



wwPDB EM Validation Summary Report ⓘ

Apr 22, 2025 – 06:37 AM EDT

PDB ID : 8VIO / pdb_00008vio
EMDB ID : EMD-43267
Title : Structure of Mycobacterium smegmatis HflX bound to a 70S ribosome
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.;
Agrawal, R.K.
Deposited on : 2024-01-05
Resolution : 3.26 Å (reported)
Based on initial models : 6DZI, 5O61

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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

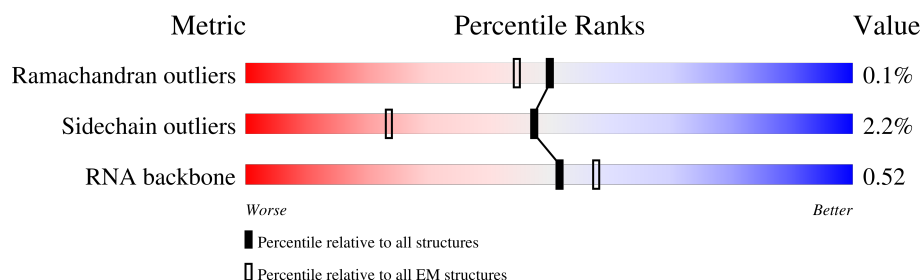
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.26 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.



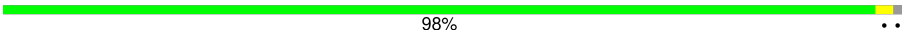

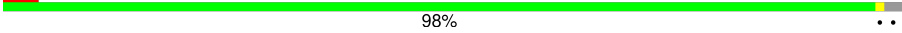
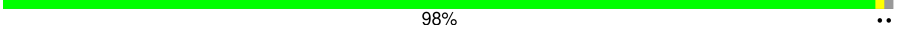


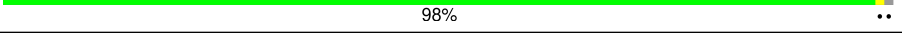



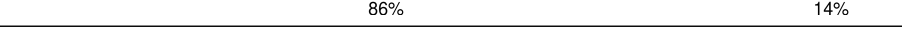
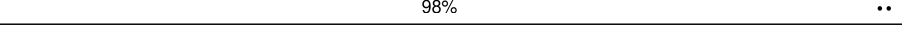
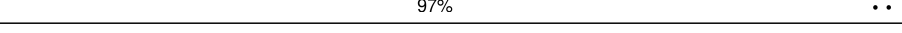
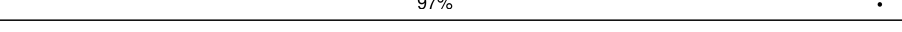
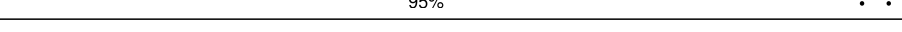
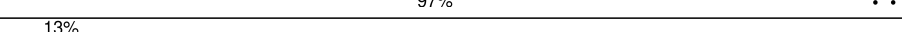
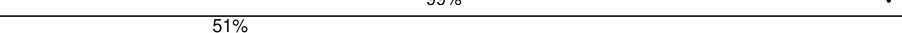








Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	Y	64	
2	c	55	
3	g	75	
4	r	84	
5	1	33	
6	j	201	
7	k	214	
8	l	96	

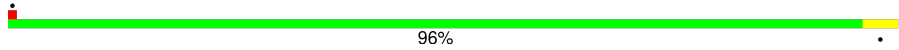
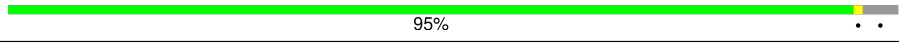
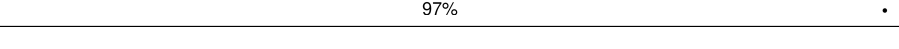

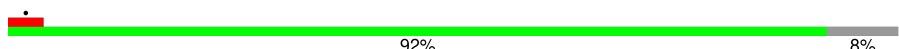


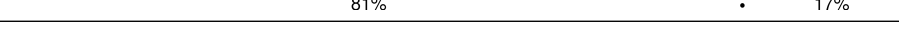
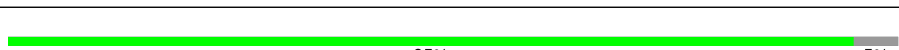
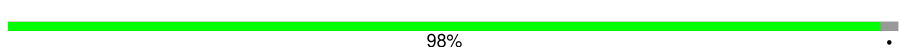
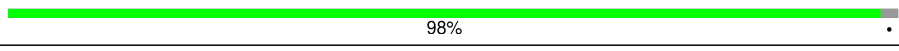
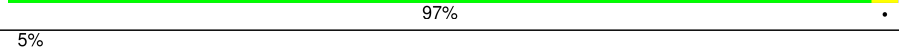

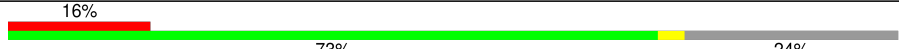
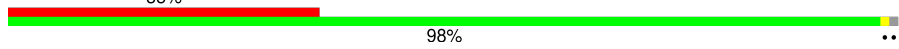

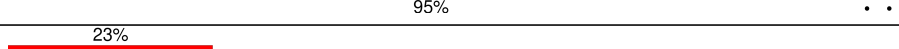


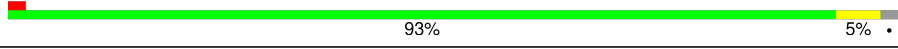




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Mol	Chain	Length	Quality of chain
9	n	132	 98%
10	q	138	 81% 17%
11	s	124	 98%
12	v	89	 98%
13	w	156	 8% 69% 28%
14	x	98	 5% 93%
15	z	86	 98%
16	h	277	 76% 81% 18%
17	3	24	 92%
18	A	3120	 80% 20%
19	B	118	 86% 14%
20	C	278	 98%
21	D	217	 97%
22	E	215	 97%
23	F	187	 95%
24	G	179	 97%
25	H	151	 13% 99%
26	I	175	 51% 70% 28%
27	J	142	 69% 92% 6%
28	K	147	 99%
29	L	122	 98%
30	M	147	 97%
31	N	138	 98%
32	O	199	 59% 41%
33	P	127	 98%

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Mol	Chain	Length	Quality of chain
34	Q	113	
35	R	129	
36	S	103	
37	T	153	
38	U	100	
39	V	105	
40	W	215	
41	X	88	
42	Z	77	
43	2	61	
44	b	57	
45	d	47	
46	e	64	
47	f	37	
48	5	77	
49	a	1528	
50	i	275	
51	m	156	
52	o	150	
53	p	101	
54	t	124	
55	y	93	
56	4	470	
57	u	61	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 152629 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 L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 2 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 3 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 4 is a protein called 30S Ribosomal Protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	r	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 5 is a protein called Conserved domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 6 is a protein called 30S ribosomal protein S4.

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

- Molecule 7 is a protein called 30S Ribosomal Protein S5.

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

- Molecule 8 is a protein called 30S ribosomal protein S6.

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

- Molecule 9 is a protein called 30S Ribosomal Protein S8.

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

- Molecule 10 is a protein called 30S ribosomal protein S11.

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

- Molecule 11 is a protein called 30S ribosomal protein S12.

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

- Molecule 12 is a protein called 30S Ribosomal Protein S15.

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

- Molecule 13 is a protein called 30S ribosomal protein S16.

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

- Molecule 14 is a protein called 30S ribosomal protein S17.

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

- Molecule 15 is a protein called 30S ribosomal protein S20.

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

- Molecule 16 is a protein called 30S Ribosomal Protein S2.

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

- Molecule 17 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	3	23	Total	C	N	O		0	0
			189	111	50	28			

- Molecule 18 is a RNA chain called 23S ribosomal RNA.

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

- Molecule 19 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 20 is a protein called 50S ribosomal protein L2.

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

- Molecule 21 is a protein called 50S ribosomal protein L3.

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

- Molecule 22 is a protein called 50S Ribosomal Protein L4.

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

- Molecule 23 is a protein called 50S Ribosomal Protein L5.

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

- Molecule 24 is a protein called 50S ribosomal protein L6.

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

- Molecule 25 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 26 is a protein called 50S ribosomal protein L10.

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

- Molecule 27 is a protein called 50S ribosomal protein L11.

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

- Molecule 28 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	K	145	Total	C	N	O	S	0	0
			1125	719	206	199	1		

- Molecule 29 is a protein called 50S ribosomal protein L14.

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

- Molecule 30 is a protein called 50S ribosomal protein L15.

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

- Molecule 31 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 32 is a protein called 50S ribosomal protein L17.

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

- Molecule 33 is a protein called 50S Ribosomal Protein L18.

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

- Molecule 34 is a protein called 50S ribosomal protein L19.

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

- Molecule 35 is a protein called 50S Ribosomal Protein L20.

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

- Molecule 36 is a protein called 50S Ribosomal Protein L21.

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

- Molecule 37 is a protein called 50S Ribosomal Protein L22.

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

- Molecule 38 is a protein called 50S Ribosomal Protein L23.

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

- Molecule 39 is a protein called 50S ribosomal protein L24.

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

- Molecule 40 is a protein called 50S ribosomal protein L25.

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

- Molecule 41 is a protein called 50S ribosomal protein L27.

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

- Molecule 42 is a protein called 50S ribosomal protein L29.

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

- Molecule 43 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 44 is a protein called 50S ribosomal protein L32.

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

- Molecule 45 is a protein called 50S ribosomal protein L34.

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

- Molecule 46 is a protein called 50S ribosomal protein L35.

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

- Molecule 47 is a protein called 50S ribosomal protein L36.

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

- Molecule 48 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 49 is a RNA chain called 16S ribosomal RNA.

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

- Molecule 50 is a protein called 30S ribosomal protein S3.

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

- Molecule 51 is a protein called 30S ribosomal protein S7.

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

- Molecule 52 is a protein called 30S ribosomal protein S9.

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

- Molecule 53 is a protein called 30S ribosomal protein S10.

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

- Molecule 54 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	t	108	Total	C	N	O	S	0	0
			877	535	180	159	3		

- Molecule 55 is a protein called 30S ribosomal protein S19.

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

- Molecule 56 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	267	Total	C	N	O	S	0	0
			2058	1275	383	397	3		

- Molecule 57 is a protein called 30S Ribosomal Protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	u	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

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 L28

Chain Y: 



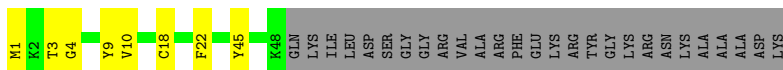
- Molecule 2: 50S Ribosomal Protein L33

Chain c: 



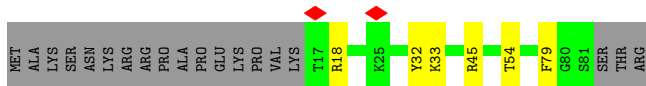
- Molecule 3: 50S Ribosomal Protein L31

Chain g: 



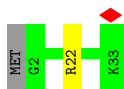
- Molecule 4: 30S Ribosomal Protein S18

Chain r: 

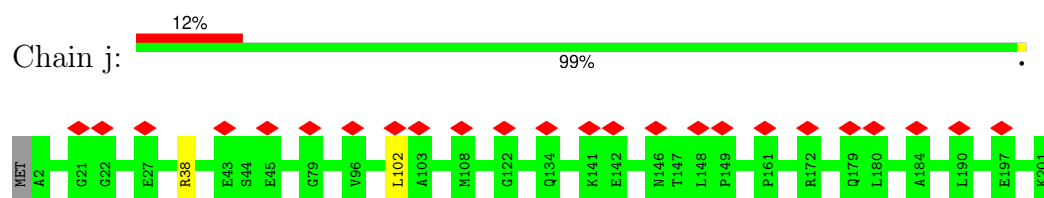


- Molecule 5: Conserved domain protein

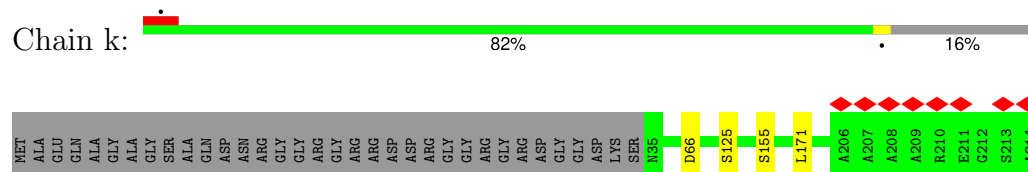
Chain 1: 



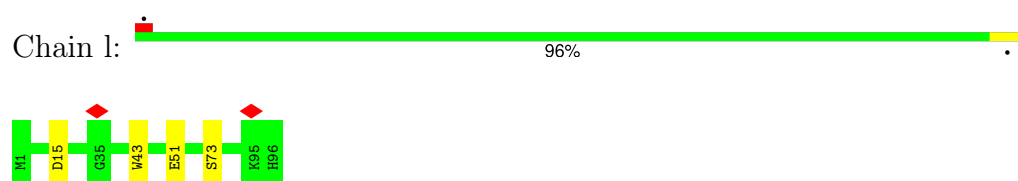
- Molecule 6: 30S ribosomal protein S4



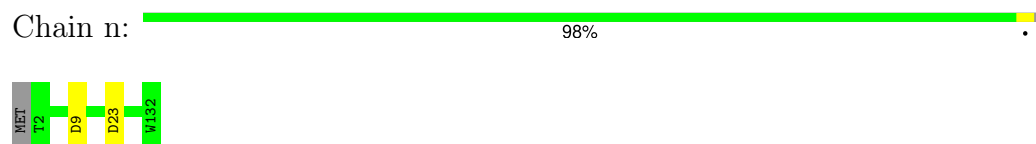
- Molecule 7: 30S Ribosomal Protein S5



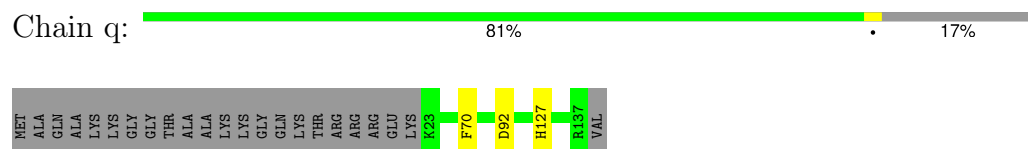
- Molecule 8: 30S ribosomal protein S6



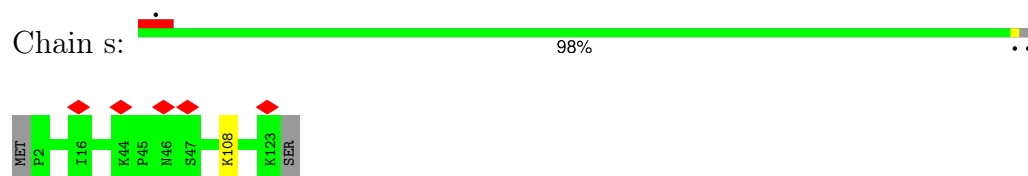
- Molecule 9: 30S Ribosomal Protein S8



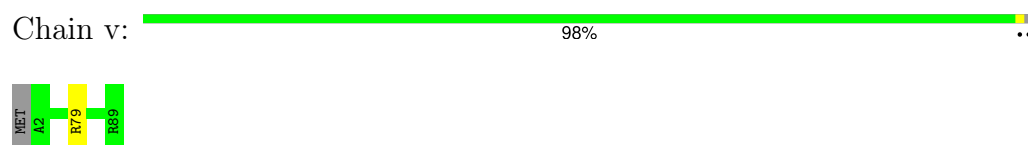
- Molecule 10: 30S ribosomal protein S11



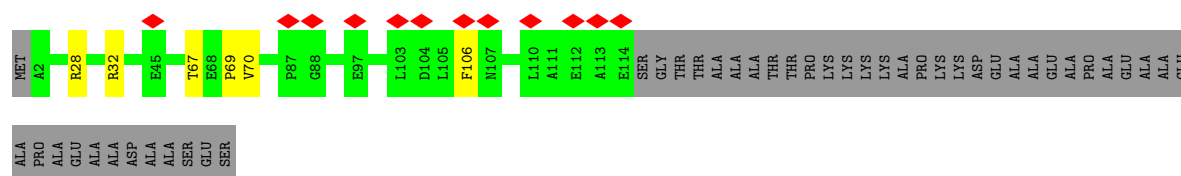
- Molecule 11: 30S ribosomal protein S12



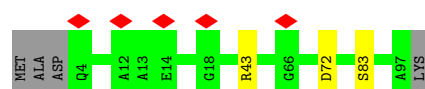
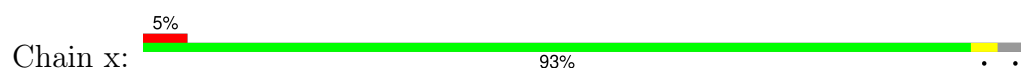
- Molecule 12: 30S Ribosomal Protein S15



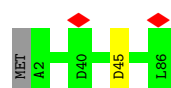
- Molecule 13: 30S ribosomal protein S16



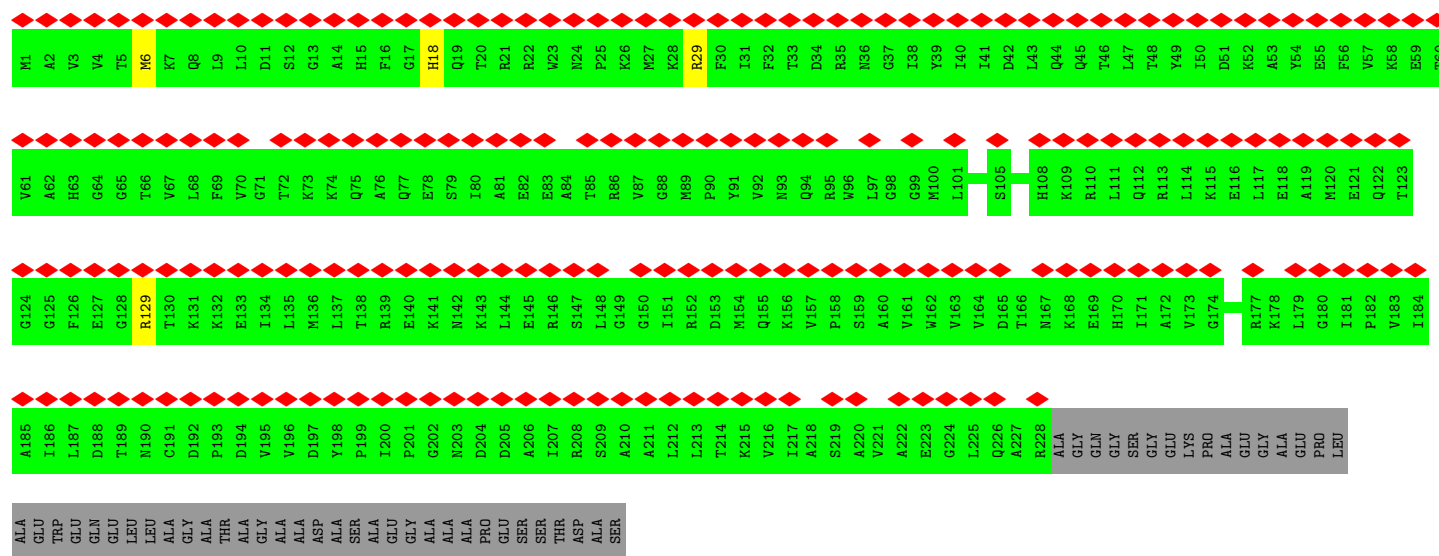
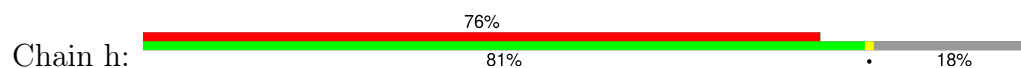
- Molecule 14: 30S ribosomal protein S17



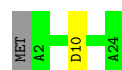
- Molecule 15: 30S ribosomal protein S20



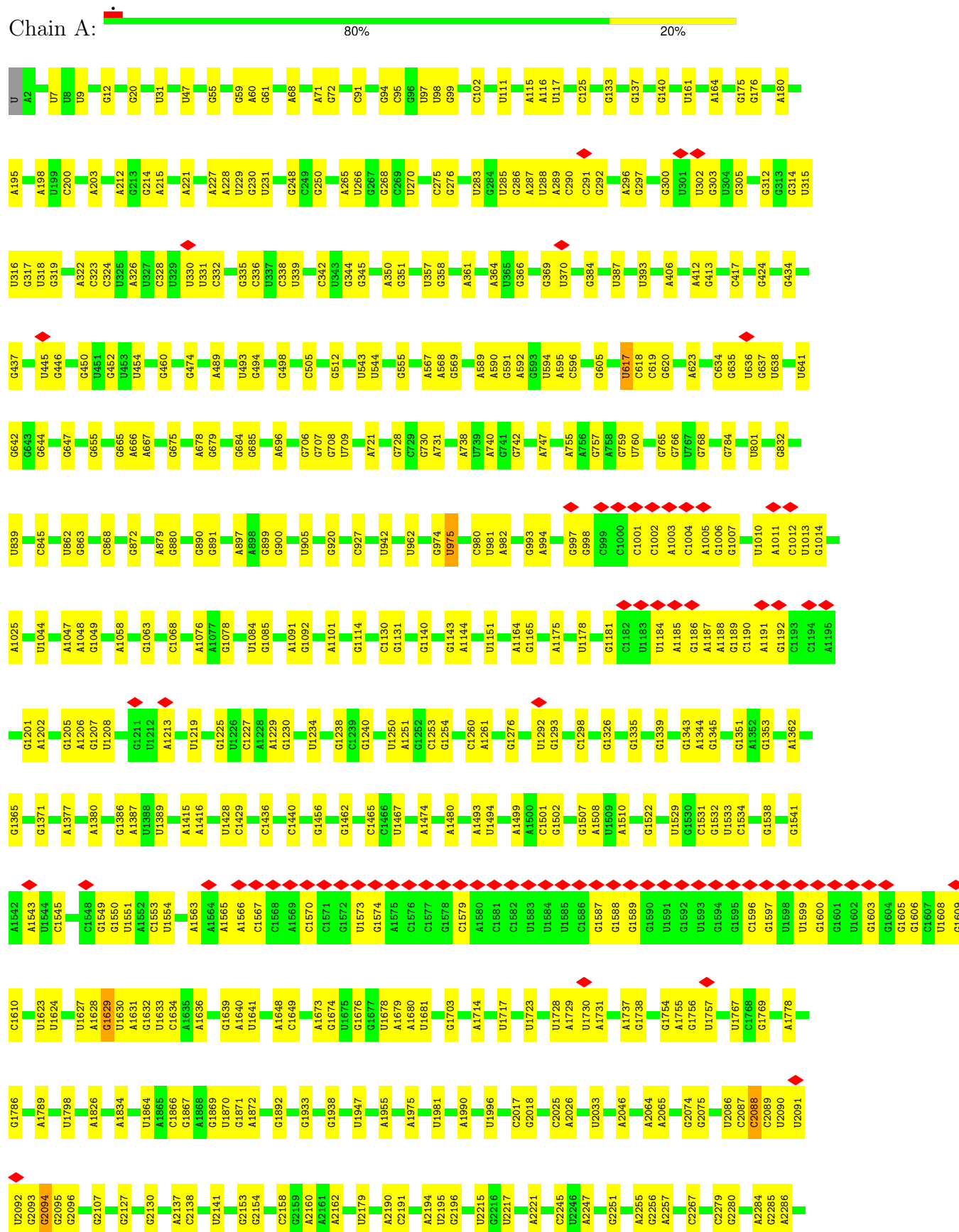
- Molecule 16: 30S Ribosomal Protein S2



- Molecule 17: 50S Ribosomal Protein L37



● Molecule 18: 23S ribosomal RNA

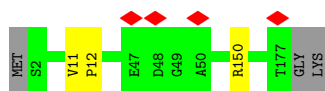






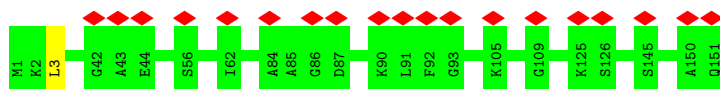
- Molecule 24: 50S ribosomal protein L6

Chain G: 97%



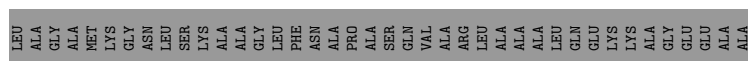
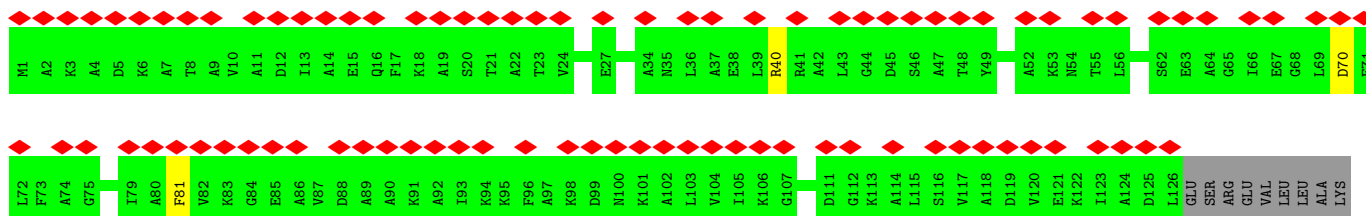
- Molecule 25: 50S ribosomal protein L9

Chain H: 13% 99%



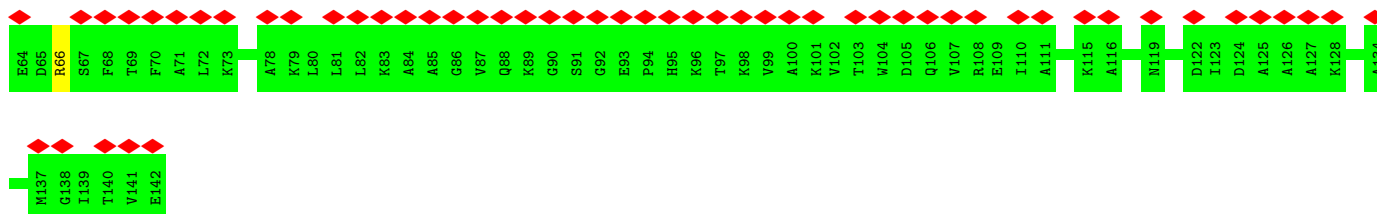
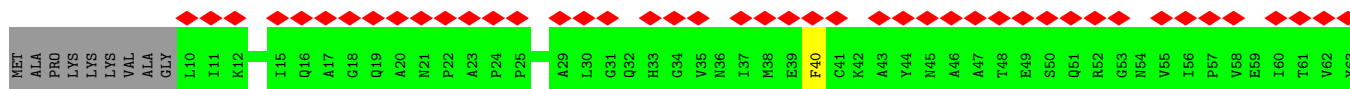
- Molecule 26: 50S ribosomal protein L10

Chain I: 51% 70% 28%



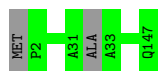
- Molecule 27: 50S ribosomal protein L11

Chain J: 69% 92% 6%



- Molecule 28: 50S Ribosomal Protein L13

Chain K: 99%



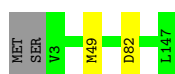
- Molecule 29: 50S ribosomal protein L14

Chain L: 98% .



- Molecule 30: 50S ribosomal protein L15

Chain M: 97% ..



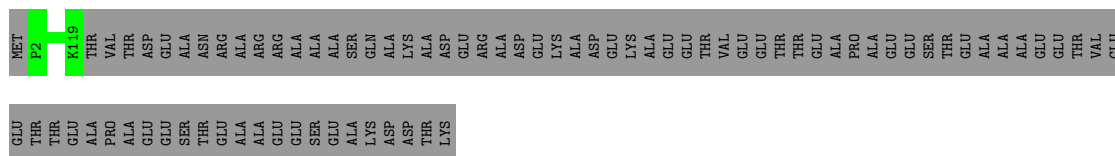
- Molecule 31: Large ribosomal subunit protein uL16

Chain N: 98% ..



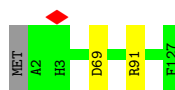
- Molecule 32: 50S ribosomal protein L17

Chain O: 59% 41%



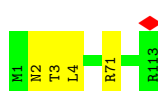
- Molecule 33: 50S Ribosomal Protein L18

Chain P: 98% ..

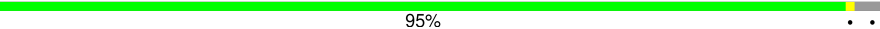


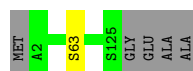
- Molecule 34: 50S ribosomal protein L19

Chain Q: 96% .



- Molecule 35: 50S Ribosomal Protein L20

Chain R:  95%



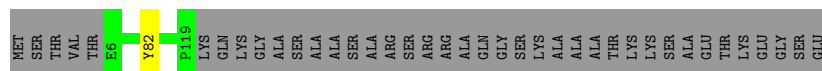
- Molecule 36: 50S Ribosomal Protein L21

Chain S:  97%



- Molecule 37: 50S Ribosomal Protein L22

Chain T:  74% 25%



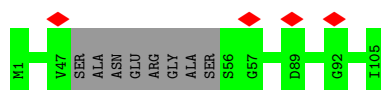
- Molecule 38: 50S Ribosomal Protein L23

Chain U:  96%



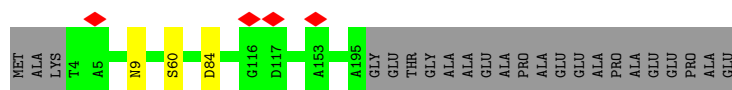
- Molecule 39: 50S ribosomal protein L24

Chain V:  92% 8%




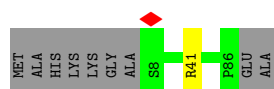
- Molecule 40: 50S ribosomal protein L25

Chain W:  88% 11%




- Molecule 41: 50S ribosomal protein L27

Chain X:  89% 10%



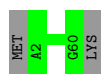
- Molecule 42: 50S ribosomal protein L29

Chain Z:  81% 17%



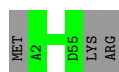
- Molecule 43: 50S ribosomal protein L30

Chain 2:  97%



- Molecule 44: 50S ribosomal protein L32

Chain b:  95% 5%



- Molecule 45: 50S ribosomal protein L34

Chain d:  98%



- Molecule 46: 50S ribosomal protein L35

Chain e:  98%



- Molecule 47: 50S ribosomal protein L36

Chain f:  97%



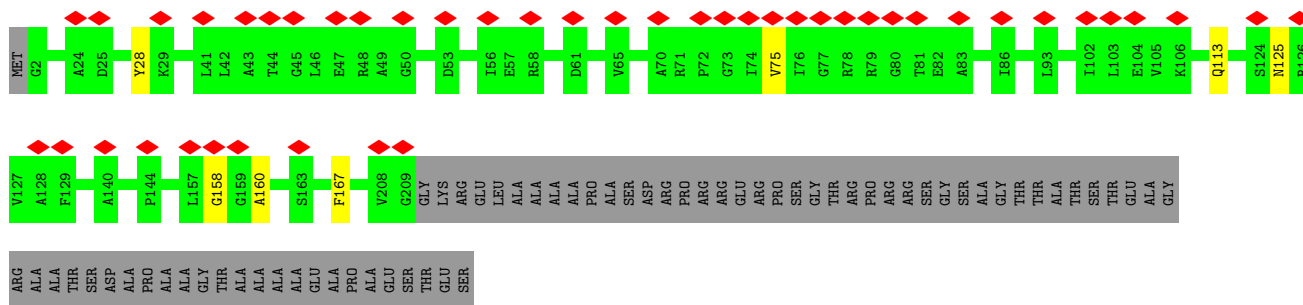
- Molecule 48: E-tRNA

Chain 5:  5% 73% 27%

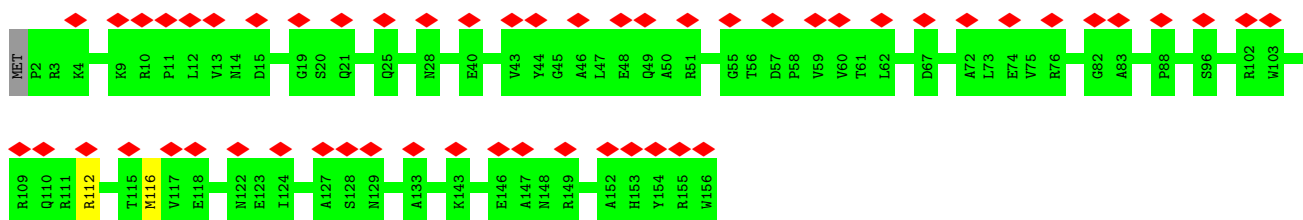


- Molecule 49: 16S ribosomal RNA

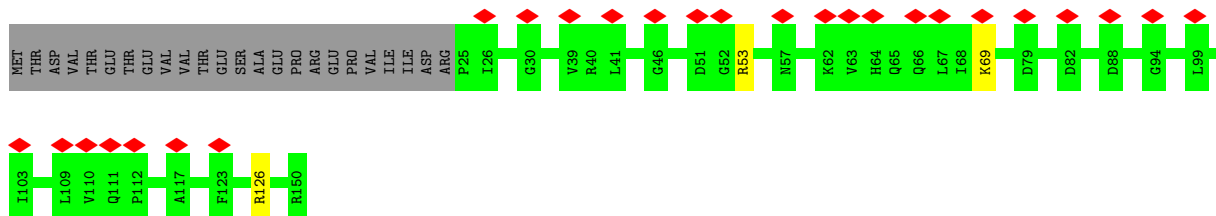
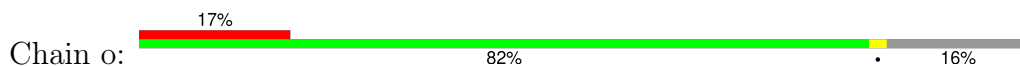




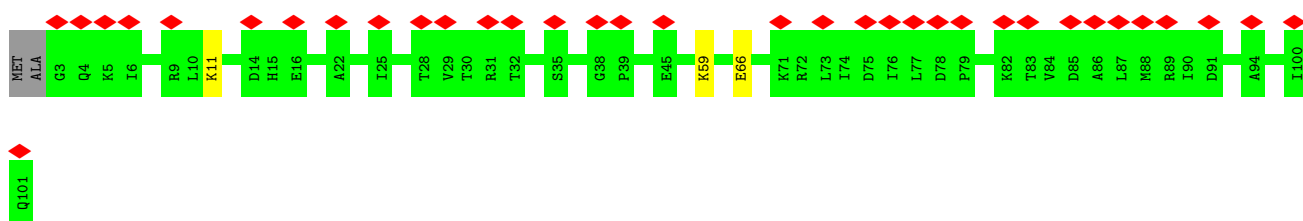
- Molecule 51: 30S ribosomal protein S7



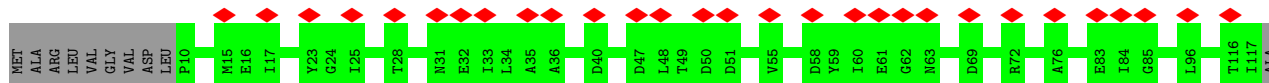
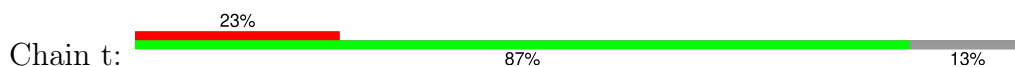
- Molecule 52: 30S ribosomal protein S9



- Molecule 53: 30S ribosomal protein S10



- Molecule 54: 30S ribosomal protein S13



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	48443	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 ($e^-/\text{\AA}^2$)	51.22	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.845	Depositor
Minimum map value	-1.224	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.083	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	433.19998, 433.19998, 433.19998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.083, 1.083, 1.083	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	Y	0.78	0/478	0.73	0/641
2	c	0.63	0/413	0.67	0/553
3	g	0.42	0/372	0.68	0/503
4	r	0.60	0/518	0.64	0/693
5	l	0.26	0/280	0.66	0/359
6	j	0.27	0/1672	0.56	0/2251
7	k	0.31	0/1312	0.57	1/1772 (0.1%)
8	l	0.31	0/782	0.55	0/1059
9	n	0.32	0/1025	0.56	0/1385
10	q	0.27	0/873	0.51	0/1180
11	s	0.29	0/969	0.60	0/1294
12	v	0.29	0/729	0.56	0/977
13	w	0.78	2/908 (0.2%)	0.91	2/1226 (0.2%)
14	x	0.27	0/759	0.59	0/1016
15	z	0.25	0/663	0.51	0/882
16	h	0.25	0/1822	0.53	0/2457
17	3	0.27	0/191	0.59	0/247
18	A	0.59	0/75001	0.84	23/117027 (0.0%)
19	B	0.46	0/2821	0.84	0/4396
20	C	0.37	0/2153	0.58	0/2895
21	D	0.39	0/1609	0.60	0/2165
22	E	0.34	0/1592	0.53	0/2153
23	F	0.49	2/1467 (0.1%)	0.93	5/1973 (0.3%)
24	G	0.35	0/1369	0.69	3/1848 (0.2%)
25	H	0.27	0/1027	0.53	0/1398
26	I	0.26	0/925	0.45	0/1246
27	J	0.24	0/1006	0.48	0/1364
28	K	0.37	0/1151	0.50	0/1557
29	L	0.37	0/946	0.57	0/1268
30	M	0.35	0/1091	0.55	0/1457
31	N	0.31	0/1118	0.54	0/1506
32	O	0.35	0/945	0.55	0/1267
33	P	0.29	0/966	0.56	0/1298
34	Q	0.53	0/921	0.63	0/1236

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	R	0.38	0/1000	0.54	0/1341
36	S	0.37	0/764	0.51	0/1030
37	T	0.37	0/887	0.56	0/1204
38	U	0.35	0/766	0.53	0/1030
39	V	0.32	0/738	0.51	0/987
40	W	0.27	0/1443	0.51	0/1970
41	X	0.35	0/595	0.58	0/798
42	Z	0.31	0/534	0.58	0/713
43	2	0.33	0/477	0.54	0/640
44	b	0.34	0/427	0.62	0/572
45	d	0.35	0/380	0.68	0/500
46	e	0.31	0/507	0.61	0/672
47	f	0.32	0/303	0.58	0/401
48	5	0.33	0/1835	0.88	0/2859
49	a	0.82	6/36309 (0.0%)	0.90	29/56657 (0.1%)
50	i	0.27	0/1684	0.60	0/2261
51	m	0.26	0/1252	0.58	0/1690
52	o	0.26	0/1012	0.60	0/1362
53	p	0.26	0/802	0.60	0/1086
54	t	0.25	0/884	0.64	0/1180
55	y	0.26	0/680	0.52	0/915
56	4	0.25	0/2085	0.56	0/2829
57	u	0.43	0/488	0.59	0/650
All	All	0.59	10/165726 (0.0%)	0.80	63/247896 (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
34	Q	0	1
50	i	0	3
All	All	0	4

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	a	587	A	N3-C4	77.76	1.81	1.34
49	a	587	A	C6-N1	64.80	1.80	1.35
49	a	587	A	N1-C2	50.10	1.79	1.34
49	a	587	A	C2-N3	48.63	1.77	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	a	587	A	C5-C4	44.03	1.69	1.38

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	a	587	A	N1-C2-N3	-48.87	104.86	129.30
49	a	587	A	C2-N3-C4	35.31	128.25	110.60
49	a	587	A	C6-N1-C2	21.22	131.33	118.60
13	w	32	ARG	CD-NE-CZ	20.47	152.26	123.60
23	F	116	PRO	CA-CB-CG	-19.04	67.83	104.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	Q	4	LEU	Mainchain
50	i	158	GLY	Peptide
50	i	160	ALA	Peptide
50	i	75	VAL	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	
1	Y	61/64 (95%)	49 (80%)	12 (20%)	0	100	100
2	c	47/55 (86%)	46 (98%)	1 (2%)	0	100	100
3	g	46/75 (61%)	33 (72%)	10 (22%)	3 (6%)	1	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	r	63/84 (75%)	53 (84%)	10 (16%)	0	100	100
5	l	30/33 (91%)	30 (100%)	0	0	100	100
6	j	198/201 (98%)	167 (84%)	31 (16%)	0	100	100
7	k	178/214 (83%)	168 (94%)	10 (6%)	0	100	100
8	l	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
9	n	129/132 (98%)	124 (96%)	5 (4%)	0	100	100
10	q	113/138 (82%)	103 (91%)	10 (9%)	0	100	100
11	s	120/124 (97%)	106 (88%)	14 (12%)	0	100	100
12	v	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
13	w	111/156 (71%)	91 (82%)	20 (18%)	0	100	100
14	x	92/98 (94%)	85 (92%)	7 (8%)	0	100	100
15	z	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
16	h	226/277 (82%)	204 (90%)	22 (10%)	0	100	100
17	3	21/24 (88%)	21 (100%)	0	0	100	100
20	C	273/278 (98%)	258 (94%)	15 (6%)	0	100	100
21	D	212/217 (98%)	195 (92%)	16 (8%)	1 (0%)	25	56
22	E	207/215 (96%)	203 (98%)	4 (2%)	0	100	100
23	F	180/187 (96%)	165 (92%)	15 (8%)	0	100	100
24	G	174/179 (97%)	165 (95%)	9 (5%)	0	100	100
25	H	149/151 (99%)	141 (95%)	8 (5%)	0	100	100
26	I	124/175 (71%)	115 (93%)	9 (7%)	0	100	100
27	J	131/142 (92%)	112 (86%)	19 (14%)	0	100	100
28	K	141/147 (96%)	133 (94%)	8 (6%)	0	100	100
29	L	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
30	M	143/147 (97%)	127 (89%)	16 (11%)	0	100	100
31	N	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
32	O	116/199 (58%)	110 (95%)	6 (5%)	0	100	100
33	P	124/127 (98%)	120 (97%)	4 (3%)	0	100	100
34	Q	111/113 (98%)	101 (91%)	10 (9%)	0	100	100
35	R	122/129 (95%)	117 (96%)	5 (4%)	0	100	100
36	S	98/103 (95%)	94 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	T	112/153 (73%)	107 (96%)	5 (4%)	0	100	100
38	U	95/100 (95%)	89 (94%)	6 (6%)	0	100	100
39	V	93/105 (89%)	84 (90%)	9 (10%)	0	100	100
40	W	190/215 (88%)	182 (96%)	8 (4%)	0	100	100
41	X	77/88 (88%)	74 (96%)	3 (4%)	0	100	100
42	Z	62/77 (80%)	62 (100%)	0	0	100	100
43	2	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
44	b	52/57 (91%)	52 (100%)	0	0	100	100
45	d	44/47 (94%)	44 (100%)	0	0	100	100
46	e	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
47	f	35/37 (95%)	35 (100%)	0	0	100	100
50	i	206/275 (75%)	173 (84%)	33 (16%)	0	100	100
51	m	153/156 (98%)	131 (86%)	22 (14%)	0	100	100
52	o	124/150 (83%)	103 (83%)	21 (17%)	0	100	100
53	p	97/101 (96%)	89 (92%)	8 (8%)	0	100	100
54	t	106/124 (86%)	88 (83%)	18 (17%)	0	100	100
55	y	80/93 (86%)	67 (84%)	13 (16%)	0	100	100
56	4	265/470 (56%)	250 (94%)	15 (6%)	0	100	100
57	u	58/61 (95%)	48 (83%)	10 (17%)	0	100	100
All	All	6224/7149 (87%)	5721 (92%)	499 (8%)	4 (0%)	50	77

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	g	4	GLY
3	g	3	THR
21	D	156	THR
3	g	10	VAL

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	Y	50/51 (98%)	46 (92%)	4 (8%)	10	31
2	c	47/52 (90%)	43 (92%)	4 (8%)	8	29
3	g	43/63 (68%)	38 (88%)	5 (12%)	4	18
4	r	55/72 (76%)	49 (89%)	6 (11%)	5	20
5	l	30/31 (97%)	29 (97%)	1 (3%)	33	58
6	j	175/176 (99%)	173 (99%)	2 (1%)	70	81
7	k	127/147 (86%)	124 (98%)	3 (2%)	44	66
8	l	85/85 (100%)	81 (95%)	4 (5%)	22	49
9	n	107/108 (99%)	105 (98%)	2 (2%)	52	71
10	q	89/105 (85%)	86 (97%)	3 (3%)	32	57
11	s	103/105 (98%)	102 (99%)	1 (1%)	73	82
12	v	76/77 (99%)	75 (99%)	1 (1%)	65	78
13	w	92/118 (78%)	87 (95%)	5 (5%)	18	45
14	x	80/83 (96%)	77 (96%)	3 (4%)	28	54
15	z	69/70 (99%)	68 (99%)	1 (1%)	62	77
16	h	191/218 (88%)	187 (98%)	4 (2%)	48	69
17	3	18/19 (95%)	17 (94%)	1 (6%)	17	44
20	C	215/218 (99%)	212 (99%)	3 (1%)	62	77
21	D	160/163 (98%)	157 (98%)	3 (2%)	52	71
22	E	169/173 (98%)	169 (100%)	0	100	100
23	F	151/156 (97%)	148 (98%)	3 (2%)	50	70
24	G	148/150 (99%)	147 (99%)	1 (1%)	81	87
25	H	90/116 (78%)	89 (99%)	1 (1%)	70	81
26	I	89/120 (74%)	86 (97%)	3 (3%)	32	57
27	J	102/108 (94%)	100 (98%)	2 (2%)	50	70
28	K	119/120 (99%)	119 (100%)	0	100	100
29	L	100/100 (100%)	97 (97%)	3 (3%)	36	60
30	M	112/114 (98%)	110 (98%)	2 (2%)	54	72
31	N	114/116 (98%)	113 (99%)	1 (1%)	75	84
32	O	97/158 (61%)	97 (100%)	0	100	100
33	P	93/94 (99%)	91 (98%)	2 (2%)	47	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Q	100/100 (100%)	97 (97%)	3 (3%)	36	60
35	R	97/99 (98%)	96 (99%)	1 (1%)	73	82
36	S	81/83 (98%)	81 (100%)	0	100	100
37	T	90/117 (77%)	89 (99%)	1 (1%)	70	81
38	U	83/85 (98%)	82 (99%)	1 (1%)	67	79
39	V	81/86 (94%)	81 (100%)	0	100	100
40	W	155/168 (92%)	152 (98%)	3 (2%)	52	71
41	X	58/63 (92%)	57 (98%)	1 (2%)	56	73
42	Z	58/66 (88%)	56 (97%)	2 (3%)	32	57
43	2	52/54 (96%)	52 (100%)	0	100	100
44	b	43/46 (94%)	43 (100%)	0	100	100
45	d	35/36 (97%)	35 (100%)	0	100	100
46	e	53/54 (98%)	53 (100%)	0	100	100
47	f	35/35 (100%)	34 (97%)	1 (3%)	37	61
50	i	170/212 (80%)	166 (98%)	4 (2%)	44	66
51	m	131/132 (99%)	129 (98%)	2 (2%)	60	75
52	o	102/125 (82%)	99 (97%)	3 (3%)	37	61
53	p	89/90 (99%)	86 (97%)	3 (3%)	32	57
54	t	93/104 (89%)	93 (100%)	0	100	100
55	y	73/84 (87%)	69 (94%)	4 (6%)	18	44
56	4	220/372 (59%)	215 (98%)	5 (2%)	45	67
57	u	49/50 (98%)	46 (94%)	3 (6%)	15	41
All	All	5144/5747 (90%)	5033 (98%)	111 (2%)	47	68

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	F	63	ASP
57	u	44	LEU
31	N	49	SER
57	u	32	SER
55	y	38	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
24	G	98	GLN
57	u	25	ASN
33	P	22	HIS
57	u	11	ASN
52	o	111	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
18	A	3118/3120 (99%)	610 (19%)	25 (0%)
19	B	117/118 (99%)	15 (12%)	1 (0%)
48	5	76/77 (98%)	21 (27%)	2 (2%)
49	a	1510/1528 (98%)	448 (29%)	0
All	All	4821/4843 (99%)	1094 (22%)	28 (0%)

5 of 1094 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
18	A	7	U
18	A	9	U
18	A	12	G
18	A	20	G
18	A	31	U

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	A	1186	G
48	5	75	C
18	A	1629	G
18	A	2626	U
18	A	1573	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

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.

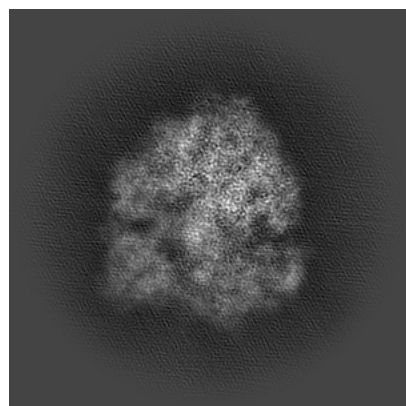
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43267. These allow visual inspection of the internal detail of the map and identification of artifacts.

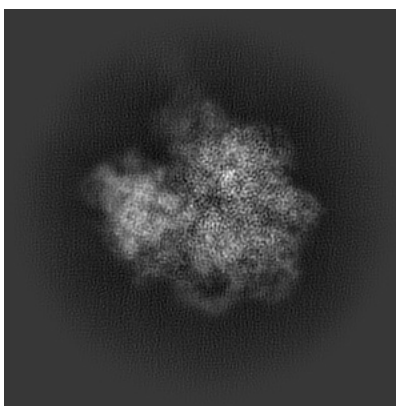
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

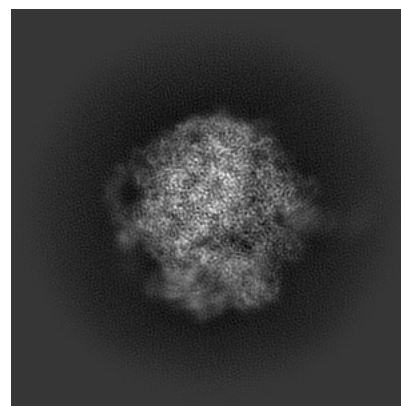
6.1.1 Primary map



X

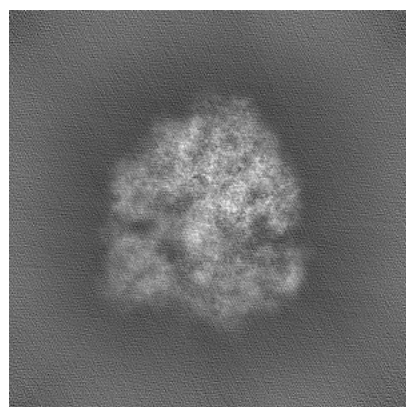


Y

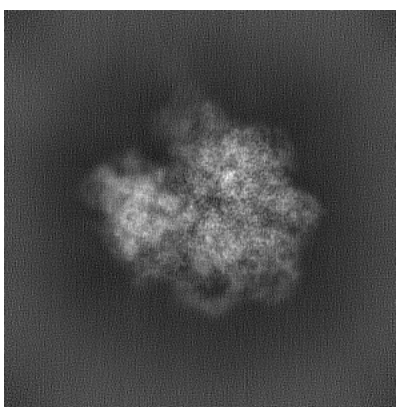


Z

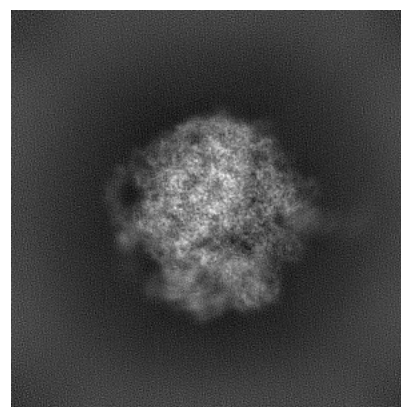
6.1.2 Raw map



X



Y

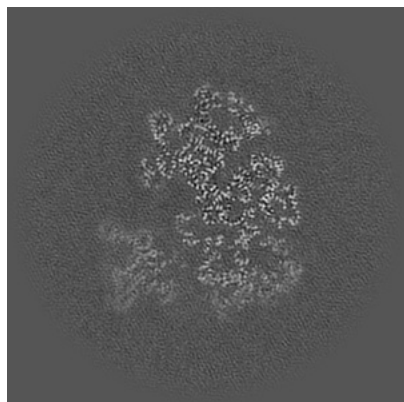


Z

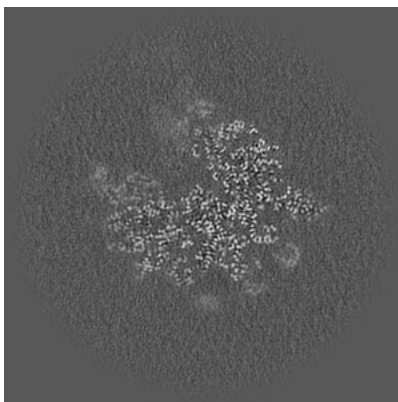
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

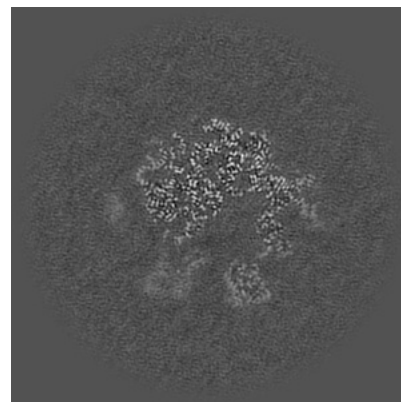
6.2.1 Primary map



X Index: 200

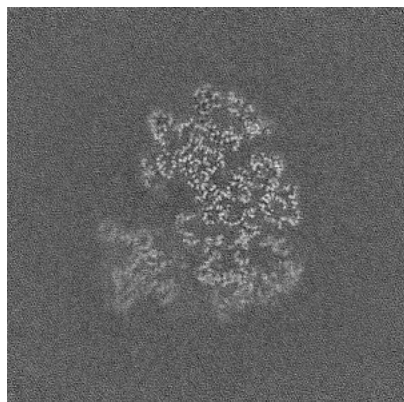


Y Index: 200

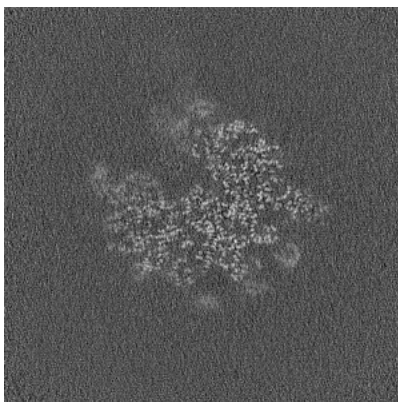


Z Index: 200

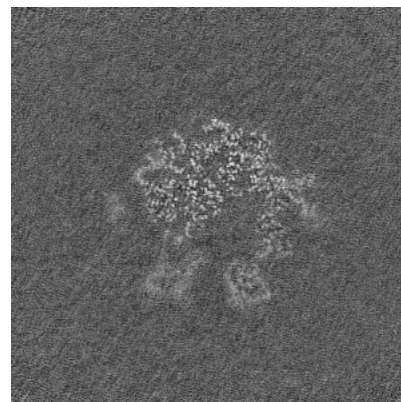
6.2.2 Raw map



X Index: 200



Y Index: 200

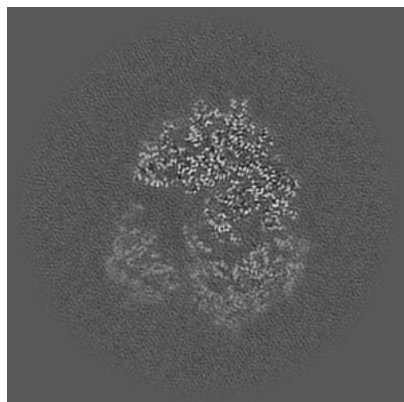


Z Index: 200

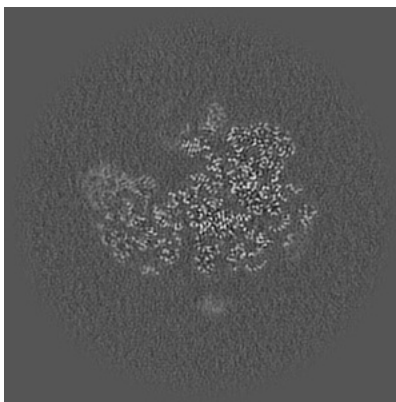
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

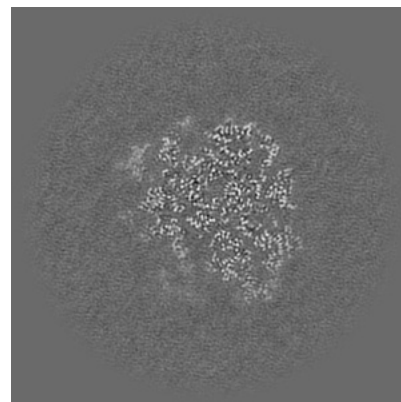
6.3.1 Primary map



X Index: 214

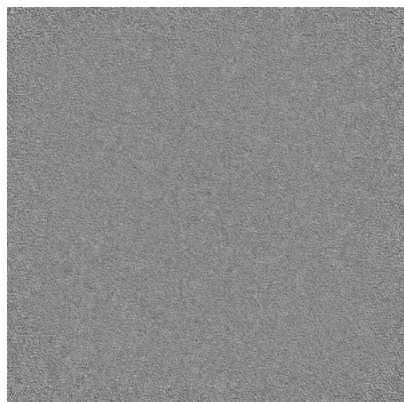


Y Index: 213

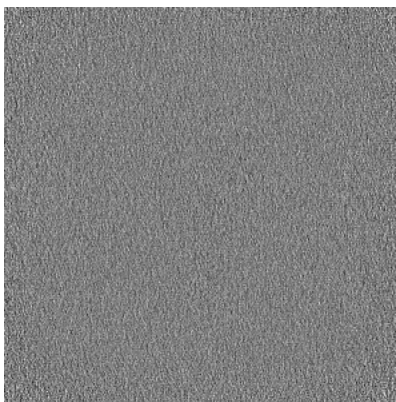


Z Index: 230

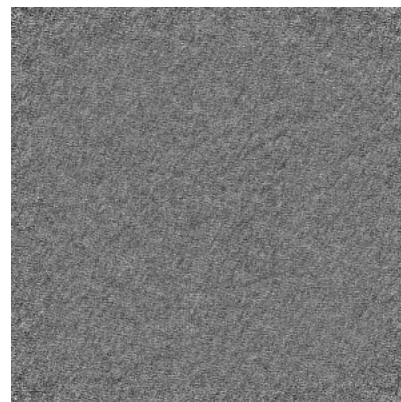
6.3.2 Raw map



X Index: 0



Y Index: 0

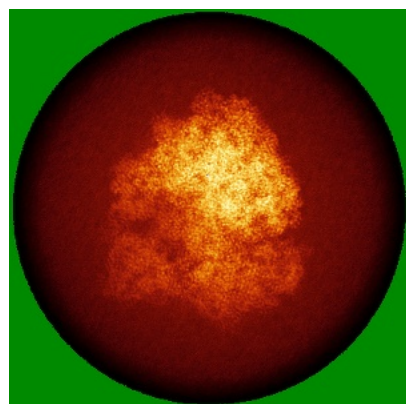


Z Index: 0

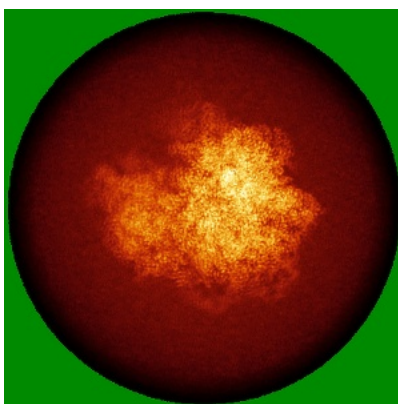
The images above show the largest variance slices of the map in three orthogonal directions.

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

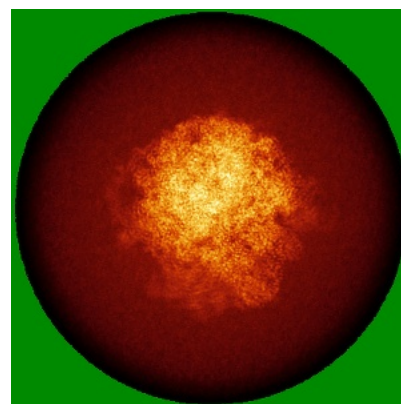
6.4.1 Primary map



X

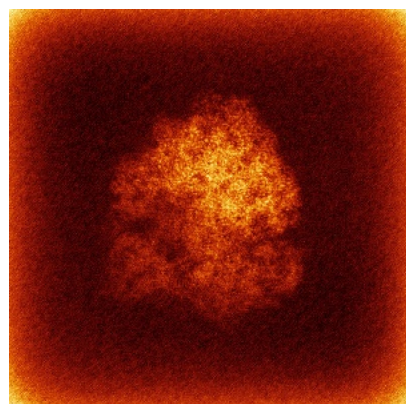


Y

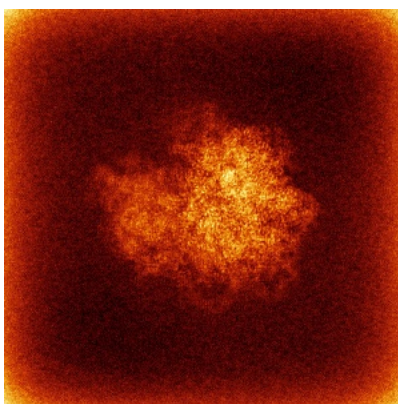


Z

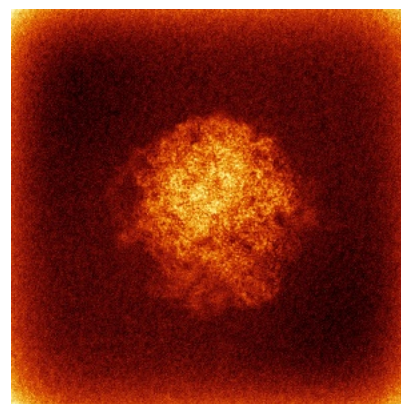
6.4.2 Raw map



X



Y

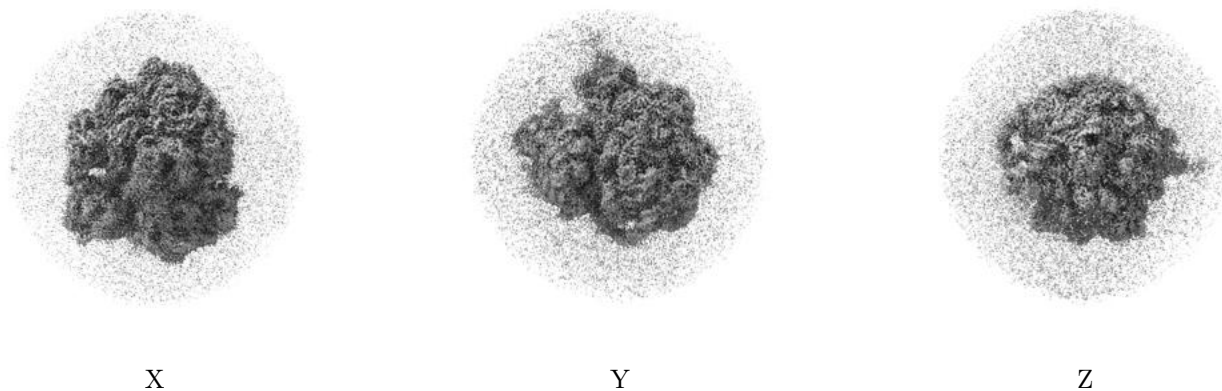


Z

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.

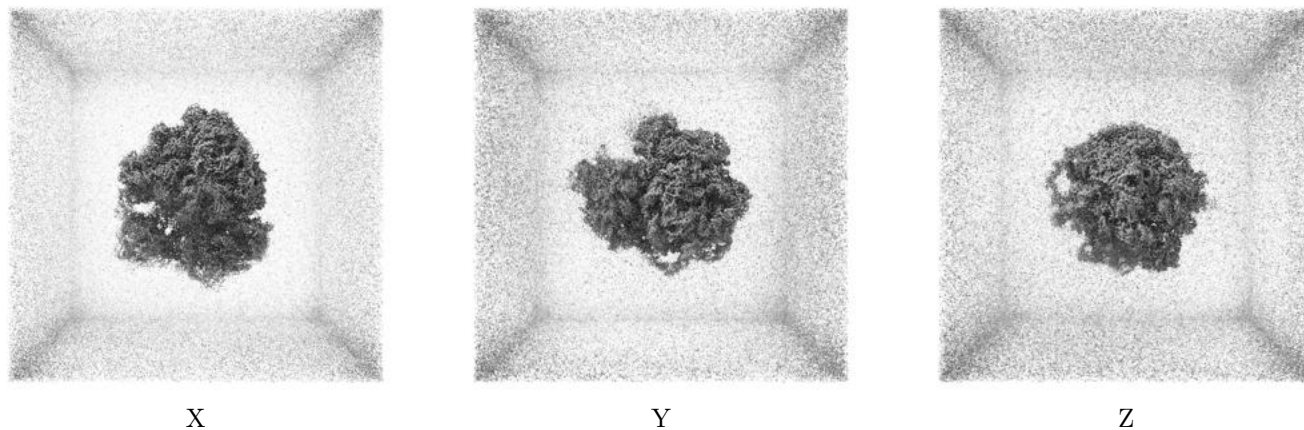
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

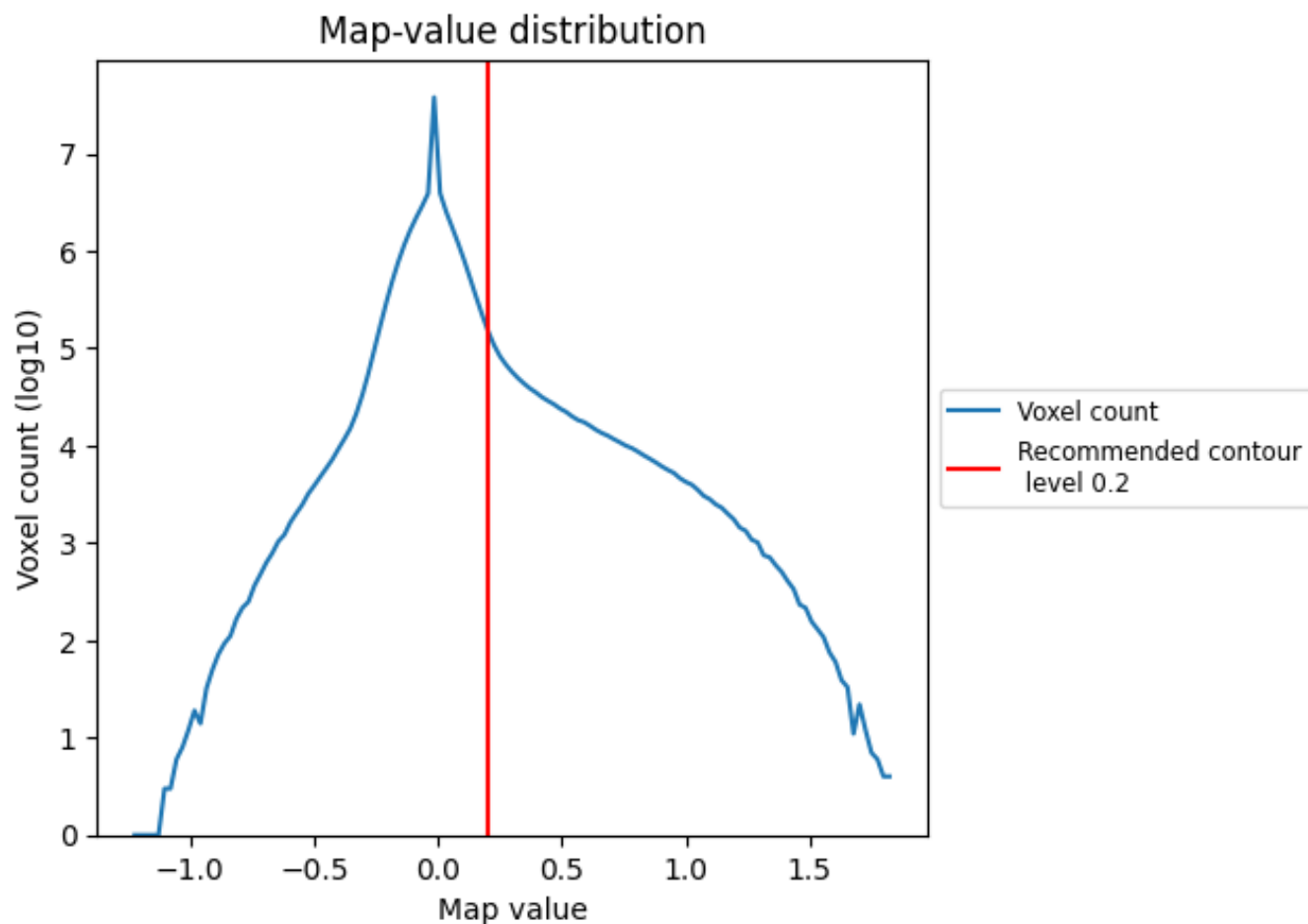
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

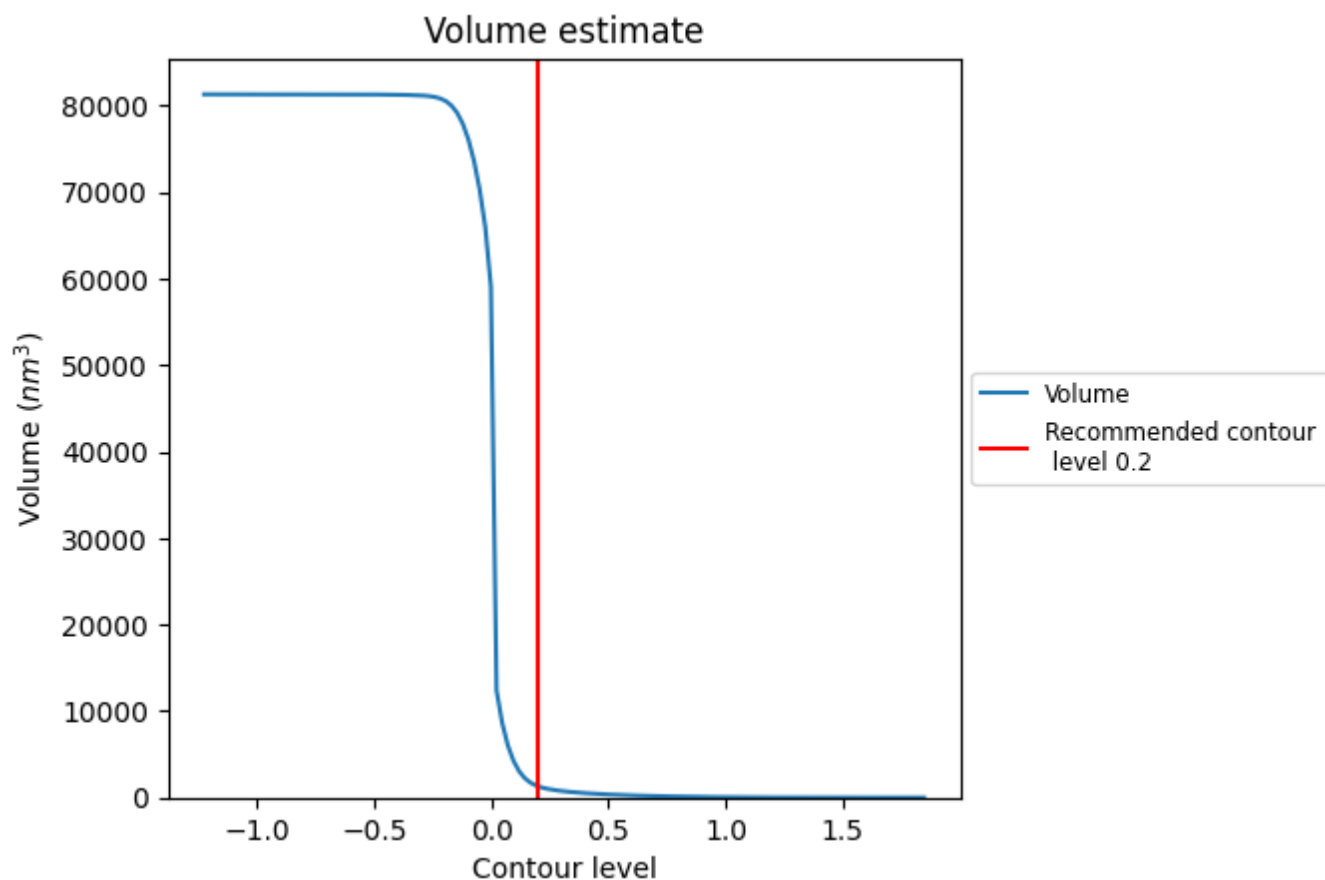
This section contains the results of statistical analysis of the map.

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.

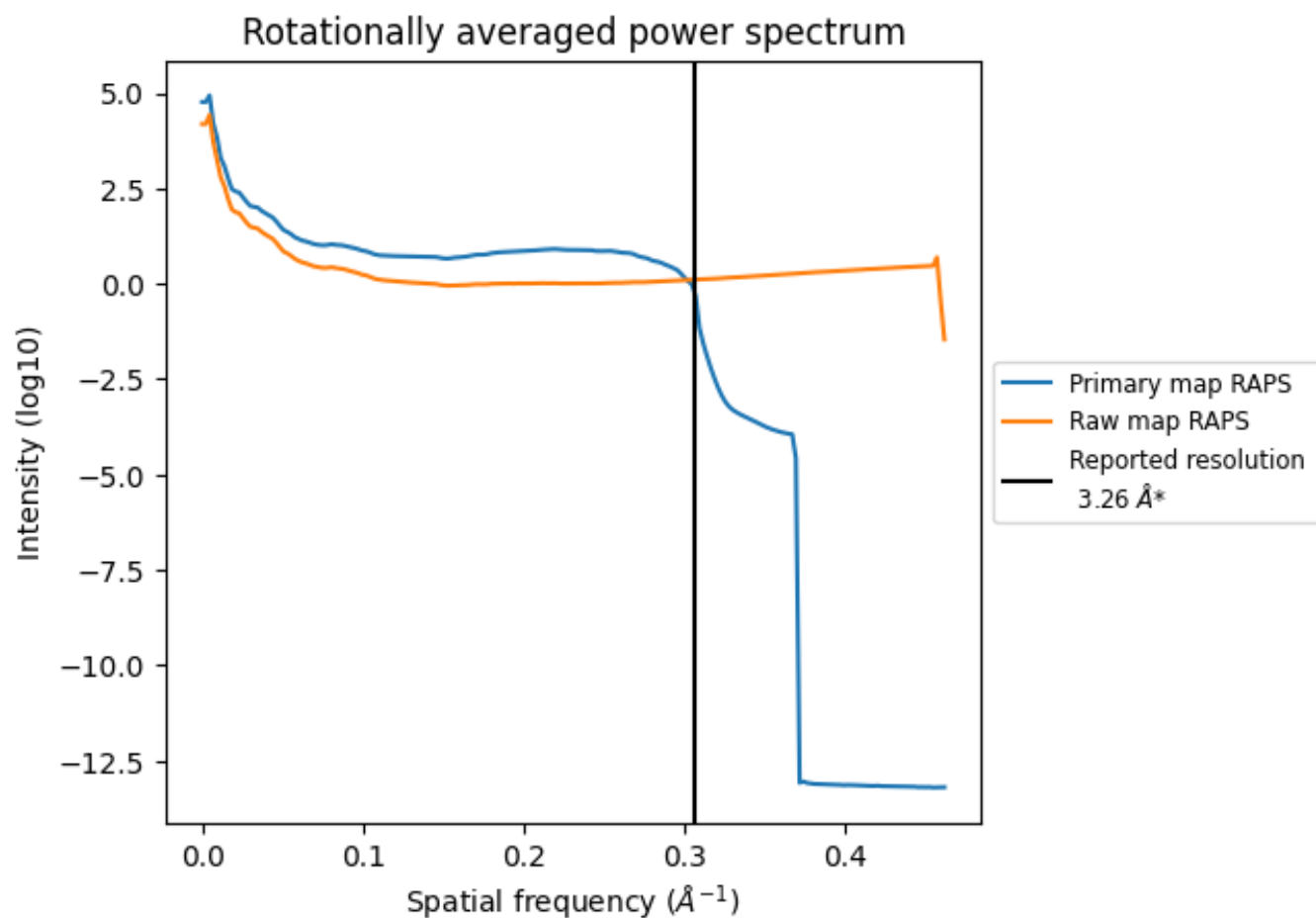
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1311 nm³; this corresponds to an approximate mass of 1184 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 ⓘ

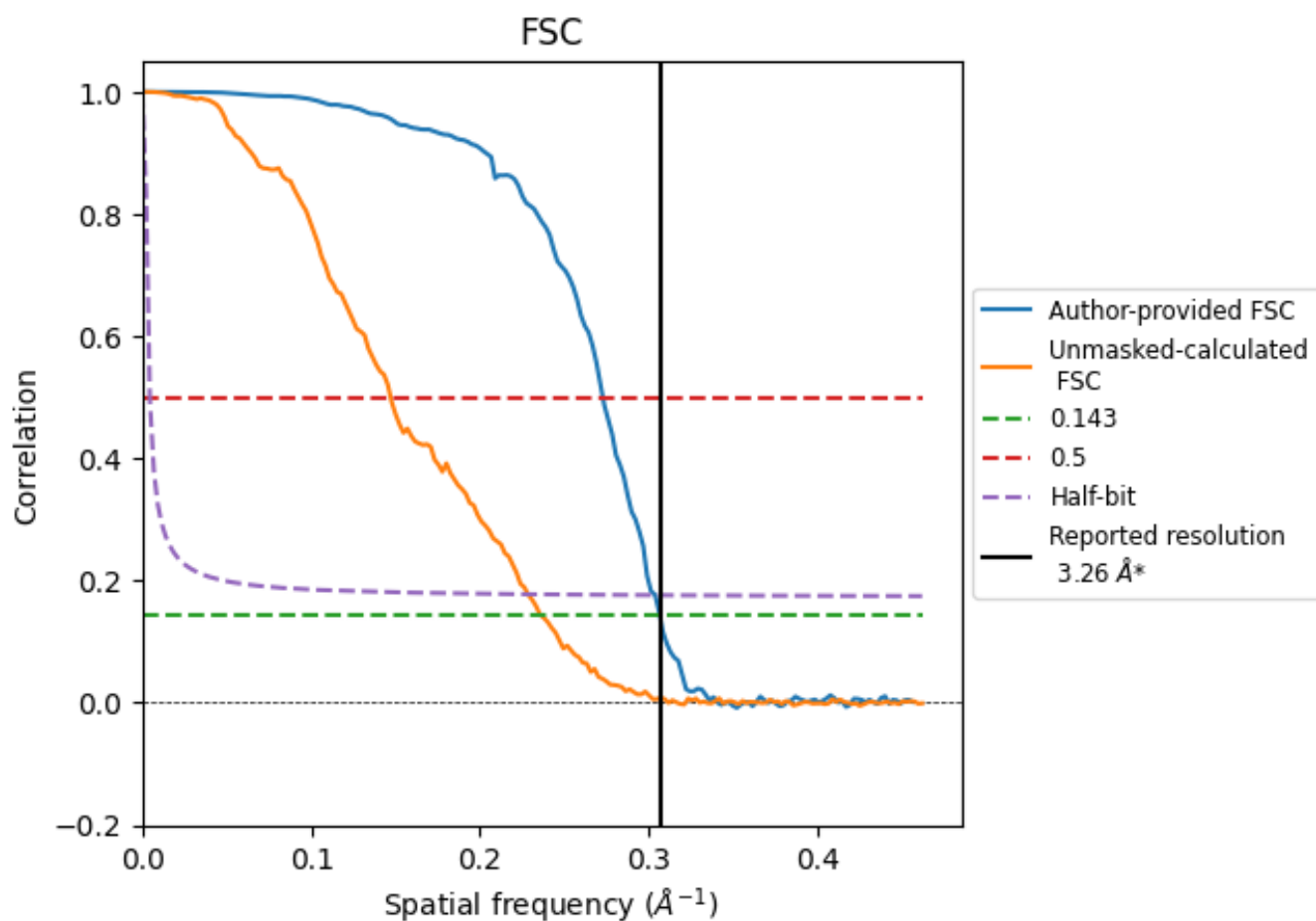


*Reported resolution corresponds to spatial frequency of 0.307 Å⁻¹

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 0.307 \AA^{-1}

8.2 Resolution estimates [i](#)

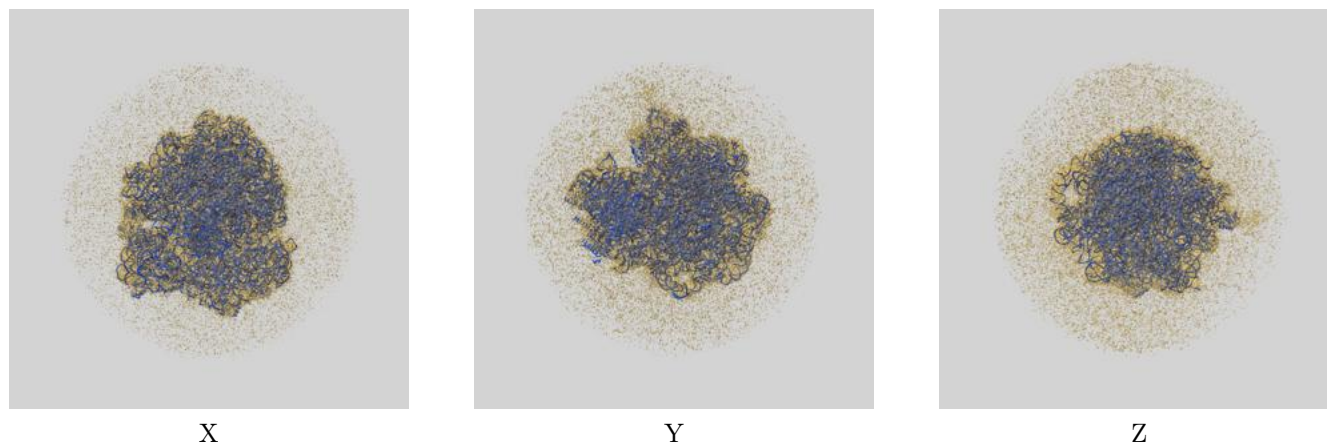
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.26	-	-
Author-provided FSC curve	3.26	3.67	3.29
Unmasked-calculated*	4.24	6.80	4.38

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.24 differs from the reported value 3.26 by more than 10 %

9 Map-model fit [i](#)

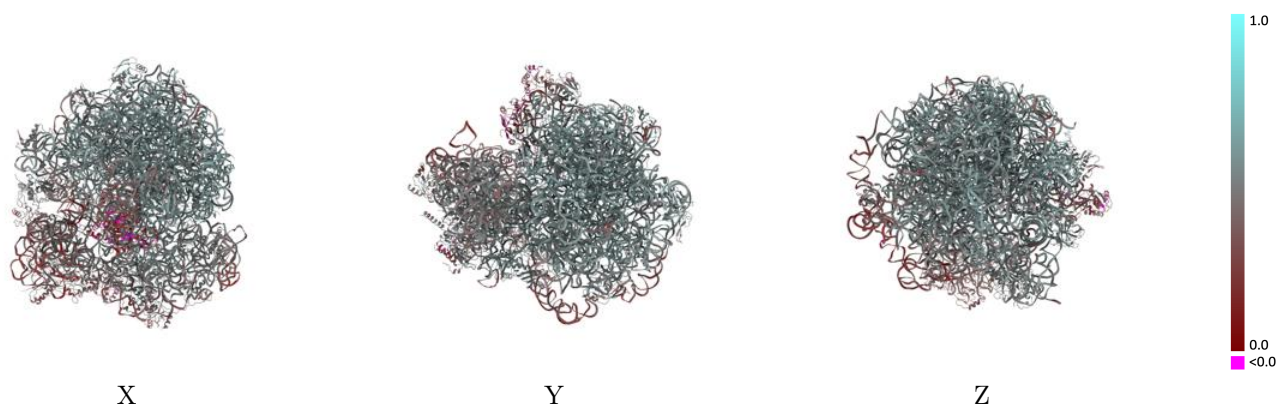
This section contains information regarding the fit between EMDB map EMD-43267 and PDB model 8VIO. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



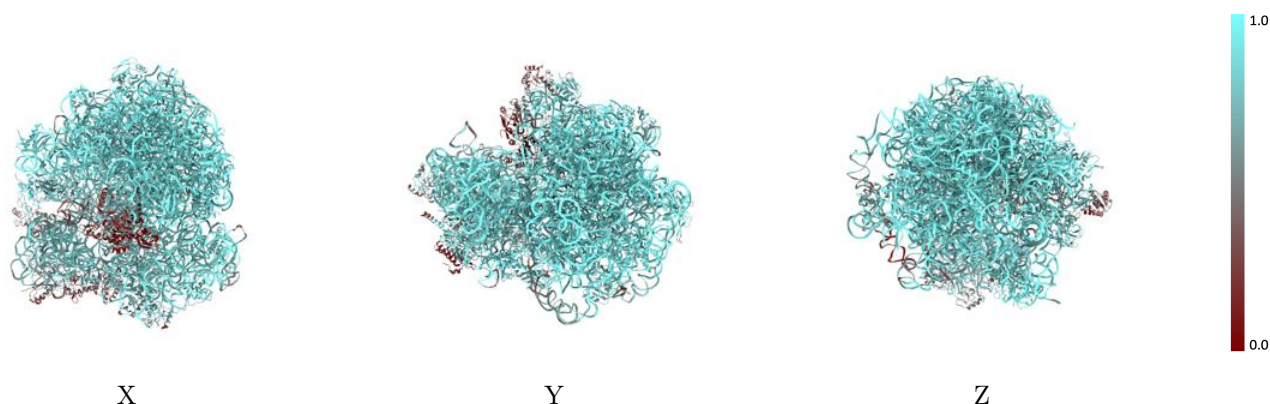
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



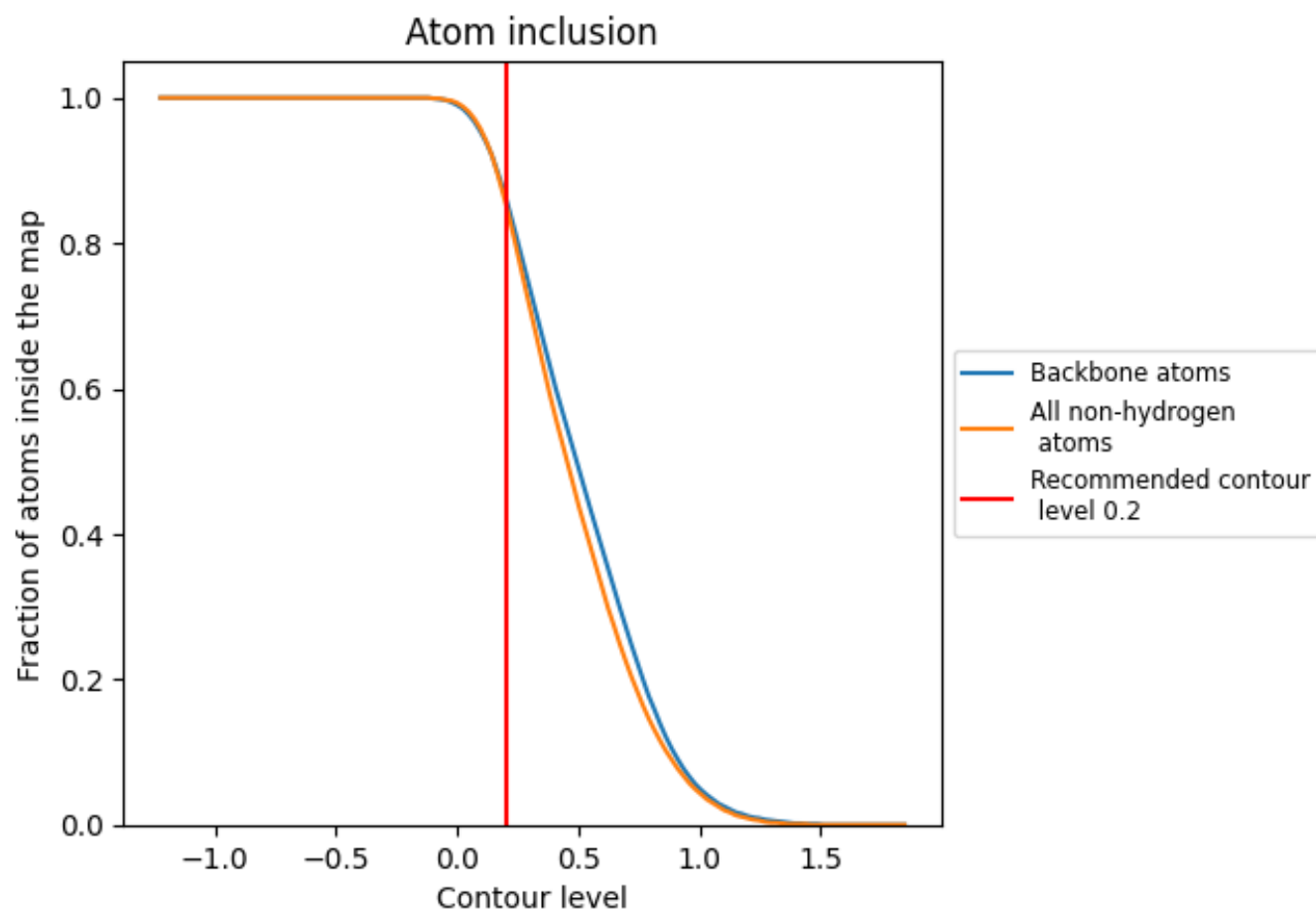
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8550	 0.4860
1	 0.8320	 0.5550
2	 0.9480	 0.5780
3	 0.9610	 0.5920
4	 0.0800	 0.3100
5	 0.8090	 0.4030
A	 0.9170	 0.5050
B	 0.9460	 0.4970
C	 0.9320	 0.5780
D	 0.9440	 0.5770
E	 0.9130	 0.5590
F	 0.8260	 0.4890
G	 0.8320	 0.4940
H	 0.7040	 0.4630
I	 0.3060	 0.2700
J	 0.2460	 0.2590
K	 0.9440	 0.5730
L	 0.9100	 0.5690
M	 0.9240	 0.5640
N	 0.8990	 0.5690
O	 0.9440	 0.5720
P	 0.8940	 0.5230
Q	 0.9140	 0.5720
R	 0.9390	 0.5750
S	 0.9310	 0.5770
T	 0.9230	 0.5690
U	 0.9050	 0.5560
V	 0.8400	 0.5230
W	 0.8030	 0.5200
X	 0.9220	 0.5760
Y	 0.9120	 0.5660
Z	 0.9180	 0.5600
a	 0.8800	 0.4460
b	 0.9450	 0.5710
c	 0.8930	 0.5680



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Chain	Atom inclusion	Q-score
d	 0.9510	 0.5870
e	 0.9480	 0.5860
f	 0.9200	 0.5790
g	 0.8000	 0.4580
h	 0.1200	 0.2780
i	 0.6000	 0.4120
j	 0.6850	 0.4460
k	 0.8260	 0.5240
l	 0.8640	 0.5170
m	 0.5080	 0.3380
n	 0.8950	 0.5450
o	 0.6040	 0.3900
p	 0.5290	 0.4030
q	 0.8900	 0.5400
r	 0.8320	 0.5140
s	 0.7800	 0.5060
t	 0.5420	 0.3710
u	 0.7830	 0.4640
v	 0.9060	 0.5430
w	 0.7340	 0.4770
x	 0.7990	 0.4900
y	 0.6340	 0.4000
z	 0.8080	 0.4710