



wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 10:38 PM EDT

PDB ID : 6V3D / pdb_00006v3d
EMDB ID : EMD-21033
Title : Cryo-EM structure of the Acinetobacter baumannii Ribosome: 50S subunit
Authors : Morgan, C.E.; Yu, E.W.
Deposited on : 2019-11-25
Resolution : 2.95 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:

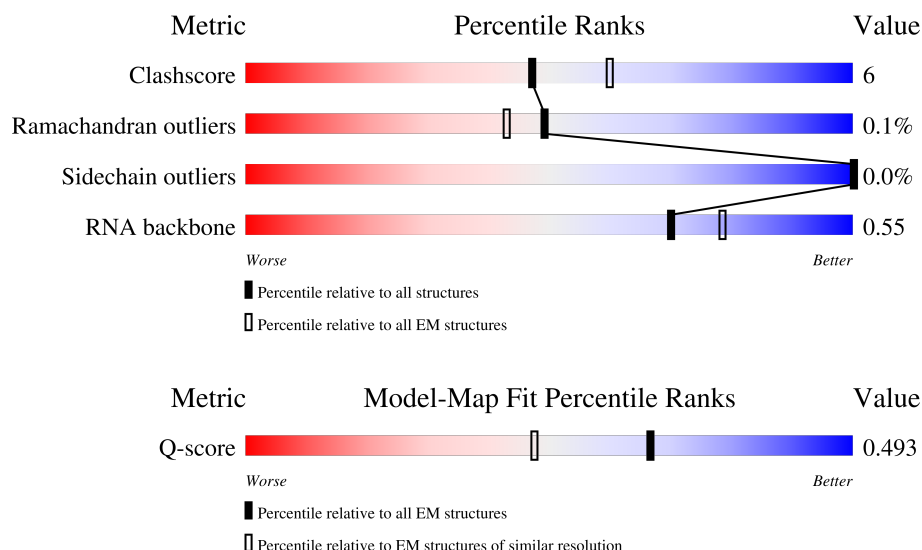
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 2.95 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.



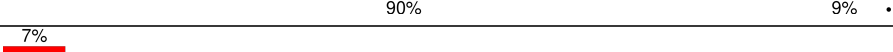
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13114 (2.45 - 3.45)

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	0	51	
2	1	44	
3	2	64	

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Mol	Chain	Length	Quality of chain
4	3	38	
5	AN1	2918	
6	B	115	
7	C	274	
8	D	212	
9	E	200	
10	F	178	
11	G	177	
12	H	148	
13	I	142	
14	J	122	
15	K	146	
16	L	137	
17	M	125	
18	N	116	
19	O	122	
20	P	119	
21	Q	103	
22	R	109	
23	S	106	
24	T	105	
25	U	98	
26	V	85	
27	W	78	
28	X	65	

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Mol	Chain	Length	Quality of chain
29	Y	58	95% 5%
30	Z	61	82% 8% 10%

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 89040 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	51	Total	C	N	O	S	0	0
			427	274	77	73	3		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	44	Total	C	N	O	S	0	0
			363	222	85	54	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			509	319	110	76	4		

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			295	179	64	48	4		

- Molecule 5 is a RNA chain called 23s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AN1	2892	Total	C	N	O	P	0	0
			62023	27689	11345	20098	2891		

- Molecule 6 is a RNA chain called 5s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	115	Total	C	N	O	P	0	0
			2450	1095	440	800	115		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	270	Total	C	N	O	S	0	0
			2096	1291	434	363	8		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	211	Total	C	N	O	S	0	0
			1572	972	297	300	3		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	186	Total	C	N	O	S	0	0
			1419	893	265	257	4		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	175	Total	C	N	O	S	0	0
			1381	877	247	249	8		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	174	Total	C	N	O	S	0	0
			1318	832	236	249	1		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	60	Total	C	N	O	S	0	0
			458	287	84	86	1		

- Molecule 13 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	142	Total	C	N	O	S	0	0
			1125	718	200	203	4		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	122	Total	C	N	O	S	0	0
			946	592	180	169	5		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	146	Total	C	N	O	S	0	0
			1089	673	215	200	1		

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	137	Total	C	N	O	S	0	0
			1087	687	210	185	5		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	119	Total	C	N	O	S	0	0
			942	590	186	163	3		

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	114	Total	C	N	O	S	0	0
			857	528	173	155	1		

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	O	117	Total	C	N	O	0	0
			919	578	177	164		

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	117	Total	C	N	O	S	0	0
			934	589	197	146	2		

- Molecule 21 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	103	Total	C	N	O	S	0	0
			807	506	155	143	3		

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	109	Total	C	N	O	S	0	0
			826	514	158	150	4		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	90	Total	C	N	O		0	0
			702	447	127	128			

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	100	Total	C	N	O		0	0
			749	465	139	145			

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	97	Total	C	N	O	S	0	0
			760	477	143	139	1		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	80	Total	C	N	O	S	0	0
			598	370	115	111	2		

- Molecule 27 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	77	Total	C	N	O	S	0	0
			632	395	130	105	2		

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	62	Total	C	N	O	S	0	0
			498	308	96	93	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	58	Total	C	N	O	S	0	0
			463	286	88	85	4		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	55	Total	C	N	O	S	0	0
			456	271	102	82	1		

- Molecule 31 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
31	3	1	Total	Zn	0
			1	1	

- Molecule 32 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
32	AN1	105	Total	Mg	0
			105	105	
32	C	1	Total	Mg	0
			1	1	

- Molecule 33 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
33	AN1	1	Total	Na	0
			1	1	

- Molecule 34 is water.

Mol	Chain	Residues	Atoms		AltConf
34	1	1	Total	O	0
			1	1	
34	AN1	218	Total	O	0
			218	218	

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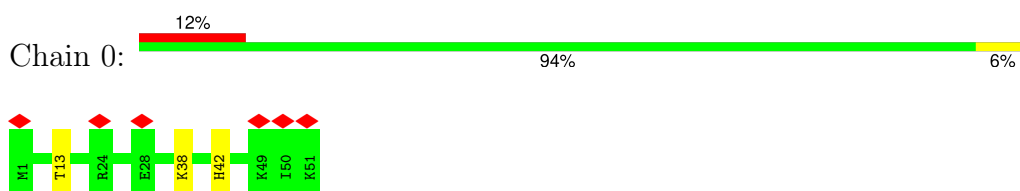
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Mol	Chain	Residues	Atoms		AltConf
34	B	3	Total 3	O 3	0
34	C	1	Total 1	O 1	0
34	D	1	Total 1	O 1	0
34	E	1	Total 1	O 1	0
34	K	1	Total 1	O 1	0
34	N	1	Total 1	O 1	0
34	R	1	Total 1	O 1	0
34	V	1	Total 1	O 1	0
34	W	1	Total 1	O 1	0
34	Z	1	Total 1	O 1	0

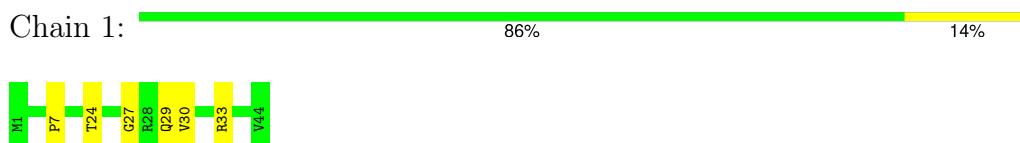
3 Residue-property plots [i](#)

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.

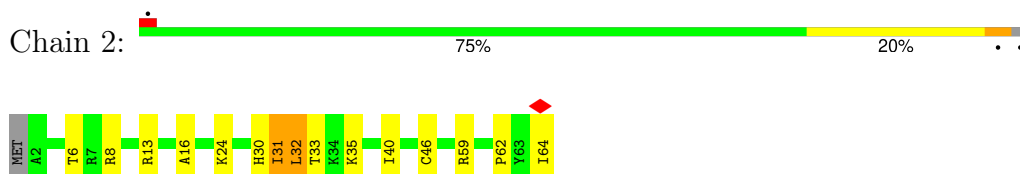
- Molecule 1: 50S ribosomal protein L33



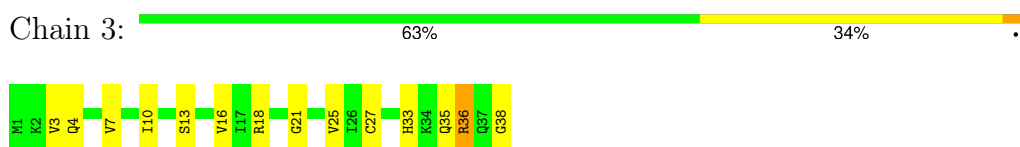
- Molecule 2: 50S ribosomal protein L34



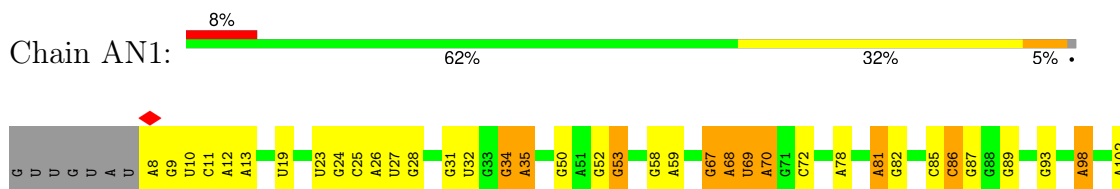
- Molecule 3: 50S ribosomal protein L35



- Molecule 4: 50S ribosomal protein L36



- Molecule 5: 23S ribosomal RNA



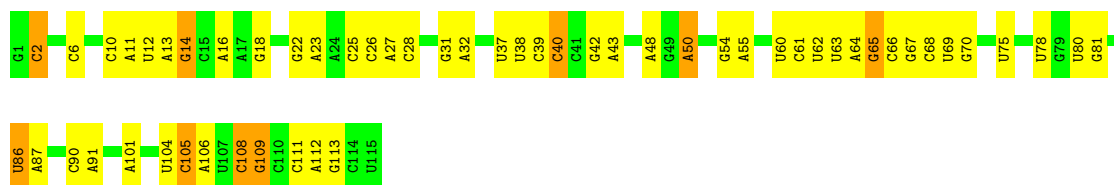






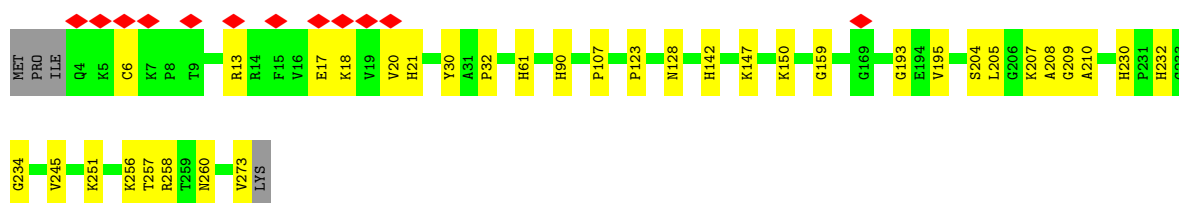
- Molecule 6: 5s ribosomal RNA

Chain B: 52% 40% 8%



- Molecule 7: 50S ribosomal protein L2

Chain C: 86% 13%



- Molecule 8: 50S ribosomal protein L3

Chain D: 88% 12%



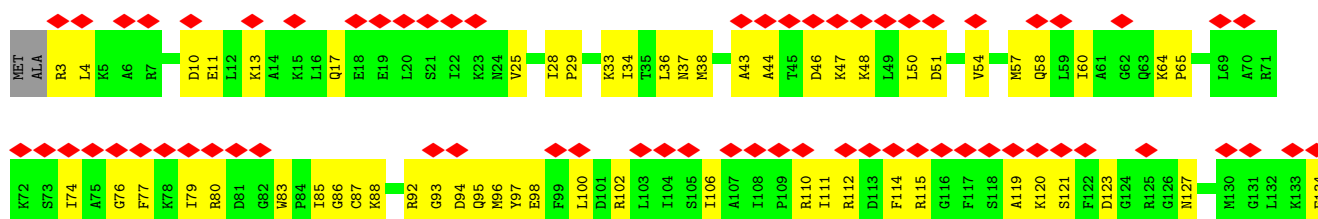
- Molecule 9: 50S ribosomal protein L4

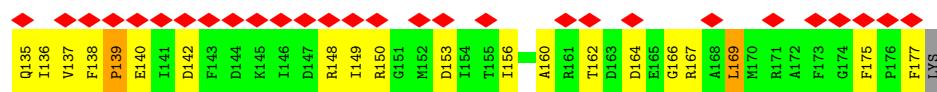
Chain E: 83% 10% 7%



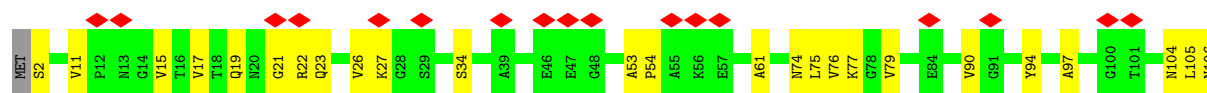
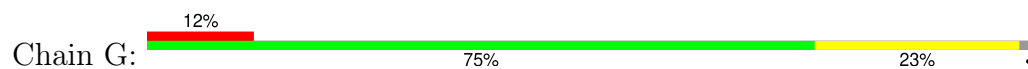
- Molecule 10: 50S ribosomal protein L5

Chain F: 53% 54% 43%

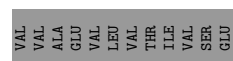
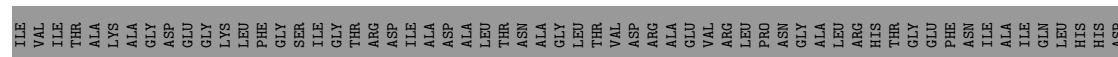
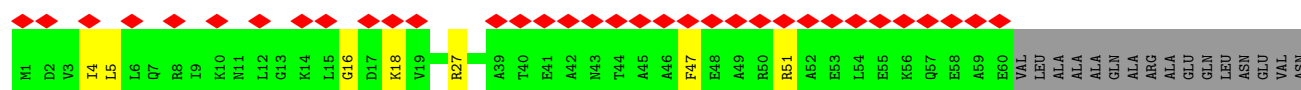
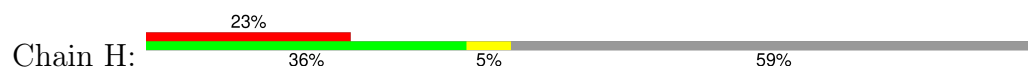




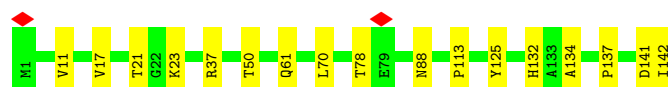
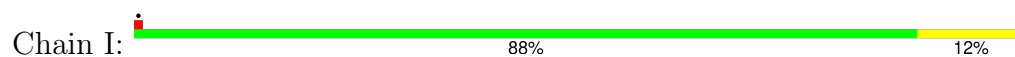
- Molecule 11: 50S ribosomal protein L6



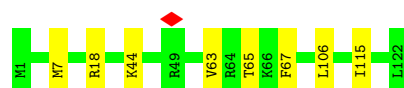
- Molecule 12: 50S ribosomal protein L9



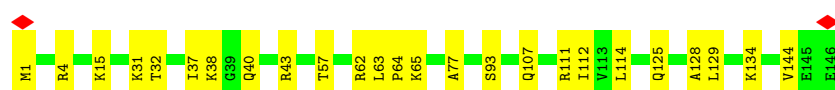
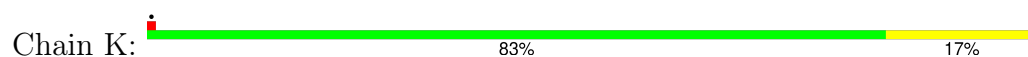
- Molecule 13: 50S ribosomal protein L13



- Molecule 14: 50S ribosomal protein L14

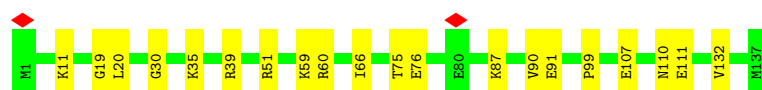


- Molecule 15: 50S ribosomal protein L15



- Molecule 16: 50S ribosomal protein L16

Chain L:  85% 15%



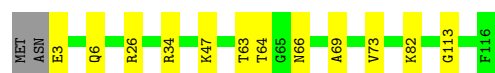
- Molecule 17: 50S ribosomal protein L17

Chain M:  92% 5%



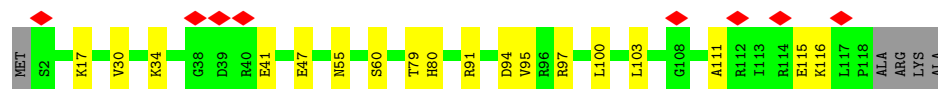
- Molecule 18: 50S ribosomal protein L18

Chain N:  88% 10%



- Molecule 19: 50S ribosomal protein L19

Chain O:  7% 81% 15%



- Molecule 20: 50S ribosomal protein L20

Chain P:  93% 5%



- Molecule 21: 50S ribosomal protein L21

Chain Q:  85% 15%

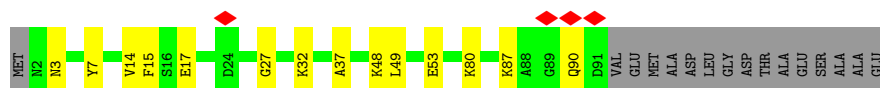


- Molecule 22: 50S ribosomal protein L22

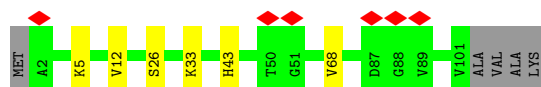
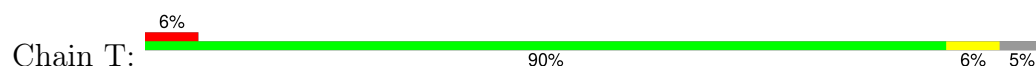
Chain R:  91% 9%



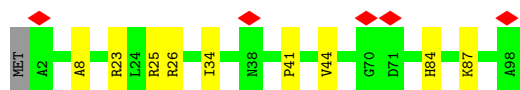
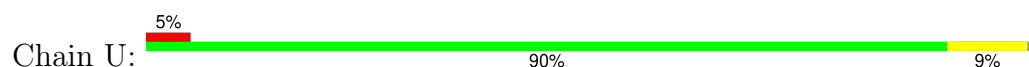
- Molecule 23: 50S ribosomal protein L23



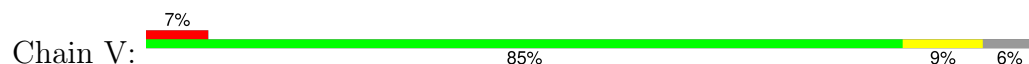
- Molecule 24: 50S ribosomal protein L24



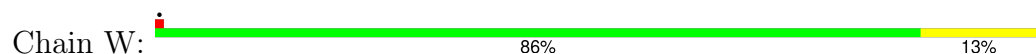
- Molecule 25: 50S ribosomal protein L25



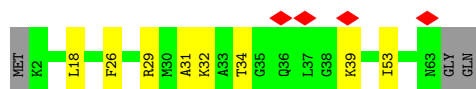
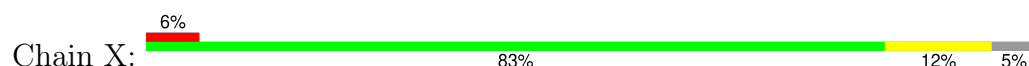
- Molecule 26: 50S ribosomal protein L27



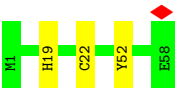
- Molecule 27: 50S ribosomal protein L28



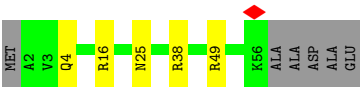
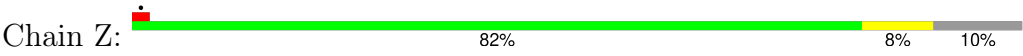
- Molecule 28: 50S ribosomal protein L29



- Molecule 29: 50S ribosomal protein L30



• Molecule 30: 50S ribosomal protein L32



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	27020	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	2.877	Depositor
Minimum map value	-1.232	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.087	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	544.768, 544.768, 544.768	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.064, 1.064, 1.064	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, OMG, 3TD, PSU, MG, 2MA, 2MG, 5MU, ZN, 7MG, OMU, 6MZ

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	0	0.13	0/434	0.34	0/573
2	1	0.12	0/367	0.33	0/481
3	2	0.15	0/515	0.42	0/678
4	3	0.11	0/296	0.40	0/389
5	AN1	0.09	0/69101	0.22	0/107780
6	B	0.08	0/2739	0.20	0/4266
7	C	0.12	0/2136	0.33	0/2869
8	D	0.12	0/1590	0.31	0/2142
9	E	0.10	0/1440	0.29	0/1944
10	F	0.18	0/1401	0.49	0/1877
11	G	0.12	0/1337	0.33	0/1807
12	H	0.14	0/461	0.40	0/616
13	I	0.10	0/1151	0.28	0/1551
14	J	0.11	0/956	0.32	0/1286
15	K	0.11	0/1097	0.31	0/1461
16	L	0.13	0/1104	0.34	0/1475
17	M	0.11	0/956	0.33	0/1282
18	N	0.11	0/865	0.32	0/1156
19	O	0.11	0/931	0.33	0/1249
20	P	0.12	0/947	0.30	0/1262
21	Q	0.11	0/818	0.34	0/1094
22	R	0.10	0/831	0.29	0/1113
23	S	0.11	0/708	0.31	0/947
24	T	0.11	0/753	0.32	0/1010
25	U	0.12	0/770	0.30	0/1036
26	V	0.10	0/606	0.29	0/810
27	W	0.11	0/642	0.31	0/856
28	X	0.13	0/499	0.31	0/662
29	Y	0.11	0/468	0.26	0/624
30	Z	0.11	0/462	0.34	0/615
All	All	0.10	0/96381	0.25	0/144911

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	3	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	3	36	ARG	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	0	427	0	462	3	0
2	1	363	0	401	4	0
3	2	509	0	566	12	0
4	3	295	0	327	7	0
5	AN1	62023	0	31192	551	0
6	B	2450	0	1241	44	0
7	C	2096	0	2157	28	0
8	D	1572	0	1610	19	0
9	E	1419	0	1464	15	0
10	F	1381	0	1433	60	0
11	G	1318	0	1373	25	0
12	H	458	0	480	4	0
13	I	1125	0	1148	11	0
14	J	946	0	1007	5	0
15	K	1089	0	1159	16	0
16	L	1087	0	1162	10	0
17	M	942	0	987	4	0
18	N	857	0	899	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	O	919	0	973	10	0
20	P	934	0	997	5	0
21	Q	807	0	842	10	0
22	R	826	0	894	7	0
23	S	702	0	756	10	0
24	T	749	0	797	4	0
25	U	760	0	783	6	0
26	V	598	0	600	6	0
27	W	632	0	667	8	0
28	X	498	0	537	7	0
29	Y	463	0	488	2	0
30	Z	456	0	448	5	0
31	3	1	0	0	0	0
32	AN1	105	0	0	0	0
32	C	1	0	0	0	0
33	AN1	1	0	0	0	0
34	1	1	0	0	0	0
34	AN1	218	0	0	4	0
34	B	3	0	0	0	0
34	C	1	0	0	0	0
34	D	1	0	0	1	0
34	E	1	0	0	0	0
34	K	1	0	0	0	0
34	N	1	0	0	0	0
34	R	1	0	0	0	0
34	V	1	0	0	0	0
34	W	1	0	0	2	0
34	Z	1	0	0	0	0
All	All	89040	0	57850	827	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 6.

The worst 5 of 827 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:1462:G:H1	5:AN1:1520:A:N6	1.49	1.10
6:B:70:G:N2	6:B:101:A:H62	1.59	1.00
6:B:70:G:H21	6:B:101:A:N6	1.64	0.96
5:AN1:2096:G:H1	5:AN1:2185:U:H3	0.91	0.89
6:B:2:C:O2	6:B:113:G:N2	2.06	0.88

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	
1	0	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
2	1	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
3	2	61/64 (95%)	57 (93%)	2 (3%)	2 (3%)	3	7
4	3	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
7	C	268/274 (98%)	258 (96%)	10 (4%)	0	100	100
8	D	209/212 (99%)	205 (98%)	4 (2%)	0	100	100
9	E	184/200 (92%)	184 (100%)	0	0	100	100
10	F	173/178 (97%)	149 (86%)	23 (13%)	1 (1%)	21	45
11	G	172/177 (97%)	167 (97%)	5 (3%)	0	100	100
12	H	58/148 (39%)	55 (95%)	3 (5%)	0	100	100
13	I	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
14	J	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
15	K	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
16	L	135/137 (98%)	133 (98%)	2 (2%)	0	100	100
17	M	117/125 (94%)	115 (98%)	2 (2%)	0	100	100
18	N	112/116 (97%)	110 (98%)	2 (2%)	0	100	100
19	O	115/122 (94%)	113 (98%)	2 (2%)	0	100	100
20	P	115/119 (97%)	115 (100%)	0	0	100	100
21	Q	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
22	R	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
23	S	88/106 (83%)	86 (98%)	2 (2%)	0	100	100
24	T	98/105 (93%)	94 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	U	95/98 (97%)	94 (99%)	1 (1%)	0	100	100
26	V	78/85 (92%)	77 (99%)	1 (1%)	0	100	100
27	W	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
28	X	60/65 (92%)	60 (100%)	0	0	100	100
29	Y	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
30	Z	53/61 (87%)	51 (96%)	2 (4%)	0	100	100
All	All	3061/3283 (93%)	2972 (97%)	86 (3%)	3 (0%)	49	72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	2	31	ILE
3	2	32	LEU
10	F	139	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/47 (100%)	47 (100%)	0	100	100
2	1	36/36 (100%)	36 (100%)	0	100	100
3	2	52/53 (98%)	52 (100%)	0	100	100
4	3	33/33 (100%)	33 (100%)	0	100	100
7	C	216/220 (98%)	216 (100%)	0	100	100
8	D	166/167 (99%)	166 (100%)	0	100	100
9	E	144/155 (93%)	144 (100%)	0	100	100
10	F	145/147 (99%)	144 (99%)	1 (1%)	76	87
11	G	139/142 (98%)	139 (100%)	0	100	100
12	H	45/112 (40%)	45 (100%)	0	100	100
13	I	118/118 (100%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	J	103/103 (100%)	103 (100%)	0	100	100
15	K	108/108 (100%)	108 (100%)	0	100	100
16	L	113/113 (100%)	113 (100%)	0	100	100
17	M	96/101 (95%)	96 (100%)	0	100	100
18	N	83/85 (98%)	83 (100%)	0	100	100
19	O	99/102 (97%)	99 (100%)	0	100	100
20	P	85/86 (99%)	85 (100%)	0	100	100
21	Q	84/84 (100%)	84 (100%)	0	100	100
22	R	88/88 (100%)	88 (100%)	0	100	100
23	S	76/87 (87%)	76 (100%)	0	100	100
24	T	82/85 (96%)	82 (100%)	0	100	100
25	U	79/80 (99%)	79 (100%)	0	100	100
26	V	60/64 (94%)	60 (100%)	0	100	100
27	W	69/70 (99%)	69 (100%)	0	100	100
28	X	54/56 (96%)	54 (100%)	0	100	100
29	Y	54/54 (100%)	54 (100%)	0	100	100
30	Z	47/50 (94%)	47 (100%)	0	100	100
All	All	2521/2646 (95%)	2520 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
10	F	169	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
15	K	107	GLN
19	O	78	GLN
27	W	35	HIS
15	K	125	GLN
18	N	66	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	AN1	2891/2918 (99%)	489 (16%)	8 (0%)
6	B	114/115 (99%)	17 (14%)	1 (0%)
All	All	3005/3033 (99%)	506 (16%)	9 (0%)

5 of 506 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	AN1	34	G
5	AN1	35	A
5	AN1	50	G
5	AN1	53	G
5	AN1	58	G

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	AN1	2379	G
6	B	108	C
5	AN1	478	A
5	AN1	782	G
5	AN1	1538	A

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

15 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
5	PSU	AN1	1907	5	18,21,22	1.14	1 (5%)	21,30,33	1.90	5 (23%)
5	OMG	AN1	2247	5	23,26,27	2.39	8 (34%)	32,38,41	1.92	8 (25%)
5	PSU	AN1	952	5	18,21,22	1.12	1 (5%)	21,30,33	1.91	5 (23%)
5	PSU	AN1	2500	5	18,21,22	1.13	1 (5%)	21,30,33	1.94	5 (23%)
5	PSU	AN1	2576	5	18,21,22	1.12	1 (5%)	21,30,33	1.90	5 (23%)
5	3TD	AN1	1911	5	19,22,23	4.31	7 (36%)	23,32,35	1.80	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	5MU	AN1	1935	5	19,22,23	5.01	7 (36%)	27,32,35	3.61	9 (33%)
5	6MZ	AN1	2026	5	22,25,26	2.48	4 (18%)	29,36,39	3.43	13 (44%)
5	PSU	AN1	2453	5	18,21,22	1.10	1 (5%)	21,30,33	1.94	5 (23%)
5	PSU	AN1	2601	5	18,21,22	1.11	1 (5%)	21,30,33	1.92	4 (19%)
5	2MA	AN1	2499	5	22,25,26	3.98	9 (40%)	32,37,40	2.80	11 (34%)
5	7MG	AN1	2065	5	23,26,27	3.58	11 (47%)	27,39,42	2.17	9 (33%)
5	2MG	AN1	2441	5	23,26,27	2.90	8 (34%)	33,38,41	2.20	11 (33%)
5	OMU	AN1	2548	5	19,22,23	3.12	8 (42%)	25,31,34	1.79	5 (20%)
5	PSU	AN1	1913	5	18,21,22	1.14	1 (5%)	21,30,33	1.81	5 (23%)

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
5	PSU	AN1	1907	5	-	1/7/25/26	0/2/2/2
5	OMG	AN1	2247	5	-	0/9/27/28	0/3/3/3
5	PSU	AN1	952	5	-	0/7/25/26	0/2/2/2
5	PSU	AN1	2500	5	-	0/7/25/26	0/2/2/2
5	PSU	AN1	2576	5	-	0/7/25/26	0/2/2/2
5	3TD	AN1	1911	5	-	5/7/25/26	0/2/2/2
5	5MU	AN1	1935	5	-	0/7/25/26	0/2/2/2
5	6MZ	AN1	2026	5	-	2/9/27/28	0/3/3/3
5	PSU	AN1	2453	5	-	0/7/25/26	0/2/2/2
5	PSU	AN1	2601	5	-	0/7/25/26	0/2/2/2
5	2MA	AN1	2499	5	-	2/7/25/26	0/3/3/3
5	7MG	AN1	2065	5	-	1/7/37/38	0/3/3/3
5	2MG	AN1	2441	5	-	0/9/27/28	0/3/3/3
5	OMU	AN1	2548	5	-	2/9/27/28	0/2/2/2
5	PSU	AN1	1913	5	-	2/7/25/26	0/2/2/2

The worst 5 of 69 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	AN1	1911	3TD	C6-C5	12.84	1.49	1.35
5	AN1	2499	2MA	C4-N3	12.18	1.50	1.34
5	AN1	1935	5MU	C2-N1	11.62	1.56	1.38
5	AN1	1935	5MU	C6-N1	10.98	1.56	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	AN1	1935	5MU	C4-C5	10.33	1.61	1.44

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	AN1	1935	5MU	C5-C4-N3	11.77	125.56	115.32
5	AN1	2026	6MZ	C4-N9-C1'	-10.00	103.25	126.63
5	AN1	2026	6MZ	C1'-N9-C8	9.79	148.81	127.09
5	AN1	1935	5MU	C5-C6-N1	-9.64	112.84	123.31
5	AN1	2499	2MA	C1'-N9-C8	-7.75	109.89	127.09

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	AN1	1913	PSU	O4'-C1'-C5-C6
5	AN1	2548	OMU	O4'-C4'-C5'-O5'
5	AN1	2548	OMU	C3'-C4'-C5'-O5'
5	AN1	1911	3TD	C3'-C4'-C5'-O5'
5	AN1	1911	3TD	O4'-C4'-C5'-O5'

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	AN1	2500	PSU	1	0
5	AN1	2576	PSU	1	0
5	AN1	1911	3TD	1	0
5	AN1	2026	6MZ	1	0
5	AN1	2499	2MA	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 108 ligands modelled in this entry, 108 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

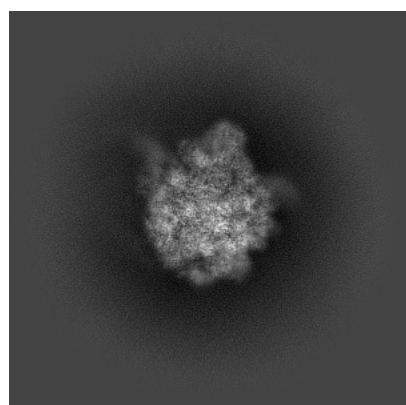
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21033. These allow visual inspection of the internal detail of the map and identification of artifacts.

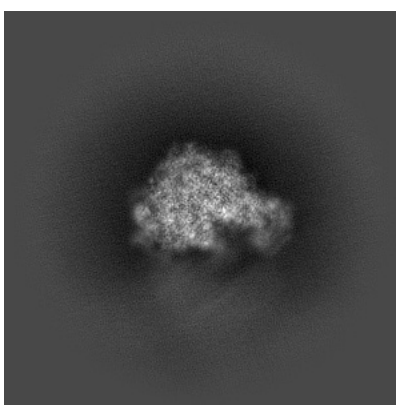
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

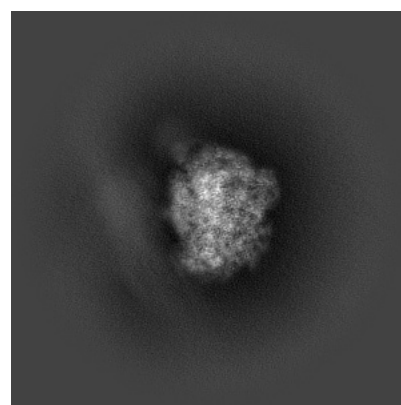
6.1.1 Primary map



X



Y

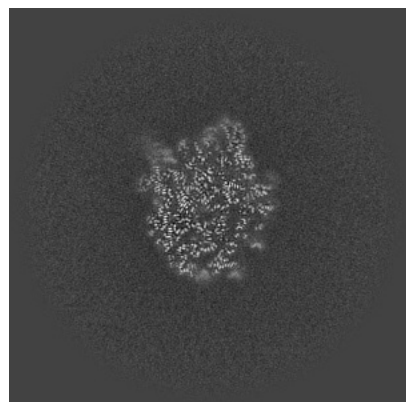


Z

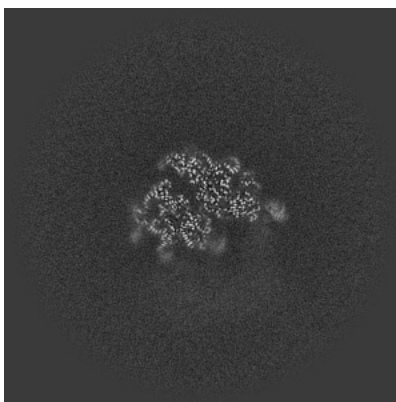
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

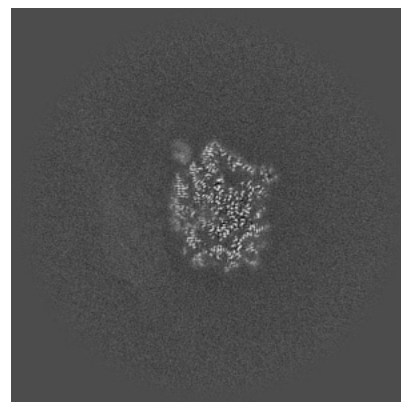
6.2.1 Primary map



X Index: 256



Y Index: 256

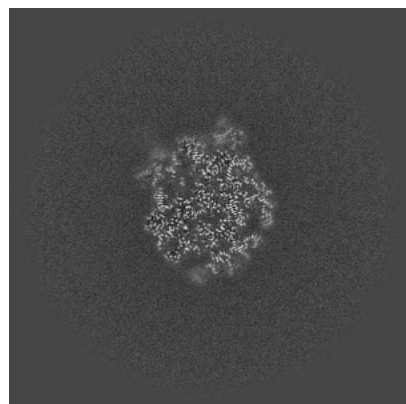


Z Index: 256

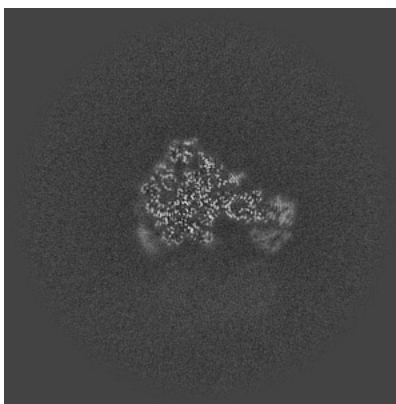
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

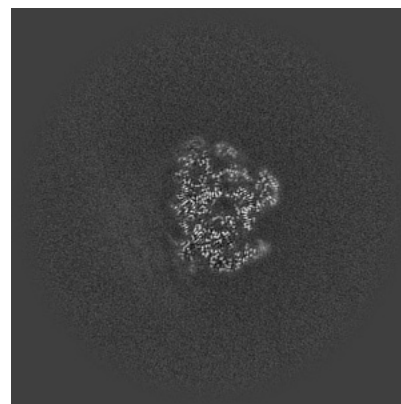
6.3.1 Primary map



X Index: 265



Y Index: 278

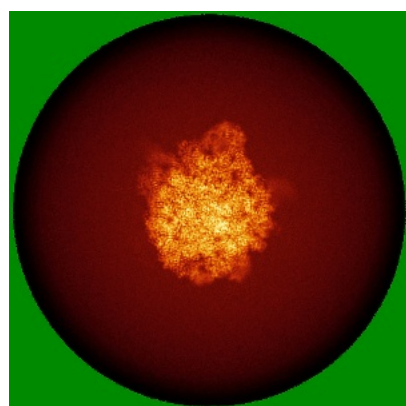


Z Index: 238

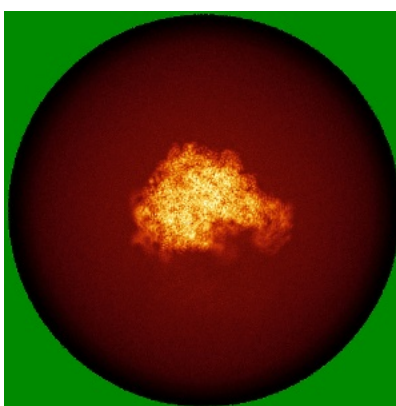
The images above show the largest variance slices of the map in three orthogonal directions.

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

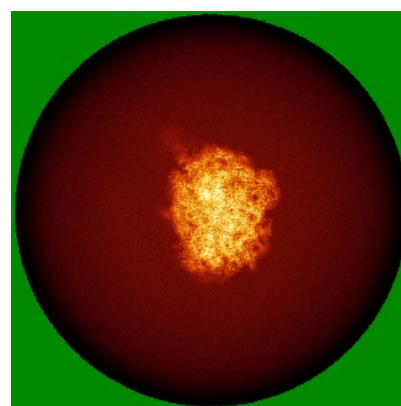
6.4.1 Primary map



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

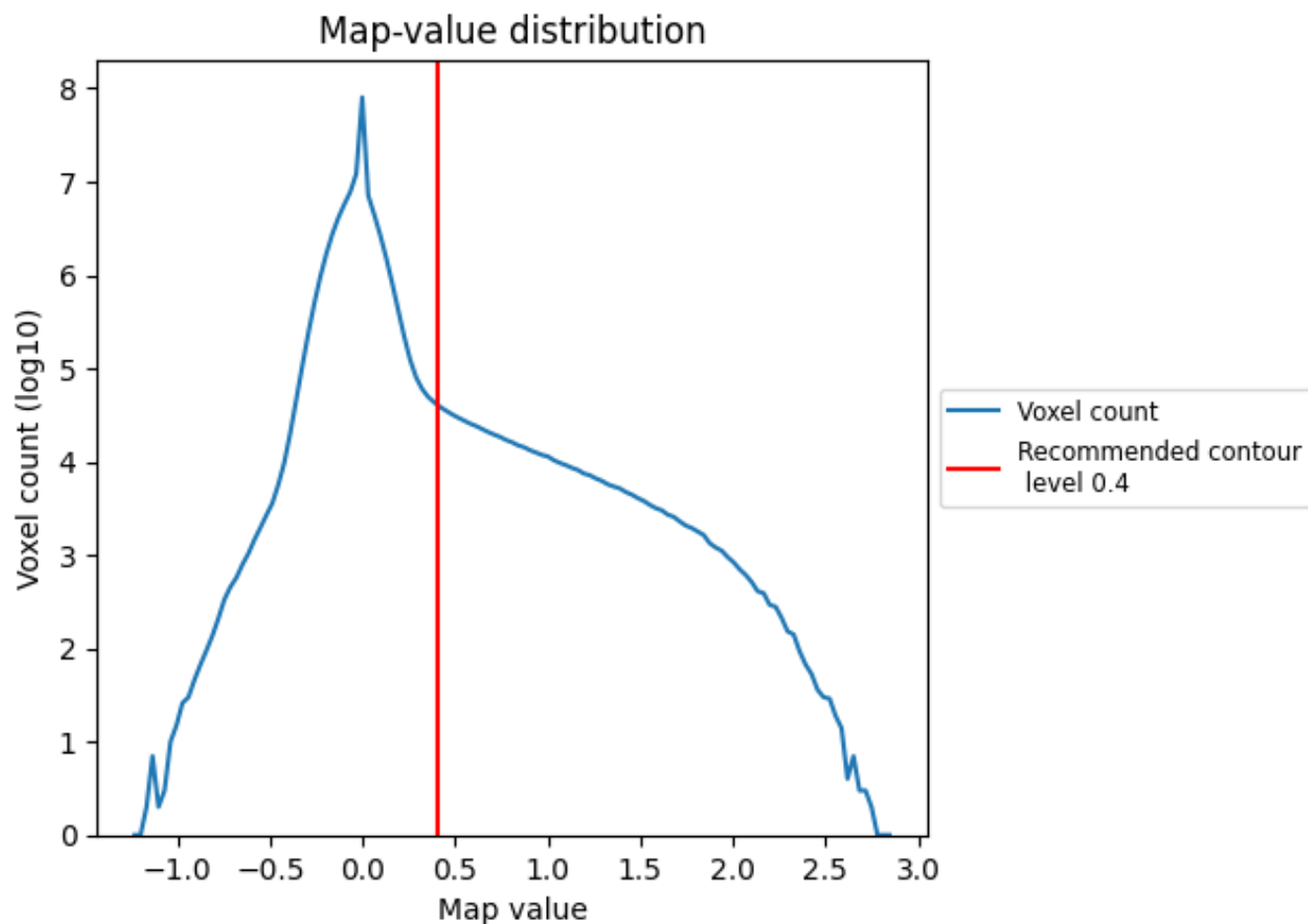
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

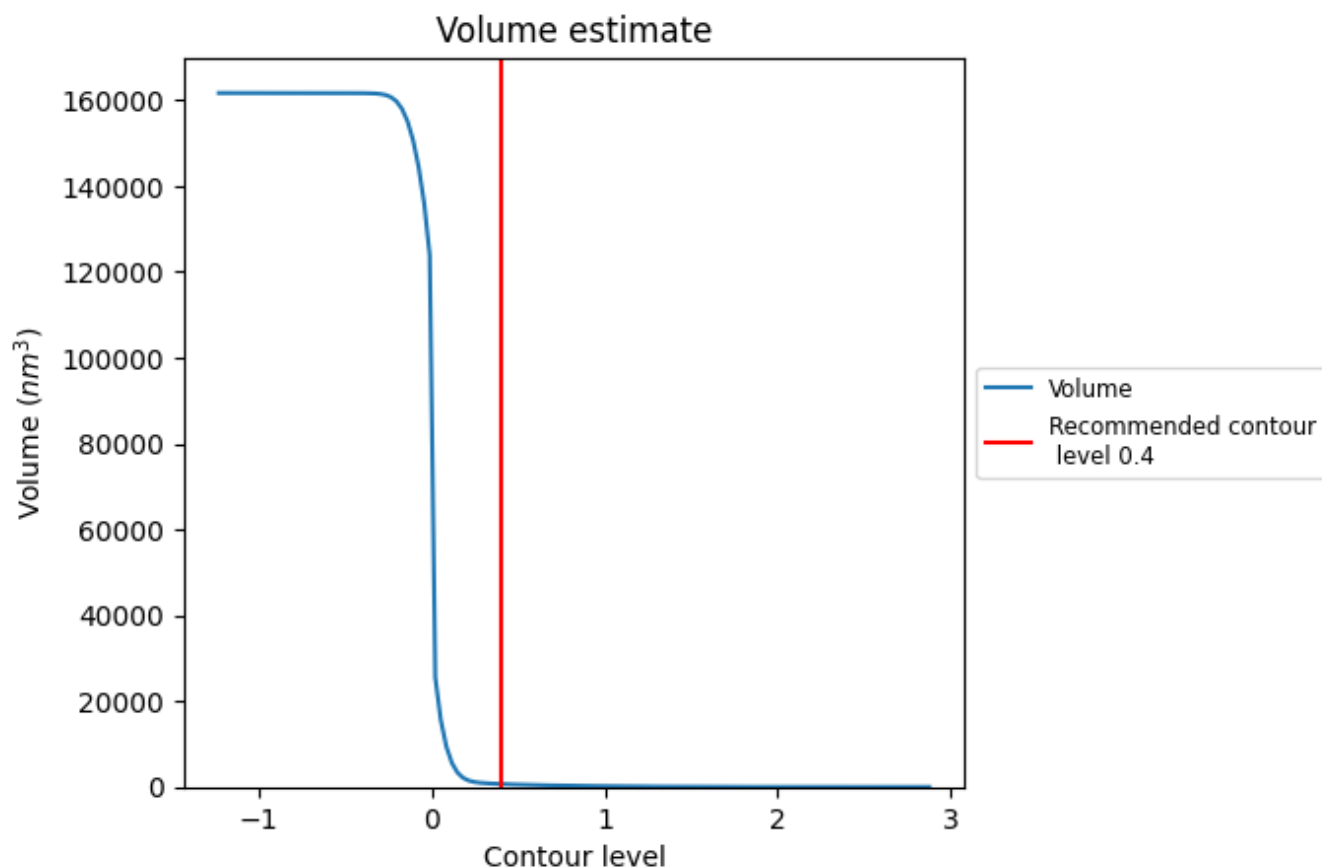
This section contains the results of statistical analysis of the map.

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.

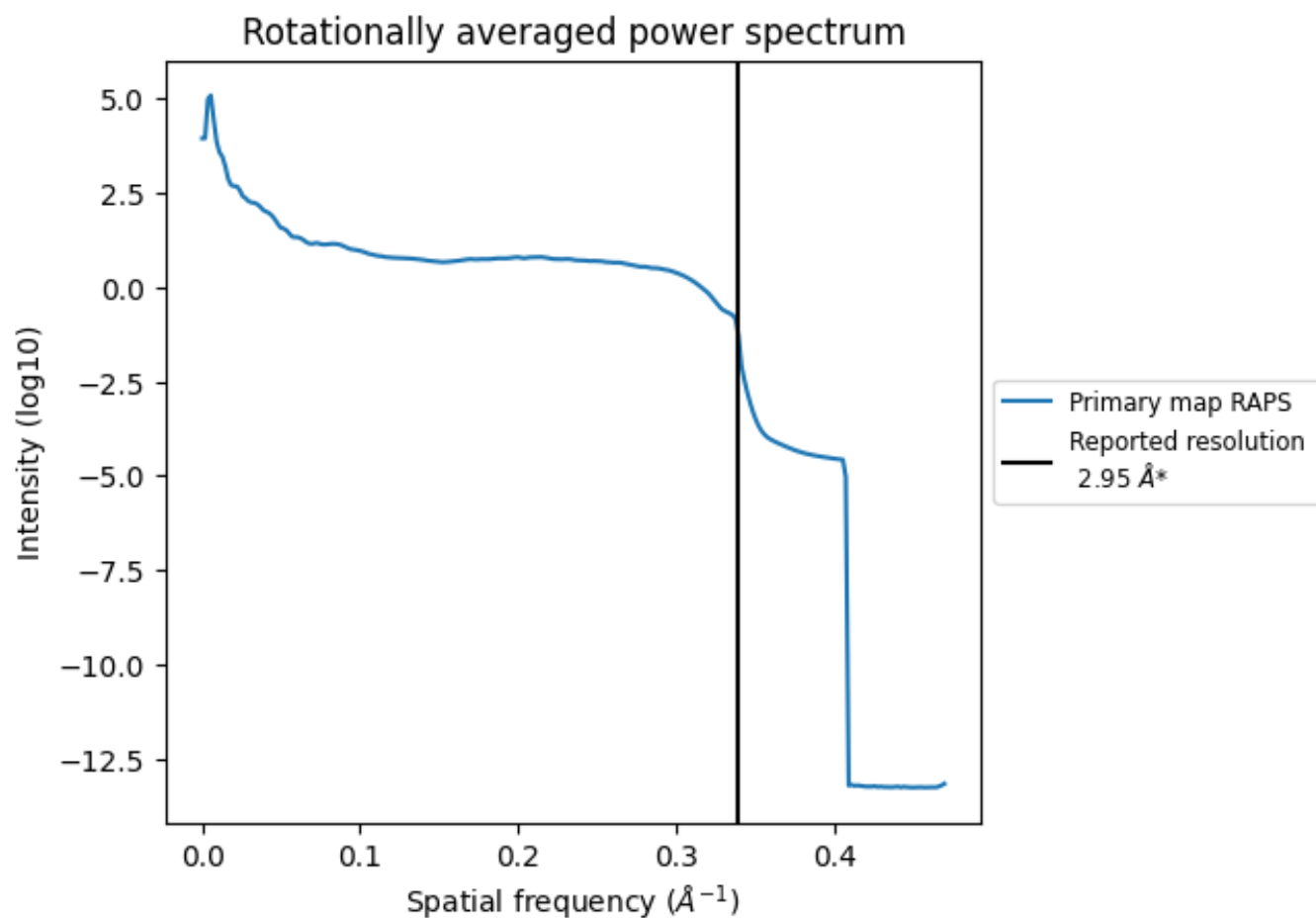
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 687 nm^3 ; this corresponds to an approximate mass of 620 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 0.339 Å⁻¹

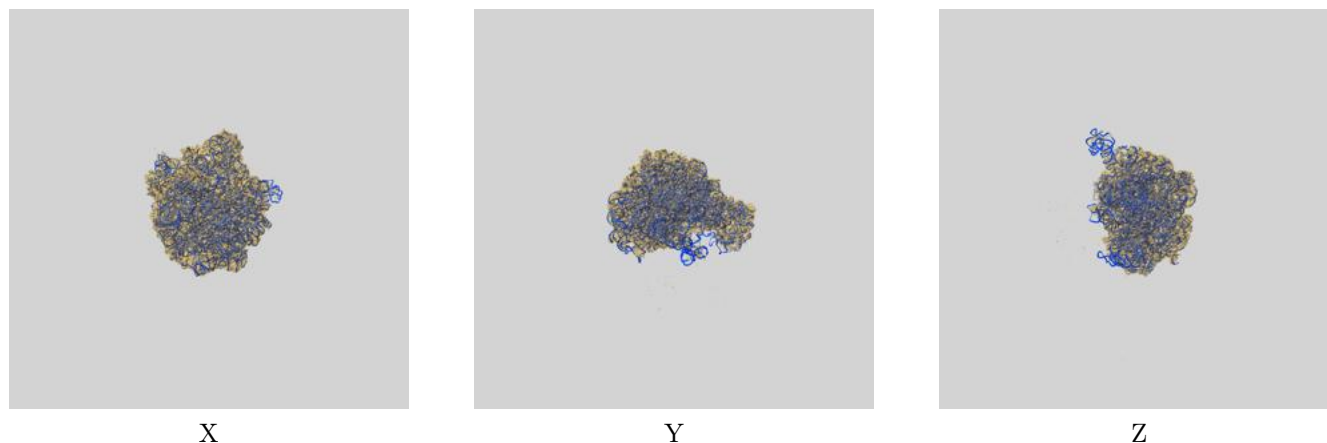
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

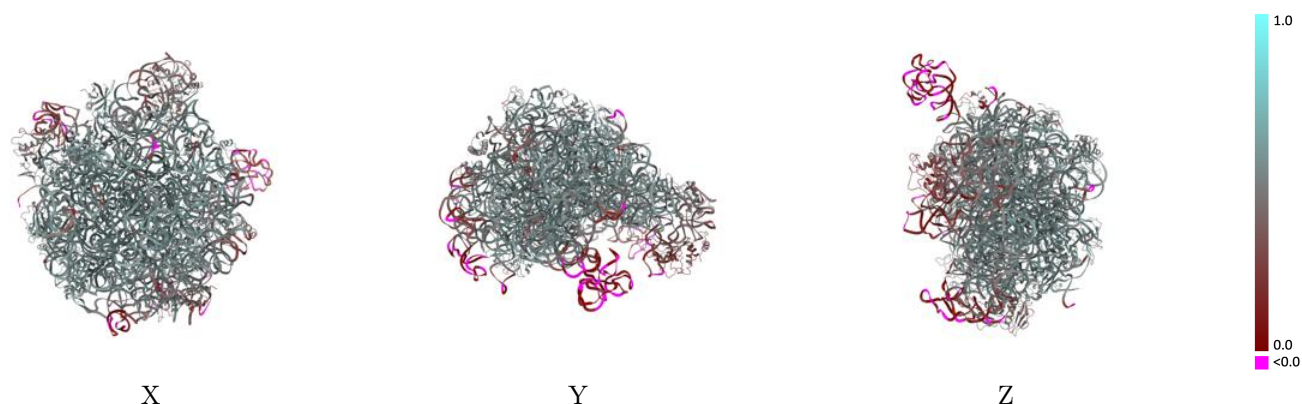
This section contains information regarding the fit between EMDB map EMD-21033 and PDB model 6V3D. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



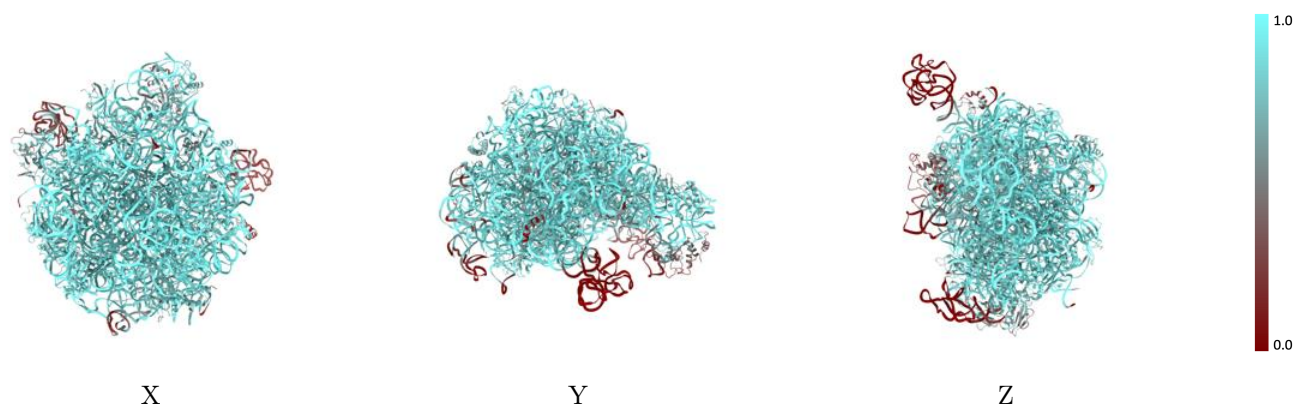
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



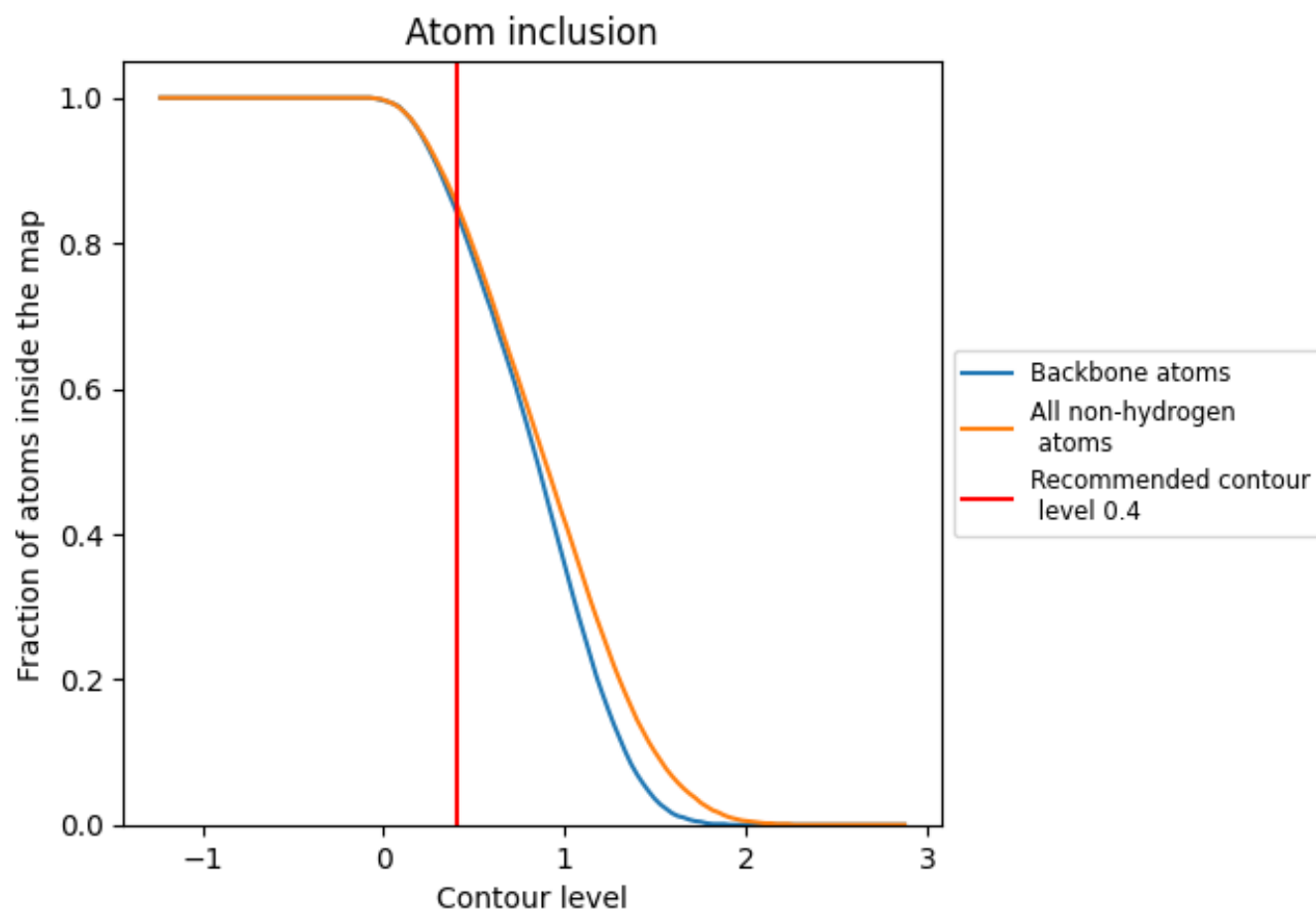
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8570	 0.4930
0	 0.7310	 0.5030
1	 0.8980	 0.5680
2	 0.8160	 0.5380
3	 0.8040	 0.5180
AN1	 0.8770	 0.4880
B	 0.9220	 0.4410
C	 0.8490	 0.5480
D	 0.9000	 0.5540
E	 0.8630	 0.5390
F	 0.3670	 0.2570
G	 0.6450	 0.4310
H	 0.3810	 0.3700
I	 0.8920	 0.5510
J	 0.8410	 0.5480
K	 0.8780	 0.5480
L	 0.8130	 0.5320
M	 0.9100	 0.5690
N	 0.8140	 0.4610
O	 0.8010	 0.5230
P	 0.9180	 0.5670
Q	 0.8920	 0.5510
R	 0.8580	 0.5560
S	 0.8130	 0.5110
T	 0.7810	 0.4910
U	 0.8220	 0.5070
V	 0.8580	 0.5510
W	 0.8630	 0.5410
X	 0.7280	 0.4210
Y	 0.8570	 0.5250
Z	 0.8410	 0.5400

