



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 06:55 PM UTC

PDB ID : 6DZP / pdb_00006dzp
EMDB ID : EMD-8937
Title : Cryo-EM Structure of Mycobacterium smegmatis C(minus) 50S ribosomal subunit
Authors : Sharma, M.R.; Li, Y.; Korripella, R.; Yang, Y.; Kaushal, P.S.; Lin, Q.; Wade, J.T.; Gray, A.G.; Derbyshire, K.M.; Agrawal, R.K.; Ojha, A.
Deposited on : 2018-07-05
Resolution : 3.42 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

A user guide is available at

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

The types of validation reports are described at

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

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

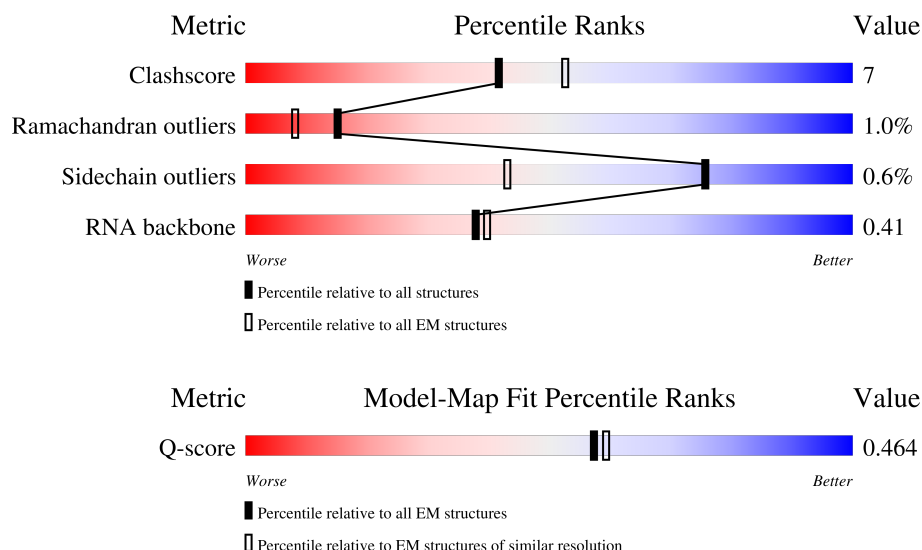
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.42 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.



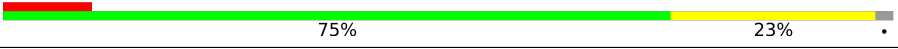
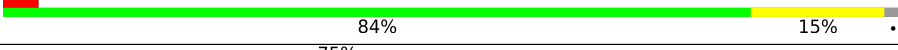
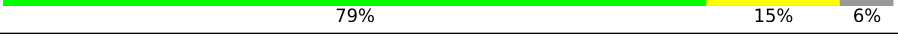
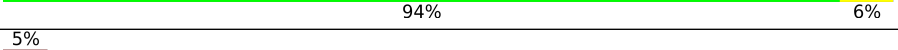
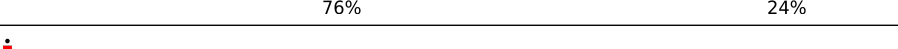
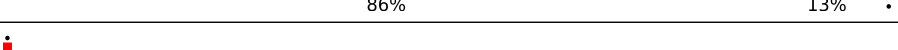
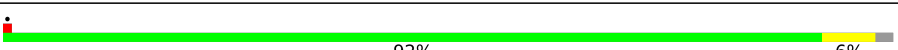
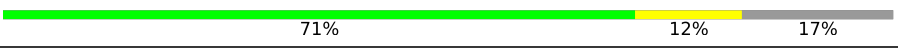
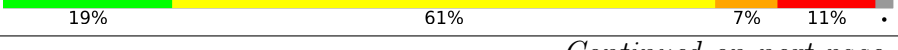
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13959 (2.92 - 3.92)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	3119	
2	B	118	
3	C	278	

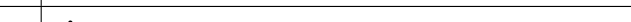
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Mol	Chain	Length	Quality of chain
4	D	217	
5	E	214	
6	F	186	
7	G	179	
8	H	151	
9	I	175	
10	J	142	
11	K	146	
12	L	122	
13	M	147	
14	N	138	
15	O	199	
16	P	126	
17	Q	113	
18	R	129	
19	S	102	
20	T	152	
21	U	99	
22	V	105	
23	W	215	
24	X	88	
25	Z	77	
26	a	61	
27	b	57	
28	c	54	

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Mol	Chain	Length	Quality of chain
29	d	47	 74% 21%
30	e	64	 75% 22%
31	f	37	 86% 14%
32	g	82	 24% 29% 40% 9% 22%
33	y	78	 10% 45% 31% 19%
34	3	23	 61% 35%

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 98097 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
1	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	151	Total	C	N	O	S	0	0
			1119	695	209	214	1		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 10 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 11 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 14 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	126	Total	C	N	O		0	0
			956	586	199	171			

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 19 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	114	Total	C	N	O		0	0
			873	543	171	159			

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 23 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 28 is a protein called 50S ribosomal protein L33 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	c	53	Total	C	N	O	0	0
			456	281	97	78		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	e	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 32 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	64	Total	C	N	O	S	0	0
			494	318	81	94	1		

- Molecule 33 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	y	77	Total	C	N	O	S	0	0
			617	377	132	106	2		

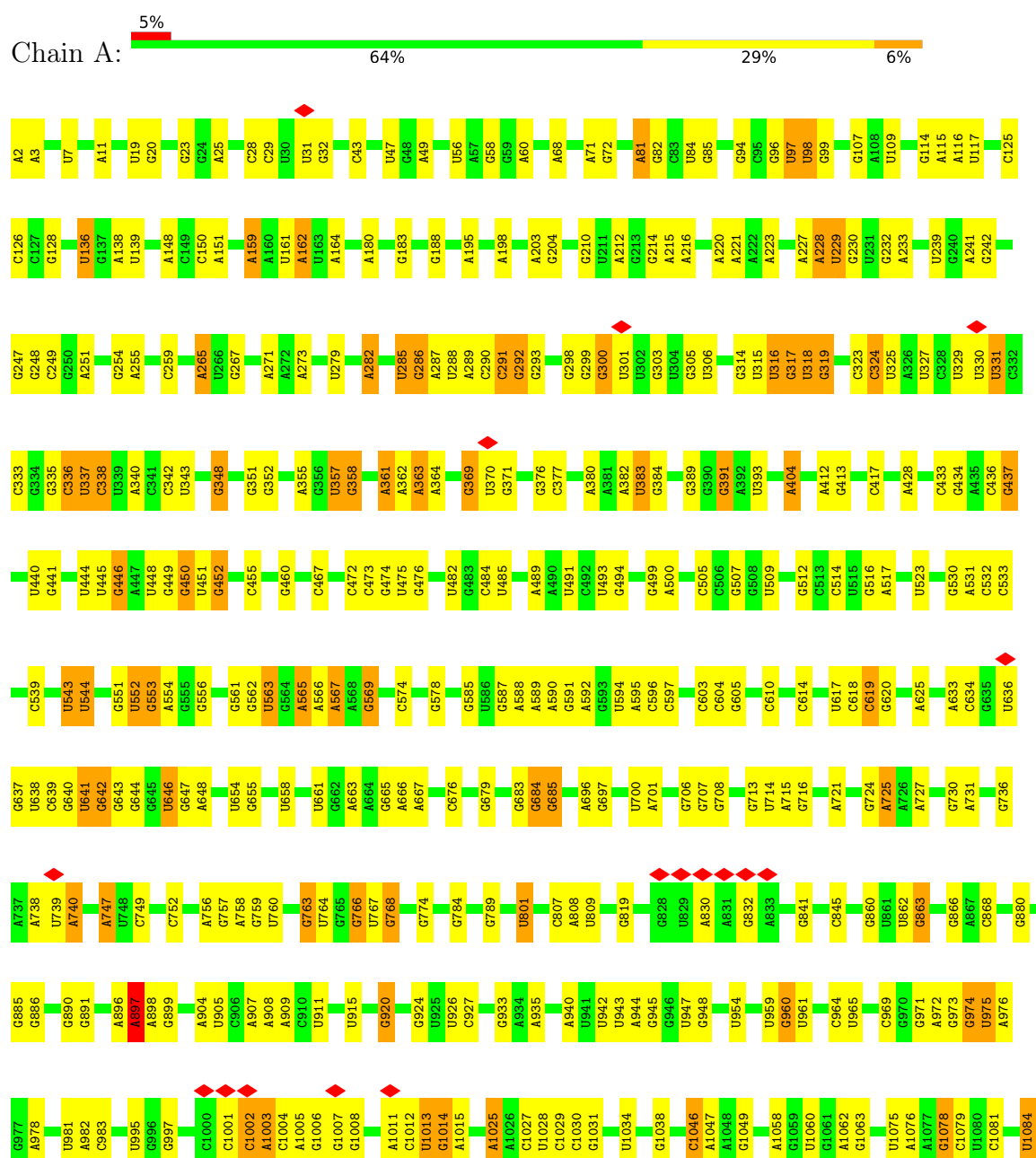
- Molecule 34 is a protein called Uncharacterized protein.

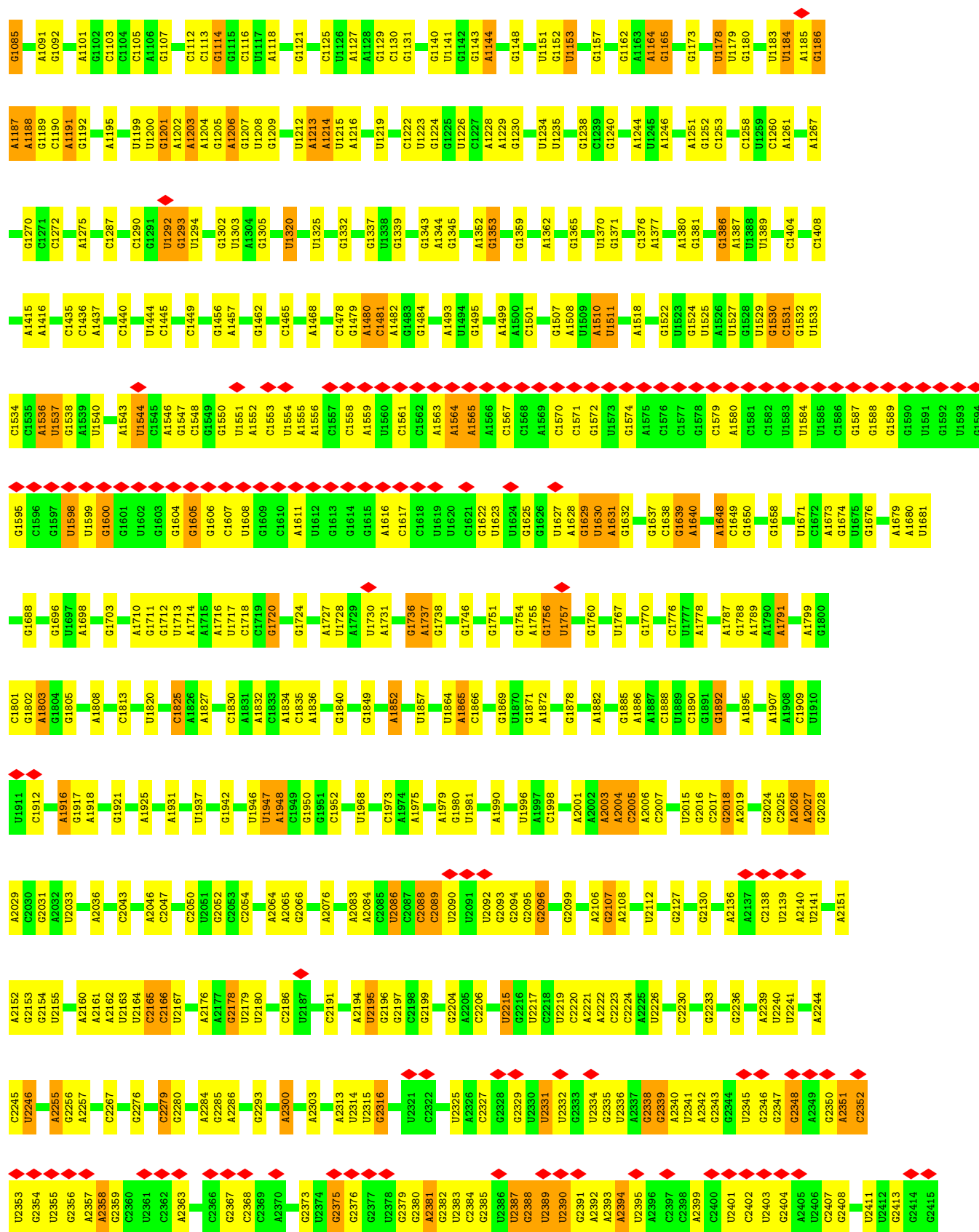
Mol	Chain	Residues	Atoms				AltConf	Trace
34	3	23	Total	C	N	O	0	0
			189	111	50	28		

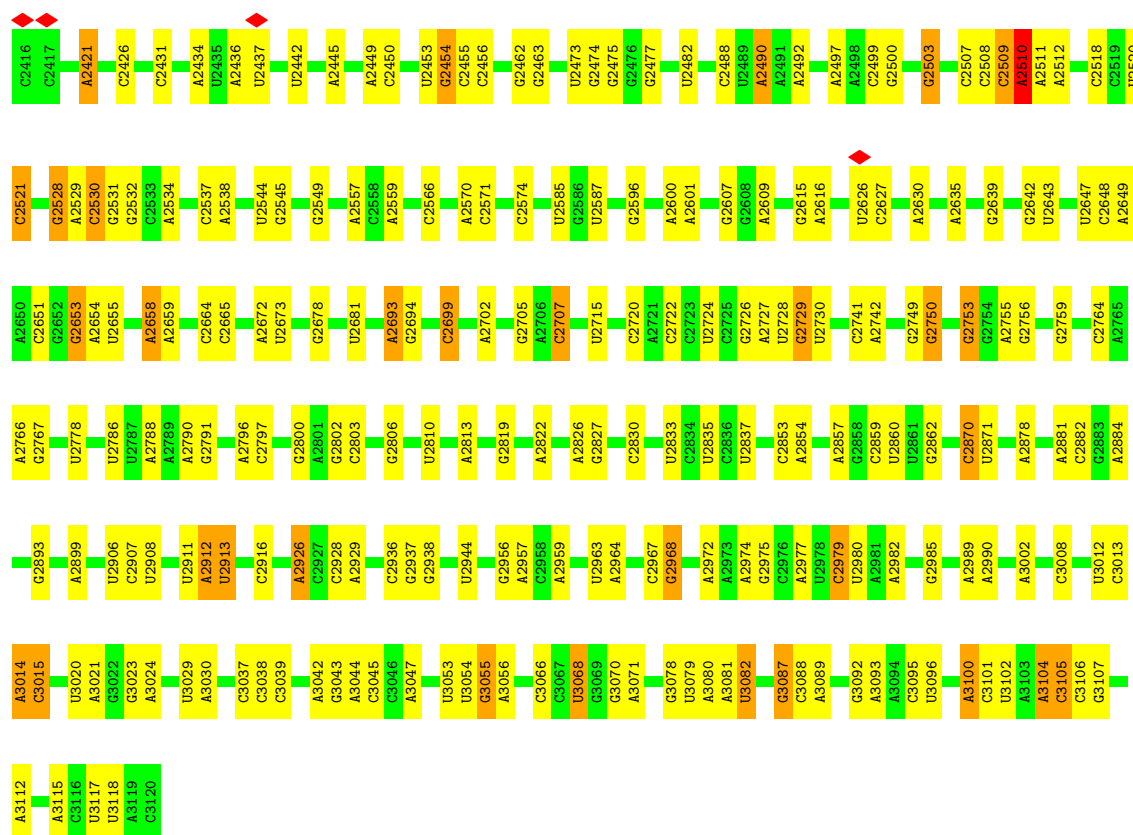
3 Residue-property plots

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.

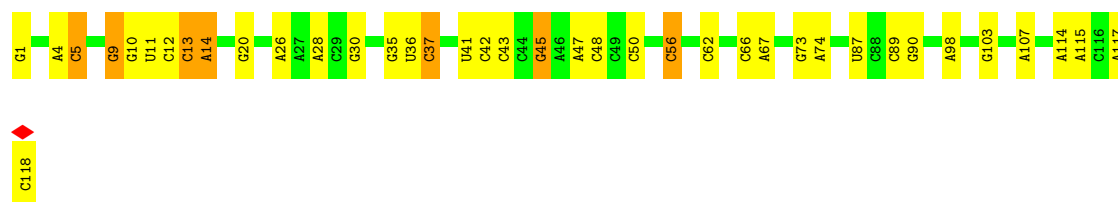
• Molecule 1: 23S rRNA



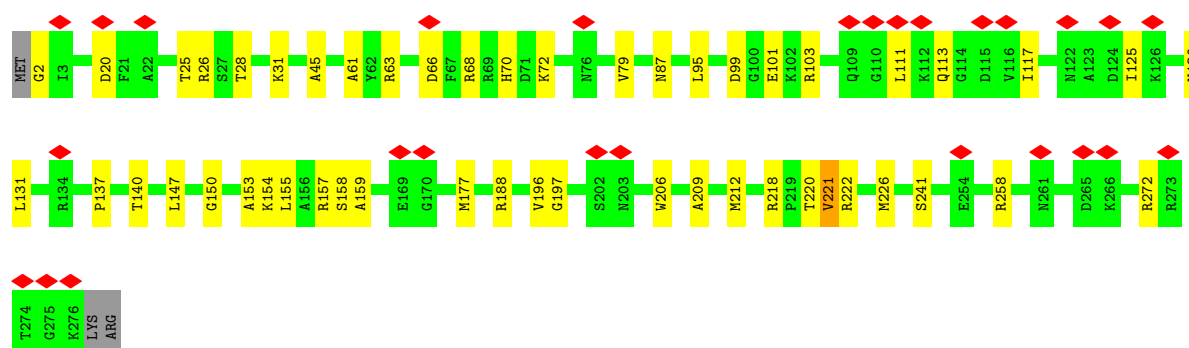
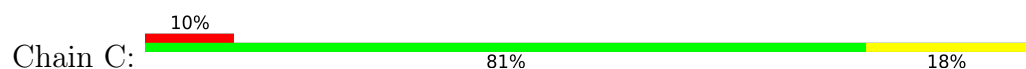




• Molecule 2: 5S rRNA

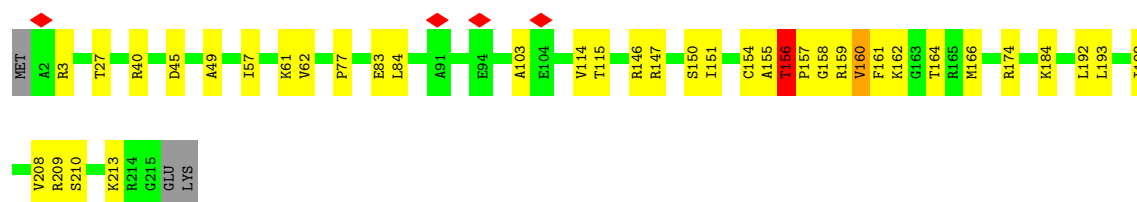


• Molecule 3: 50S ribosomal protein L2



- Molecule 4: 50S ribosomal protein L3

Chain D:  81% 17%



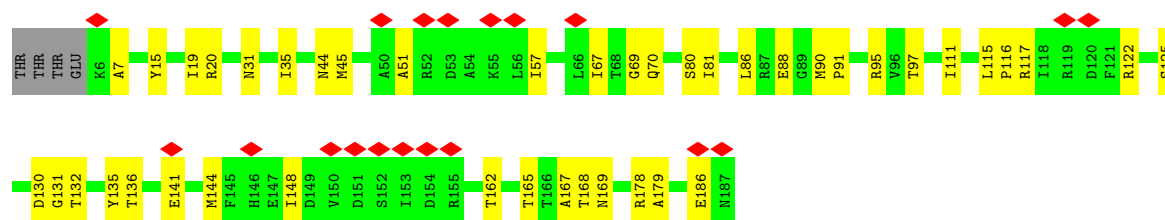
- Molecule 5: 50S ribosomal protein L4

Chain E:  86% 12%



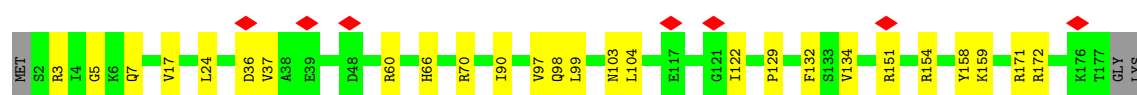
- Molecule 6: 50S ribosomal protein L5

Chain F:  10% 75% 23%



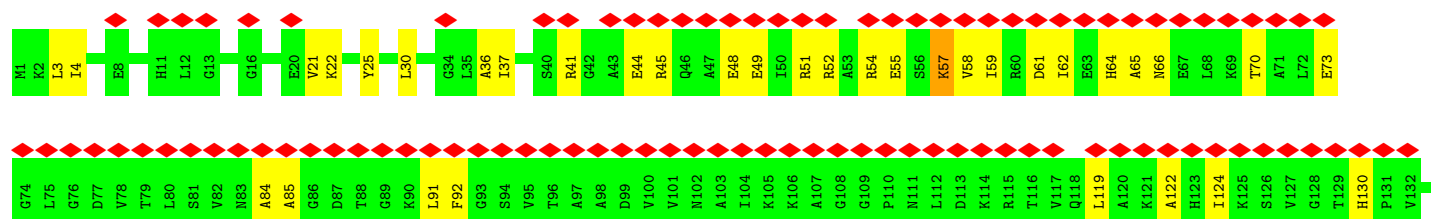
- Molecule 7: 50S ribosomal protein L6

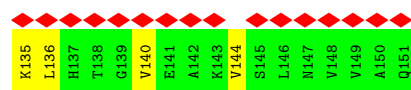
Chain G:  84% 15%



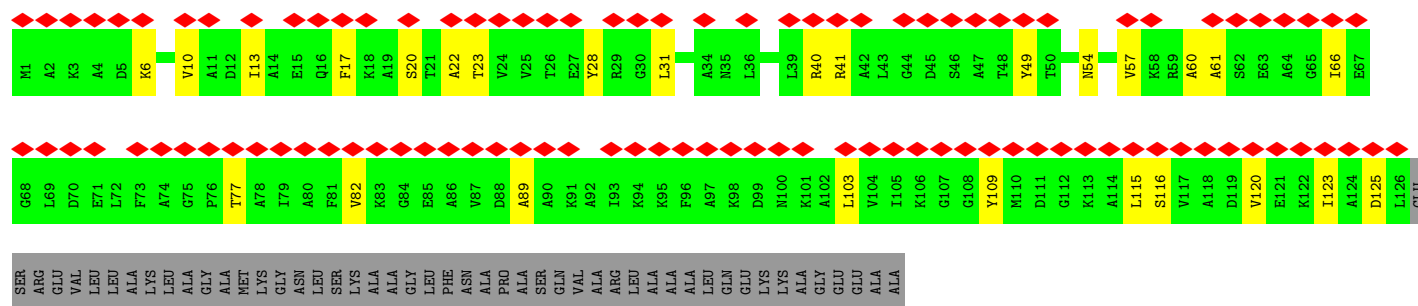
- Molecule 8: 50S ribosomal protein L9

Chain H:  75% 74% 25%

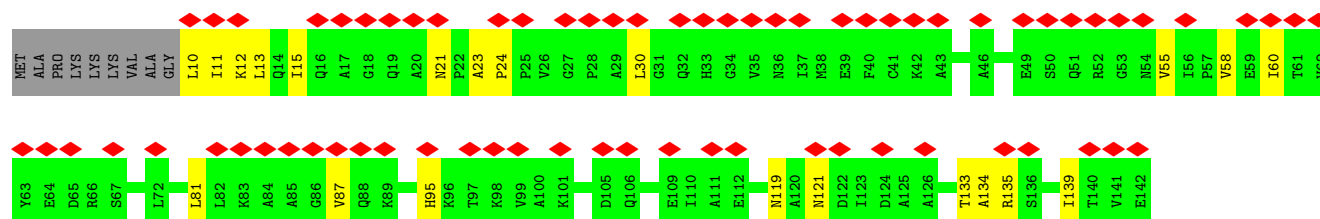
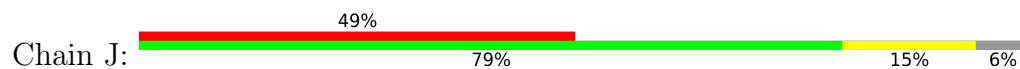




• Molecule 9: 50S ribosomal protein L10



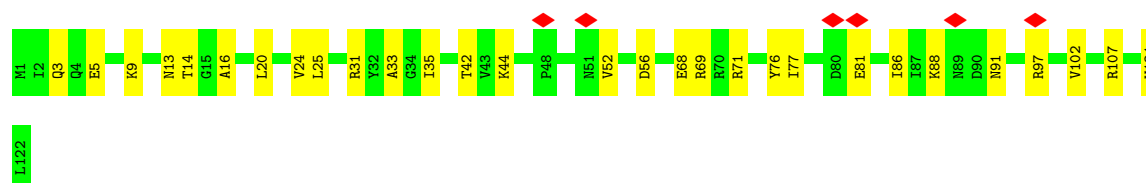
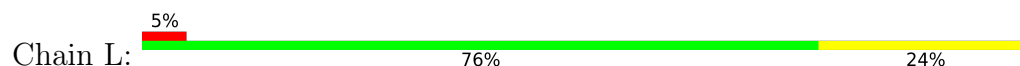
• Molecule 10: 50S ribosomal protein L11



• Molecule 11: 50S ribosomal protein L13



• Molecule 12: 50S ribosomal protein L14



• Molecule 13: 50S ribosomal protein L15





- Molecule 14: 50S ribosomal protein L16

Chain N: 87% 12%



- Molecule 15: 50S ribosomal protein L17

Chain O: 50% 9% 41%



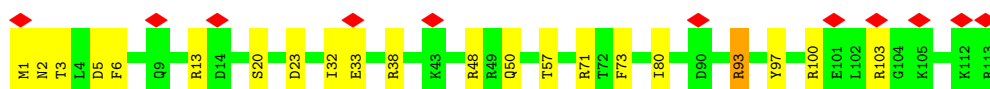
- Molecule 16: 50S ribosomal protein L18

Chain P: 88% 12%



- Molecule 17: 50S ribosomal protein L19

Chain Q: 10% 81% 18%



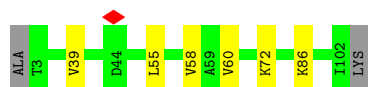
- Molecule 18: 50S ribosomal protein L20

Chain R: 83% 13%

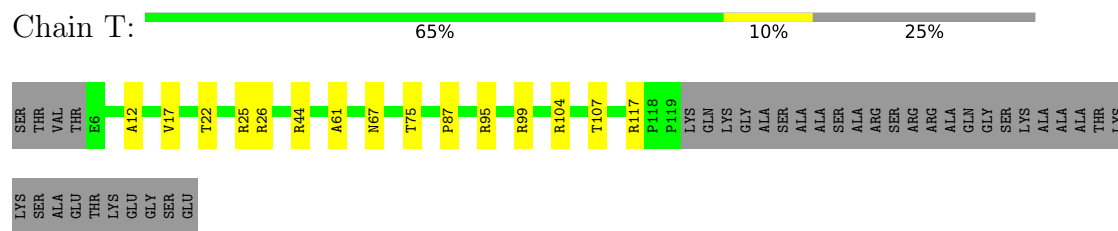


- Molecule 19: 50S ribosomal protein L21

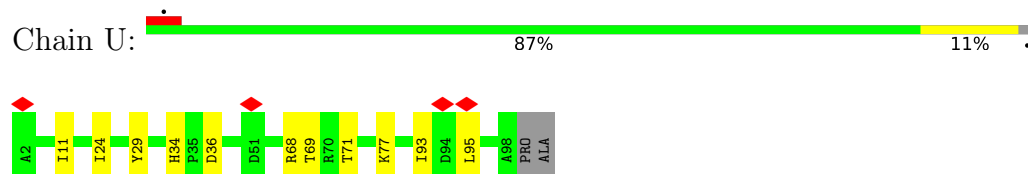
Chain S: 92% 6%



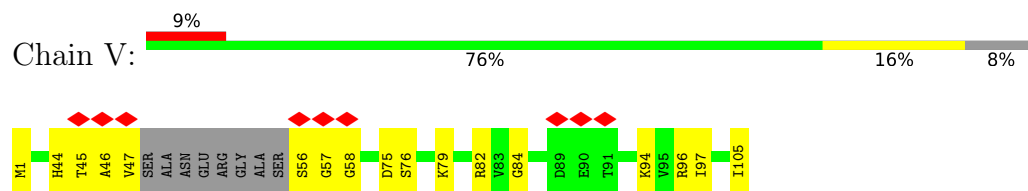
- Molecule 20: 50S ribosomal protein L22



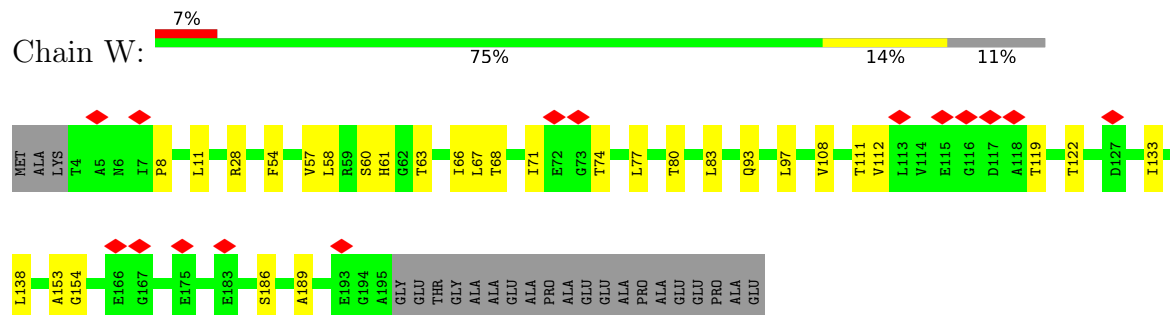
- Molecule 21: 50S ribosomal protein L23



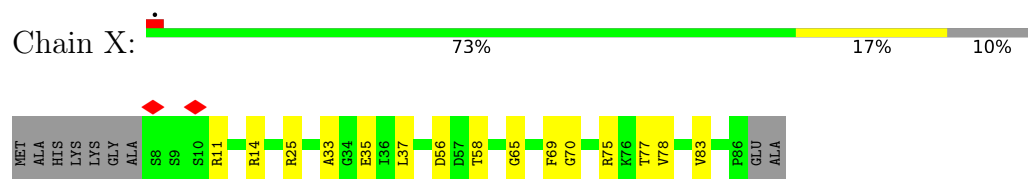
- Molecule 22: 50S ribosomal protein L24



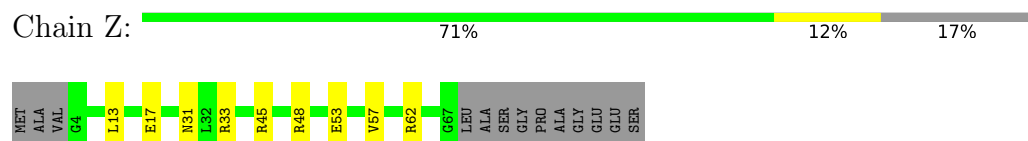
- Molecule 23: 50S ribosomal protein L25



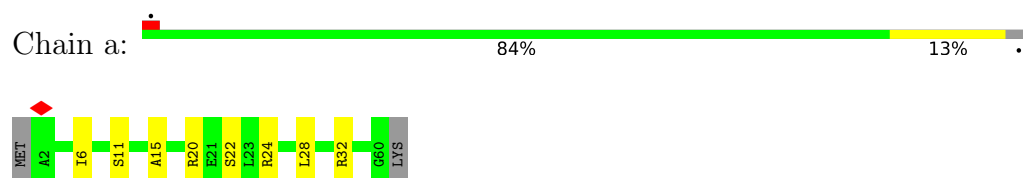
- Molecule 24: 50S ribosomal protein L27



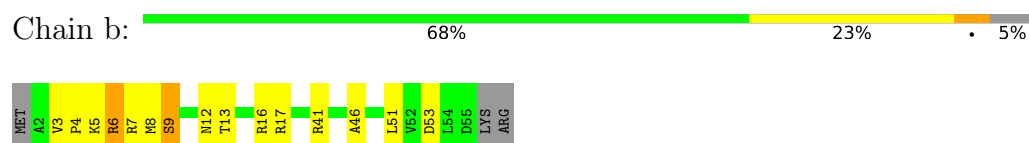
- Molecule 25: 50S ribosomal protein L29



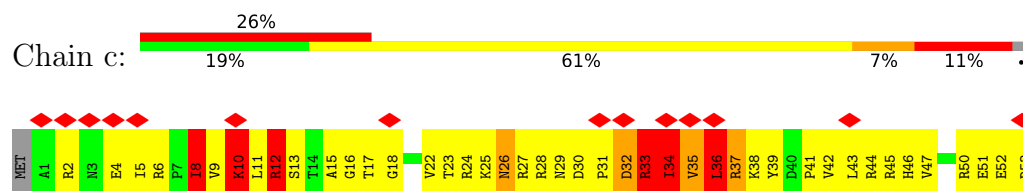
- Molecule 26: 50S ribosomal protein L30



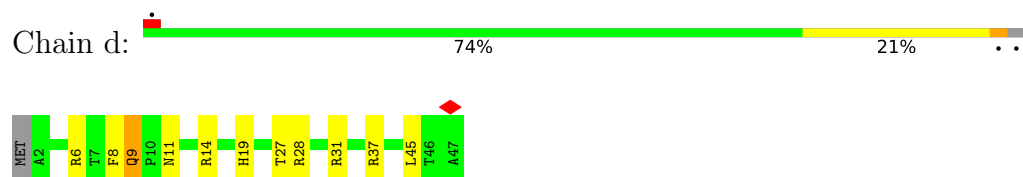
- Molecule 27: 50S ribosomal protein L32



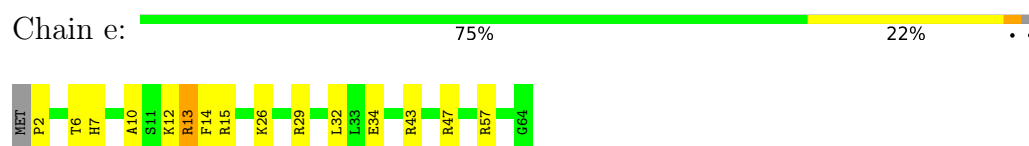
- Molecule 28: 50S ribosomal protein L33 2



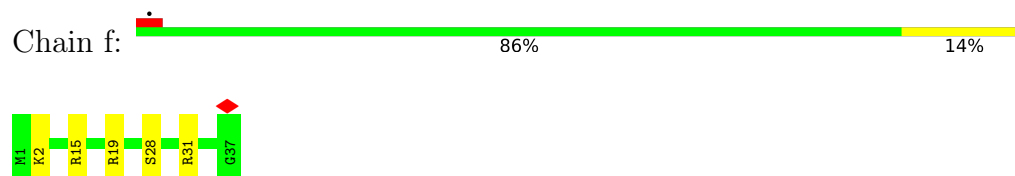
- Molecule 29: 50S ribosomal protein L34



- Molecule 30: 50S ribosomal protein L35

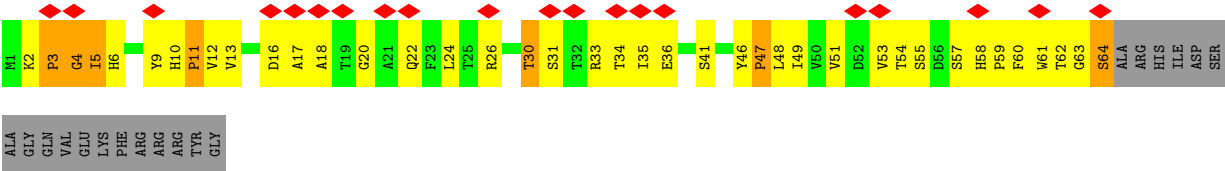


- Molecule 31: 50S ribosomal protein L36



- Molecule 32: 50S ribosomal protein L31

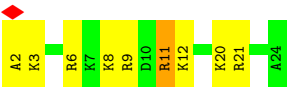




● Molecule 33: 50S ribosomal protein L28



● Molecule 34: Uncharacterized protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	66840	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 ($e^-/\text{\AA}^2$)	67	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	0.300	Depositor
Minimum map value	-0.194	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.033	Depositor
Map size (Å)	485.78003, 485.78003, 485.78003	wwPDB
Map dimensions	454, 454, 454	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	0.57	0/75001	0.51	11/117027 (0.0%)
2	B	0.44	0/2821	0.43	0/4396
3	C	0.74	1/2153 (0.0%)	0.68	3/2895 (0.1%)
4	D	0.74	0/1609	0.75	3/2165 (0.1%)
5	E	0.64	0/1592	0.57	0/2153
6	F	0.45	0/1467	0.55	0/1973
7	G	0.47	0/1369	0.60	0/1848
8	H	0.40	0/1129	0.65	0/1524
9	I	0.30	0/925	0.50	0/1246
10	J	0.32	0/1006	0.58	0/1364
11	K	0.68	0/1157	0.58	0/1567
12	L	0.73	0/946	0.63	0/1268
13	M	0.65	0/1091	0.65	0/1457
14	N	0.67	0/1118	0.62	0/1506
15	O	0.75	0/945	0.64	0/1267
16	P	0.55	0/966	0.58	0/1298
17	Q	0.74	1/921 (0.1%)	0.72	2/1236 (0.2%)
18	R	0.83	0/1000	0.63	0/1341
19	S	0.63	0/764	0.55	0/1030
20	T	0.74	0/887	0.62	0/1204
21	U	0.62	0/766	0.58	0/1030
22	V	0.48	0/738	0.58	0/987
23	W	0.49	0/1443	0.55	0/1970
24	X	0.75	0/595	0.59	0/798
25	Z	0.57	0/534	0.57	0/713
26	a	0.69	0/477	0.57	0/640
27	b	0.69	0/427	0.77	0/572
28	c	0.57	0/463	1.15	4/621 (0.6%)
29	d	0.86	0/380	0.90	3/500 (0.6%)
30	e	0.70	0/507	0.59	0/672
31	f	0.77	0/303	0.55	0/401
32	g	0.45	0/513	0.92	1/707 (0.1%)
33	y	0.56	0/629	1.09	7/843 (0.8%)
34	3	0.76	0/191	0.73	1/247 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.58	2/106833 (0.0%)	0.55	35/160466 (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
10	J	0	1
23	W	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	Q	50	GLN	CA-CB	-10.16	1.35	1.53
3	C	45	ALA	CA-C	-5.54	1.45	1.52

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	Q	93	ARG	CA-C-N	8.72	138.16	122.46
17	Q	93	ARG	C-N-CA	8.72	138.16	122.46
3	C	221	VAL	CA-C-N	8.70	137.42	121.06
3	C	221	VAL	C-N-CA	8.70	137.42	121.06
28	c	8	ILE	N-CA-C	-8.43	97.72	108.84

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	147	ARG	Peptide
10	J	21	ASN	Peptide
23	W	153	ALA	Peptide

5.2 Too-close contacts ⓘ

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	66981	0	33700	396	0
2	B	2522	0	1285	15	0
3	C	2110	0	2165	35	0
4	D	1587	0	1630	31	0
5	E	1569	0	1607	18	0
6	F	1445	0	1476	38	0
7	G	1348	0	1399	20	0
8	H	1119	0	1165	55	0
9	I	918	0	959	19	0
10	J	990	0	1021	18	0
11	K	1130	0	1167	6	0
12	L	938	0	1000	22	0
13	M	1078	0	1151	26	0
14	N	1092	0	1128	10	0
15	O	928	0	972	18	0
16	P	956	0	991	12	0
17	Q	907	0	938	12	0
18	R	988	0	1038	13	0
19	S	754	0	802	4	0
20	T	873	0	909	12	0
21	U	756	0	802	10	0
22	V	732	0	782	20	0
23	W	1428	0	1443	17	0
24	X	586	0	601	10	0
25	Z	531	0	541	8	0
26	a	474	0	500	6	0
27	b	423	0	460	23	0
28	c	456	0	474	111	0
29	d	377	0	411	12	0
30	e	502	0	541	32	0
31	f	299	0	324	6	0
32	g	494	0	470	94	0
33	y	617	0	625	79	0
34	3	189	0	205	14	0
All	All	98097	0	64682	1015	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1015 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)
33:y:14:GLY:HA3	33:y:28:TRP:CZ3	1.28	1.66
32:g:35:ILE:CD1	32:g:49:ILE:HG23	1.12	1.58
33:y:14:GLY:CA	33:y:28:TRP:CZ3	1.97	1.47
32:g:60:PHE:HE1	32:g:62:THR:CG2	1.12	1.45
33:y:14:GLY:CA	33:y:28:TRP:HZ3	1.29	1.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	273/278 (98%)	232 (85%)	41 (15%)	0	100	100
4	D	212/217 (98%)	182 (86%)	28 (13%)	2 (1%)	14	41
5	E	207/214 (97%)	192 (93%)	15 (7%)	0	100	100
6	F	180/186 (97%)	165 (92%)	14 (8%)	1 (1%)	21	49
7	G	174/179 (97%)	157 (90%)	17 (10%)	0	100	100
8	H	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
9	I	124/175 (71%)	117 (94%)	6 (5%)	1 (1%)	16	44
10	J	131/142 (92%)	116 (88%)	15 (12%)	0	100	100
11	K	144/146 (99%)	135 (94%)	9 (6%)	0	100	100
12	L	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
13	M	143/147 (97%)	120 (84%)	21 (15%)	2 (1%)	9	31
14	N	134/138 (97%)	119 (89%)	15 (11%)	0	100	100
15	O	116/199 (58%)	107 (92%)	9 (8%)	0	100	100
16	P	124/126 (98%)	116 (94%)	8 (6%)	0	100	100
17	Q	111/113 (98%)	94 (85%)	15 (14%)	2 (2%)	6	26
18	R	122/129 (95%)	117 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	S	98/102 (96%)	93 (95%)	5 (5%)	0	100	100
20	T	112/152 (74%)	105 (94%)	7 (6%)	0	100	100
21	U	95/99 (96%)	81 (85%)	14 (15%)	0	100	100
22	V	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
23	W	190/215 (88%)	169 (89%)	20 (10%)	1 (0%)	24	54
24	X	77/88 (88%)	69 (90%)	8 (10%)	0	100	100
25	Z	62/77 (80%)	62 (100%)	0	0	100	100
26	a	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
27	b	52/57 (91%)	47 (90%)	4 (8%)	1 (2%)	6	26
28	c	51/54 (94%)	26 (51%)	15 (29%)	10 (20%)	0	0
29	d	44/47 (94%)	40 (91%)	4 (9%)	0	100	100
30	e	61/64 (95%)	56 (92%)	5 (8%)	0	100	100
31	f	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
32	g	62/82 (76%)	43 (69%)	14 (23%)	5 (8%)	1	4
33	y	75/78 (96%)	56 (75%)	8 (11%)	11 (15%)	0	1
34	3	21/23 (91%)	18 (86%)	3 (14%)	0	100	100
All	All	3649/4003 (91%)	3255 (89%)	358 (10%)	36 (1%)	15	39

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	156	THR
6	F	131	GLY
27	b	9	SER
28	c	10	LYS
28	c	12	ARG

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	
3	C	215/218 (99%)	215 (100%)	0	100	100
4	D	160/163 (98%)	160 (100%)	0	100	100
5	E	169/172 (98%)	169 (100%)	0	100	100
6	F	151/155 (97%)	151 (100%)	0	100	100
7	G	148/150 (99%)	148 (100%)	0	100	100
8	H	116/116 (100%)	115 (99%)	1 (1%)	70	75
9	I	89/120 (74%)	89 (100%)	0	100	100
10	J	102/108 (94%)	102 (100%)	0	100	100
11	K	119/119 (100%)	118 (99%)	1 (1%)	73	76
12	L	100/100 (100%)	100 (100%)	0	100	100
13	M	112/114 (98%)	112 (100%)	0	100	100
14	N	114/116 (98%)	114 (100%)	0	100	100
15	O	97/158 (61%)	97 (100%)	0	100	100
16	P	93/93 (100%)	93 (100%)	0	100	100
17	Q	100/100 (100%)	100 (100%)	0	100	100
18	R	97/99 (98%)	97 (100%)	0	100	100
19	S	81/82 (99%)	81 (100%)	0	100	100
20	T	90/116 (78%)	89 (99%)	1 (1%)	65	73
21	U	83/84 (99%)	83 (100%)	0	100	100
22	V	81/86 (94%)	80 (99%)	1 (1%)	63	72
23	W	155/168 (92%)	155 (100%)	0	100	100
24	X	58/63 (92%)	58 (100%)	0	100	100
25	Z	58/66 (88%)	58 (100%)	0	100	100
26	a	52/54 (96%)	52 (100%)	0	100	100
27	b	43/46 (94%)	42 (98%)	1 (2%)	44	62
28	c	49/50 (98%)	45 (92%)	4 (8%)	10	34
29	d	35/36 (97%)	35 (100%)	0	100	100
30	e	53/54 (98%)	52 (98%)	1 (2%)	50	66
31	f	35/35 (100%)	35 (100%)	0	100	100
32	g	55/70 (79%)	53 (96%)	2 (4%)	31	55
33	y	64/65 (98%)	58 (91%)	6 (9%)	8	28
34	3	18/18 (100%)	18 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2992/3194 (94%)	2974 (99%)	18 (1%)	76 80

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	y	33	GLN
33	y	56	LYS
33	y	53	LYS
28	c	34	ILE
33	y	26	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
22	V	4	HIS
32	g	58	HIS
28	c	46	HIS
33	y	5	GLN
5	E	151	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3118/3119 (99%)	770 (24%)	32 (1%)
2	B	117/118 (99%)	23 (19%)	1 (0%)
All	All	3235/3237 (99%)	793 (24%)	33 (1%)

5 of 793 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	U
1	A	11	A
1	A	19	U
1	A	20	G
1	A	23	G

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2350	G

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Mol	Chain	Res	Type
1	A	2384	C
2	B	10	G
1	A	1002	C
1	A	974	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 [i](#)

There are no chain breaks in this entry.

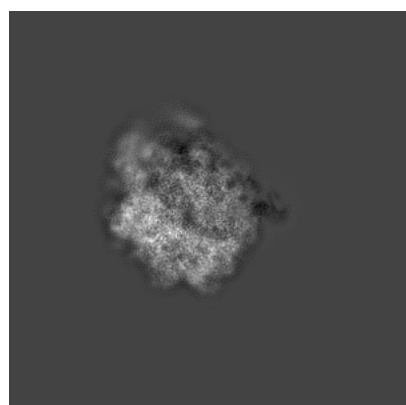
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8937. These allow visual inspection of the internal detail of the map and identification of artifacts.

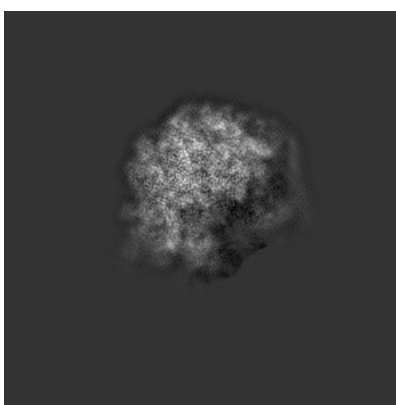
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

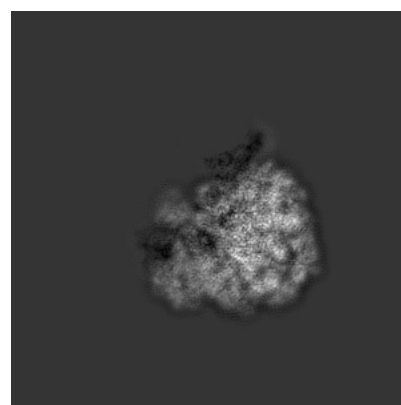
6.1.1 Primary map



X



Y

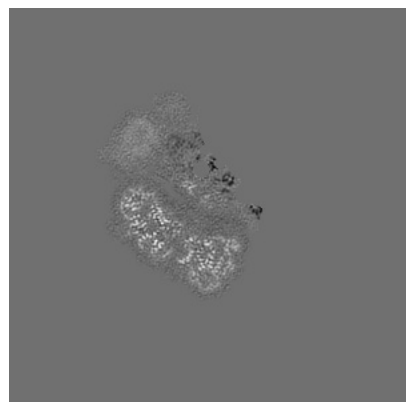


Z

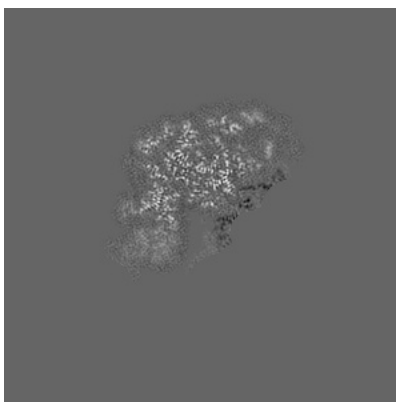
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

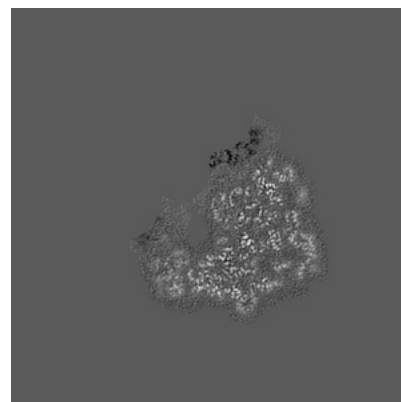
6.2.1 Primary map



X Index: 227



Y Index: 227

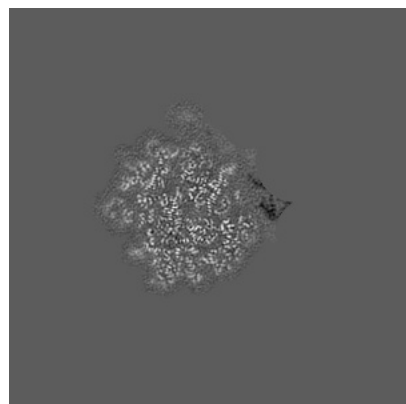


Z Index: 227

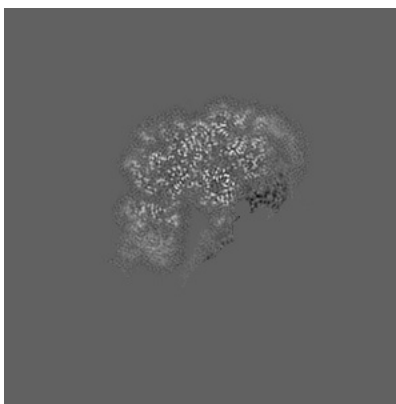
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

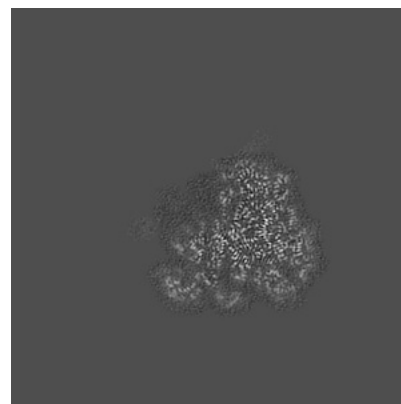
6.3.1 Primary map



X Index: 270



Y Index: 216

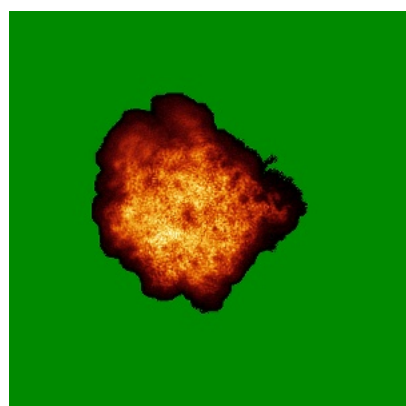


Z Index: 201

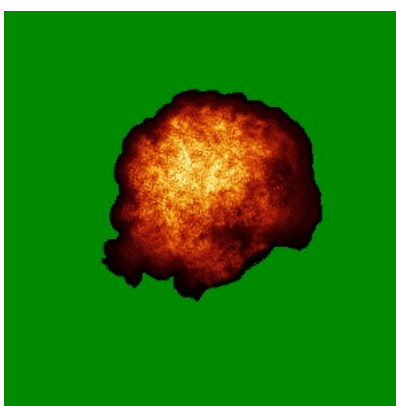
The images above show the largest variance slices of the map in three orthogonal directions.

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

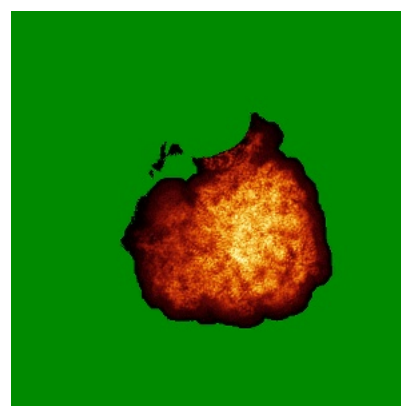
6.4.1 Primary map



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

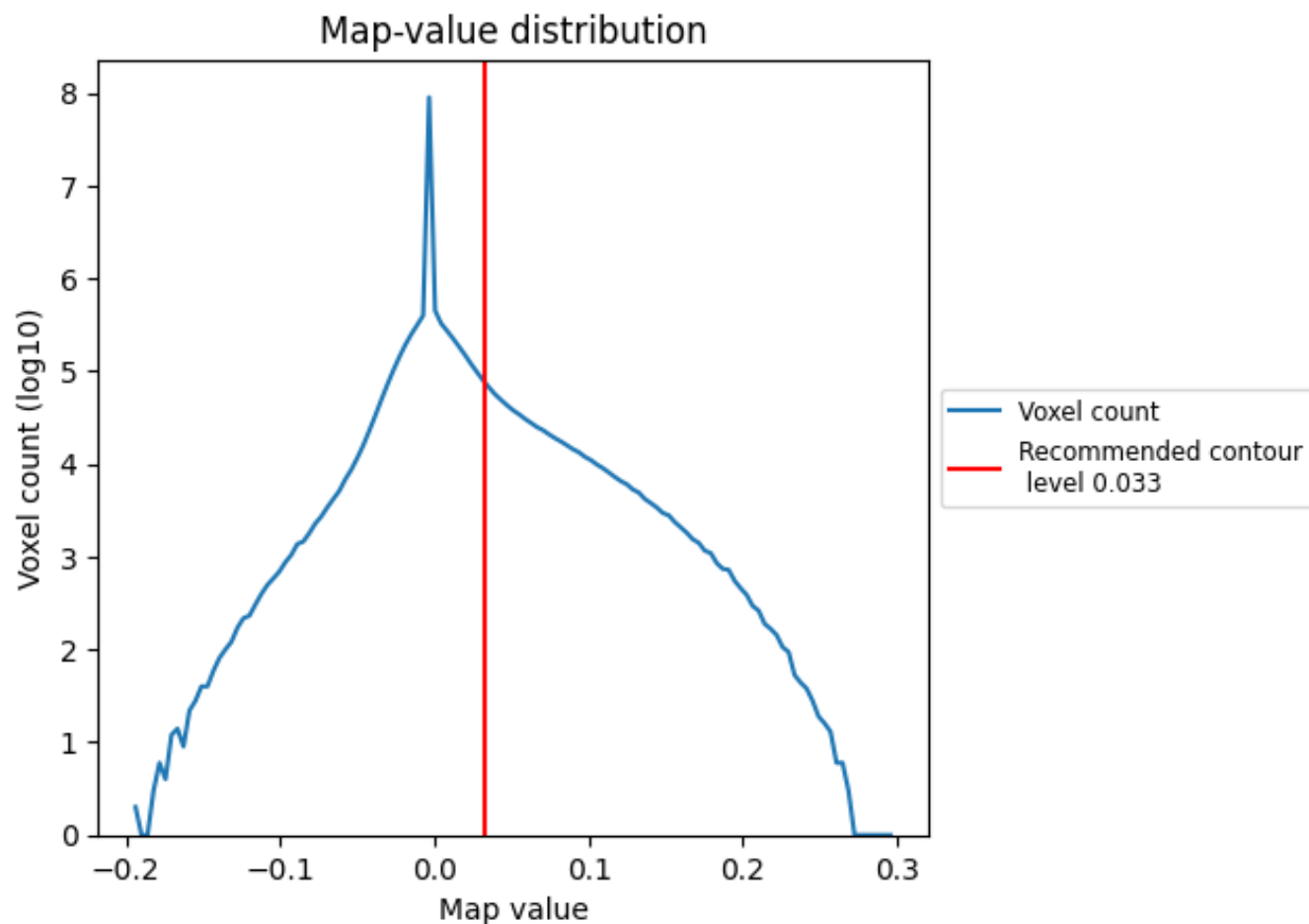
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

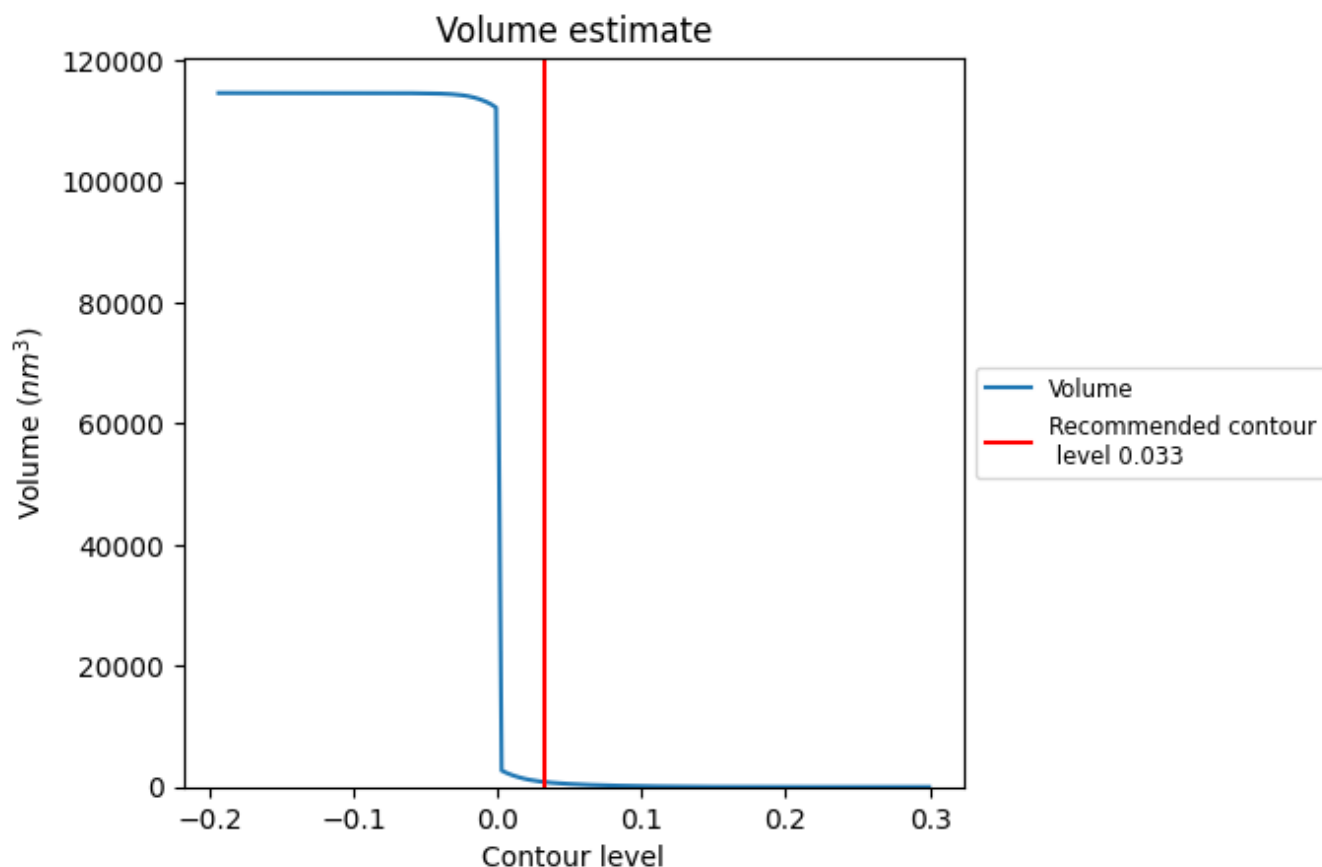
This section contains the results of statistical analysis of the map.

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.

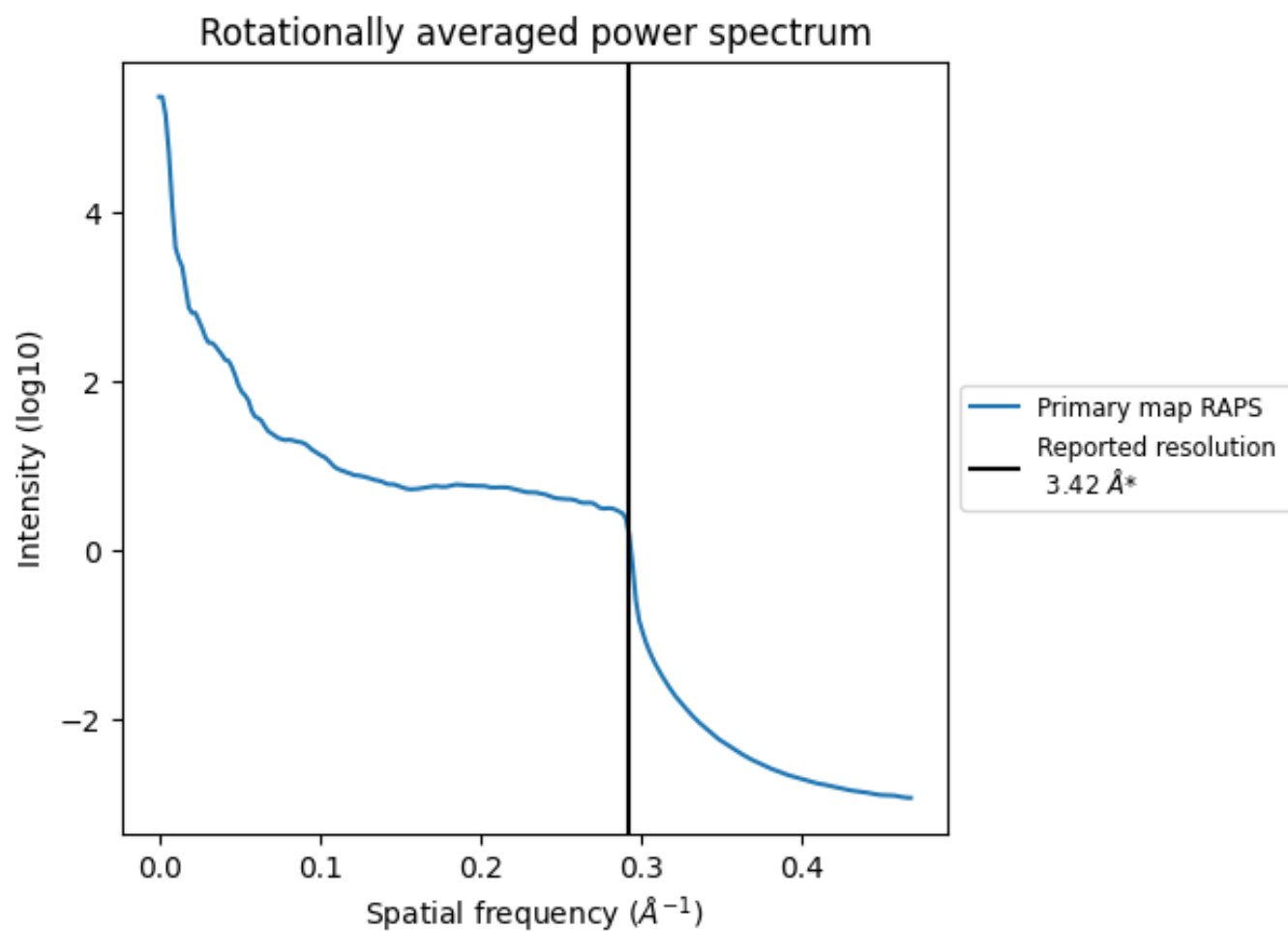
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 804 nm³; this corresponds to an approximate mass of 726 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 ⓘ

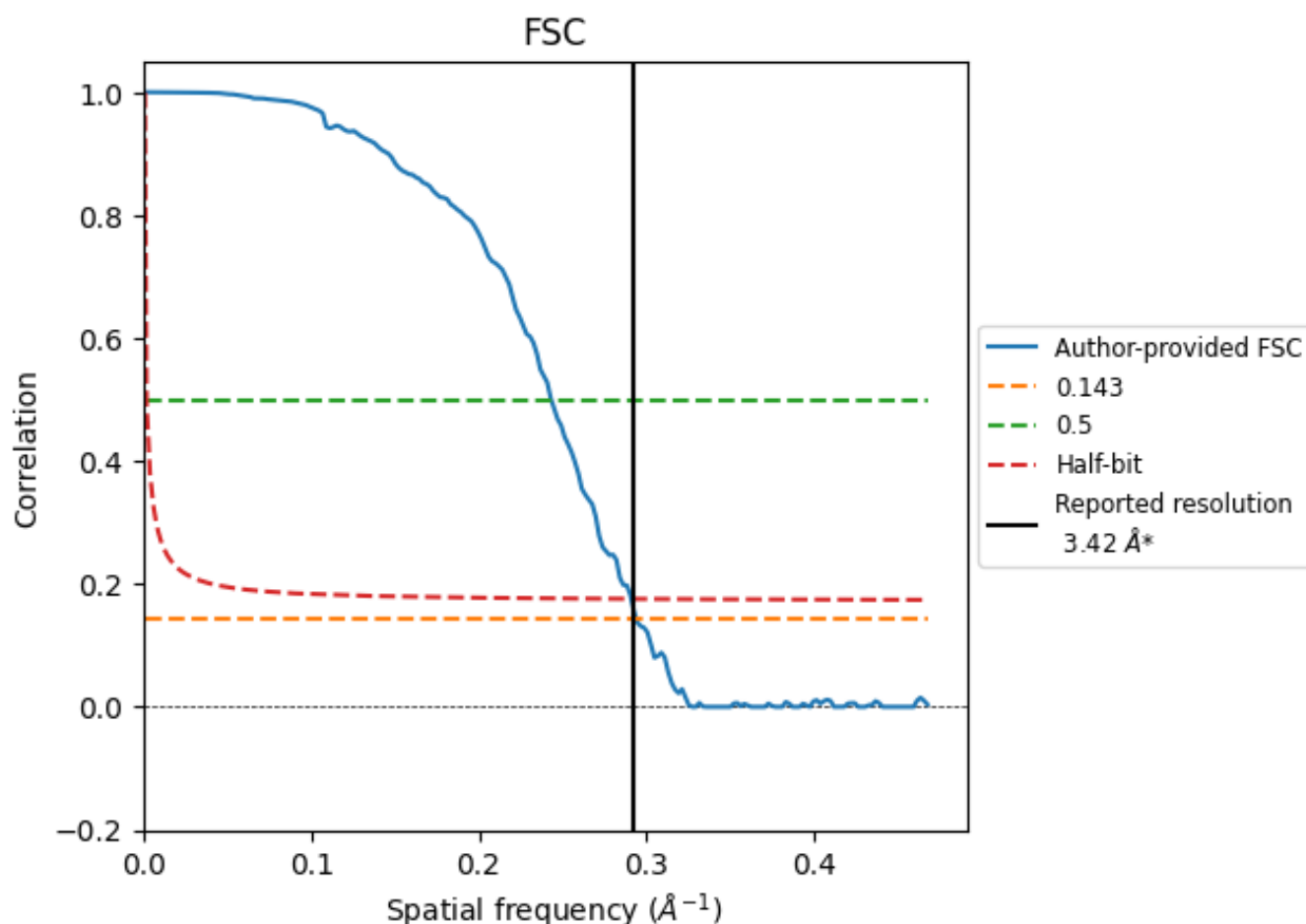


*Reported resolution corresponds to spatial frequency of 0.292 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.292 Å⁻¹

8.2 Resolution estimates [i](#)

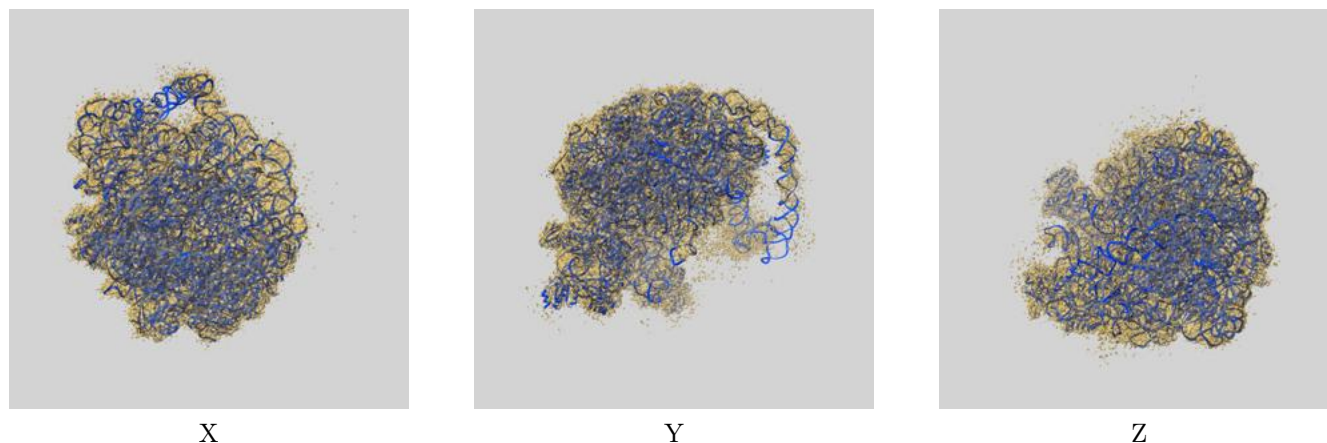
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.42	-	-
Author-provided FSC curve	3.40	4.11	3.44
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

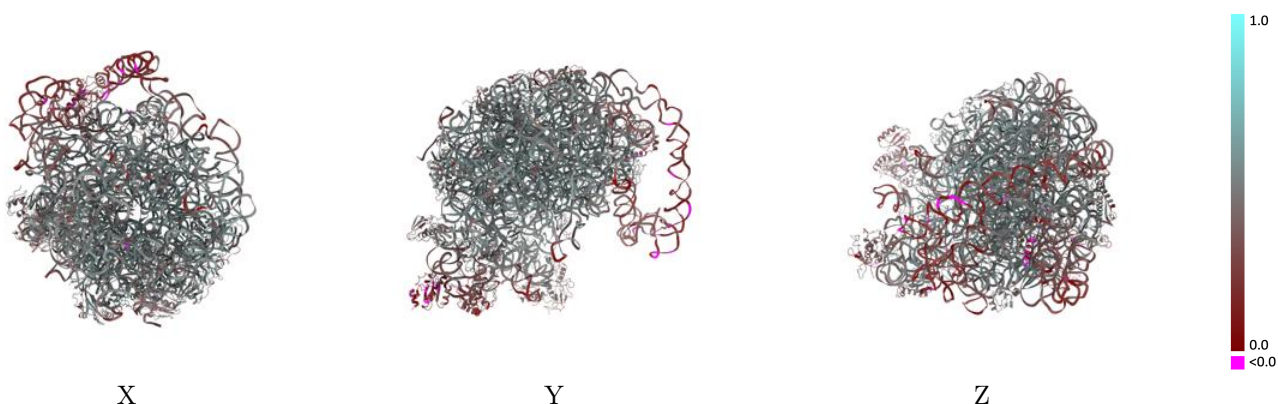
This section contains information regarding the fit between EMDB map EMD-8937 and PDB model 6DZP. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



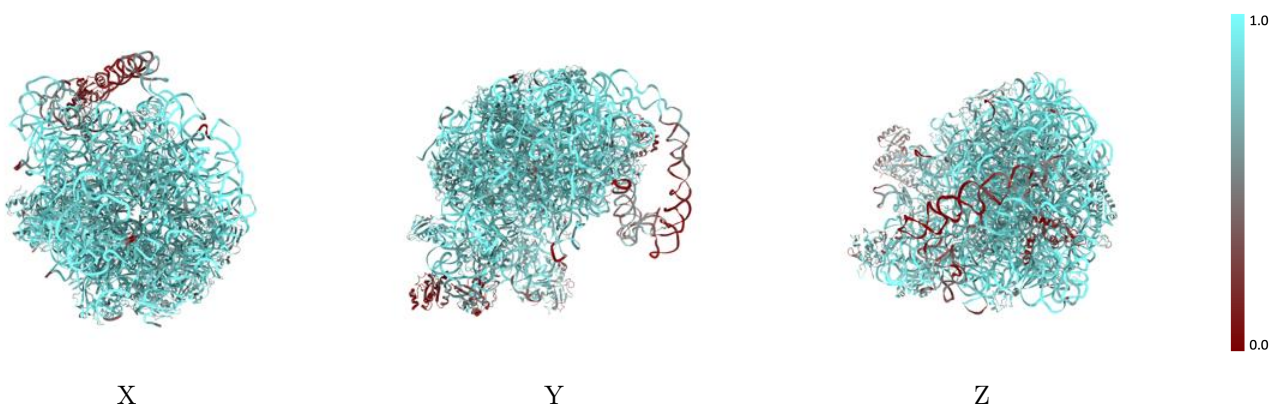
The images above show the 3D surface view of the map at the recommended contour level 0.033 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



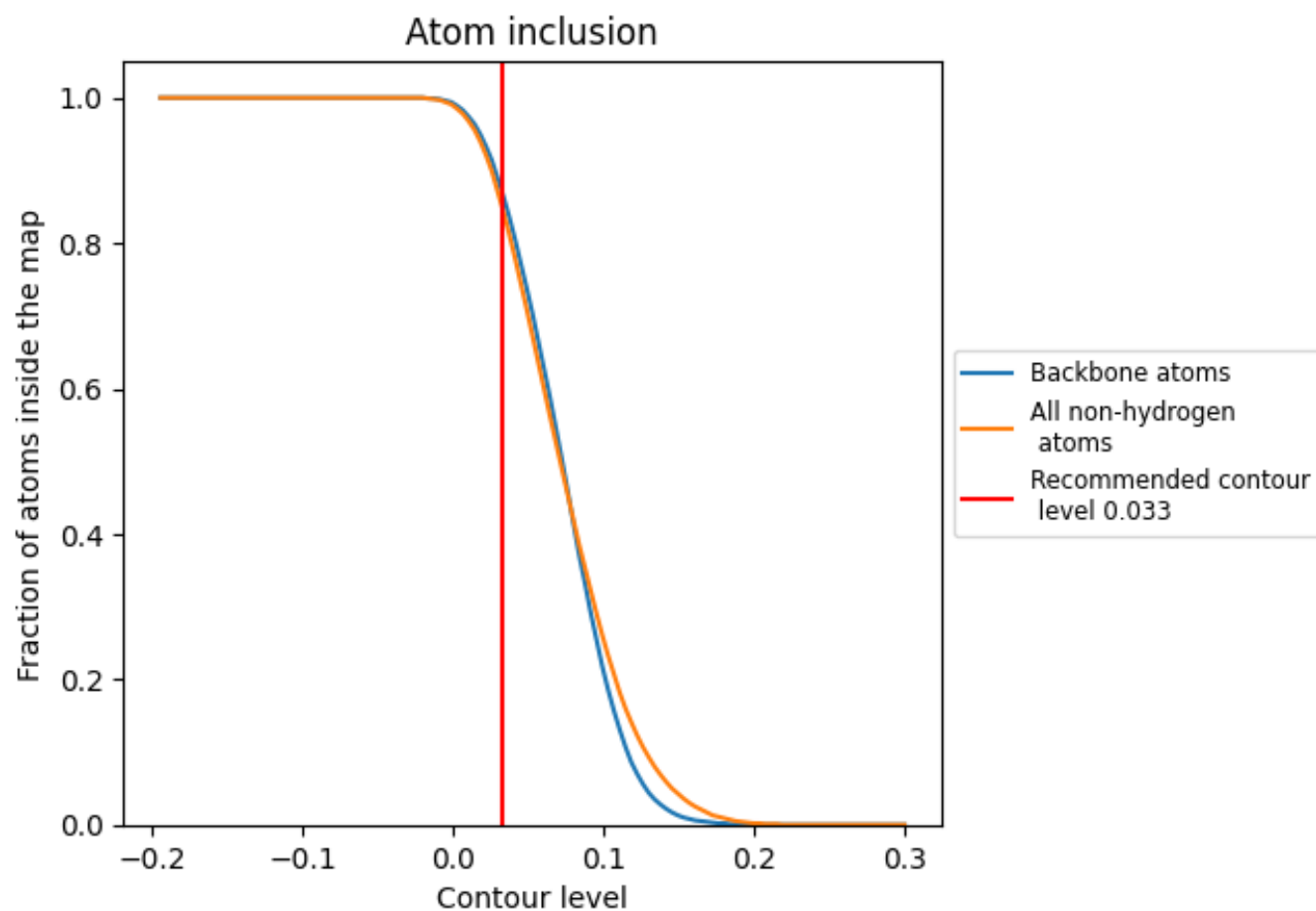
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.033).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 85% 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 (0.033) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8480	 0.4640
3	 0.8100	 0.5200
A	 0.8920	 0.4710
B	 0.9450	 0.4600
C	 0.7410	 0.4900
D	 0.8320	 0.5100
E	 0.8020	 0.4780
F	 0.7000	 0.3860
G	 0.7750	 0.4300
H	 0.2950	 0.2840
I	 0.2240	 0.2020
J	 0.4180	 0.2760
K	 0.8370	 0.5050
L	 0.7460	 0.4880
M	 0.8050	 0.4890
N	 0.8030	 0.5030
O	 0.8430	 0.4980
P	 0.8380	 0.4540
Q	 0.7350	 0.4610
R	 0.8440	 0.5080
S	 0.8620	 0.5060
T	 0.8140	 0.4880
U	 0.7740	 0.4620
V	 0.7400	 0.4210
W	 0.7340	 0.4470
X	 0.8220	 0.5170
Z	 0.8080	 0.4390
a	 0.8130	 0.5030
b	 0.8060	 0.4800
c	 0.6010	 0.3370
d	 0.7990	 0.5120
e	 0.8190	 0.5110
f	 0.8430	 0.5200
g	 0.5620	 0.2850
y	 0.7500	 0.4270

