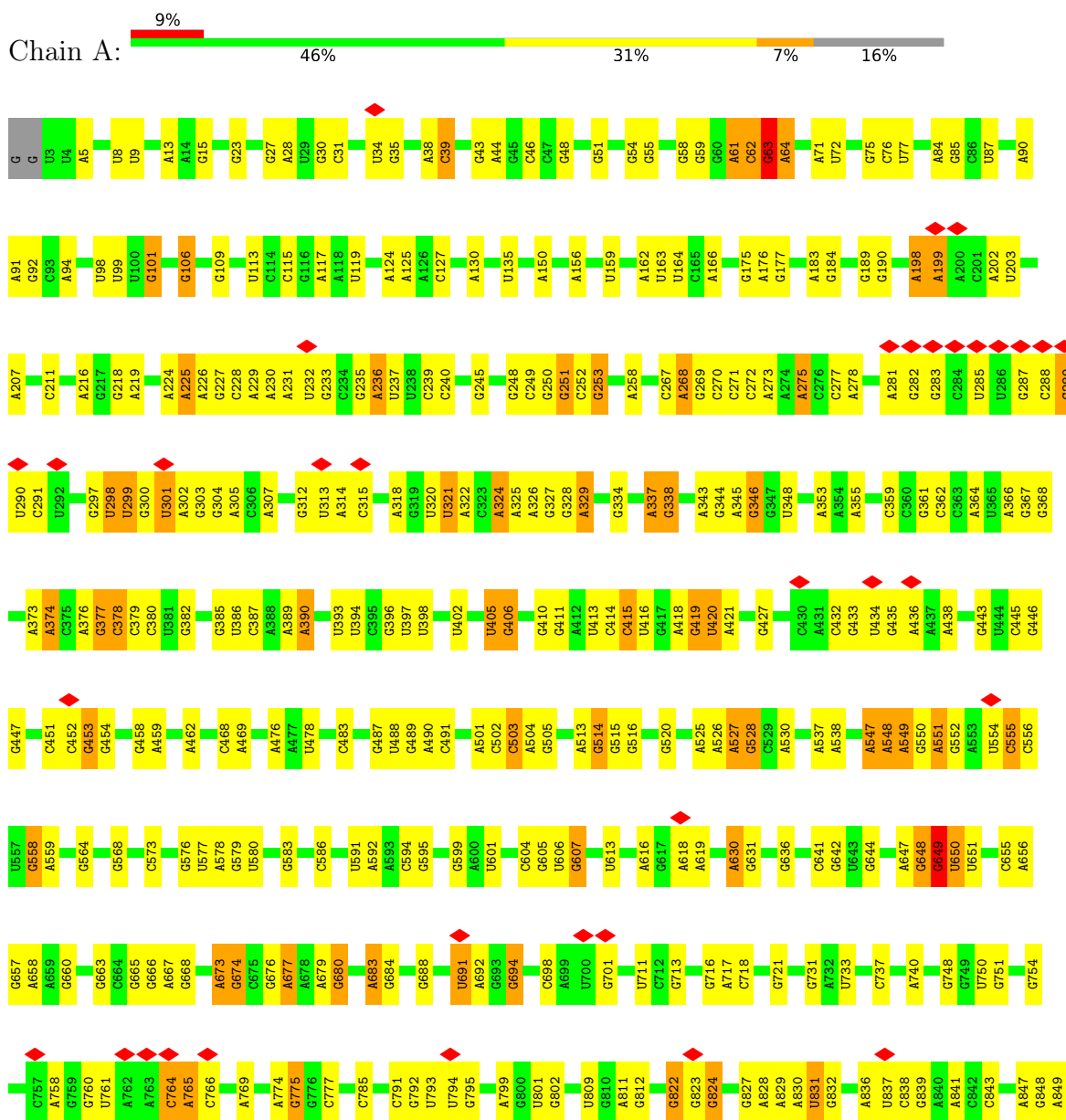
- Molecule 22 is water.

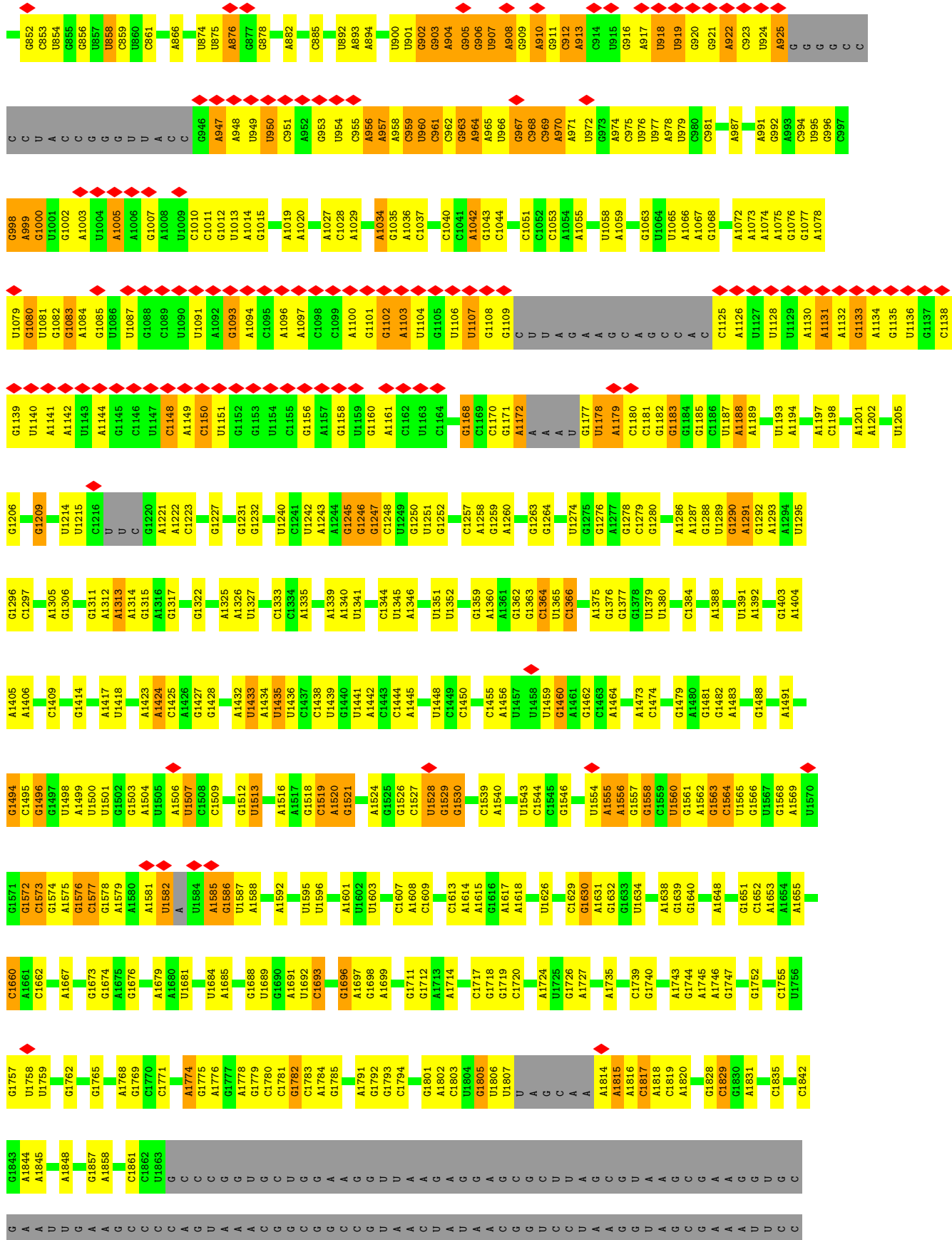
Mol	Chain	Residues	Atoms		AltConf
22	A	13	Total	O	0
			13	13	

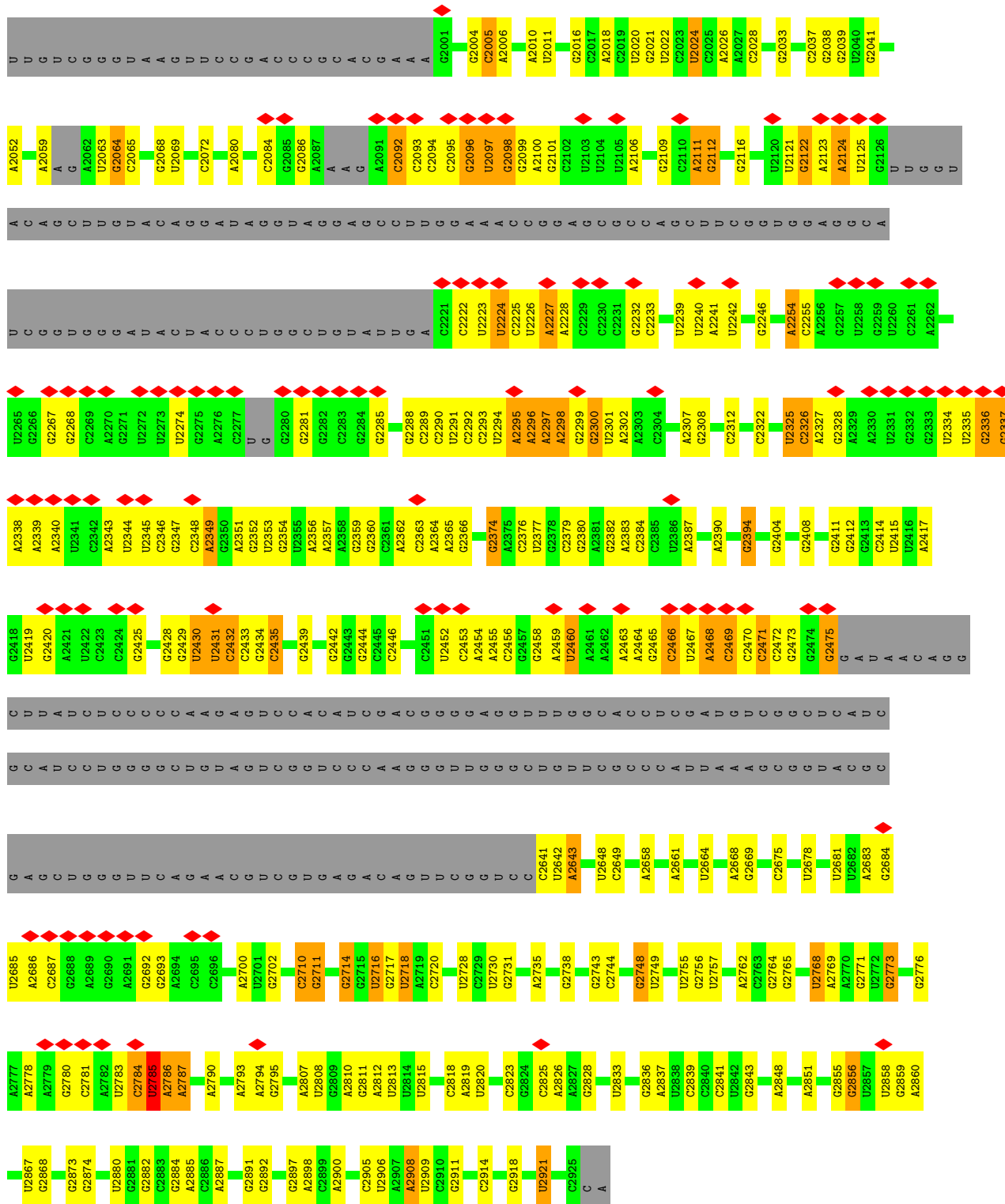
### 3 Residue-property plots

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: 23S rRNA



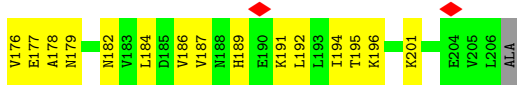




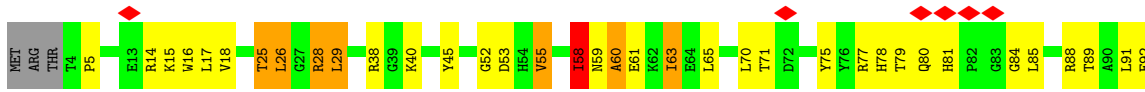
● Molecule 2: 5S rRNA



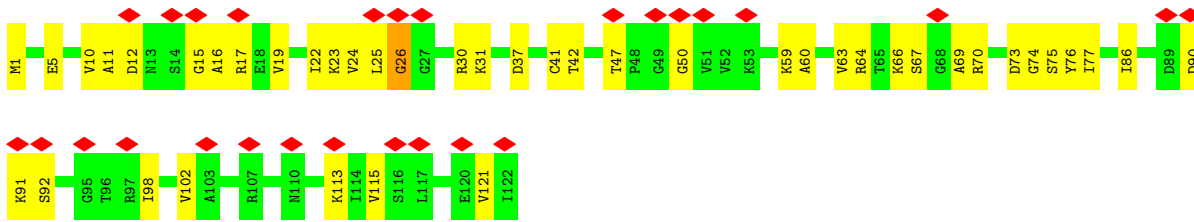




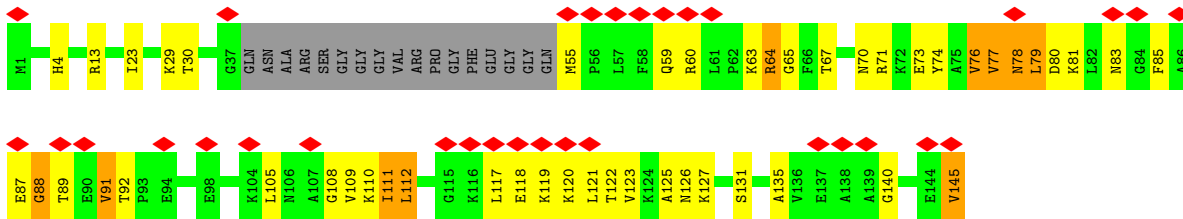
• Molecule 6: 50S ribosomal protein L13



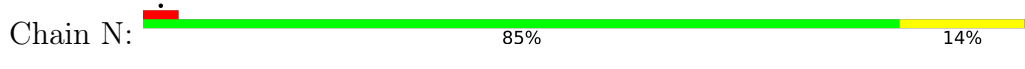
• Molecule 7: 50S ribosomal protein L14



• Molecule 8: 50S ribosomal protein L15

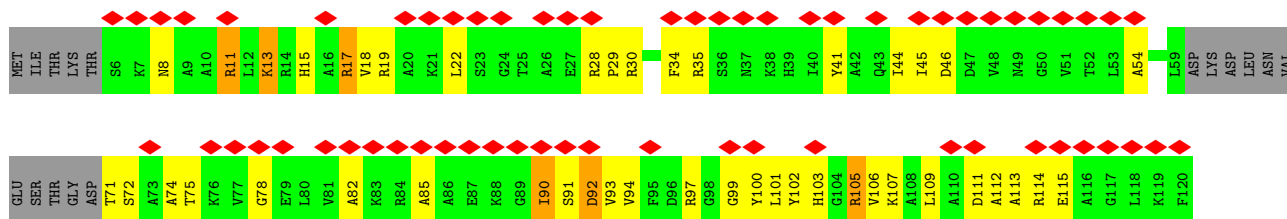


• Molecule 9: 50S ribosomal protein L17

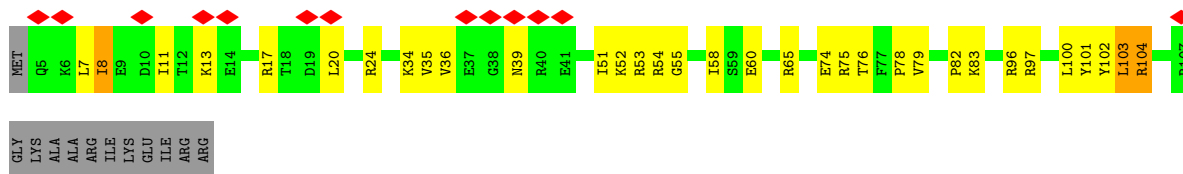


• Molecule 10: 50S ribosomal protein L18

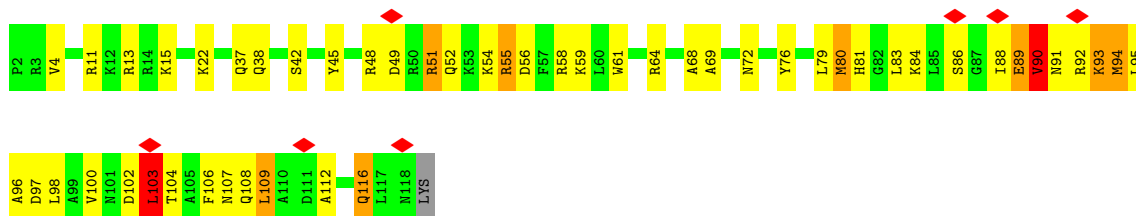




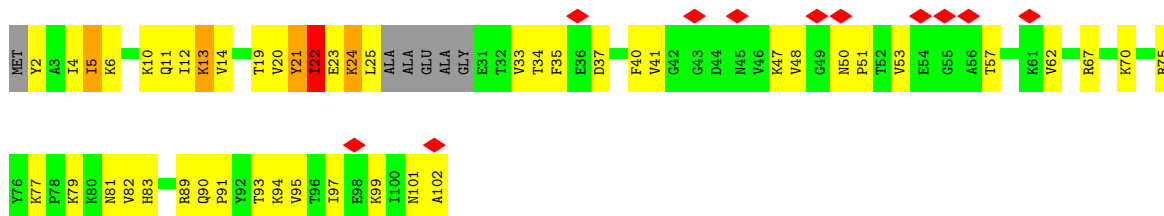
• Molecule 11: 50S ribosomal protein L19



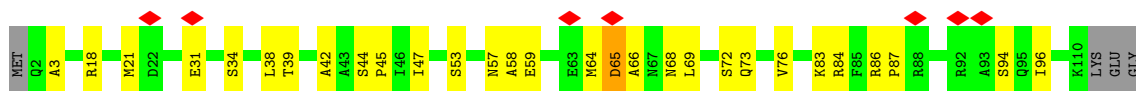
• Molecule 12: 50S ribosomal protein L20



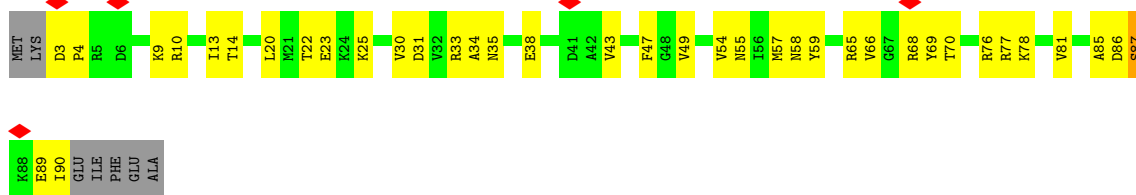
• Molecule 13: 50S ribosomal protein L21



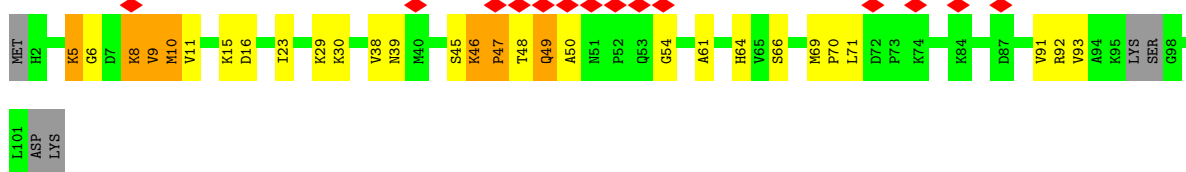
• Molecule 14: 50S ribosomal protein L22



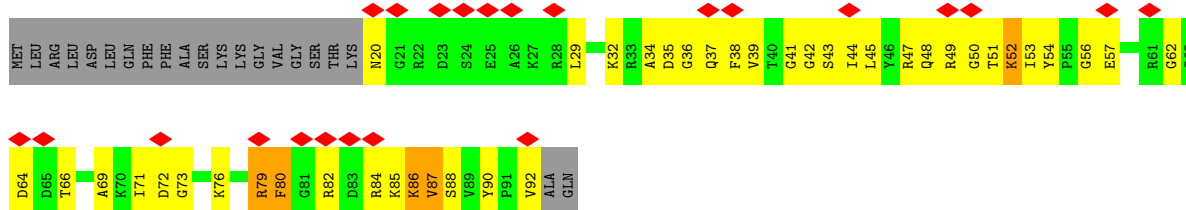
• Molecule 15: 50S ribosomal protein L23



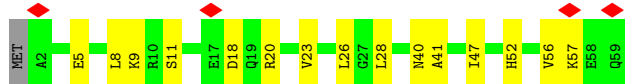
• Molecule 16: 50S ribosomal protein L24



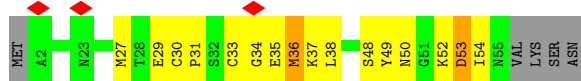
• Molecule 17: 50S ribosomal protein L27



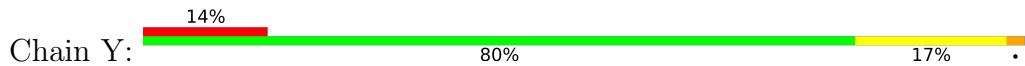
• Molecule 18: 50S ribosomal protein L30

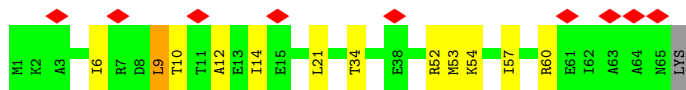


• Molecule 19: 50S ribosomal protein L32

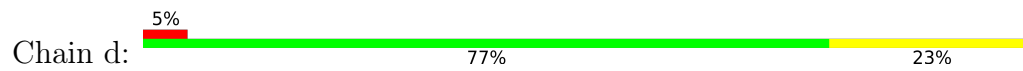


• Molecule 20: 50S ribosomal protein L29





- Molecule 21: 50S ribosomal protein L34



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	546297	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.640	Depositor
Minimum map value	-0.343	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.0732	Depositor
Map size (Å)	360.52798, 360.52798, 360.52798	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.073, 1.073, 1.073	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	0.36	0/59472	0.42	6/92759 (0.0%)
2	B	0.23	0/2678	0.44	0/4174
3	C	0.29	0/1709	0.62	2/2296 (0.1%)
4	D	0.31	0/1276	0.80	8/1709 (0.5%)
5	E	0.30	0/1501	0.79	4/2025 (0.2%)
6	J	0.35	0/1142	0.70	4/1537 (0.3%)
7	K	0.27	0/927	0.53	0/1245
8	L	0.26	0/961	0.92	10/1281 (0.8%)
9	N	0.39	0/960	0.56	0/1284
10	O	0.22	0/799	0.84	2/1070 (0.2%)
11	P	0.29	0/859	0.57	0/1152
12	Q	0.36	0/952	0.82	3/1266 (0.2%)
13	R	0.31	0/768	0.85	4/1029 (0.4%)
14	S	0.33	0/851	0.60	0/1146
15	T	0.31	0/713	0.49	0/951
16	U	0.28	0/748	0.65	1/1000 (0.1%)
17	V	0.23	0/563	0.66	0/753
18	Z	0.29	0/457	0.48	0/613
19	b	0.32	0/433	0.57	0/574
20	Y	0.29	0/531	0.57	0/707
21	d	0.39	0/370	0.54	0/483
All	All	0.34	0/78670	0.48	44/119054 (0.0%)

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
4	D	0	1
12	Q	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	Q	103	LEU	CB-CA-C	18.24	139.72	110.90
10	O	90	ILE	CB-CA-C	-14.73	87.14	111.29
5	E	84	ARG	N-CA-C	13.53	128.33	111.69
13	R	22	ILE	CB-CA-C	-12.93	92.04	110.91
8	L	85	PHE	CB-CA-C	-11.87	85.95	109.33

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	56	LYS	Peptide
12	Q	103	LEU	Peptide

## 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	53094	0	26707	704	0
2	B	2395	0	1212	53	0
3	C	1684	0	1754	82	0
4	D	1265	0	1332	101	0
5	E	1484	0	1565	82	0
6	J	1119	0	1159	50	0
7	K	920	0	977	54	0
8	L	952	0	1002	105	0
9	N	953	0	983	13	0
10	O	791	0	824	40	0
11	P	846	0	902	53	0
12	Q	940	0	1005	124	0
13	R	758	0	801	98	0
14	S	842	0	899	31	0
15	T	707	0	751	36	0
16	U	739	0	790	43	0
17	V	555	0	540	83	0
18	Z	455	0	491	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	b	426	0	445	9	0
20	Y	530	0	568	19	0
21	d	367	0	410	9	0
22	A	13	0	0	0	0
All	All	71835	0	45117	1548	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 15.

The worst 5 of 1548 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)
12:Q:61:TRP:CZ2	12:Q:94:MET:HB2	1.27	1.60
12:Q:95:LEU:HD22	13:R:11:GLN:CB	1.28	1.57
1:A:901:U:H2'	1:A:902:G:C8	1.36	1.56
1:A:2465:G:H2'	1:A:2466:C:C5'	1.38	1.52
12:Q:95:LEU:CD2	13:R:11:GLN:HB3	1.30	1.52

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	
3	C	219/277 (79%)	199 (91%)	20 (9%)	0	100	100
4	D	161/209 (77%)	138 (86%)	20 (12%)	3 (2%)	6	26
5	E	188/207 (91%)	159 (85%)	28 (15%)	1 (0%)	24	54
6	J	139/145 (96%)	122 (88%)	14 (10%)	3 (2%)	5	24
7	K	120/122 (98%)	110 (92%)	9 (8%)	1 (1%)	16	44
8	L	124/145 (86%)	115 (93%)	6 (5%)	3 (2%)	4	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	N	117/120 (98%)	107 (92%)	10 (8%)	0	100	100
10	O	100/120 (83%)	92 (92%)	7 (7%)	1 (1%)	12	40
11	P	101/115 (88%)	92 (91%)	9 (9%)	0	100	100
12	Q	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	42
13	R	92/102 (90%)	77 (84%)	15 (16%)	0	100	100
14	S	107/113 (95%)	100 (94%)	7 (6%)	0	100	100
15	T	86/95 (90%)	79 (92%)	7 (8%)	0	100	100
16	U	94/103 (91%)	82 (87%)	9 (10%)	3 (3%)	3	17
17	V	71/94 (76%)	62 (87%)	8 (11%)	1 (1%)	9	31
18	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
19	b	52/59 (88%)	47 (90%)	4 (8%)	1 (2%)	6	26
20	Y	63/66 (96%)	58 (92%)	5 (8%)	0	100	100
21	d	42/44 (96%)	42 (100%)	0	0	100	100
All	All	2047/2313 (88%)	1844 (90%)	185 (9%)	18 (1%)	16	42

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	O	102	TYR
4	D	93	VAL
6	J	59	ASN
7	K	26	GLY
12	Q	90	VAL

### 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	
3	C	177/225 (79%)	168 (95%)	9 (5%)	21	48
4	D	135/170 (79%)	114 (84%)	21 (16%)	2	10
5	E	162/170 (95%)	147 (91%)	15 (9%)	8	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	J	120/123 (98%)	111 (92%)	9 (8%)	12	38
7	K	101/101 (100%)	100 (99%)	1 (1%)	68	75
8	L	98/109 (90%)	87 (89%)	11 (11%)	6	21
9	N	99/100 (99%)	99 (100%)	0	100	100
10	O	78/93 (84%)	67 (86%)	11 (14%)	3	13
11	P	91/100 (91%)	86 (94%)	5 (6%)	19	46
12	Q	96/97 (99%)	83 (86%)	13 (14%)	4	15
13	R	82/84 (98%)	75 (92%)	7 (8%)	10	33
14	S	90/93 (97%)	86 (96%)	4 (4%)	25	51
15	T	79/85 (93%)	76 (96%)	3 (4%)	29	54
16	U	82/87 (94%)	77 (94%)	5 (6%)	17	43
17	V	54/74 (73%)	46 (85%)	8 (15%)	3	12
18	Z	52/53 (98%)	52 (100%)	0	100	100
19	b	48/53 (91%)	43 (90%)	5 (10%)	7	24
20	Y	56/57 (98%)	55 (98%)	1 (2%)	51	67
21	d	39/39 (100%)	39 (100%)	0	100	100
All	All	1739/1913 (91%)	1611 (93%)	128 (7%)	15	38

5 of 128 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	V	53	ILE
17	V	82	ARG
6	J	29	LEU
6	J	28	ARG
17	V	87	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
10	O	49	ASN
17	V	20	ASN
12	Q	72	ASN
18	Z	52	HIS
16	U	44	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2458/2927 (83%)	792 (32%)	50 (2%)
2	B	111/119 (93%)	45 (40%)	3 (2%)
All	All	2569/3046 (84%)	837 (32%)	53 (2%)

5 of 837 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	U
1	A	9	U
1	A	13	A
1	A	15	G
1	A	23	G

5 of 53 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1245	G
1	A	1527	C
1	A	2812	A
1	A	1250	G
1	A	1362	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](#)

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

There are no chain breaks in this entry.

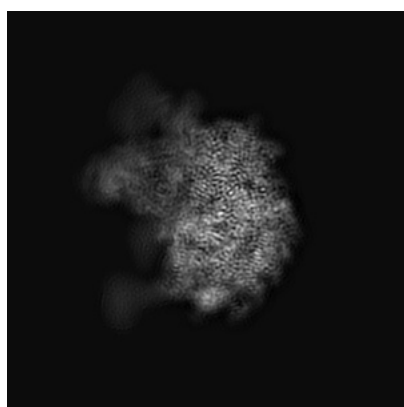
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20435. These allow visual inspection of the internal detail of the map and identification of artifacts.

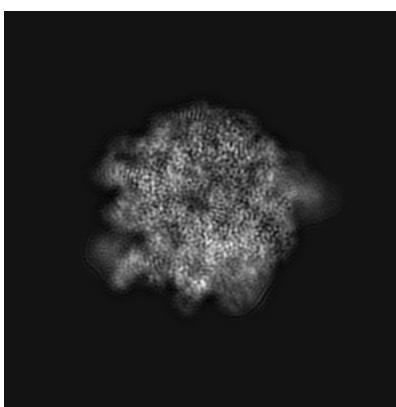
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

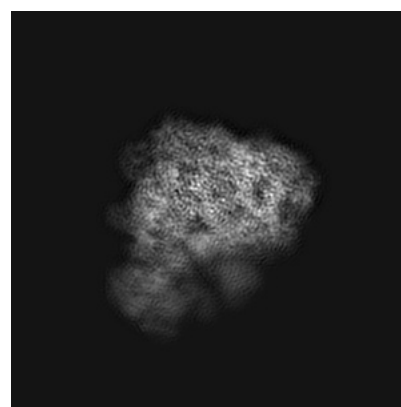
#### 6.1.1 Primary map



X



Y

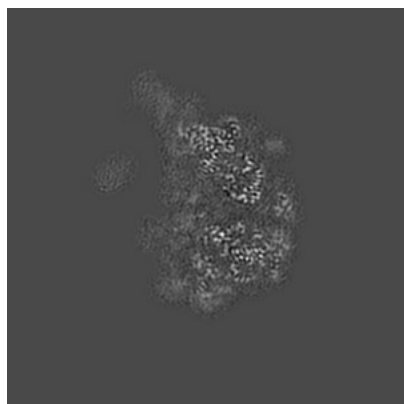


Z

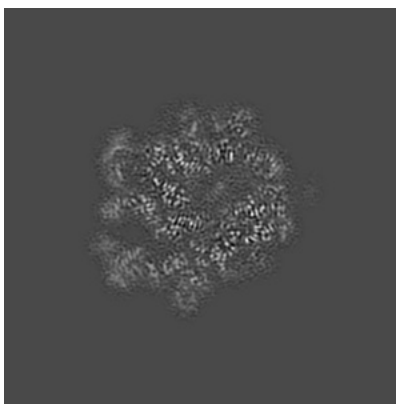
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

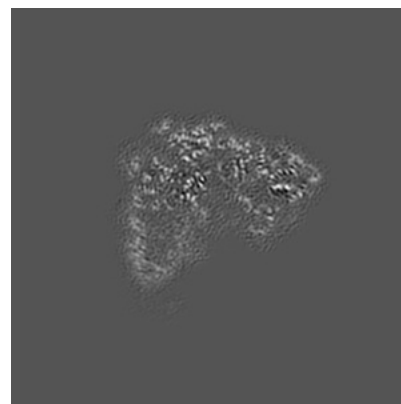
#### 6.2.1 Primary map



X Index: 168



Y Index: 168

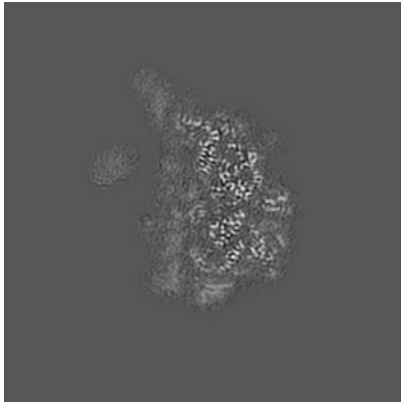


Z Index: 168

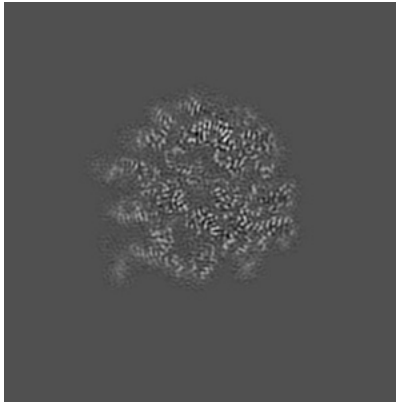
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

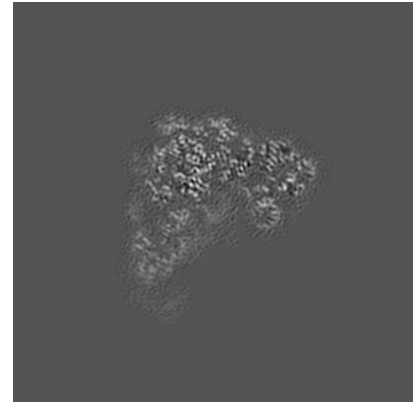
### 6.3.1 Primary map



X Index: 164



Y Index: 185

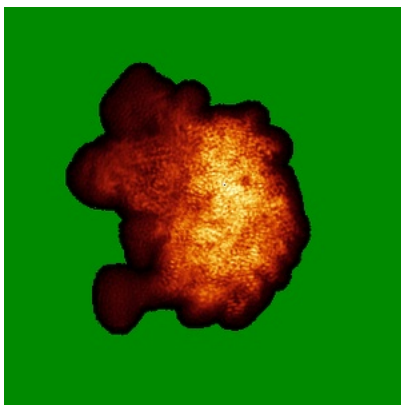


Z Index: 173

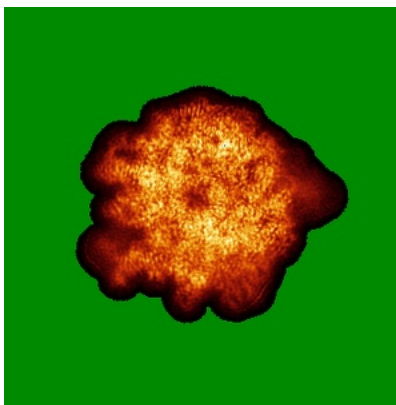
The images above show the largest variance slices of the map in three orthogonal directions.

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

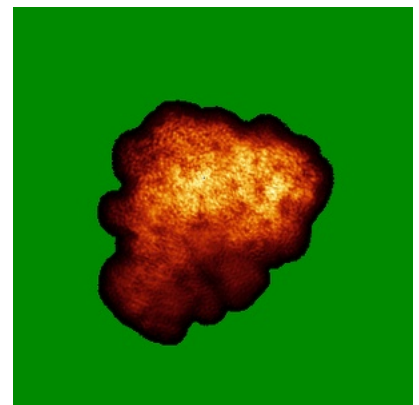
### 6.4.1 Primary map



X



Y

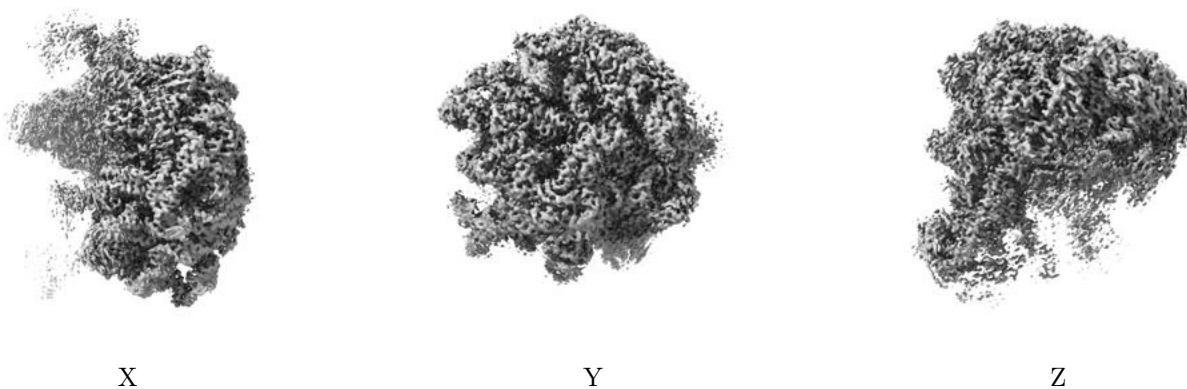


Z

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 0.0732. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

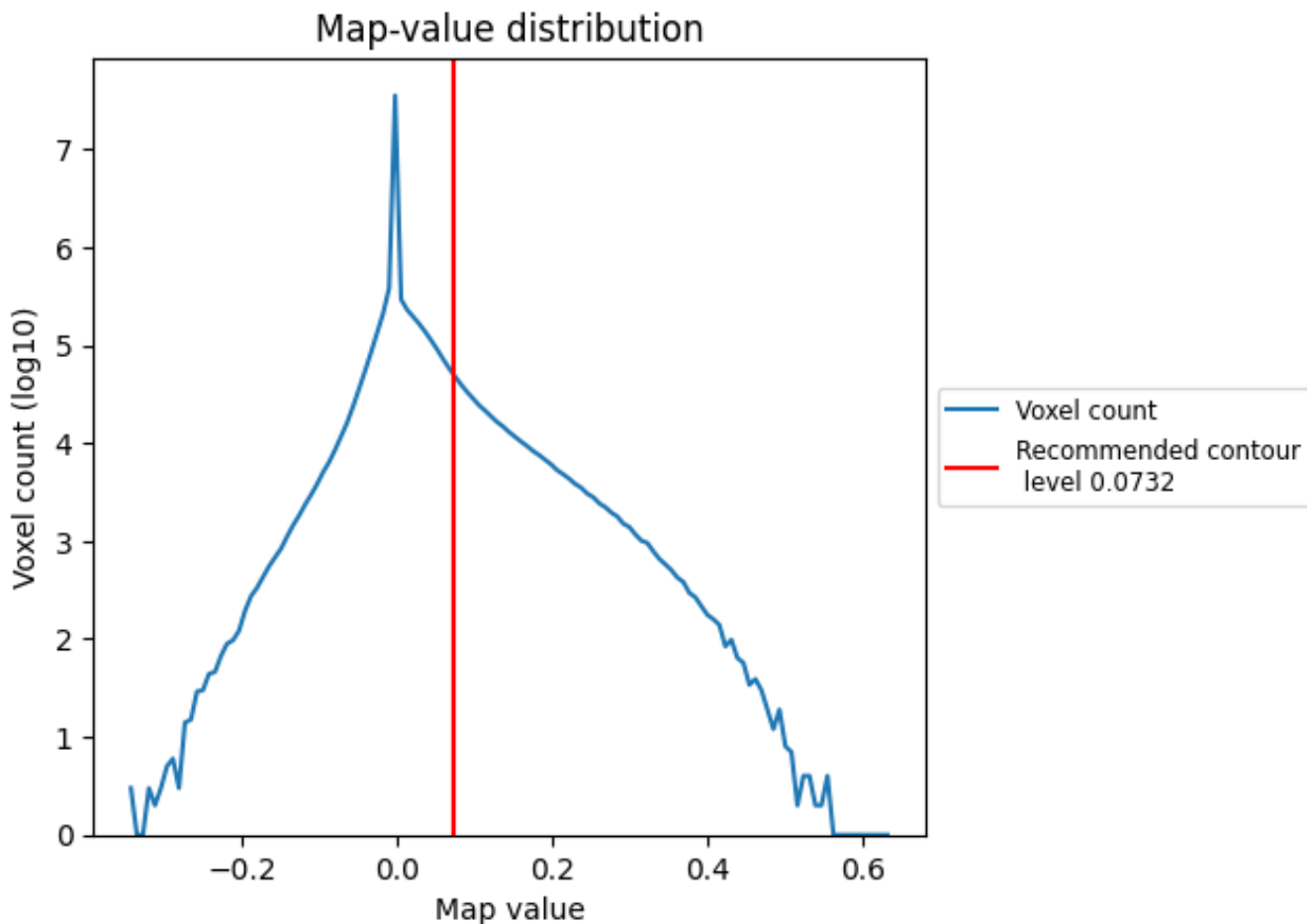
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

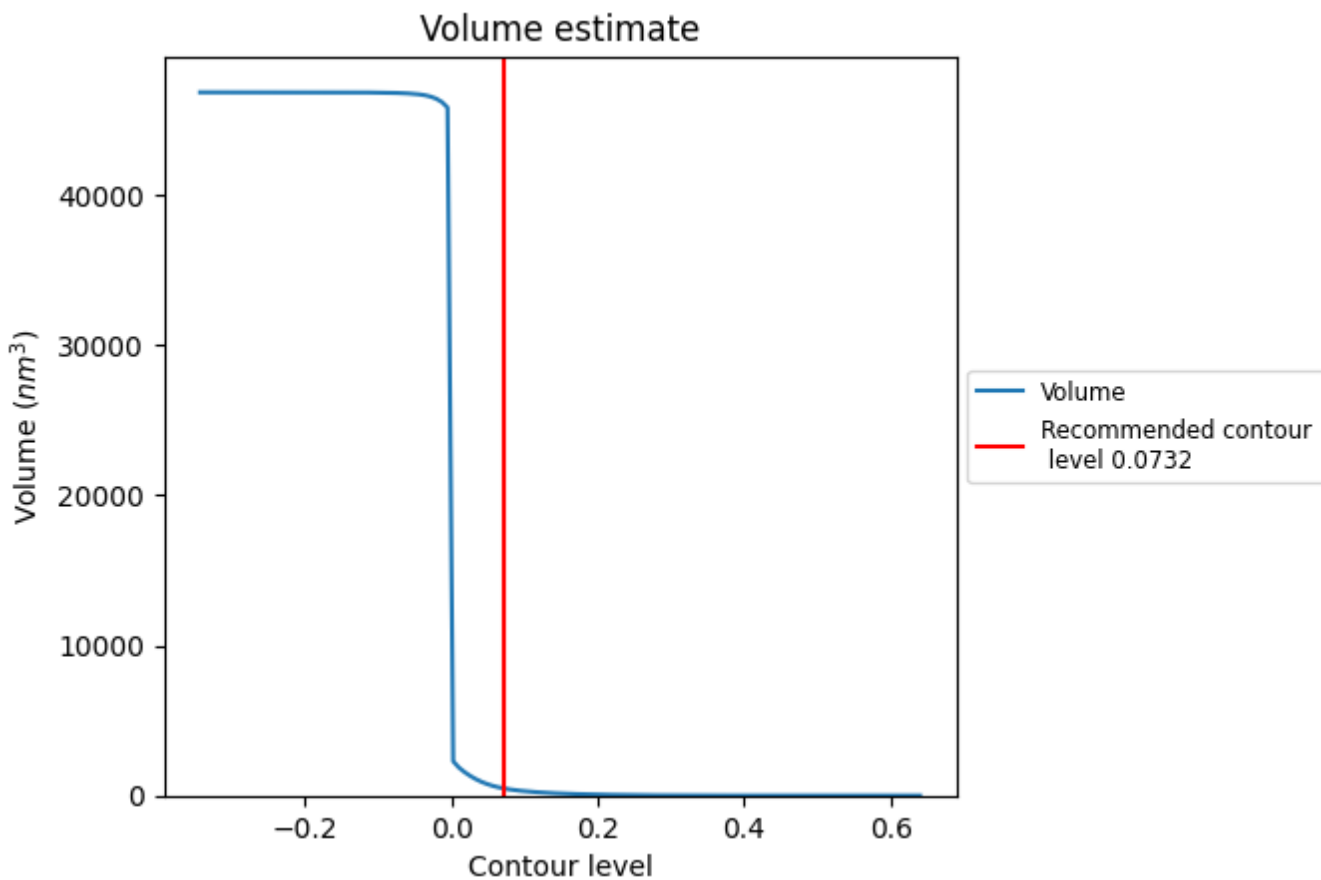
This section contains the results of statistical analysis of the map.

### 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.

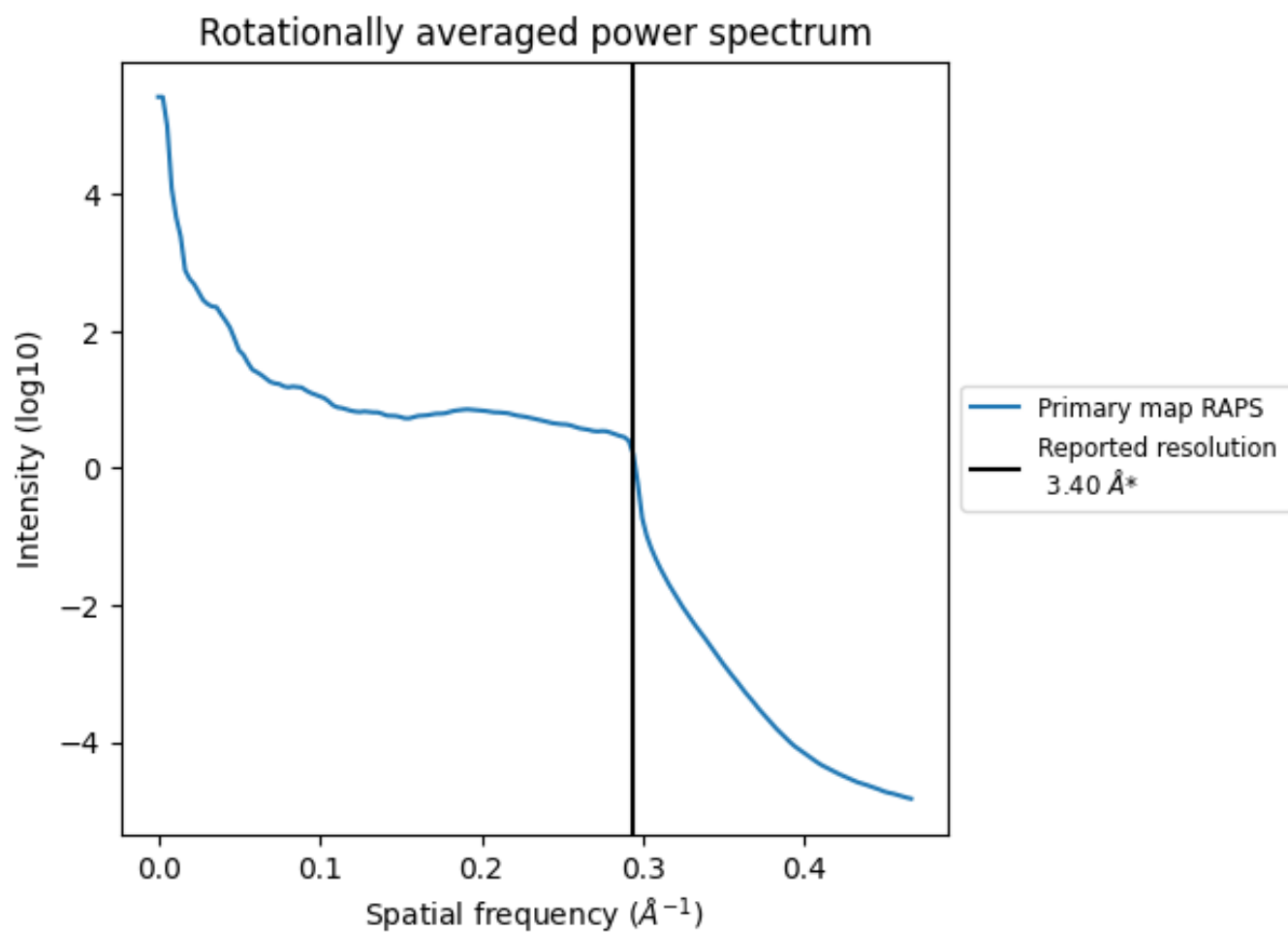
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 466  $\text{nm}^3$ ; this corresponds to an approximate mass of 421 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 [i](#)

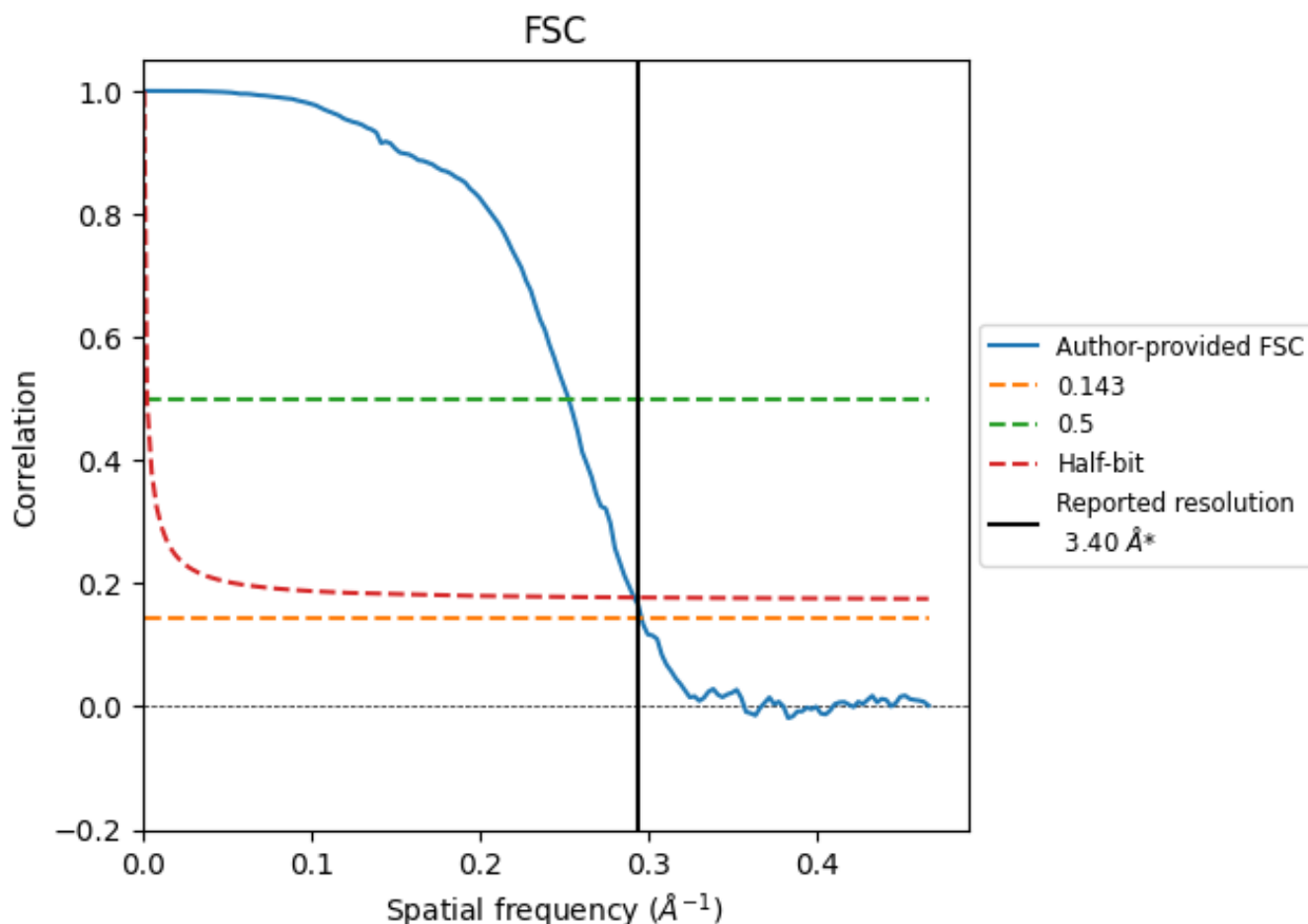


\*Reported resolution corresponds to spatial frequency of  $0.294 \text{\AA}^{-1}$

## 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 0.294 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

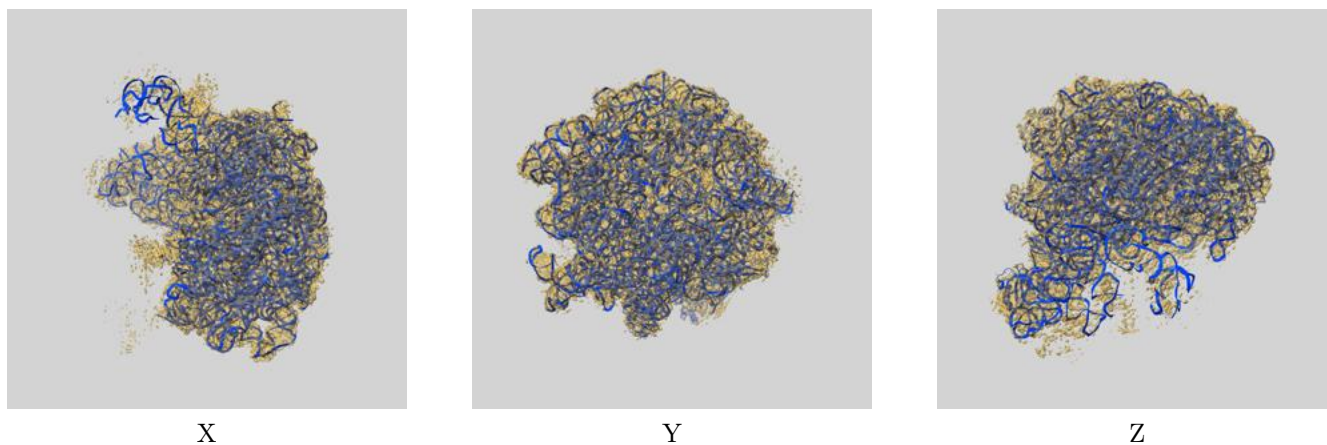
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.38	3.96	3.43
Unmasked-calculated*	-	-	-

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

## 9 Map-model fit [i](#)

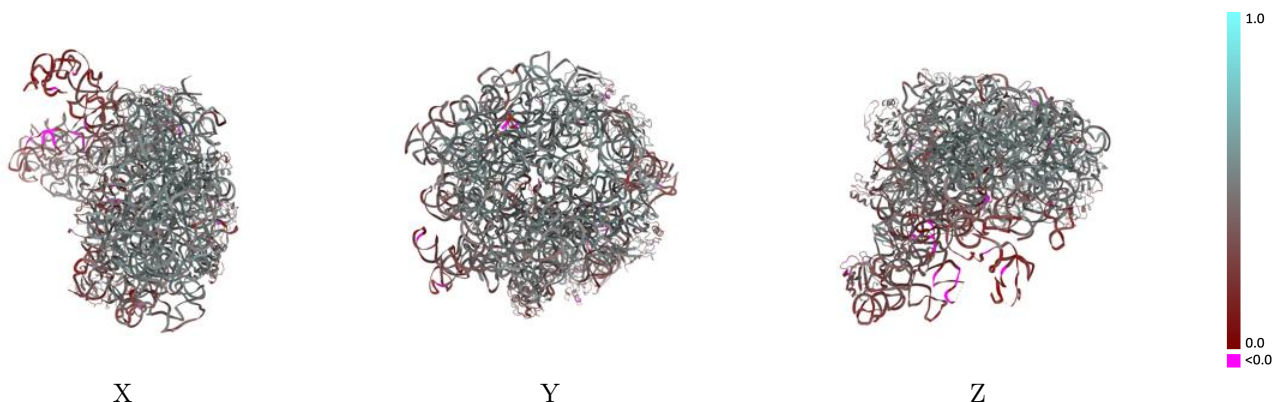
This section contains information regarding the fit between EMDB map EMD-20435 and PDB model 6PPF. Per-residue inclusion information can be found in section 3 on page 8.

### 9.1 Map-model overlay [i](#)



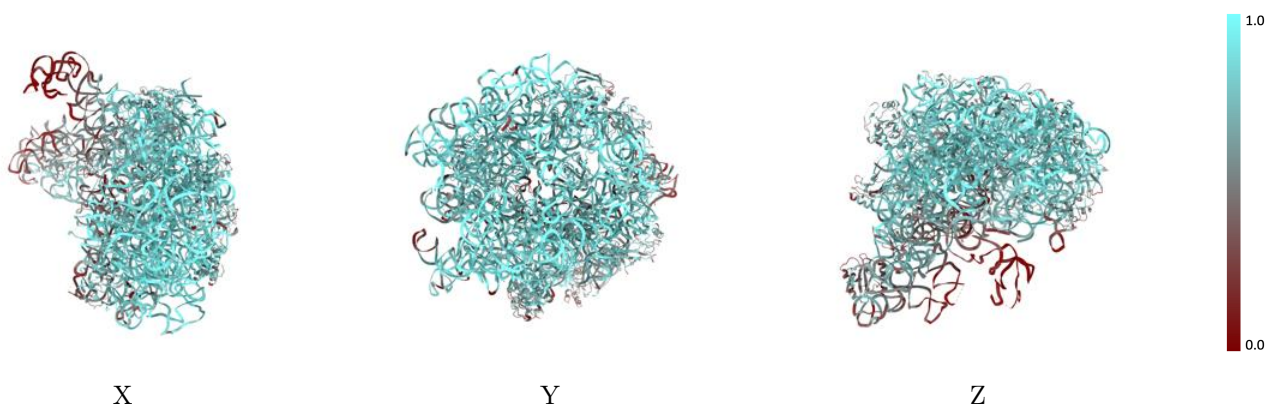
The images above show the 3D surface view of the map at the recommended contour level 0.0732 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



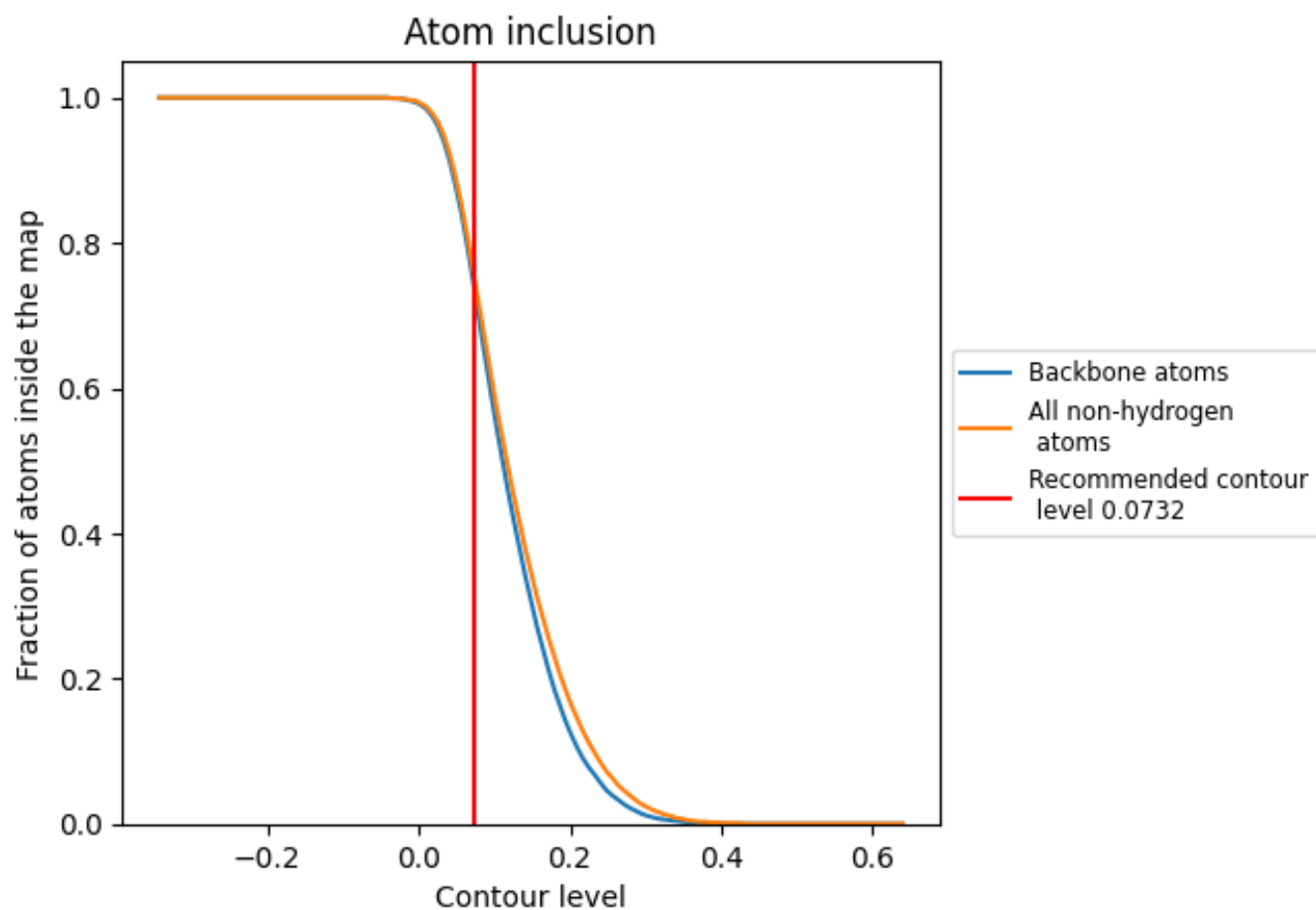
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0732).













































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 76% 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 (0.0732) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7550	 0.4360
A	 0.7930	 0.4390
B	 0.4920	 0.2950
C	 0.6980	 0.4540
D	 0.7240	 0.4550
E	 0.6840	 0.4380
J	 0.7540	 0.4760
K	 0.5840	 0.4320
L	 0.5830	 0.4040
N	 0.7950	 0.5070
O	 0.3550	 0.2810
P	 0.6730	 0.4300
Q	 0.7770	 0.4730
R	 0.6930	 0.4500
S	 0.7580	 0.4970
T	 0.7230	 0.4630
U	 0.6430	 0.4180
V	 0.4910	 0.3820
Y	 0.6540	 0.4400
Z	 0.6970	 0.4780
b	 0.7430	 0.4760
d	 0.7910	 0.5210

