



wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 09:29 AM EST

PDB ID : 6DZI
EMDB ID : EMD-8932
Title : Cryo-EM Structure of Mycobacterium smegmatis 70S C(minus) ribosome 70S-MPY complex
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 : 3.46 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

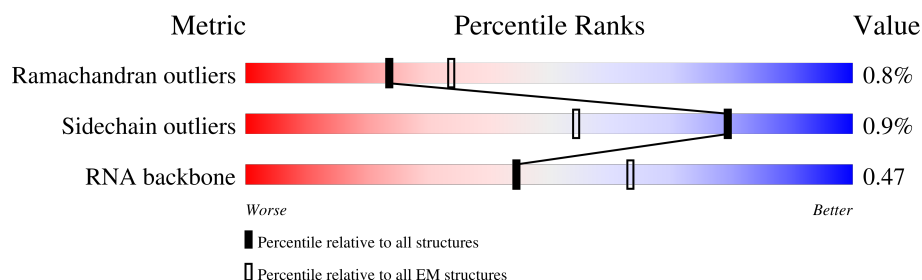
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.46 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.



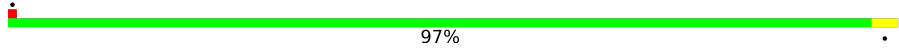
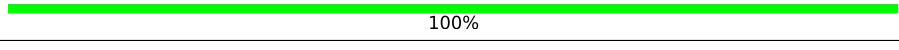
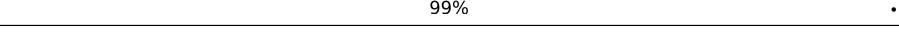
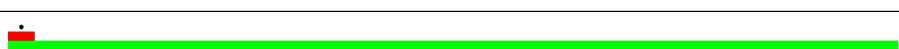
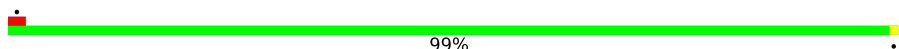
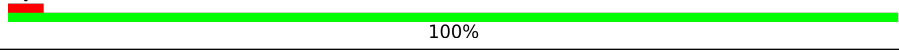
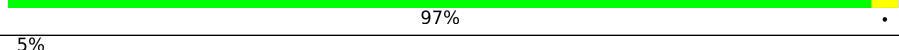
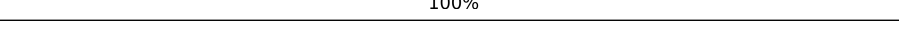


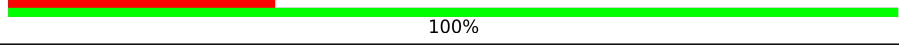
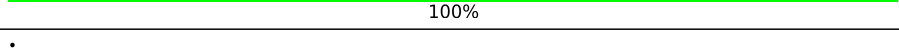

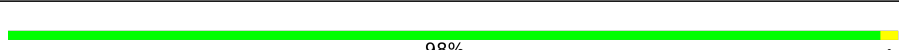
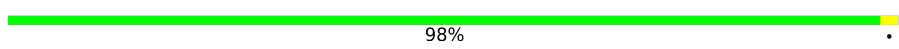
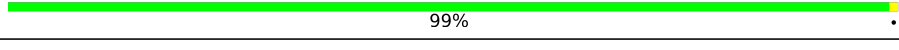
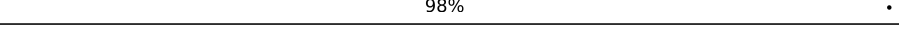

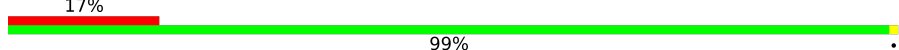
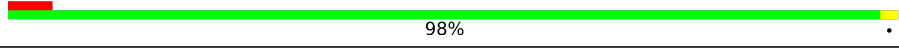
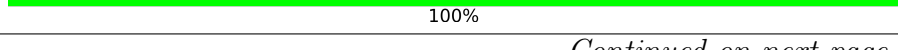



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	h	1511	
2	j	32	
3	k	208	
4	l	200	
5	m	180	
6	n	96	
7	p	155	
8	q	131	

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Mol	Chain	Length	Quality of chain
9	4	126	 97%
10	s	99	 100%
11	t	115	 99%
12	u	122	 98%
13	v	116	 100%
14	x	88	 99%
15	z	113	 100%
16	5	94	 97%
17	6	82	 100%
18	7	85	 95%
19	8	228	 83%
20	r	84	 100%
21	Y	103	 100%
22	9	100	 100%
23	A	3119	 69%
24	B	118	 79%
25	C	275	 98%
26	D	214	 98%
27	E	209	 99%
28	F	182	 98%
29	G	176	 99%
30	H	151	 99%
31	I	126	 99%
32	J	133	 98%
33	K	146	100%

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Mol	Chain	Length	Quality of chain
34	L	122	100%
35	M	145	98% .
36	N	136	99% ..
37	O	118	100%
38	P	126	98% .
39	Q	113	96% . .
40	R	124	100%
41	S	100	99% .
42	T	114	97% .
43	U	97	100%
44	V	105	91% . 8%
45	W	192	99% .
46	X	79	97% .
47	Z	64	98% .
48	a	59	100%
49	b	54	94% 6%
50	c	53	19% 79% 19% .
51	d	46	98% .
52	e	63	100%
53	f	37	100%
54	g	82	82% 10% 9%
55	y	77	83% 14% .
56	3	23	100%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 150868 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	h	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 2 is a protein called CONSERVED PROTEIN DOMAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	j	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	k	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	m	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	p	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
9	4	126	Total	C	N	O	0	0
			994	630	194	170		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	s	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	u	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

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

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

- Molecule 14 is a protein called 30S ribosomal protein S15.

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

- Molecule 15 is a protein called 30S ribosomal protein S16.

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

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	5	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 17 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	6	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 18 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	7	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 19 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	8	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 20 is a protein called 30S ribosomal protein S18 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	r	84	Total	C	N	O	S	0	0
			659	408	131	116	4		

- Molecule 21 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	103	Total	C	N	O	S	0	0
			861	529	175	155	2		

- Molecule 22 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	9	100	Total	C	N	O	S	0	0
			819	497	183	138	1		

- Molecule 23 is a RNA chain called 23 S rRNA (3119-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

- Molecule 24 is a RNA chain called 5S RNA (118-MER).

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

- Molecule 25 is a protein called 50S ribosomal protein L2.

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

- Molecule 26 is a protein called 50S ribosomal protein L3.

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

- Molecule 27 is a protein called 50S ribosomal protein L4.

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

- Molecule 28 is a protein called 50S ribosomal protein L5.

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

- Molecule 29 is a protein called 50S ribosomal protein L6.

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

- Molecule 30 is a protein called 50S ribosomal protein L9.

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

- Molecule 31 is a protein called 50S ribosomal protein L10.

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

- Molecule 32 is a protein called 50S ribosomal protein L11.

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

- Molecule 33 is a protein called 50S ribosomal protein L13.

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

- Molecule 34 is a protein called 50S ribosomal protein L14.

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

- Molecule 35 is a protein called 50S ribosomal protein L15.

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

- Molecule 36 is a protein called 50S ribosomal protein L16.

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

- Molecule 37 is a protein called 50S ribosomal protein L17.

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

- Molecule 38 is a protein called 50S ribosomal protein L18.

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

- Molecule 39 is a protein called 50S ribosomal protein L19.

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

- Molecule 40 is a protein called 50S ribosomal protein L20.

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

- Molecule 41 is a protein called 50S ribosomal protein L21.

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

- Molecule 42 is a protein called 50S ribosomal protein L22.

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

- Molecule 43 is a protein called 50S ribosomal protein L23.

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

- Molecule 44 is a protein called 50S ribosomal protein L24.

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

- Molecule 45 is a protein called 50S ribosomal protein L25.

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

- Molecule 46 is a protein called 50S ribosomal protein L27.

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

- Molecule 47 is a protein called 50S ribosomal protein L29.

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

- Molecule 48 is a protein called 50S ribosomal protein L30.

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

- Molecule 49 is a protein called 50S ribosomal protein L32.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L34.

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

- Molecule 52 is a protein called 50S ribosomal protein L35.

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

- Molecule 53 is a protein called 50S ribosomal protein L36.

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

- Molecule 54 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	g	75	Total	C	N	O	S	0	0
			593	379	103	110	1		

- Molecule 55 is a protein called 50S ribosomal protein L28.

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

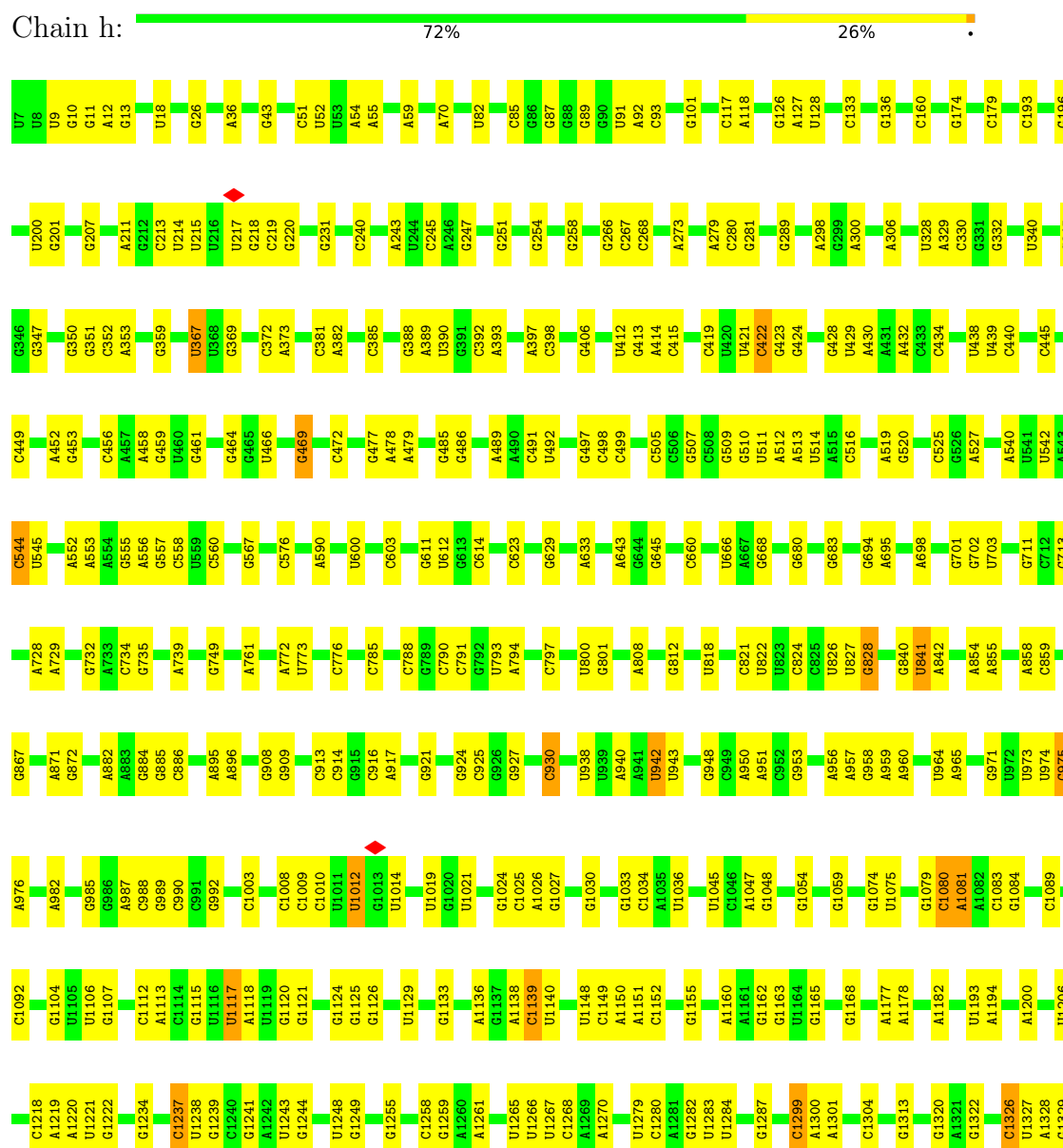
- Molecule 56 is a protein called Uncharacterized protein.

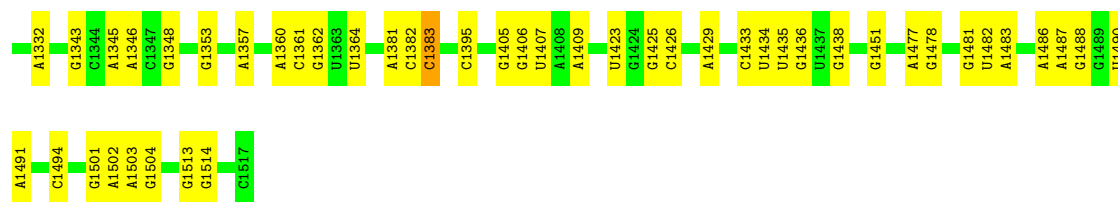
Mol	Chain	Residues	Atoms				AltConf	Trace
56	3	23	Total	C	N	O	0	0
			189	111	50	28		

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: 16S rRNA

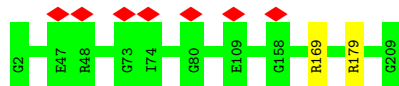




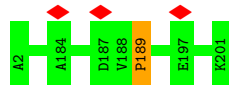
- Molecule 2: CONSERVED PROTEIN DOMAIN



- Molecule 3: 30S ribosomal protein S3



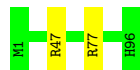
- Molecule 4: 30S ribosomal protein S4



- Molecule 5: 30S ribosomal protein S5

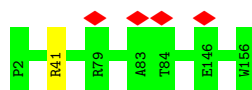


- Molecule 6: 30S ribosomal protein S6



- Molecule 7: 30S ribosomal protein S7





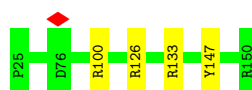
- Molecule 8: 30S ribosomal protein S8

Chain q: 98%



- Molecule 9: 30S ribosomal protein S9

Chain 4: 97%



- Molecule 10: 30S ribosomal protein S10

Chain s: 100%

There are no outlier residues recorded for this chain.

- Molecule 11: 30S ribosomal protein S11

Chain t: 99%



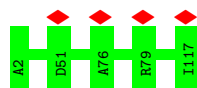
- Molecule 12: 30S ribosomal protein S12

Chain u: 98%



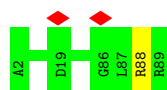
- Molecule 13: 30S ribosomal protein S13

Chain v: 100%

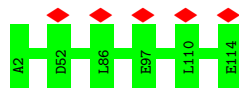


- Molecule 14: 30S ribosomal protein S15

Chain x: 99%



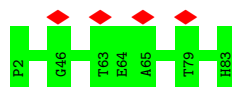
- Molecule 15: 30S ribosomal protein S16



- Molecule 16: 30S ribosomal protein S17



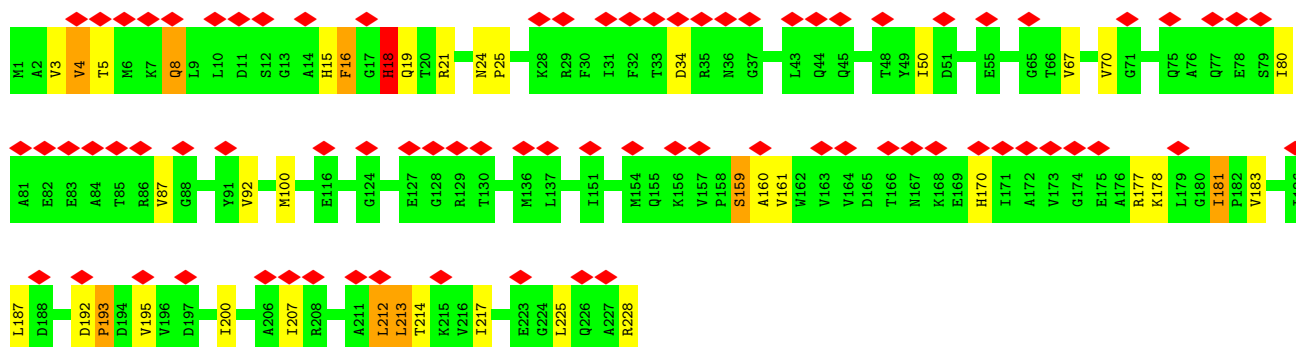
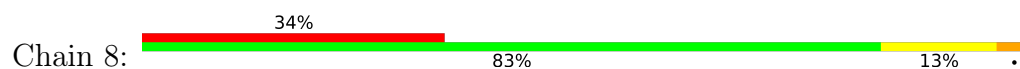
- Molecule 17: 30S ribosomal protein S19



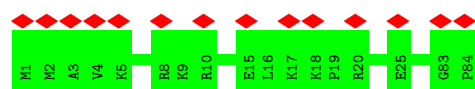
- Molecule 18: 30S ribosomal protein S20



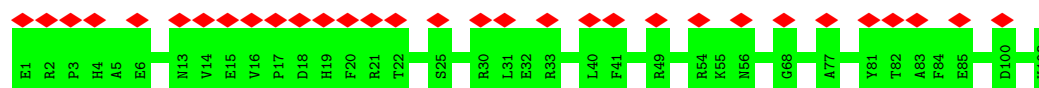
- Molecule 19: 30S ribosomal protein S2



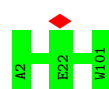
- Molecule 20: 30S ribosomal protein S18 1



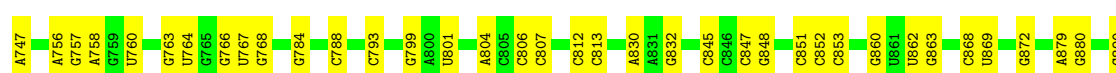
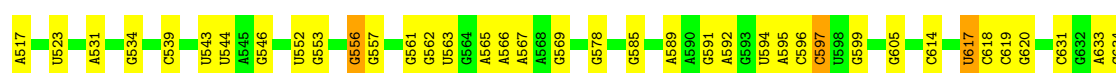
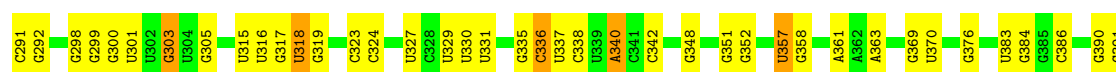
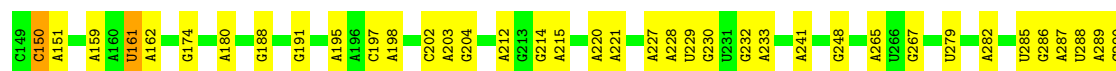
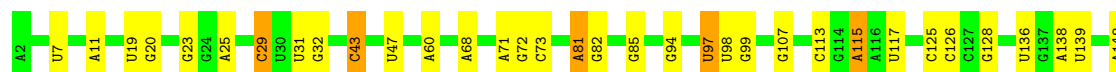
- Molecule 21: Ribosome hibernation promoting factor



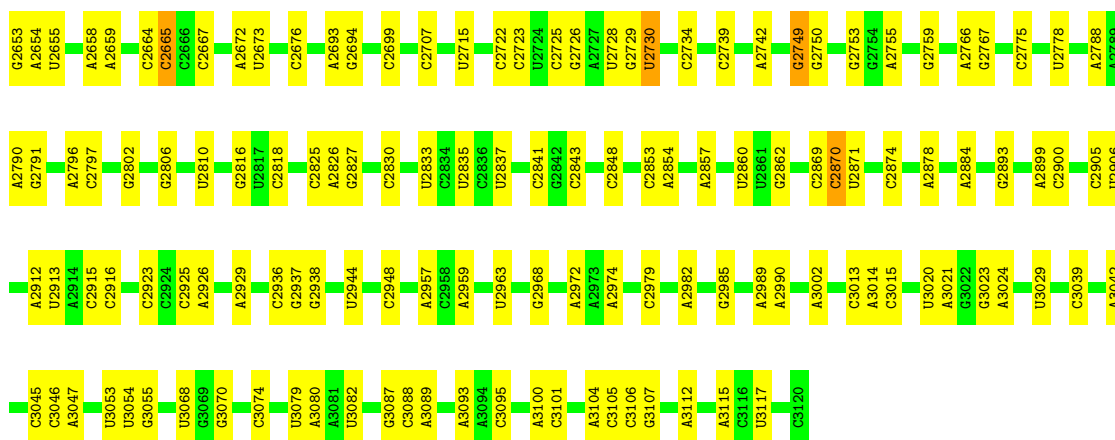
- Molecule 22: 30S ribosomal protein S14



- Molecule 23: 23 S rRNA (3119-MER)



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C2507	U2373	G2276	G2169	U2033	C1893	U1756	A1627	U1560	C1465	G1345	U1219	G1121	C1003
C2509	G2375	G2280	U2180	A2036	A1894	U1757	A1628	C1561	C1466	A1352	U1223	G1122	C1004
A2510	G2380	A2284	C2181	C2043	C1901	G1760	U1630	C1562	G1472	G1353	G1224	C1123	C1005
A2511	G2385	G2285	U2180	A2036	C1902	U1767	G1632	A1564	G1473	G1359	U1226	C1124	G1006
C2519	A2380	A2286	C2181	A2046	C1909	C1775	G1637	A1565	A1480	A1362	G1230	G1130	G1007
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A2609	U2331	U2331	A1982	A2129	A1982	C1838	G1718	C1594	C1536	C1421	U1294	G1192	C1081
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	U2344	U2344	A1995	A2142	A1995	C1851	G1731	C1607	C1549	C1440	U1325	U1212	
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• Molecule 24: 5S RNA (118-MER)

Chain B:  79% 20%



• Molecule 25: 50S ribosomal protein L2

Chain C:  98%



• Molecule 26: 50S ribosomal protein L3

Chain D:  98%



• Molecule 27: 50S ribosomal protein L4

Chain E:  99%



• Molecule 28: 50S ribosomal protein L5

Chain F:  98%



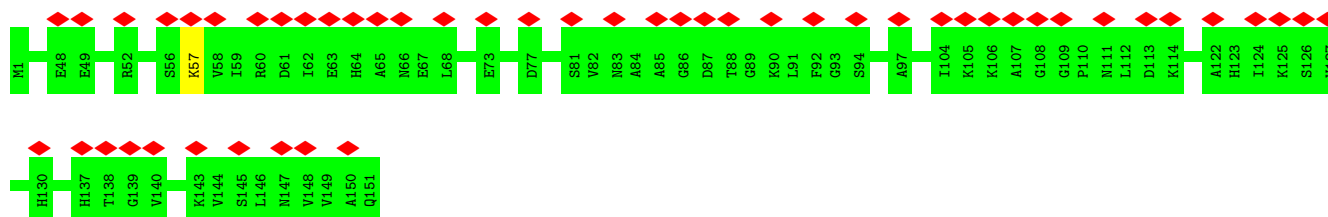
• Molecule 29: 50S ribosomal protein L6

Chain G:  99%



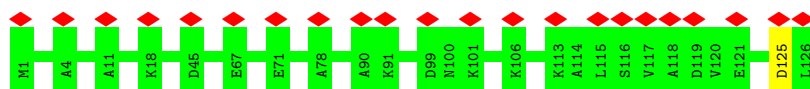
- Molecule 30: 50S ribosomal protein L9

Chain H:  33%  99%



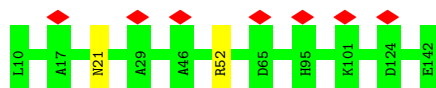
- Molecule 31: 50S ribosomal protein L10

Chain I:  17%  99%



- Molecule 32: 50S ribosomal protein L11

Chain J:  5%  98%



- Molecule 33: 50S ribosomal protein L13

Chain K:  100%

There are no outlier residues recorded for this chain.

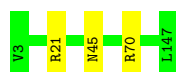
- Molecule 34: 50S ribosomal protein L14

Chain L:  100%

There are no outlier residues recorded for this chain.

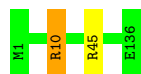
- Molecule 35: 50S ribosomal protein L15

Chain M:  98%



- Molecule 36: 50S ribosomal protein L16

Chain N:  99% ..



- Molecule 37: 50S ribosomal protein L17

Chain O:  100%

There are no outlier residues recorded for this chain.

- Molecule 38: 50S ribosomal protein L18

Chain P:  98% .



- Molecule 39: 50S ribosomal protein L19

Chain Q:  96% ..



- Molecule 40: 50S ribosomal protein L20

Chain R:  100%

There are no outlier residues recorded for this chain.

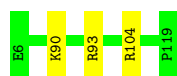
- Molecule 41: 50S ribosomal protein L21

Chain S:  99% .



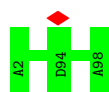
- Molecule 42: 50S ribosomal protein L22

Chain T:  97% .

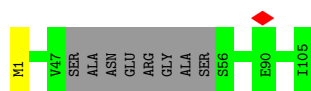
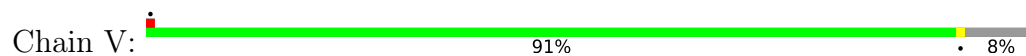


- Molecule 43: 50S ribosomal protein L23

Chain U:  100%



- Molecule 44: 50S ribosomal protein L24



- Molecule 45: 50S ribosomal protein L25



- Molecule 46: 50S ribosomal protein L27



- Molecule 47: 50S ribosomal protein L29



- Molecule 48: 50S ribosomal protein L30

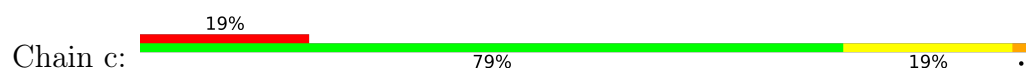


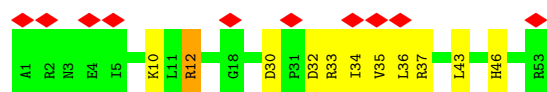
There are no outlier residues recorded for this chain.

- Molecule 49: 50S ribosomal protein L32

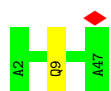


- Molecule 50: 50S ribosomal protein L33 2





- Molecule 51: 50S ribosomal protein L34



- Molecule 52: 50S ribosomal protein L35



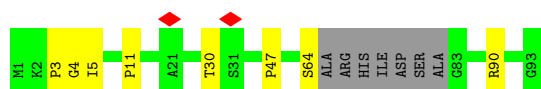
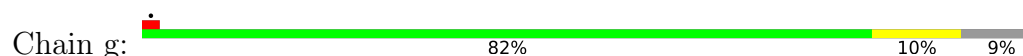
There are no outlier residues recorded for this chain.

- Molecule 53: 50S ribosomal protein L36

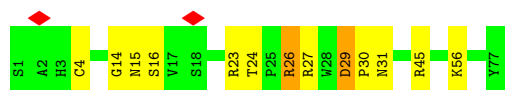
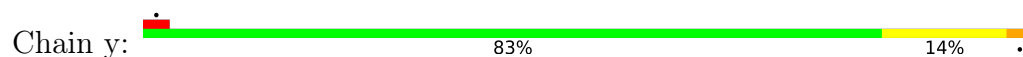


There are no outlier residues recorded for this chain.

- Molecule 54: 50S ribosomal protein L31



- Molecule 55: 50S ribosomal protein L28



- Molecule 56: Uncharacterized protein



There are no outlier residues recorded for this chain.

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 ($e^-/\text{\AA}^2$)	67.10	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	0.313	Depositor
Minimum map value	-0.175	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	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	h	0.75	0/36309	1.06	78/56657 (0.1%)
2	j	0.54	0/280	0.87	0/359
3	k	0.37	0/1684	0.62	0/2261
4	l	0.38	0/1672	0.65	0/2251
5	m	0.42	0/1312	0.63	0/1772
6	n	0.44	0/782	0.61	0/1059
7	p	0.35	0/1252	0.67	0/1690
8	q	0.44	0/1025	0.65	1/1385 (0.1%)
9	4	0.34	0/1012	0.66	0/1362
10	s	0.35	0/802	0.62	0/1086
11	t	0.42	0/873	0.65	0/1180
12	u	0.47	0/969	0.79	2/1294 (0.2%)
13	v	0.35	0/942	0.72	0/1260
14	x	0.47	0/729	0.73	0/977
15	z	0.41	0/908	0.65	0/1226
16	5	0.42	0/759	0.69	0/1016
17	6	0.37	0/680	0.62	0/915
18	7	0.44	0/663	0.65	0/882
19	8	0.46	0/1822	1.21	28/2457 (1.1%)
20	r	0.41	0/665	0.72	0/889
21	Y	0.36	0/875	0.67	0/1169
22	9	0.36	0/830	0.65	0/1106
23	A	1.26	88/75001 (0.1%)	1.23	313/117027 (0.3%)
24	B	0.99	0/2821	1.12	5/4396 (0.1%)
25	C	0.76	1/2153 (0.0%)	0.77	4/2895 (0.1%)
26	D	0.80	0/1609	0.79	1/2165 (0.0%)
27	E	0.66	0/1592	0.67	1/2153 (0.0%)
28	F	0.49	0/1467	0.67	0/1973
29	G	0.53	0/1369	0.70	1/1848 (0.1%)
30	H	0.42	0/1129	0.75	0/1524
31	I	0.34	0/925	0.58	0/1246
32	J	0.34	0/1006	0.62	0/1364
33	K	0.71	0/1157	0.65	0/1567
34	L	0.80	0/946	0.74	0/1268

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	M	0.70	0/1091	0.76	1/1457 (0.1%)
36	N	0.70	0/1118	0.75	2/1506 (0.1%)
37	O	0.75	0/945	0.73	0/1267
38	P	0.60	0/966	0.74	1/1298 (0.1%)
39	Q	0.80	1/921 (0.1%)	0.73	1/1236 (0.1%)
40	R	0.86	0/1000	0.75	0/1341
41	S	0.69	0/764	0.63	0/1030
42	T	0.76	0/887	0.76	0/1204
43	U	0.68	0/766	0.64	0/1030
44	V	0.55	0/738	0.63	0/987
45	W	0.52	0/1443	0.64	0/1970
46	X	0.80	0/595	0.73	0/798
47	Z	0.60	0/534	0.74	1/713 (0.1%)
48	a	0.70	0/477	0.69	0/640
49	b	0.67	0/427	0.79	1/572 (0.2%)
50	c	0.50	0/463	0.88	1/621 (0.2%)
51	d	0.84	0/380	0.99	2/500 (0.4%)
52	e	0.69	0/507	0.75	0/672
53	f	0.85	0/303	0.71	0/401
54	g	0.42	0/613	0.76	2/835 (0.2%)
55	y	0.53	0/629	0.82	1/843 (0.1%)
56	3	0.72	0/191	0.79	0/247
All	All	0.98	90/163778 (0.1%)	1.07	447/244847 (0.2%)

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	l	0	1
19	8	0	10
26	D	0	1
32	J	0	1
45	W	0	1
All	All	0	14

The worst 5 of 90 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	Q	50	GLN	CA-CB	-8.43	1.35	1.53
23	A	1081	C	N1-C6	-6.45	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	2841	C	N1-C6	-6.26	1.33	1.37
23	A	901	C	N1-C6	-6.19	1.33	1.37
23	A	202	C	N1-C6	-6.10	1.33	1.37

The worst 5 of 447 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	8	213	LEU	CA-CB-CG	14.81	149.37	115.30
1	h	1081	A	O4'-C1'-N9	11.00	117.00	108.20
23	A	2509	C	O4'-C1'-N1	10.71	116.77	108.20
23	A	1012	C	C2-N1-C1'	10.54	130.39	118.80
23	A	2245	C	C2-N1-C1'	10.28	130.10	118.80

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
19	8	24	ASN	Peptide
19	8	4	VAL	Peptide
19	8	5	THR	Peptide
19	8	8	GLN	Peptide
4	1	189	PRO	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	j	30/32 (94%)	29 (97%)	1 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	k	206/208 (99%)	182 (88%)	24 (12%)	0	100	100
4	l	198/200 (99%)	178 (90%)	19 (10%)	1 (0%)	29	66
5	m	178/180 (99%)	154 (86%)	22 (12%)	2 (1%)	14	50
6	n	94/96 (98%)	86 (92%)	8 (8%)	0	100	100
7	p	153/155 (99%)	146 (95%)	7 (5%)	0	100	100
8	q	129/131 (98%)	113 (88%)	16 (12%)	0	100	100
9	4	124/126 (98%)	111 (90%)	12 (10%)	1 (1%)	19	57
10	s	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
11	t	113/115 (98%)	100 (88%)	13 (12%)	0	100	100
12	u	120/122 (98%)	102 (85%)	18 (15%)	0	100	100
13	v	114/116 (98%)	100 (88%)	14 (12%)	0	100	100
14	x	86/88 (98%)	81 (94%)	5 (6%)	0	100	100
15	z	111/113 (98%)	98 (88%)	13 (12%)	0	100	100
16	5	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
17	6	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
18	7	83/85 (98%)	82 (99%)	1 (1%)	0	100	100
19	8	226/228 (99%)	196 (87%)	23 (10%)	7 (3%)	4	29
20	r	82/84 (98%)	75 (92%)	7 (8%)	0	100	100
21	Y	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
22	9	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
25	C	273/275 (99%)	232 (85%)	41 (15%)	0	100	100
26	D	212/214 (99%)	182 (86%)	28 (13%)	2 (1%)	17	54
27	E	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
28	F	180/182 (99%)	165 (92%)	14 (8%)	1 (1%)	25	62
29	G	174/176 (99%)	157 (90%)	17 (10%)	0	100	100
30	H	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
31	I	124/126 (98%)	117 (94%)	6 (5%)	1 (1%)	19	57
32	J	131/133 (98%)	116 (88%)	15 (12%)	0	100	100
33	K	144/146 (99%)	135 (94%)	9 (6%)	0	100	100
34	L	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
35	M	143/145 (99%)	120 (84%)	21 (15%)	2 (1%)	11	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	N	134/136 (98%)	119 (89%)	15 (11%)	0	100	100
37	O	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
38	P	124/126 (98%)	116 (94%)	8 (6%)	0	100	100
39	Q	111/113 (98%)	94 (85%)	15 (14%)	2 (2%)	8	39
40	R	122/124 (98%)	117 (96%)	5 (4%)	0	100	100
41	S	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
42	T	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
43	U	95/97 (98%)	81 (85%)	14 (15%)	0	100	100
44	V	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
45	W	190/192 (99%)	169 (89%)	20 (10%)	1 (0%)	29	66
46	X	77/79 (98%)	69 (90%)	8 (10%)	0	100	100
47	Z	62/64 (97%)	62 (100%)	0	0	100	100
48	a	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
49	b	52/54 (96%)	47 (90%)	4 (8%)	1 (2%)	8	38
50	c	51/53 (96%)	26 (51%)	15 (29%)	10 (20%)	0	1
51	d	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
52	e	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
53	f	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
54	g	71/82 (87%)	50 (70%)	16 (22%)	5 (7%)	1	11
55	y	75/77 (97%)	56 (75%)	8 (11%)	11 (15%)	0	2
56	3	21/23 (91%)	18 (86%)	3 (14%)	0	100	100
All	All	6173/6298 (98%)	5524 (90%)	602 (10%)	47 (1%)	24	57

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	m	103	GLY
19	8	16	PHE
19	8	25	PRO
19	8	161	VAL
26	D	156	THR

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	j	30/30 (100%)	30 (100%)	0	100	100
3	k	170/170 (100%)	168 (99%)	2 (1%)	71	87
4	l	175/175 (100%)	175 (100%)	0	100	100
5	m	127/127 (100%)	126 (99%)	1 (1%)	81	92
6	n	85/85 (100%)	83 (98%)	2 (2%)	49	76
7	p	131/131 (100%)	130 (99%)	1 (1%)	81	92
8	q	107/107 (100%)	106 (99%)	1 (1%)	78	91
9	4	102/102 (100%)	99 (97%)	3 (3%)	42	71
10	s	89/89 (100%)	89 (100%)	0	100	100
11	t	89/89 (100%)	88 (99%)	1 (1%)	73	88
12	u	103/103 (100%)	102 (99%)	1 (1%)	76	89
13	v	99/99 (100%)	99 (100%)	0	100	100
14	x	76/76 (100%)	75 (99%)	1 (1%)	69	86
15	z	92/92 (100%)	92 (100%)	0	100	100
16	5	80/80 (100%)	77 (96%)	3 (4%)	33	64
17	6	73/73 (100%)	73 (100%)	0	100	100
18	7	69/69 (100%)	65 (94%)	4 (6%)	20	52
19	8	191/191 (100%)	185 (97%)	6 (3%)	40	70
20	r	70/70 (100%)	70 (100%)	0	100	100
21	Y	91/91 (100%)	91 (100%)	0	100	100
22	9	85/85 (100%)	85 (100%)	0	100	100
25	C	215/215 (100%)	215 (100%)	0	100	100
26	D	160/160 (100%)	159 (99%)	1 (1%)	86	95
27	E	169/169 (100%)	168 (99%)	1 (1%)	86	95
28	F	151/151 (100%)	149 (99%)	2 (1%)	69	86
29	G	148/148 (100%)	148 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	H	116/116 (100%)	115 (99%)	1 (1%)	78	91
31	I	89/89 (100%)	89 (100%)	0	100	100
32	J	102/102 (100%)	101 (99%)	1 (1%)	76	89
33	K	119/119 (100%)	119 (100%)	0	100	100
34	L	100/100 (100%)	100 (100%)	0	100	100
35	M	112/112 (100%)	112 (100%)	0	100	100
36	N	114/114 (100%)	113 (99%)	1 (1%)	78	91
37	O	97/97 (100%)	97 (100%)	0	100	100
38	P	93/93 (100%)	92 (99%)	1 (1%)	73	88
39	Q	100/100 (100%)	99 (99%)	1 (1%)	76	89
40	R	97/97 (100%)	97 (100%)	0	100	100
41	S	81/81 (100%)	80 (99%)	1 (1%)	71	87
42	T	90/90 (100%)	87 (97%)	3 (3%)	38	68
43	U	83/83 (100%)	83 (100%)	0	100	100
44	V	81/86 (94%)	80 (99%)	1 (1%)	71	87
45	W	155/155 (100%)	155 (100%)	0	100	100
46	X	58/58 (100%)	56 (97%)	2 (3%)	37	67
47	Z	58/58 (100%)	58 (100%)	0	100	100
48	a	52/52 (100%)	52 (100%)	0	100	100
49	b	43/43 (100%)	42 (98%)	1 (2%)	50	76
50	c	49/49 (100%)	48 (98%)	1 (2%)	55	79
51	d	35/35 (100%)	35 (100%)	0	100	100
52	e	53/53 (100%)	53 (100%)	0	100	100
53	f	35/35 (100%)	35 (100%)	0	100	100
54	g	64/70 (91%)	63 (98%)	1 (2%)	62	83
55	y	64/64 (100%)	61 (95%)	3 (5%)	26	59
56	3	18/18 (100%)	18 (100%)	0	100	100
All	All	5135/5146 (100%)	5087 (99%)	48 (1%)	79	91

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	F	78	ARG

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Mol	Chain	Res	Type
41	S	81	LYS
28	F	95	ARG
36	N	10	ARG
42	T	93	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
28	F	31	ASN
30	H	46	GLN
55	y	33	GLN
55	y	19	HIS
55	y	21	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	h	1510/1511 (99%)	391 (25%)	0
23	A	3118/3119 (99%)	771 (24%)	32 (1%)
24	B	117/118 (99%)	23 (19%)	1 (0%)
All	All	4745/4748 (99%)	1185 (24%)	33 (0%)

5 of 1185 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	h	9	U
1	h	10	G
1	h	11	G
1	h	12	A
1	h	13	G

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	A	2350	G
23	A	2384	C
24	B	10	G
23	A	1002	C
23	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 monosaccharides 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.

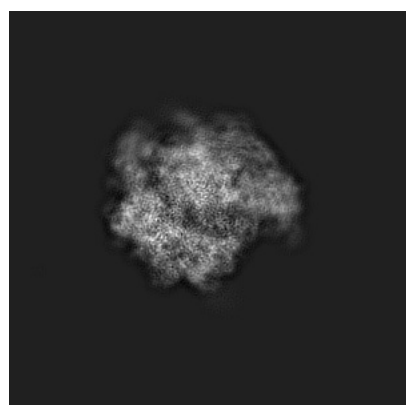
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8932. These allow visual inspection of the internal detail of the map and identification of artifacts.

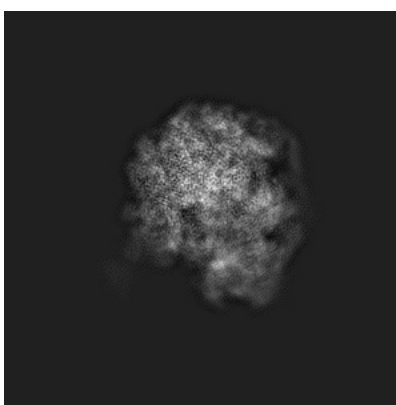
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

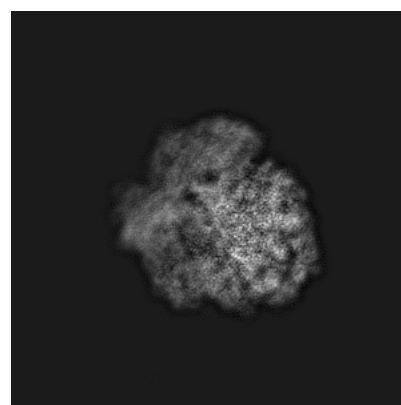
6.1.1 Primary map



X



Y

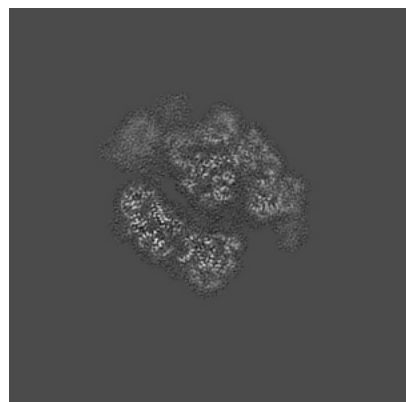


Z

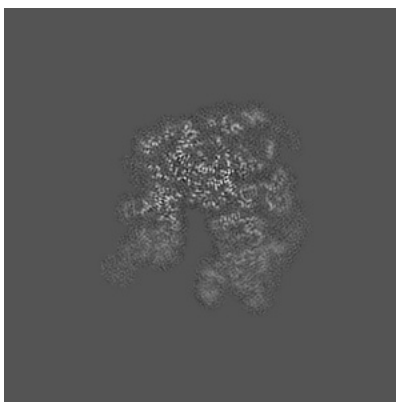
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

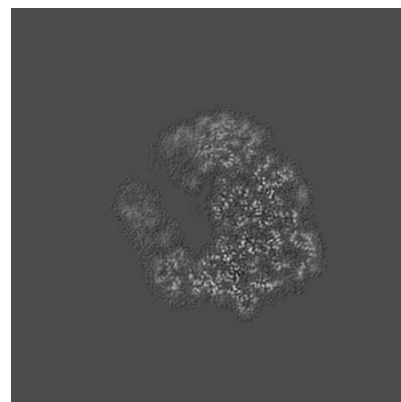
6.2.1 Primary map



X Index: 227



Y Index: 227

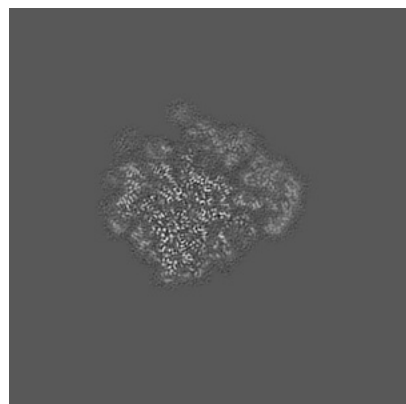


Z Index: 227

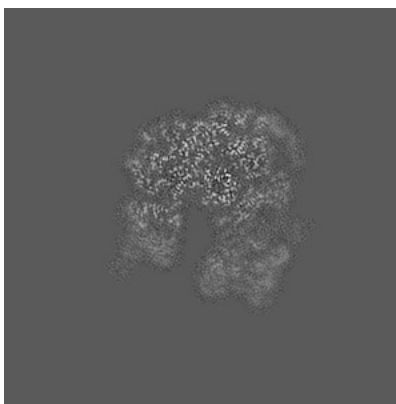
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

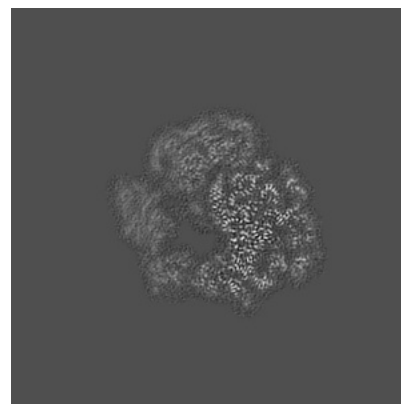
6.3.1 Primary map



X Index: 255



Y Index: 216

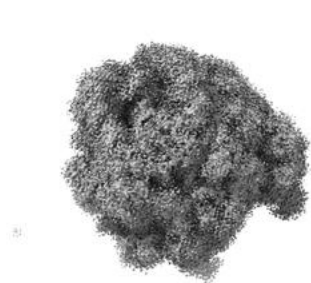


Z Index: 238

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

6.4 Orthogonal surface views [i](#)

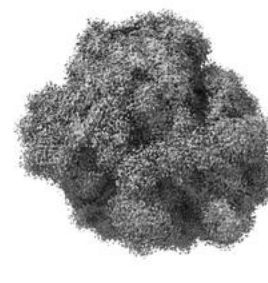
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

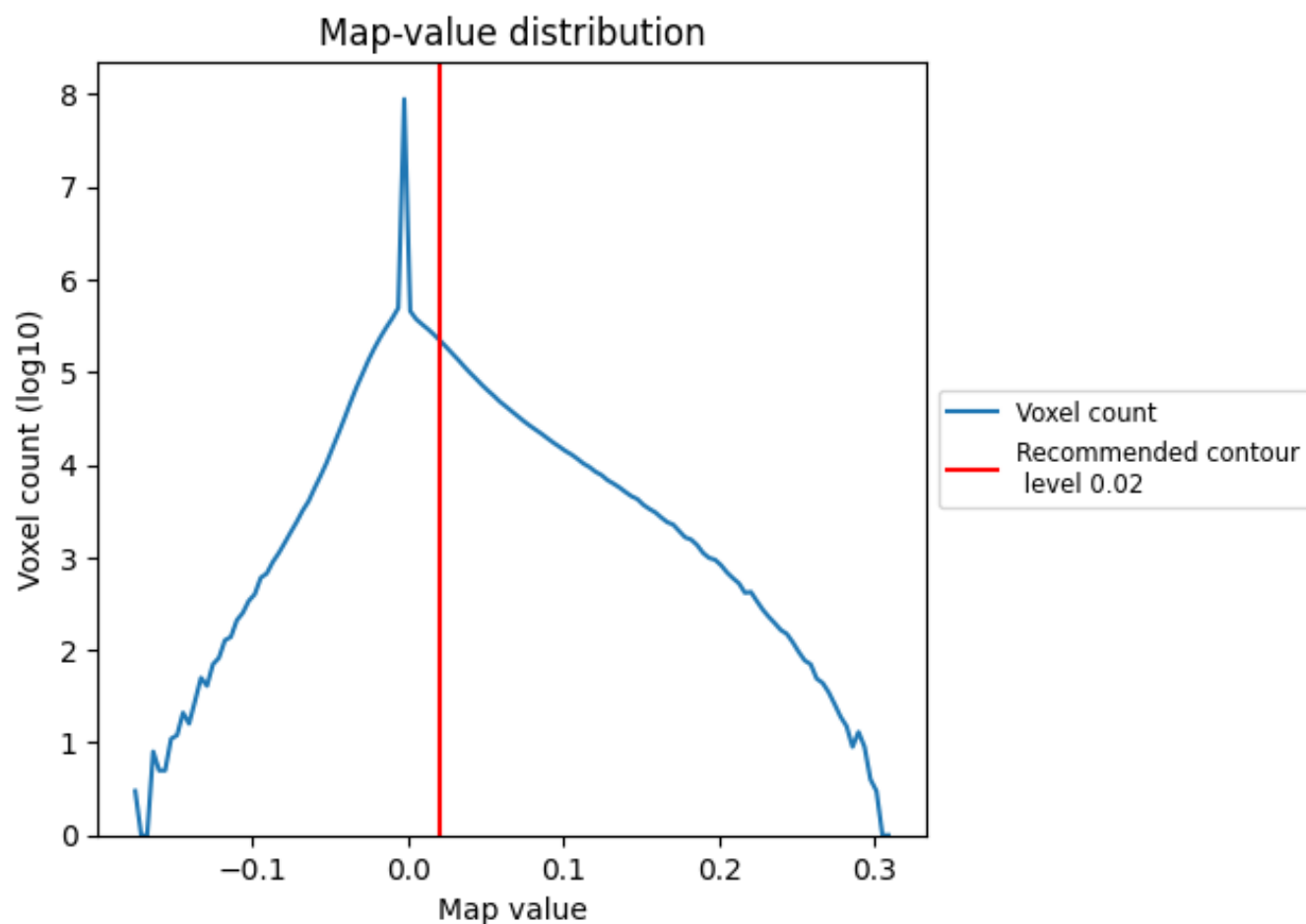
6.5 Mask visualisation

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

7 Map analysis [i](#)

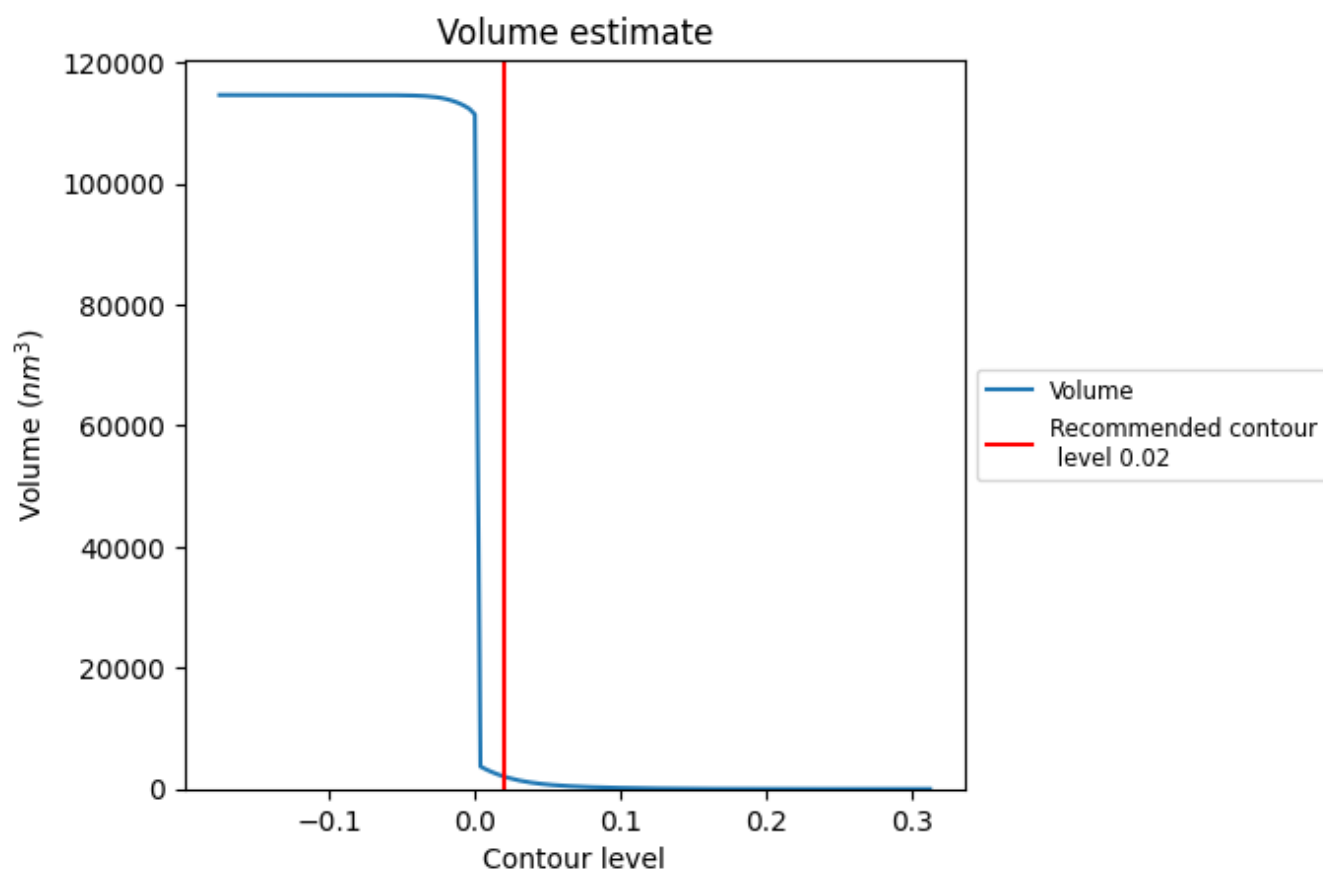
This section contains the results of statistical analysis of the map.

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.

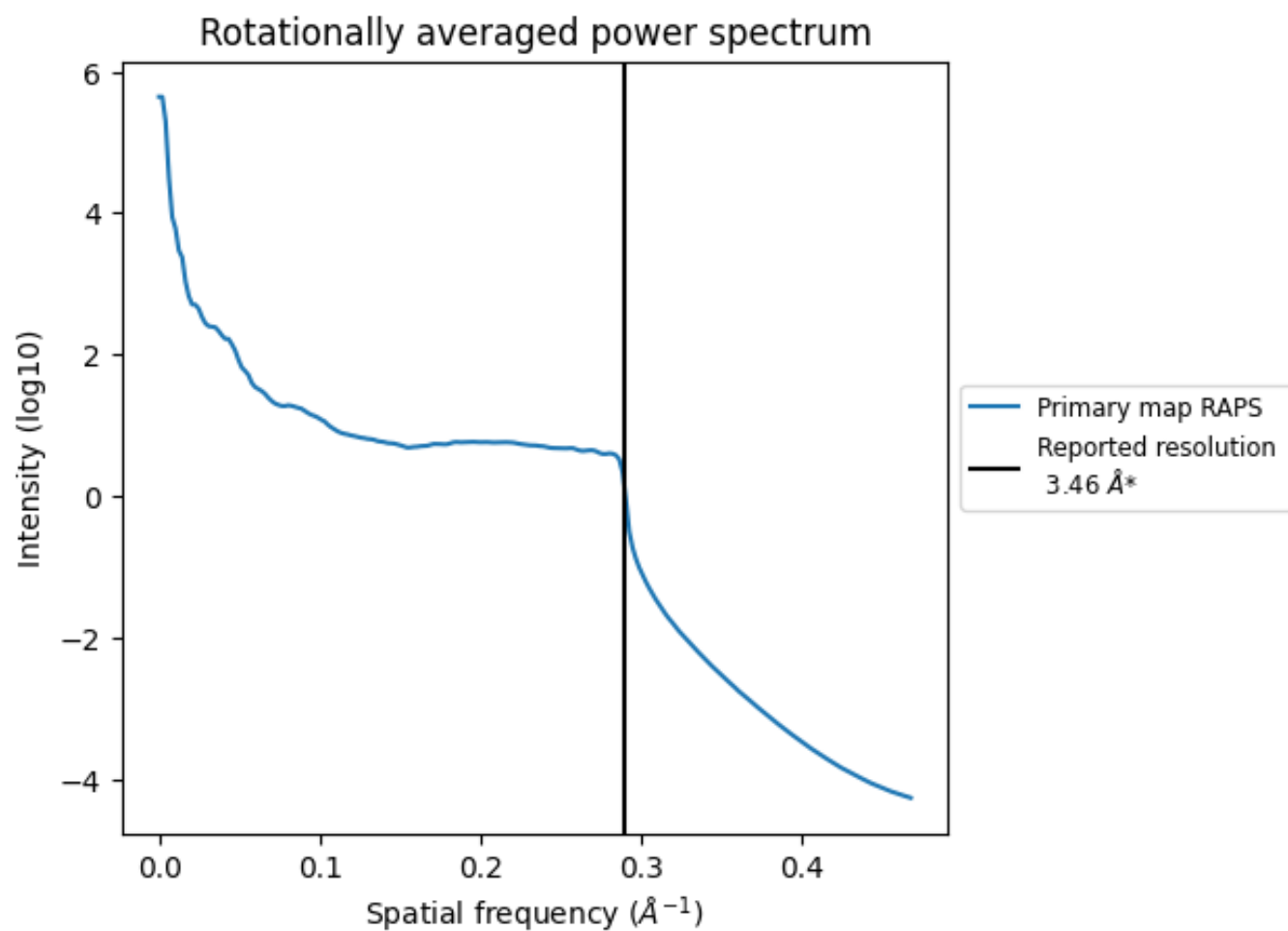
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2059 nm³; this corresponds to an approximate mass of 1860 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 ⓘ

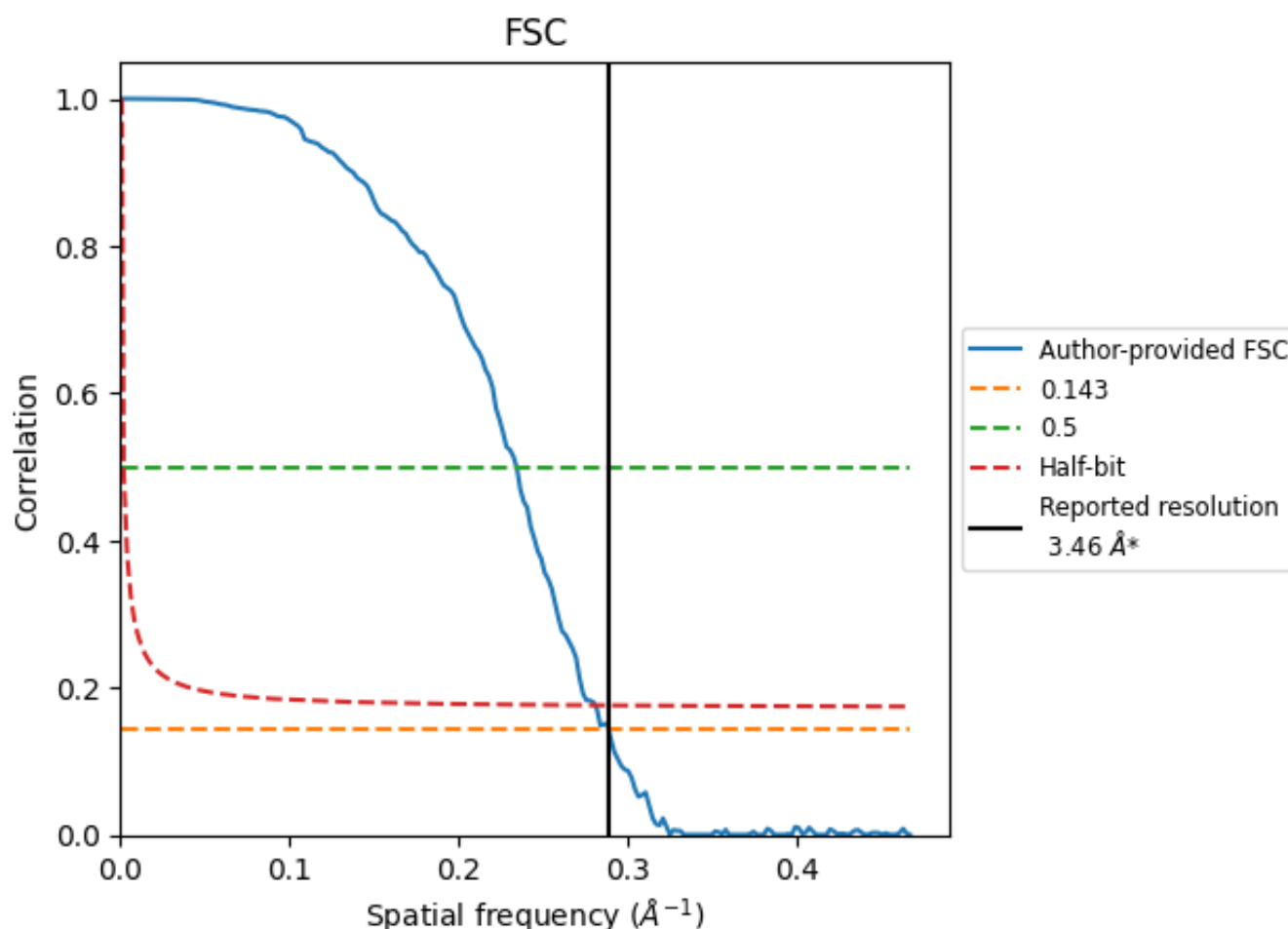


*Reported resolution corresponds to spatial frequency of 0.289 Å⁻¹

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 0.289 Å⁻¹

8.2 Resolution estimates [i](#)

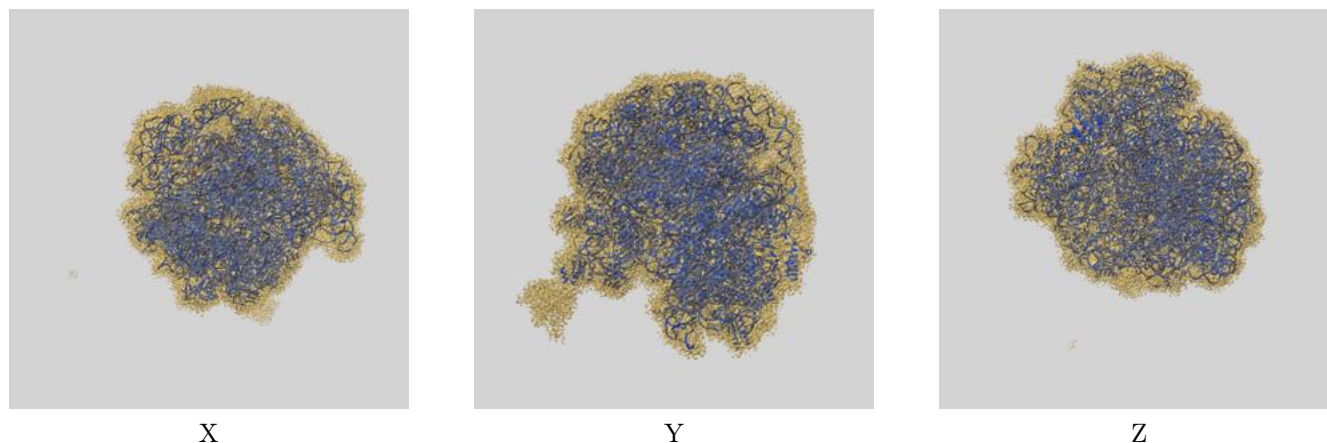
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.46	-	-
Author-provided FSC curve	3.46	4.27	3.56
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

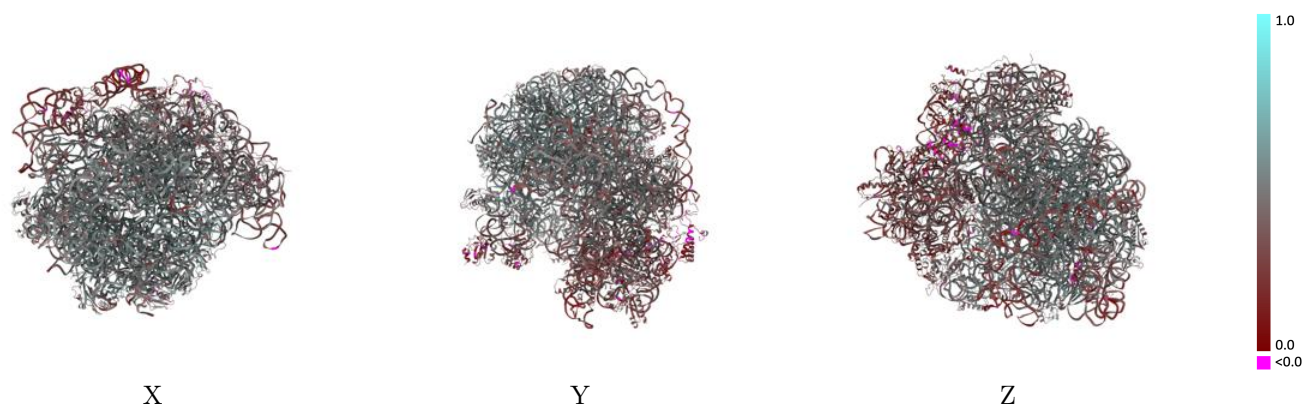
This section contains information regarding the fit between EMDB map EMD-8932 and PDB model 6DZI. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



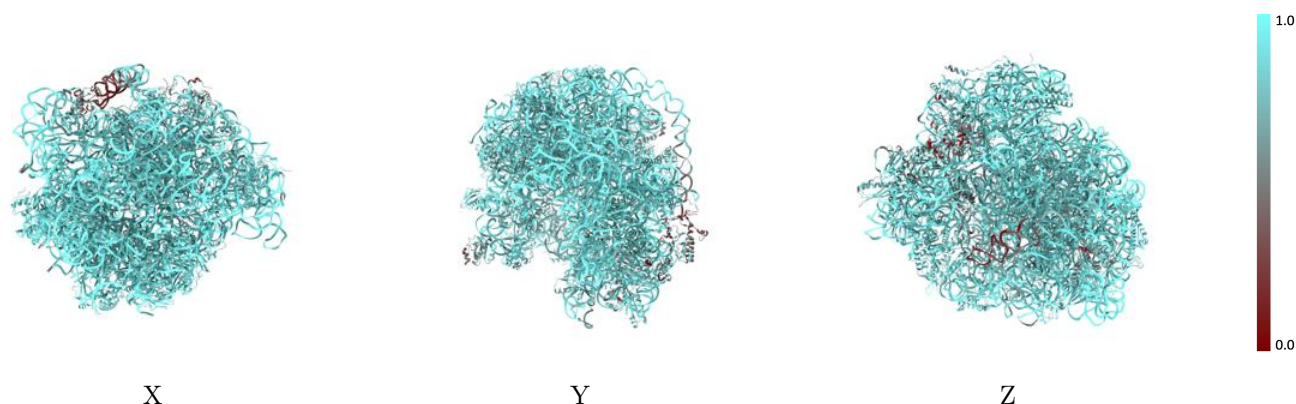
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



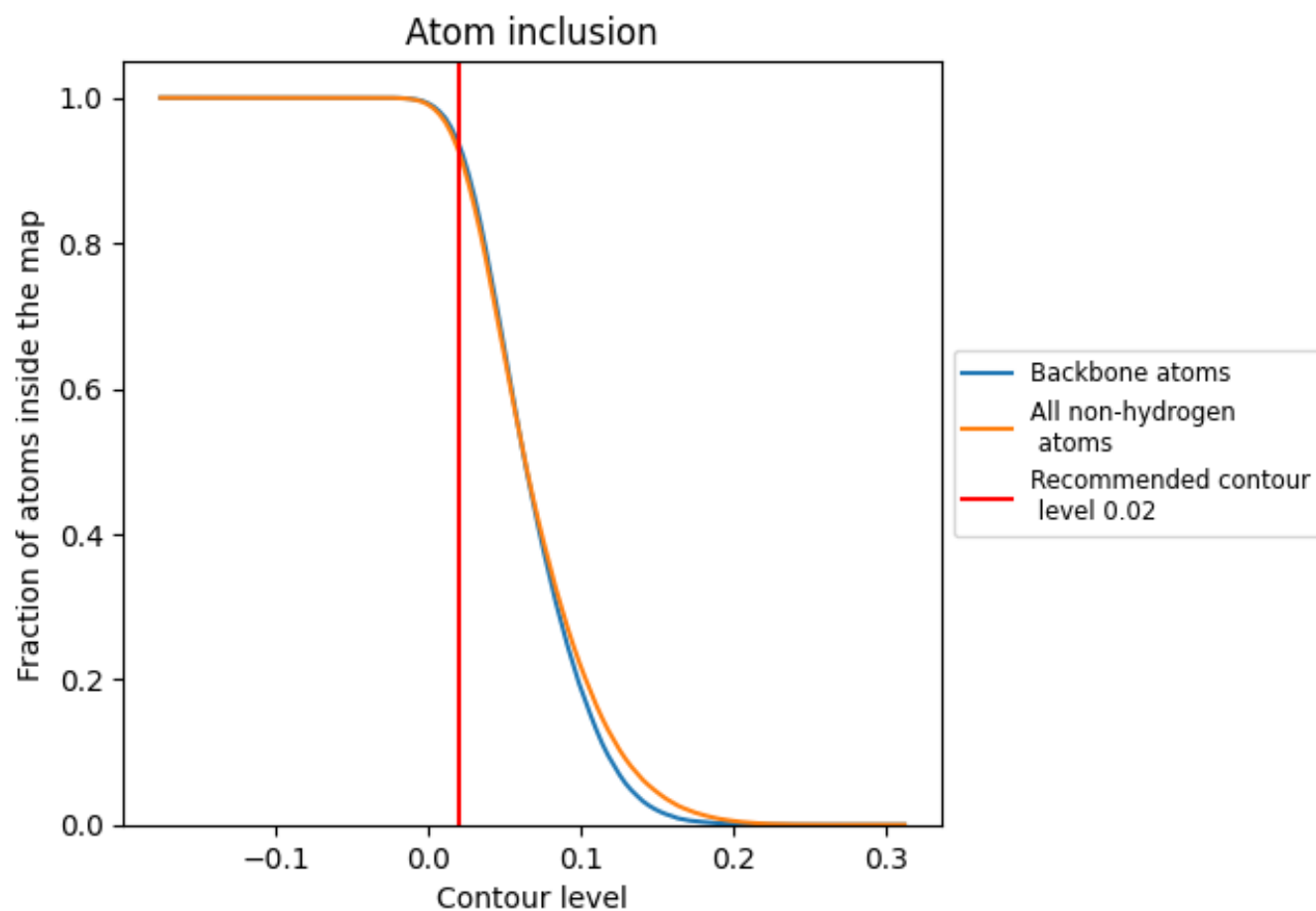
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ













































The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9277	 0.4380
3	 0.9106	 0.5190
4	 0.8929	 0.3240
5	 0.8733	 0.4370
6	 0.7957	 0.3270
7	 0.8875	 0.3630
8	 0.5225	 0.1690
9	 0.8693	 0.3250
A	 0.9617	 0.4760
B	 0.9826	 0.4620
C	 0.8919	 0.5100
D	 0.9333	 0.5100
E	 0.9213	 0.4830
F	 0.9158	 0.4010
G	 0.9261	 0.4290
H	 0.5669	 0.2940
I	 0.6284	 0.2350
J	 0.7937	 0.2780
K	 0.9377	 0.5090
L	 0.8934	 0.5020
M	 0.9292	 0.4940
N	 0.9112	 0.5050
O	 0.9247	 0.5030
P	 0.9469	 0.4560
Q	 0.8920	 0.4730
R	 0.9123	 0.5060
S	 0.9503	 0.5090
T	 0.9109	 0.4950
U	 0.9108	 0.4620
V	 0.9028	 0.4270
W	 0.8955	 0.4510
X	 0.9329	 0.5160
Y	 0.5182	 0.2720
Z	 0.9333	 0.4440
a	 0.9346	 0.4990



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Chain	Atom inclusion	Q-score
b	 0.9353	 0.4940
c	 0.7622	 0.3500
d	 0.8997	 0.5200
e	 0.9146	 0.5140
f	 0.9373	 0.5230
g	 0.8478	 0.2800
h	 0.9635	 0.4050
j	 0.7824	 0.4360
k	 0.8206	 0.3330
l	 0.8405	 0.3100
m	 0.8562	 0.3790
n	 0.8545	 0.3930
p	 0.8081	 0.3130
q	 0.9253	 0.4160
r	 0.7210	 0.3310
s	 0.8305	 0.3250
t	 0.8556	 0.4150
u	 0.8755	 0.4180
v	 0.8499	 0.3210
x	 0.8846	 0.4130
y	 0.8739	 0.4340
z	 0.8537	 0.3830