



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 07:39 PM UTC

PDB ID : 6V3E / pdb_00006v3e
EMDB ID : EMD-21034
Title : Cryo-EM structure of the Acinetobacter baumannii Ribosome: 30S subunit
Authors : Morgan, C.E.; Yu, E.W.
Deposited on : 2019-11-25
Resolution : 4.40 Å(reported)
Based on initial model : 5AFI

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:

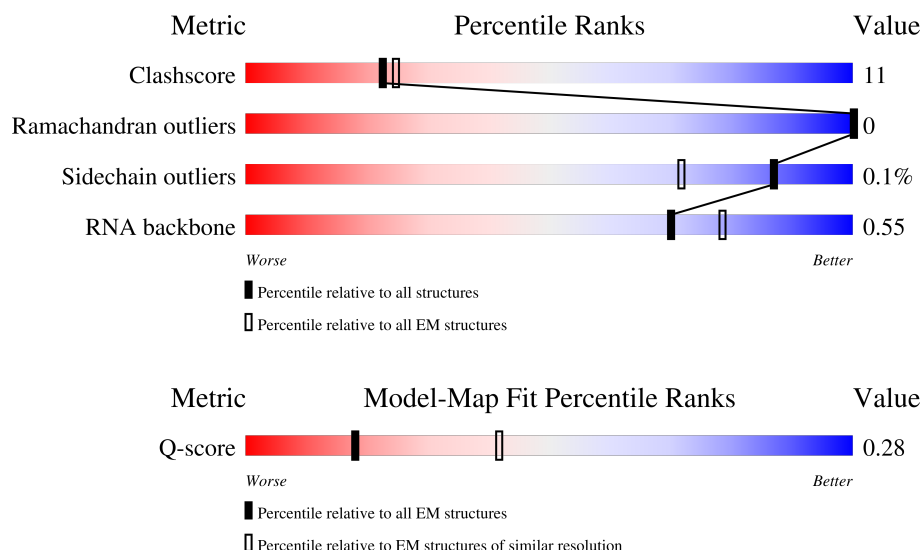
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 4.40 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	3132 (3.91 - 4.90)

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 ≥ 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	sN1	1544	
2	b	250	
3	c	250	

Continued on next page...

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Mol	Chain	Length	Quality of chain
4	d	208	
5	e	165	
6	f	127	
7	g	156	
8	h	131	
9	i	128	
10	j	103	
11	k	128	
12	l	124	
13	m	118	
14	n	101	
15	o	89	
16	p	101	
17	q	85	
18	r	75	
19	s	91	
20	t	88	

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 50850 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 Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	sN1	1528	Total	C	N	O	P	0	0
			32782	14631	5994	10630	1527		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	225	Total	C	N	O	S	0	0
			1769	1110	328	325	6		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	215	Total	C	N	O	S	0	0
			1690	1065	318	299	8		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	207	Total	C	N	O	S	0	0
			1631	1017	313	299	2		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	155	Total	C	N	O	S	0	0
			1129	700	217	207	5		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	94	Total	C	N	O	S	0	0
			793	499	147	143	4		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	133	Total	C	N	O	S	0	0
			1047	657	193	191	6		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	130	Total	C	N	O	S	0	0
			985	615	177	187	6		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	127	Total	C	N	O	S	0	0
			995	621	198	175	1		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	100	Total	C	N	O	S	0	0
			801	500	150	148	3		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	117	Total	C	N	O	S	0	0
			862	535	167	159	1		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	122	Total	C	N	O	S	0	0
			945	580	193	167	5		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	115	Total	C	N	O	S	0	0
			903	558	184	158	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	100	Total	C	N	O	S	0	0
			792	493	158	137	4		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O	S	0	0
			705	434	144	126	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	83	Total	C	N	O	S	0	0
			649	406	129	113	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	80	Total	C	N	O	S	0	0
			630	396	118	115	1		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	r	53	Total	C	N	O	0	0
			438	282	75	81		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	82	Total	C	N	O	S	0	0
			646	412	125	107	2		

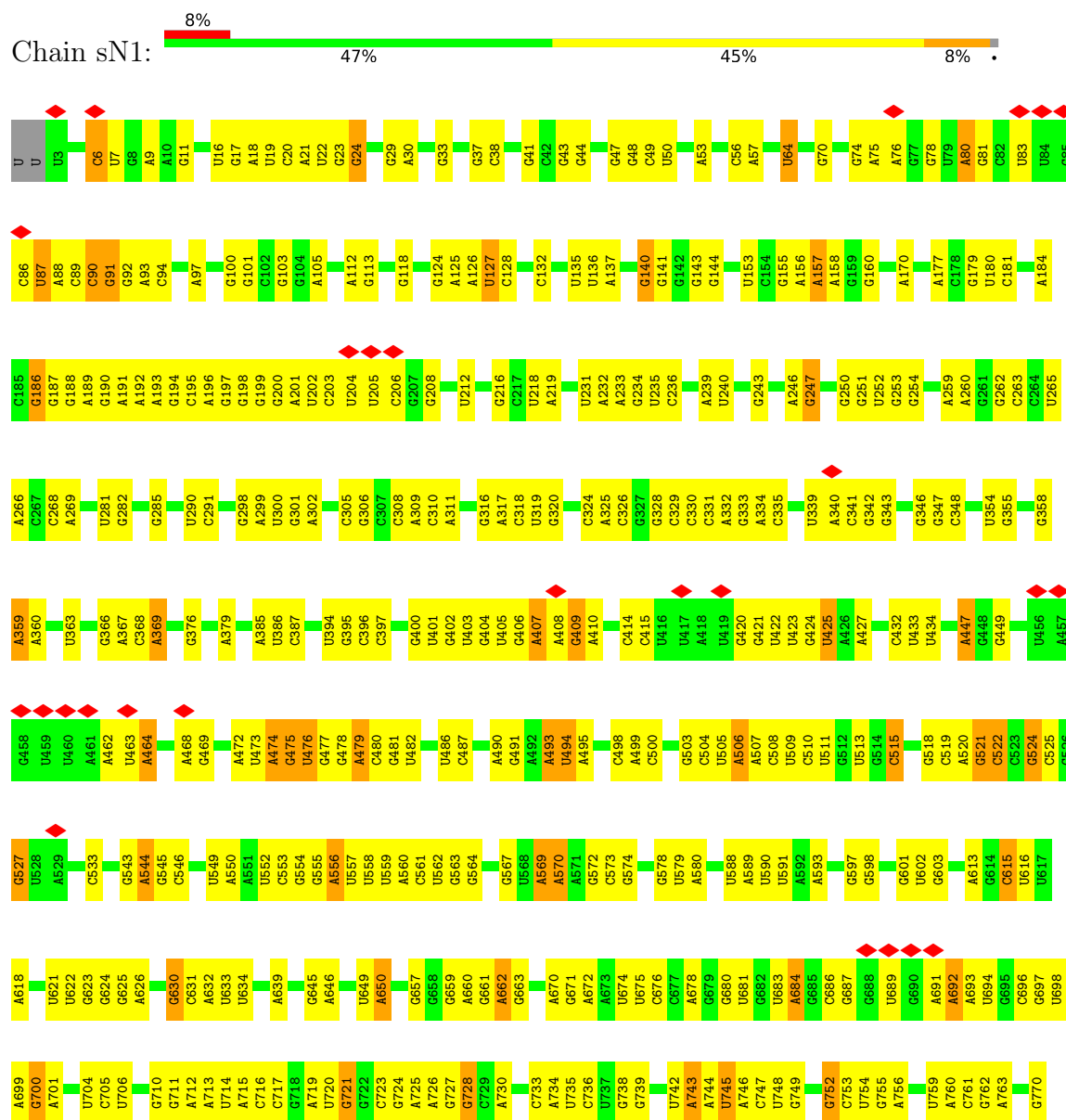
- Molecule 20 is a protein called 30S ribosomal protein S20.

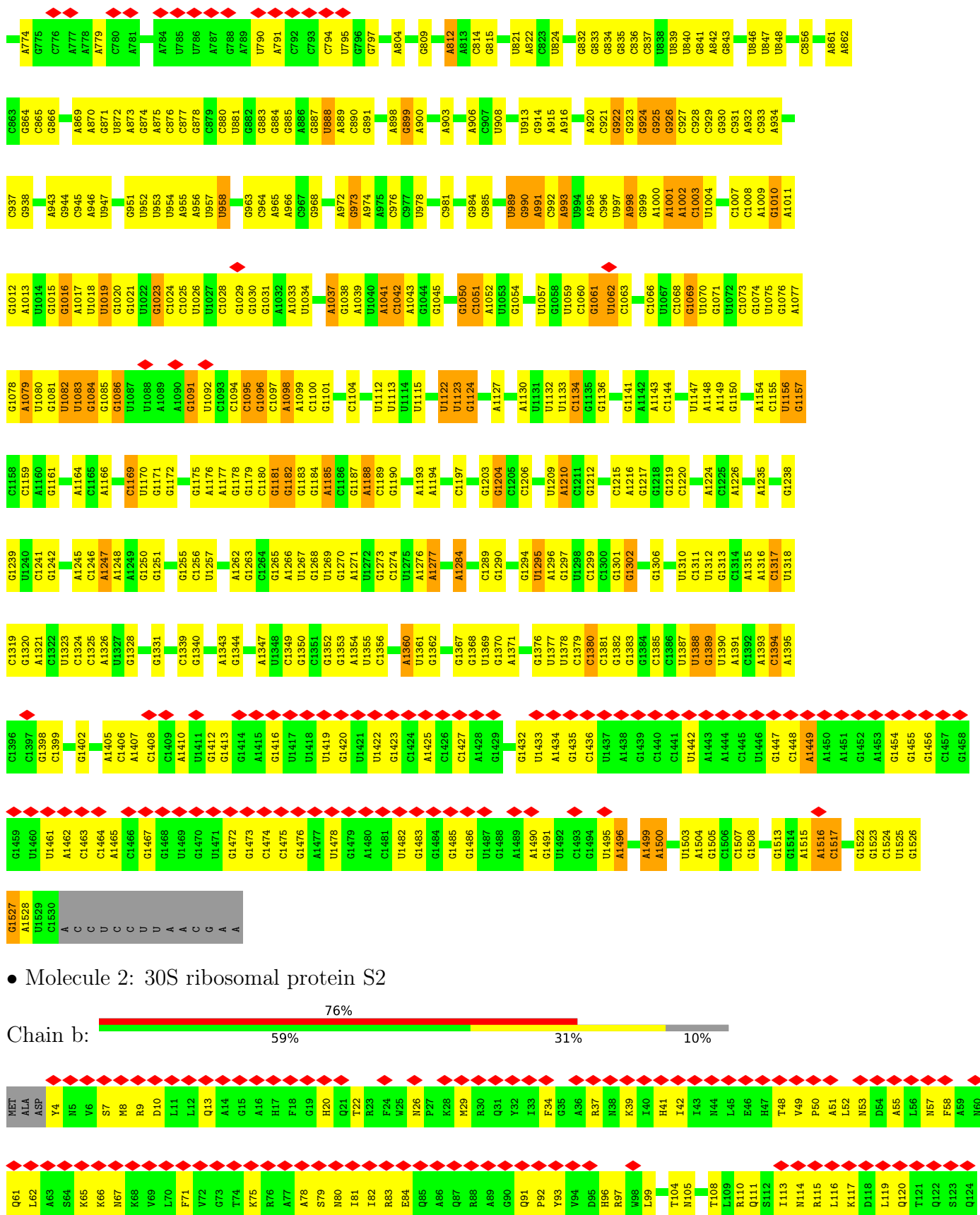
Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	85	Total	C	N	O	S	0	0
			658	406	138	112	2		

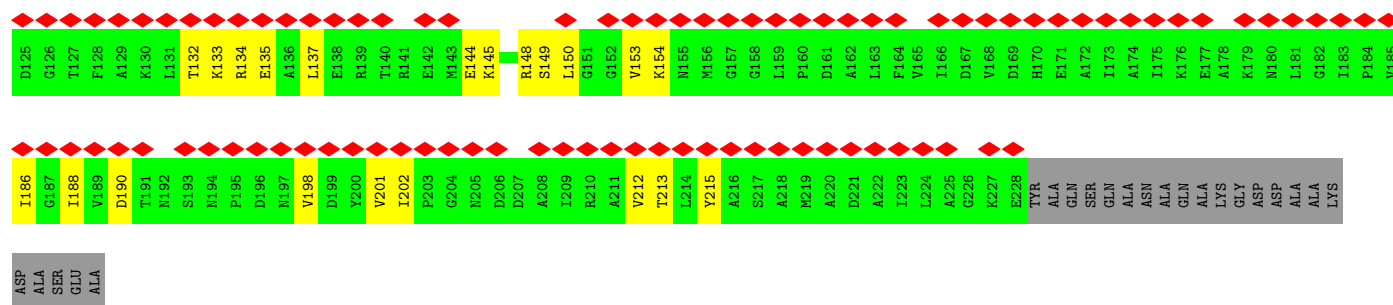
3 Residue-property plots

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: 16s Ribosomal RNA

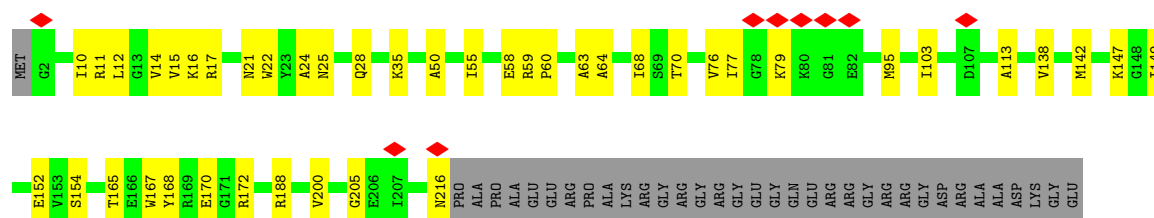






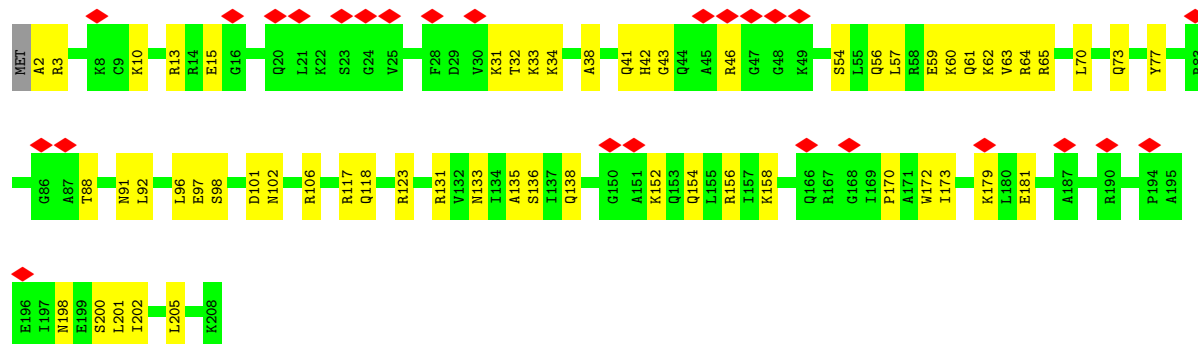
- Molecule 3: 30S ribosomal protein S3

Chain c: 69% 17% 14%



- Molecule 4: 30S ribosomal protein S4

Chain d: 12% 72% 28%



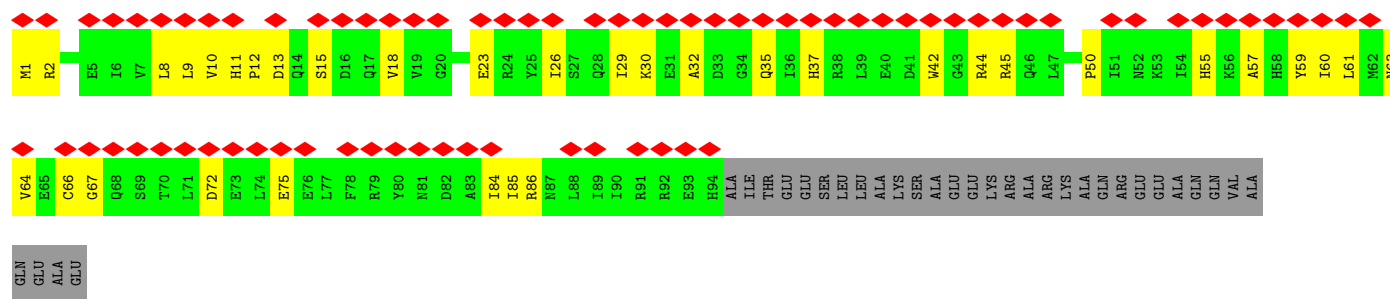
- Molecule 5: 30S ribosomal protein S5

Chain e: 79% 15% 6%

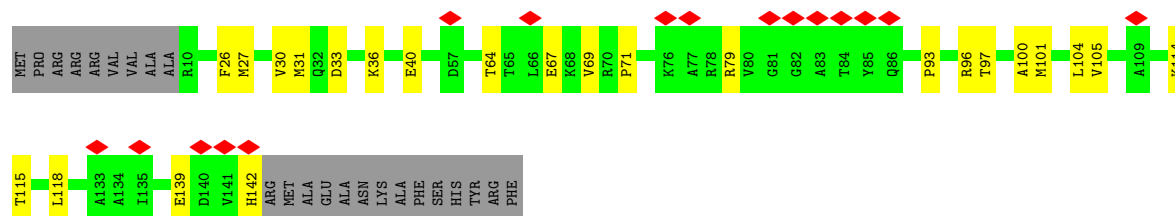


- Molecule 6: 30S ribosomal protein S6

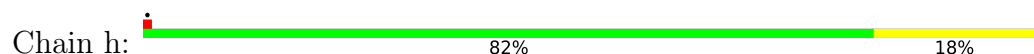
Chain f: 46% 28% 26%



• Molecule 7: 30S ribosomal protein S7



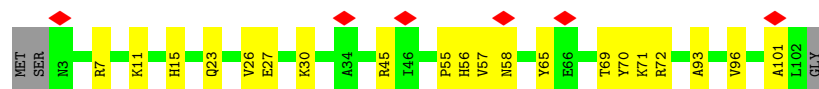
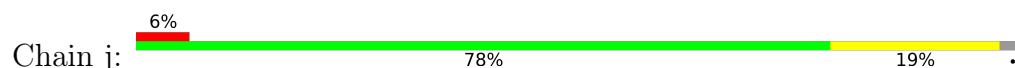
• Molecule 8: 30S ribosomal protein S8



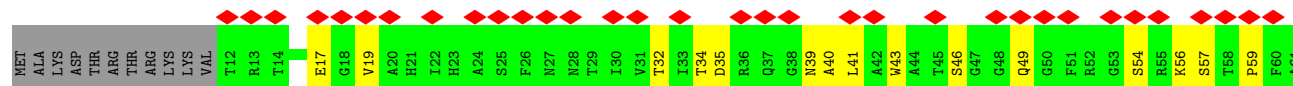
• Molecule 9: 30S ribosomal protein S9

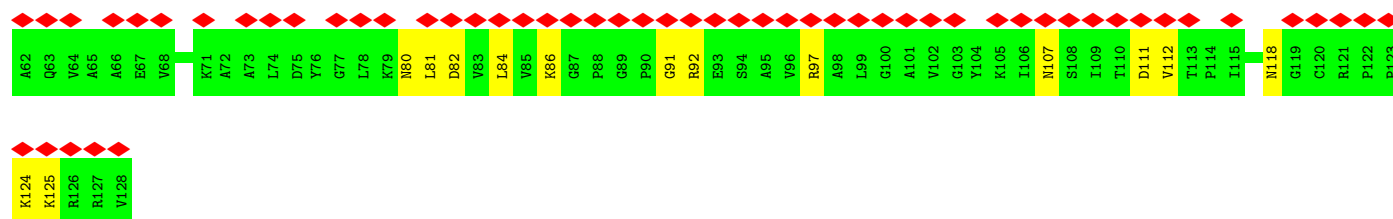


• Molecule 10: 30S ribosomal protein S10

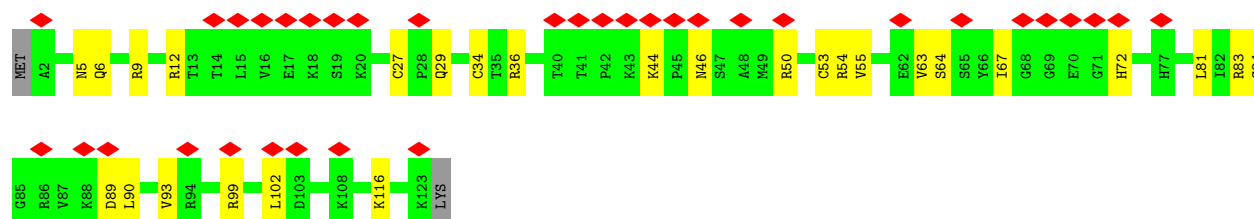
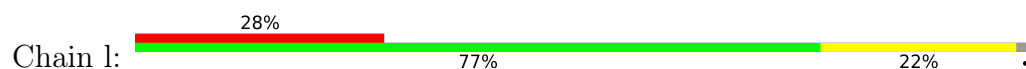


• Molecule 11: 30S ribosomal protein S11

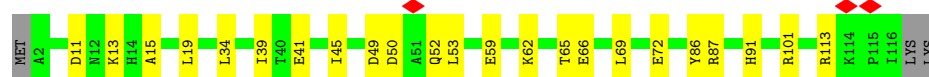
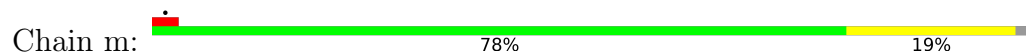




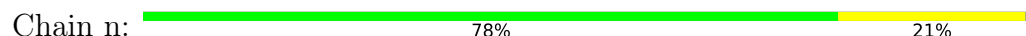
- Molecule 12: 30S ribosomal protein S12



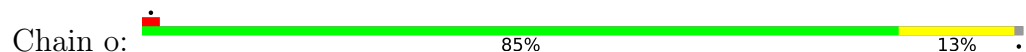
- Molecule 13: 30S ribosomal protein S13



- Molecule 14: 30S ribosomal protein S14



- Molecule 15: 30S ribosomal protein S15



- Molecule 16: 30S ribosomal protein S16



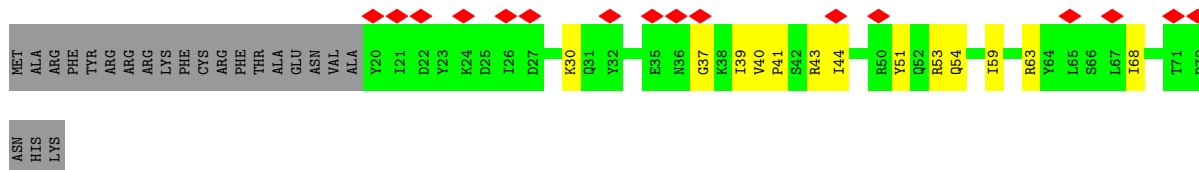
- Molecule 17: 30S ribosomal protein S17

Chain q:  74% 20% 6%



- Molecule 18: 30S ribosomal protein S18

Chain r:  21% 53% 17% 29%



- Molecule 19: 30S ribosomal protein S19

Chain s:  8% 74% 16% 10%



- Molecule 20: 30S ribosomal protein S20

Chain t:  89% 8% 1%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10555	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	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.777	Depositor
Minimum map value	-0.324	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.25	Depositor
Map size ($\text{\AA}$)	544.768, 544.768, 544.768	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.064, 1.064, 1.064	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: PSU, 5MC, UR3, MA6, 4OC, 2MG, 7MG

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	sN1	0.09	1/36476 (0.0%)	0.20	0/56895
2	b	0.17	0/1799	0.43	0/2429
3	c	0.11	0/1714	0.31	0/2304
4	d	0.12	0/1653	0.33	0/2213
5	e	0.13	0/1141	0.34	0/1537
6	f	0.12	0/808	0.37	0/1089
7	g	0.11	0/1062	0.31	0/1424
8	h	0.10	0/993	0.28	0/1331
9	i	0.12	0/1006	0.32	0/1346
10	j	0.11	0/811	0.36	0/1096
11	k	0.13	0/878	0.36	0/1189
12	l	0.15	0/958	0.39	0/1284
13	m	0.12	0/913	0.36	0/1226
14	n	0.11	0/803	0.33	0/1071
15	o	0.09	0/715	0.27	0/958
16	p	0.11	0/660	0.32	0/886
17	q	0.11	0/637	0.29	0/858
18	r	0.10	0/445	0.28	0/601
19	s	0.11	0/664	0.32	0/897
20	t	0.10	0/664	0.28	0/885
All	All	0.10	1/54800 (0.0%)	0.25	0/81519

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	sN1	1495	UR3	O3'-P	5.07	1.61	1.56

There are no bond angle outliers.

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	sN1	32782	0	16508	639	0
2	b	1769	0	1787	50	0
3	c	1690	0	1774	30	0
4	d	1631	0	1691	47	0
5	e	1129	0	1174	18	0
6	f	793	0	788	25	0
7	g	1047	0	1088	15	0
8	h	985	0	1047	15	0
9	i	995	0	1053	17	0
10	j	801	0	832	13	0
11	k	862	0	877	19	0
12	l	945	0	996	22	0
13	m	903	0	962	16	0
14	n	792	0	833	16	0
15	o	705	0	712	9	0
16	p	649	0	660	10	0
17	q	630	0	678	12	0
18	r	438	0	456	8	0
19	s	646	0	663	10	0
20	t	658	0	710	7	0
All	All	50850	0	35289	909	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 909 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)
19:s:30:PRO:HA	19:s:48:THR:O	1.58	1.02
1:sN1:883:G:H1	1:sN1:908:U:H3	1.08	0.98
1:sN1:1157:G:N7	1:sN1:1179:G:N2	2.14	0.93
1:sN1:1112:U:H3	1:sN1:1182:G:H1	1.15	0.90
1:sN1:832:G:H1	1:sN1:848:U:H3	0.95	0.90

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	223/250 (89%)	212 (95%)	11 (5%)	0	100	100
3	c	213/250 (85%)	210 (99%)	3 (1%)	0	100	100
4	d	205/208 (99%)	203 (99%)	2 (1%)	0	100	100
5	e	153/165 (93%)	149 (97%)	4 (3%)	0	100	100
6	f	92/127 (72%)	87 (95%)	5 (5%)	0	100	100
7	g	131/156 (84%)	130 (99%)	1 (1%)	0	100	100
8	h	128/131 (98%)	124 (97%)	4 (3%)	0	100	100
9	i	125/128 (98%)	122 (98%)	3 (2%)	0	100	100
10	j	98/103 (95%)	93 (95%)	5 (5%)	0	100	100
11	k	115/128 (90%)	112 (97%)	3 (3%)	0	100	100
12	l	120/124 (97%)	116 (97%)	4 (3%)	0	100	100
13	m	113/118 (96%)	109 (96%)	4 (4%)	0	100	100
14	n	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
15	o	86/89 (97%)	86 (100%)	0	0	100	100
16	p	81/101 (80%)	81 (100%)	0	0	100	100
17	q	78/85 (92%)	76 (97%)	2 (3%)	0	100	100
18	r	51/75 (68%)	51 (100%)	0	0	100	100
19	s	80/91 (88%)	79 (99%)	1 (1%)	0	100	100
20	t	83/88 (94%)	83 (100%)	0	0	100	100
All	All	2273/2518 (90%)	2219 (98%)	54 (2%)	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	185/200 (92%)	184 (100%)	1 (0%)	81	81
3	c	175/198 (88%)	175 (100%)	0	100	100
4	d	170/171 (99%)	170 (100%)	0	100	100
5	e	113/120 (94%)	113 (100%)	0	100	100
6	f	86/111 (78%)	86 (100%)	0	100	100
7	g	110/128 (86%)	110 (100%)	0	100	100
8	h	108/109 (99%)	108 (100%)	0	100	100
9	i	99/100 (99%)	99 (100%)	0	100	100
10	j	89/91 (98%)	89 (100%)	0	100	100
11	k	88/98 (90%)	88 (100%)	0	100	100
12	l	104/106 (98%)	104 (100%)	0	100	100
13	m	95/98 (97%)	95 (100%)	0	100	100
14	n	81/82 (99%)	81 (100%)	0	100	100
15	o	71/72 (99%)	71 (100%)	0	100	100
16	p	63/77 (82%)	63 (100%)	0	100	100
17	q	72/76 (95%)	72 (100%)	0	100	100
18	r	47/66 (71%)	47 (100%)	0	100	100
19	s	70/78 (90%)	70 (100%)	0	100	100
20	t	65/67 (97%)	65 (100%)	0	100	100
All	All	1891/2048 (92%)	1890 (100%)	1 (0%)	87	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	b	153	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
6	f	55	HIS
9	i	79	HIS
20	t	21	ASN
7	g	21	GLN
8	h	53	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	sN1	1527/1544 (98%)	222 (14%)	0

5 of 222 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	sN1	6	C
1	sN1	9	A
1	sN1	11	G
1	sN1	24	G
1	sN1	33	G

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

9 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	MA6	sN1	1515	1	23,26,27	1.37	4 (17%)	33,38,41	3.30	12 (36%)
1	7MG	sN1	524	1	23,26,27	3.64	11 (47%)	27,39,42	2.17	9 (33%)
1	2MG	sN1	1204	1	23,26,27	2.92	8 (34%)	33,38,41	2.19	11 (33%)
1	UR3	sN1	1495	1	19,22,23	2.98	6 (31%)	26,32,35	1.59	3 (11%)
1	4OC	sN1	1399	1	20,23,24	3.24	8 (40%)	25,32,35	0.91	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MA6	sN1	1516	1	23,26,27	1.37	4 (17%)	33,38,41	3.32	12 (36%)
1	2MG	sN1	963	1	23,26,27	2.92	8 (34%)	33,38,41	2.22	12 (36%)
1	5MC	sN1	964	1	19,22,23	3.95	8 (42%)	26,32,35	0.99	2 (7%)
1	PSU	sN1	513	1	18,21,22	1.17	1 (5%)	21,30,33	1.70	4 (19%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MA6	sN1	1515	1	-	0/11/29/30	0/3/3/3
1	7MG	sN1	524	1	-	3/7/37/38	0/3/3/3
1	2MG	sN1	1204	1	-	0/9/27/28	0/3/3/3
1	UR3	sN1	1495	1	-	2/7/25/26	0/2/2/2
1	4OC	sN1	1399	1	-	0/9/29/30	0/2/2/2
1	MA6	sN1	1516	1	-	3/11/29/30	0/3/3/3
1	2MG	sN1	963	1	-	0/9/27/28	0/3/3/3
1	5MC	sN1	964	1	-	0/7/25/26	0/2/2/2
1	PSU	sN1	513	1	-	0/7/25/26	0/2/2/2

The worst 5 of 58 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	sN1	964	5MC	C6-C5	9.27	1.49	1.34
1	sN1	524	7MG	C8-N9	8.70	1.51	1.45
1	sN1	1204	2MG	C2-N3	7.74	1.46	1.32
1	sN1	963	2MG	C2-N3	7.69	1.46	1.32
1	sN1	1495	UR3	C2-N1	7.44	1.48	1.38

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	sN1	1516	MA6	N1-C6-N6	-12.23	101.96	116.86
1	sN1	1515	MA6	N1-C6-N6	-12.06	102.16	116.86
1	sN1	1516	MA6	C5-C6-N6	8.17	138.27	125.33
1	sN1	1515	MA6	C5-C6-N6	8.04	138.06	125.33
1	sN1	1204	2MG	C2-N3-C4	6.50	120.14	112.00

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	sN1	1516	MA6	C5-C6-N6-C9
1	sN1	524	7MG	C3'-C4'-C5'-O5'
1	sN1	524	7MG	O4'-C4'-C5'-O5'
1	sN1	1495	UR3	O4'-C4'-C5'-O5'
1	sN1	1516	MA6	N1-C6-N6-C9

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	sN1	1204	2MG	1	0
1	sN1	1516	MA6	1	0

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.

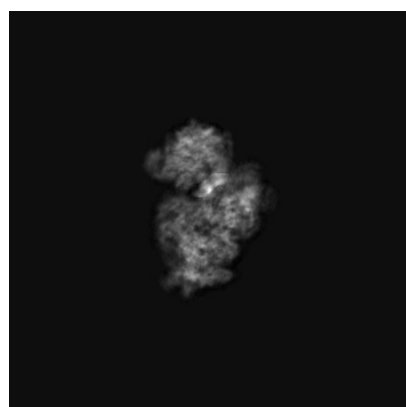
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21034. These allow visual inspection of the internal detail of the map and identification of artifacts.

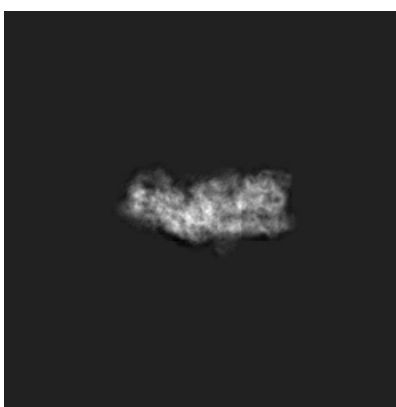
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

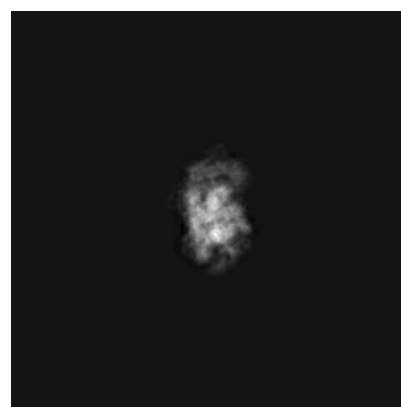
6.1.1 Primary map



X



Y

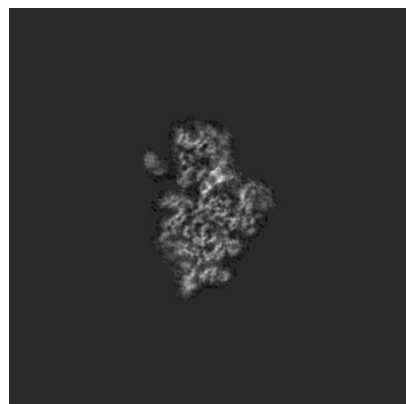


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 256



Y Index: 256

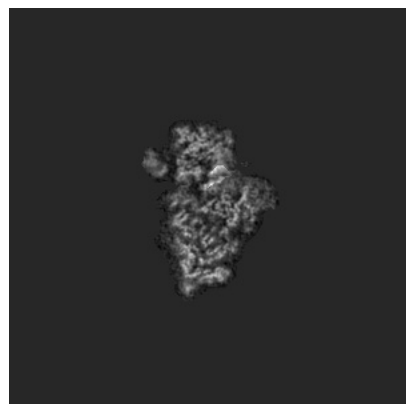


Z Index: 256

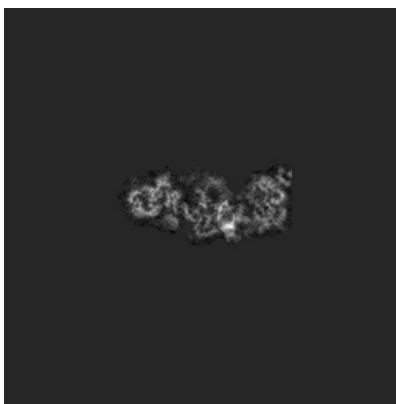
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

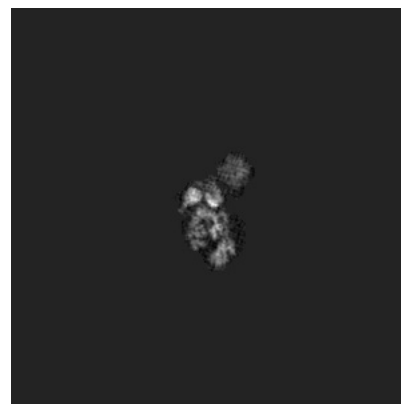
6.3.1 Primary map



X Index: 261



Y Index: 251

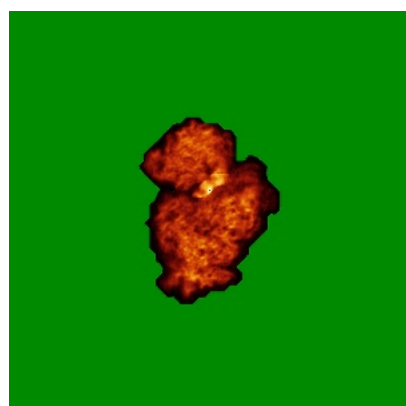


Z Index: 301

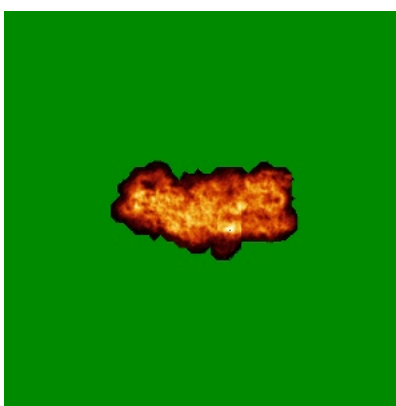
The images above show the largest variance slices of the map in three orthogonal directions.

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

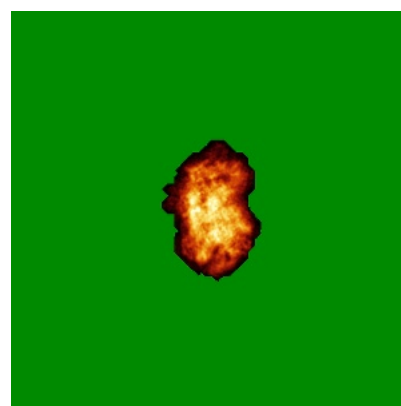
6.4.1 Primary map



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](#)

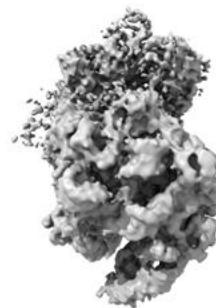
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

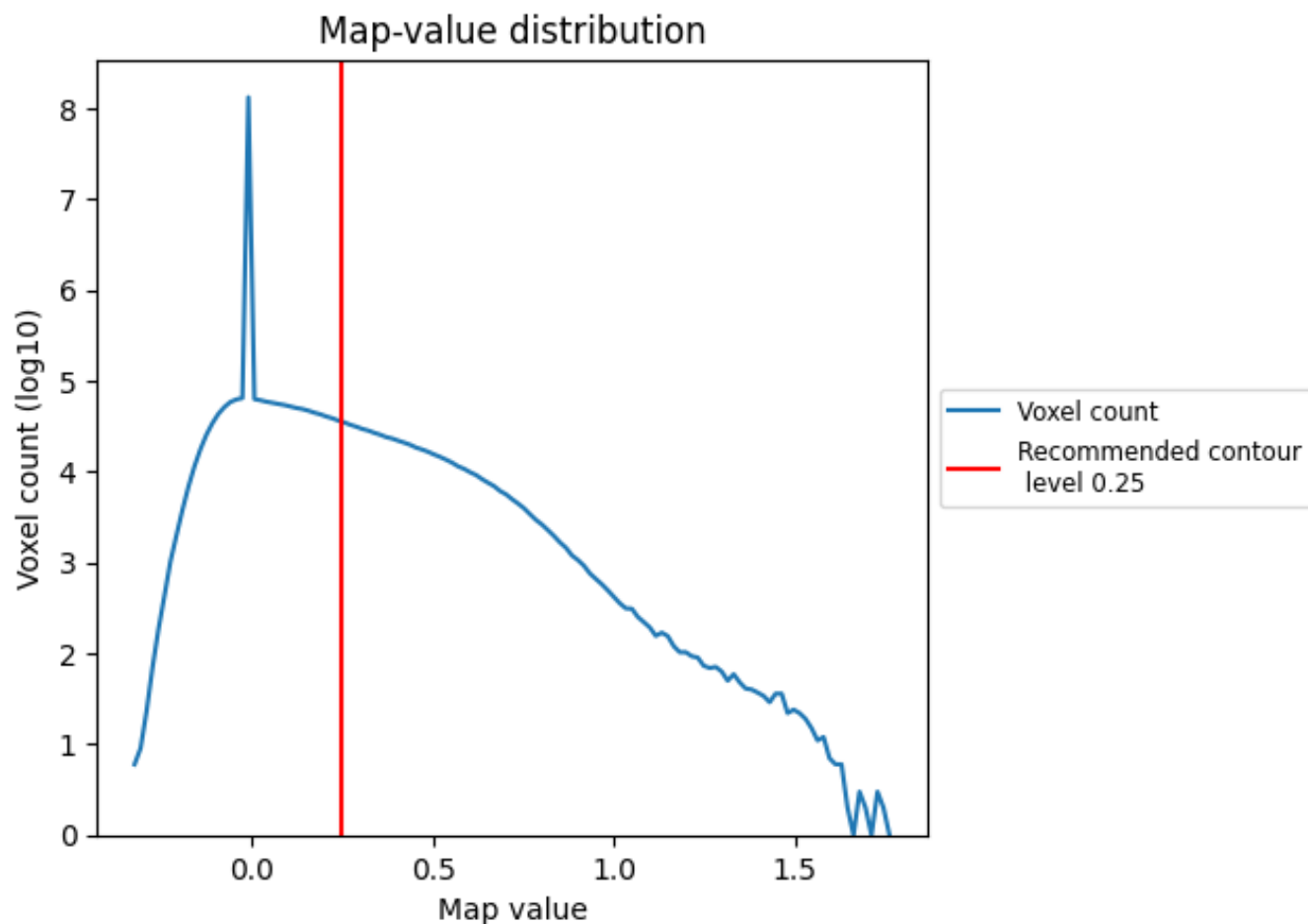
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

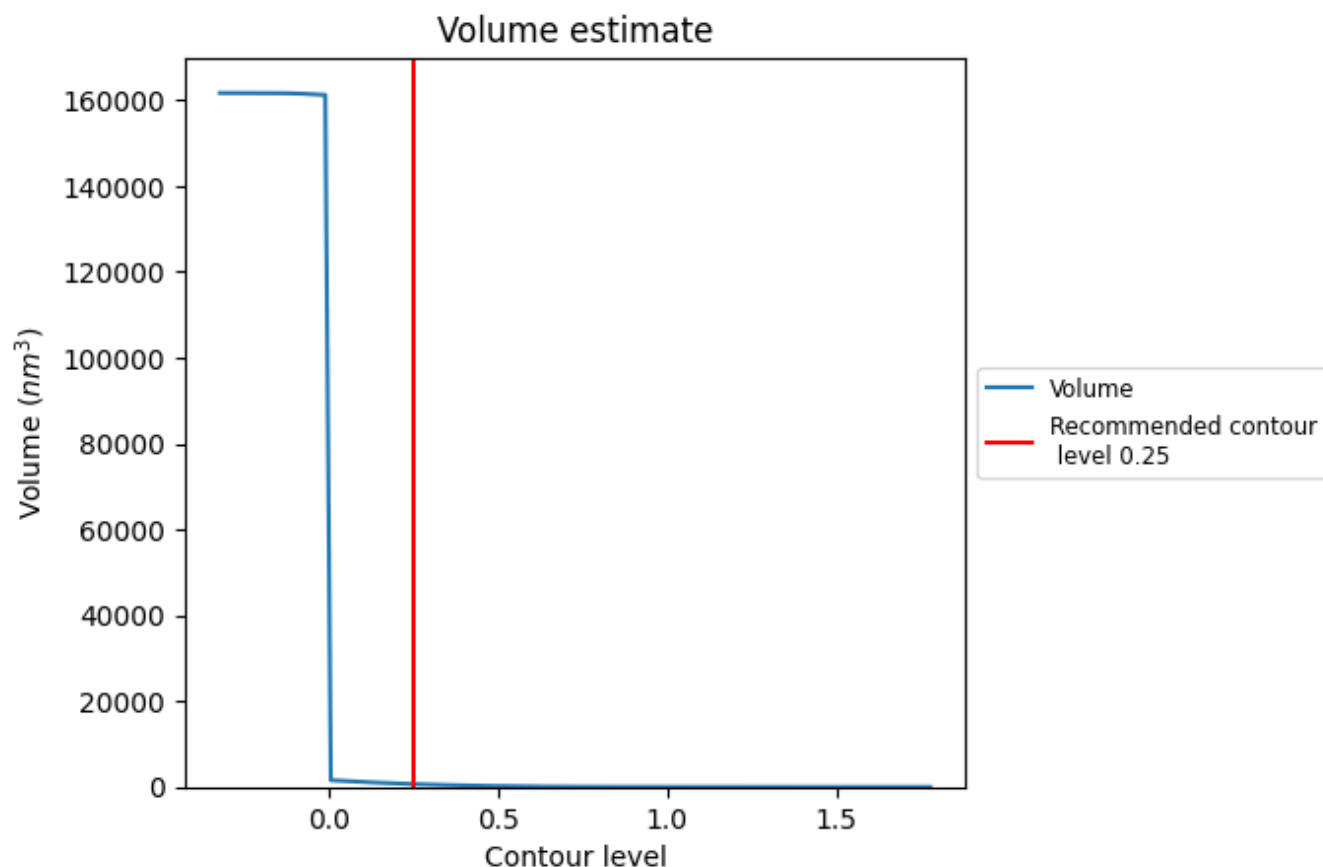
This section contains the results of statistical analysis of the map.

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.

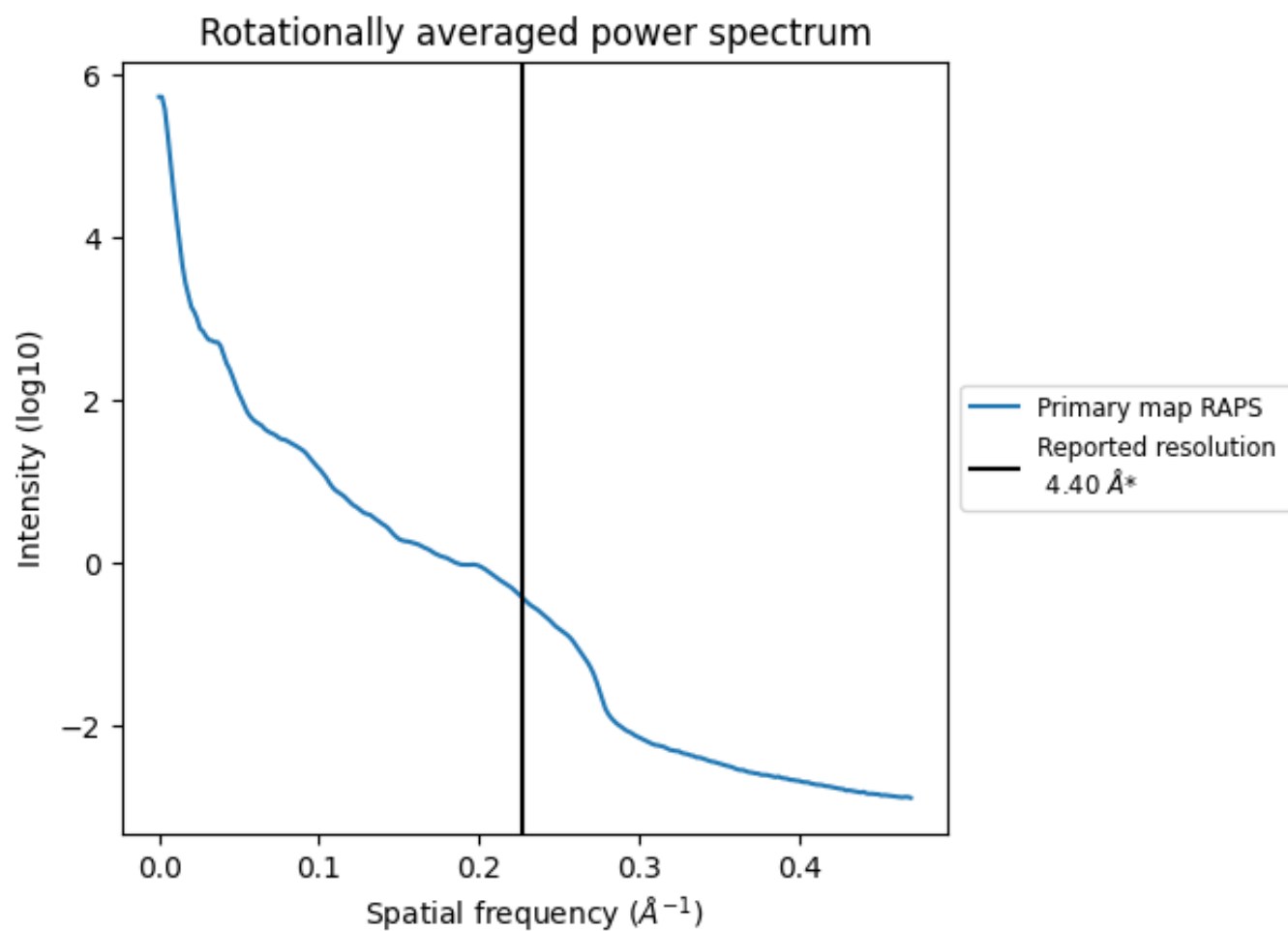
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 668 nm^3 ; this corresponds to an approximate mass of 603 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 0.227 Å⁻¹

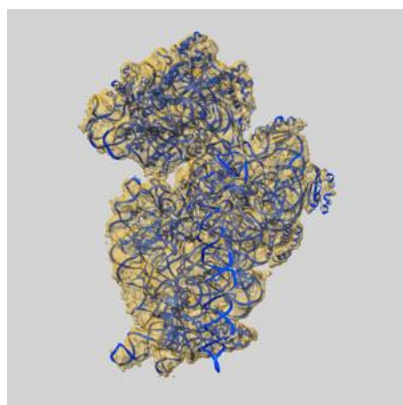
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

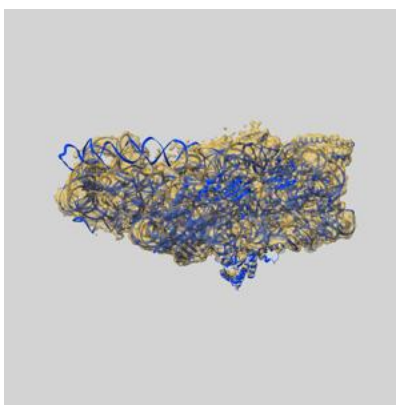
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21034 and PDB model 6V3E. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

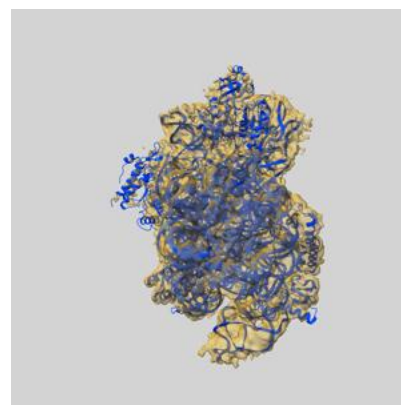
9.1 Map-model overlay [i](#)



X



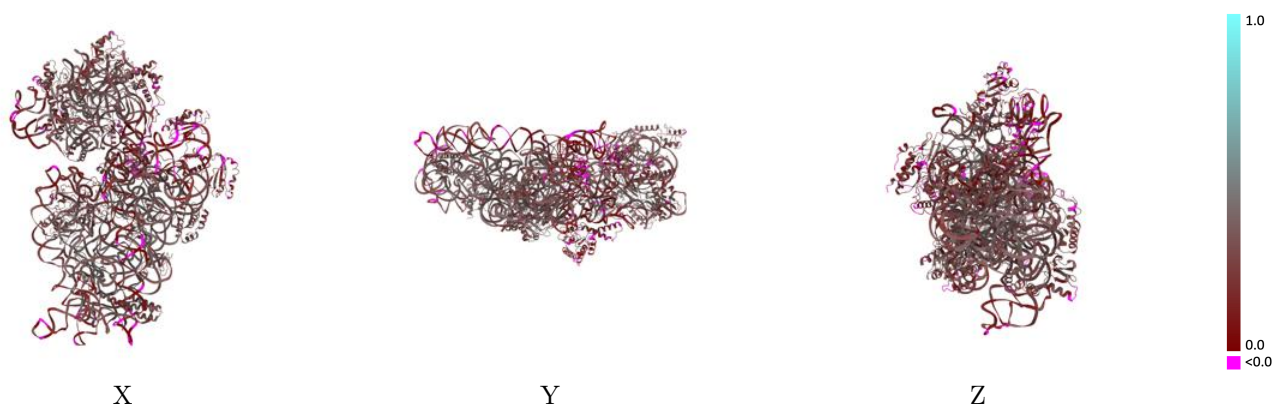
Y



Z

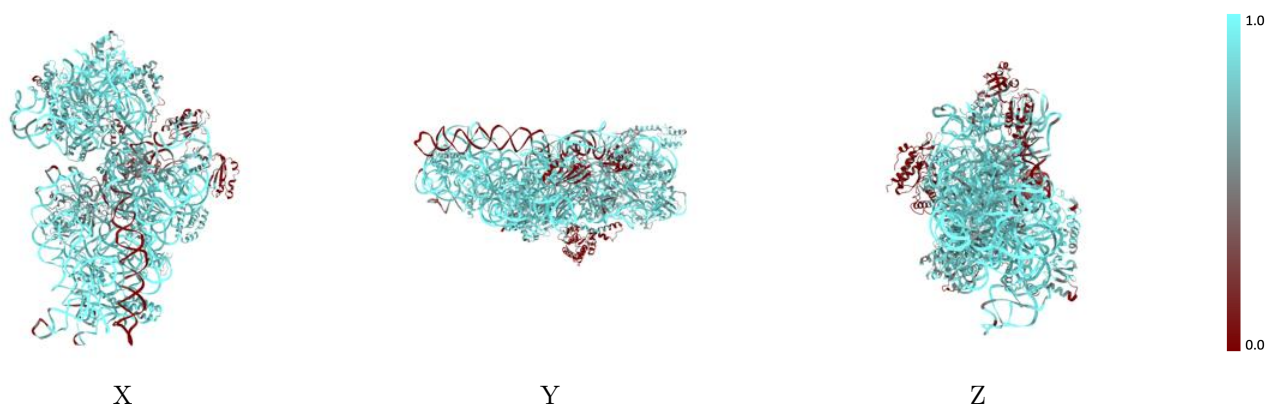
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



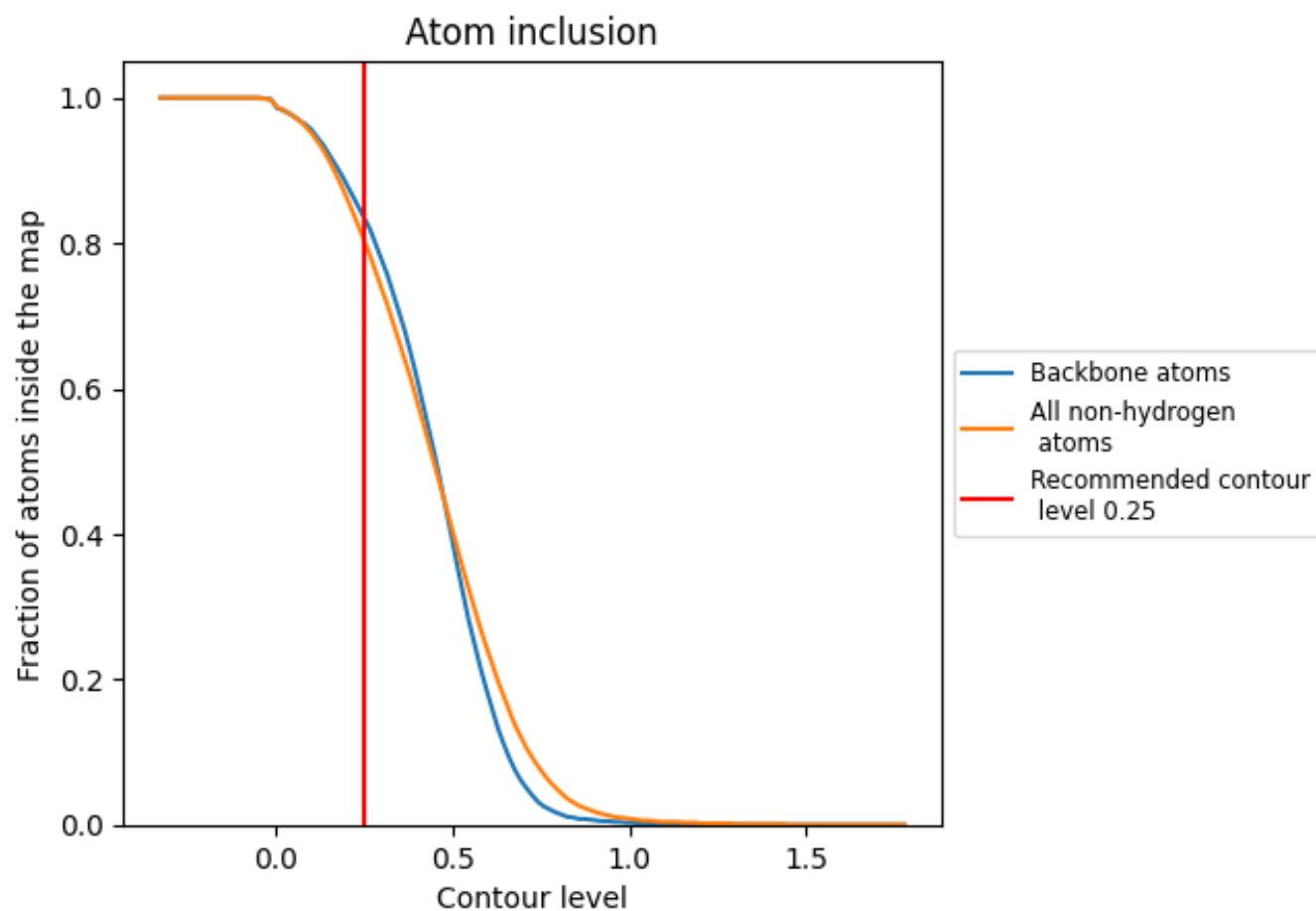
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 81% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8060	 0.2800
b	 0.1850	 0.1510
c	 0.7820	 0.2980
d	 0.6910	 0.2580
e	 0.8430	 0.3070
f	 0.2050	 0.1800
g	 0.6920	 0.2140
h	 0.8520	 0.3580
i	 0.8040	 0.3100
j	 0.7800	 0.3270
k	 0.2150	 0.1300
l	 0.5510	 0.3120
m	 0.7870	 0.2850
n	 0.8050	 0.3280
o	 0.8400	 0.3050
p	 0.9200	 0.3740
q	 0.8880	 0.3500
r	 0.5970	 0.1980
s	 0.7710	 0.2840
sN1	 0.8810	 0.2850
t	 0.8930	 0.3290

