



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 01:29 PM UTC

PDB ID : 6WDM / pdb_00006wdm
EMDB ID : EMD-21641
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Non-cognate Structure V-B2)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.60 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

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

The types of validation reports are described at
<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

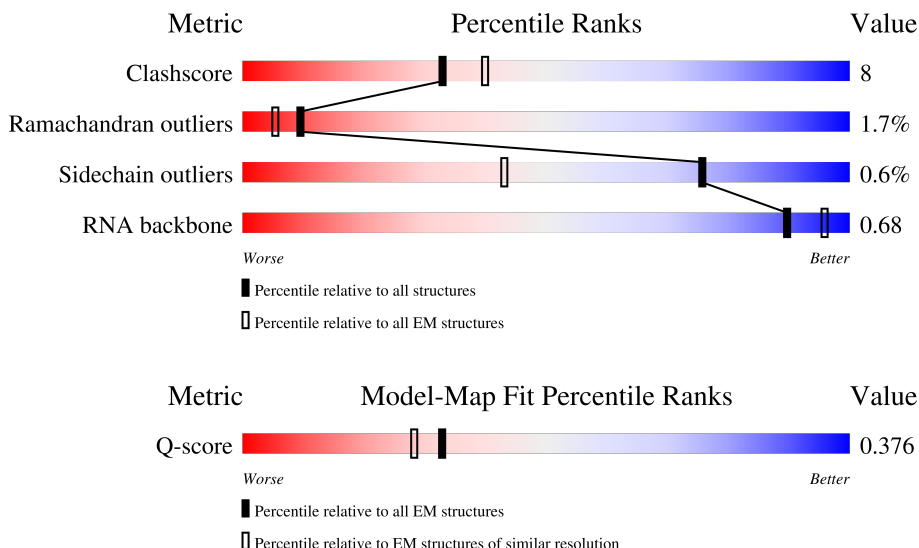
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



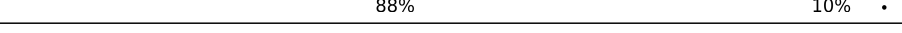
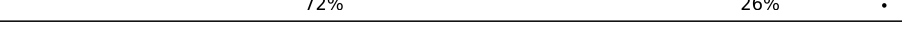
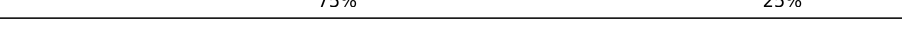
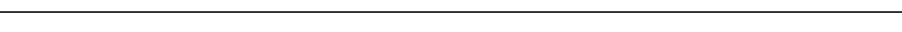
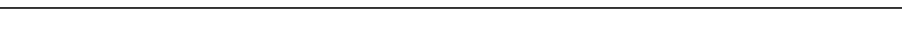
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	b	271	
2	c	209	
3	d	201	

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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	

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Mol	Chain	Length	Quality of chain
29	E	64	
30	F	38	
31	G	225	
32	H	206	
33	I	205	
34	J	157	
35	K	100	
36	L	151	
37	M	129	
38	N	127	
39	O	98	
40	P	116	
41	Q	123	
42	R	114	
43	S	100	
44	T	88	
45	U	82	
46	V	80	
47	W	65	
48	X	79	
49	Y	85	
50	Z	65	
51	a	223	
52	3	1539	
53	1	2903	

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Mol	Chain	Length	Quality of chain
54	2	120	 61%32%7%
55	5	77	 78%19%•
55	6	77	 5%75%23%•
56	4	18	 6%67%33%
57	7	77	 69%22%8%•

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 150220 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 L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	t	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	u	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	v	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	x	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	D	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	E	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 31 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 33 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	I	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 35 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 36 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 37 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	M	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 38 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 39 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 40 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 41 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 43 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 44 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	T	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 45 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	U	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 46 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 47 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 48 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 49 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 50 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 51 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 55 is a RNA chain called tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
55	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

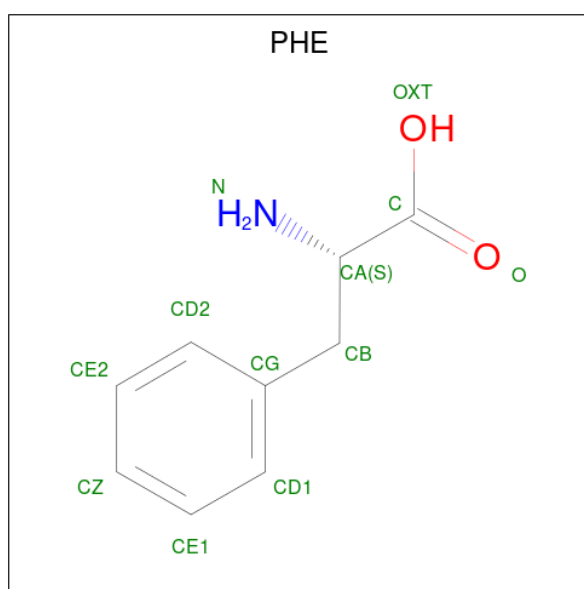
- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	77	119	17		

- Molecule 57 is a RNA chain called tRNA^{Phe}.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 58 is PHENYLALANINE (CCD ID: PHE) (formula: C₉H₁₁NO₂).



Mol	Chain	Residues	Atoms				AltConf
58	7	1	Total	C	N	O	0
			11	9	1	1	

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).

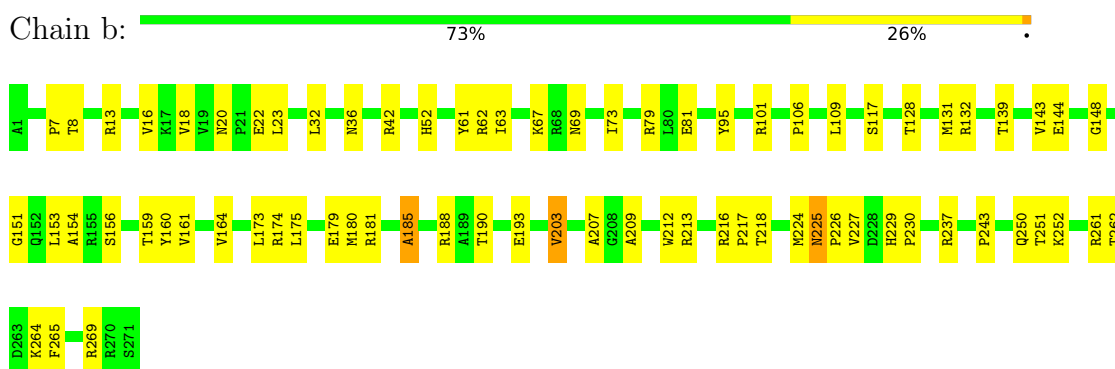


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
59	7	1	8	5	1	1	1	0

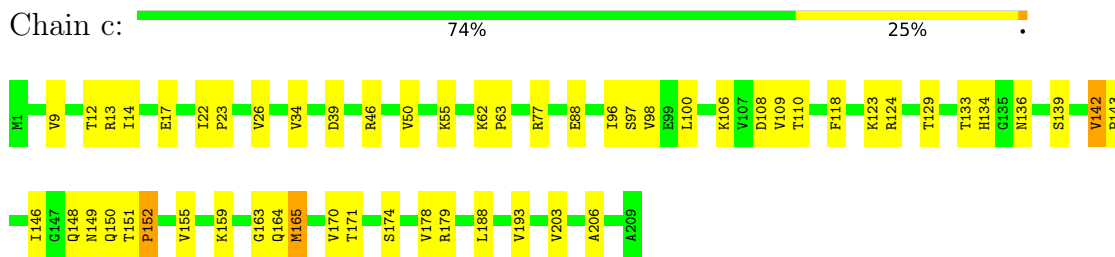
3 Residue-property plots

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.

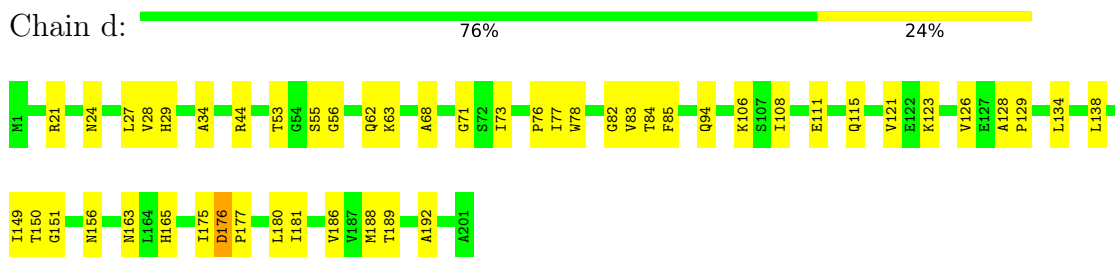
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3



- Molecule 3: 50S ribosomal protein L4



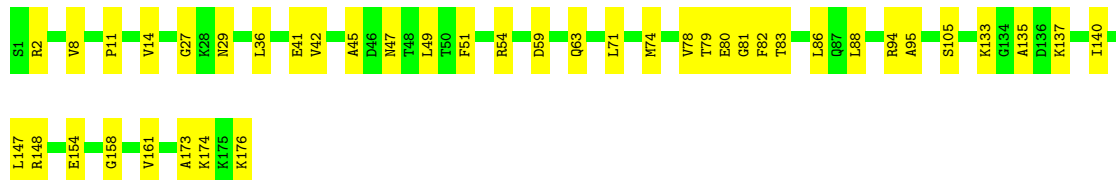
- Molecule 4: 50S ribosomal protein L5





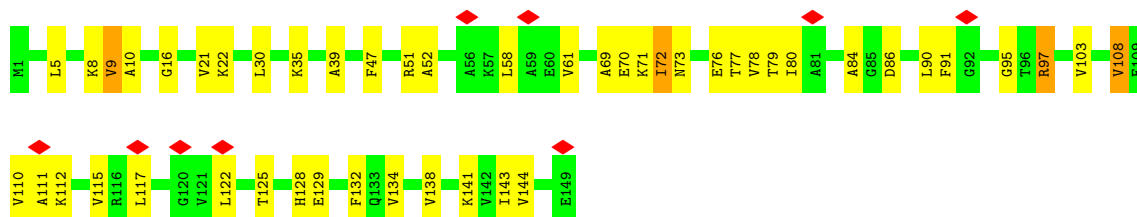
- Molecule 5: 50S ribosomal protein L6

Chain f: 77% 23%



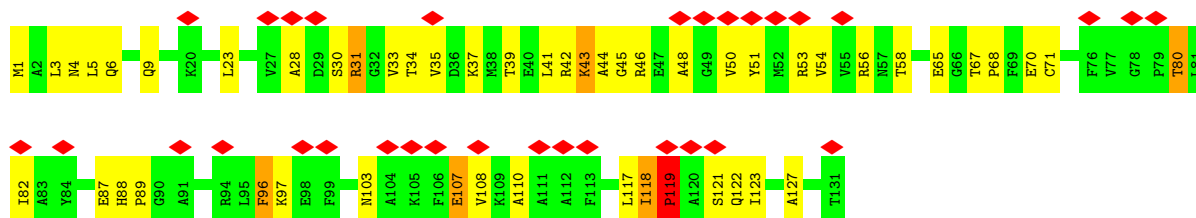
- Molecule 6: 50S ribosomal protein L9

Chain g: 6% 68% 30%



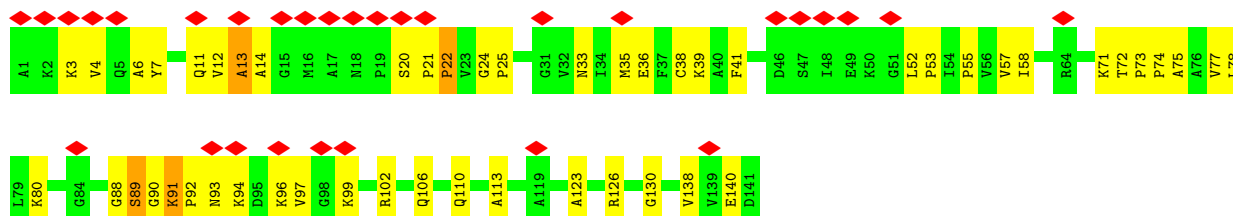
- Molecule 7: 50S ribosomal protein L10

Chain h: 24% 61% 34% 5%

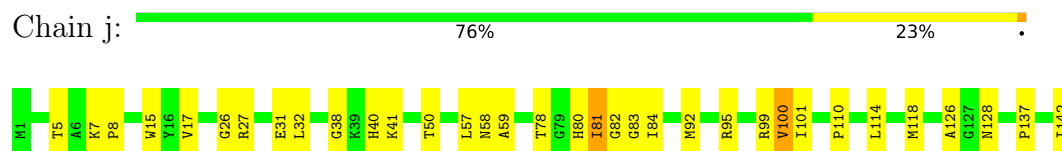


- Molecule 8: 50S ribosomal protein L11

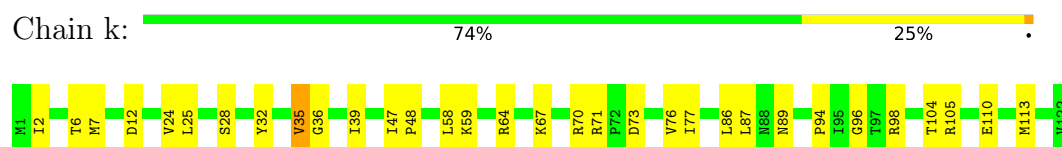
Chain i: 21% 64% 33%



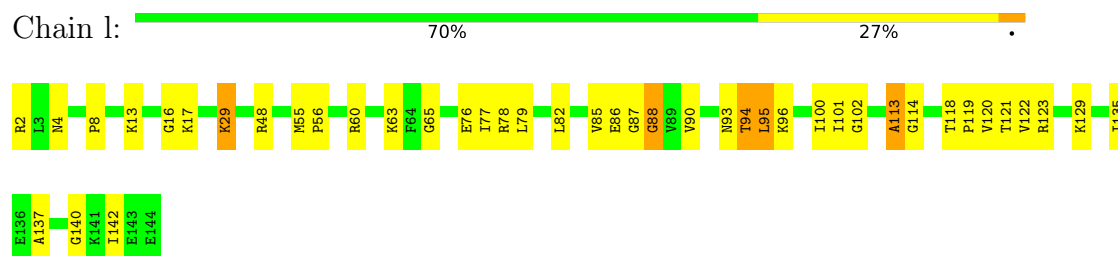
- Molecule 9: 50S ribosomal protein L13



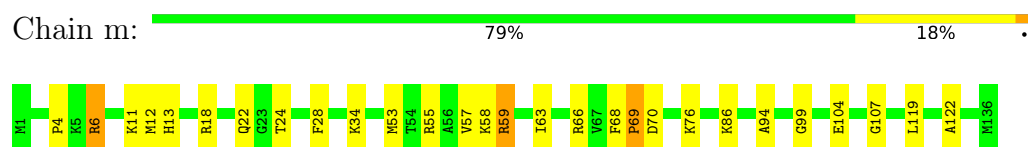
- Molecule 10: 50S ribosomal protein L14



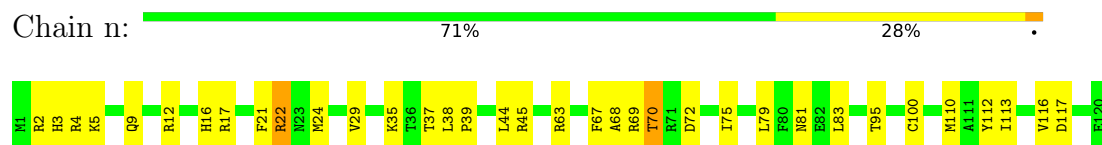
- Molecule 11: 50S ribosomal protein L15



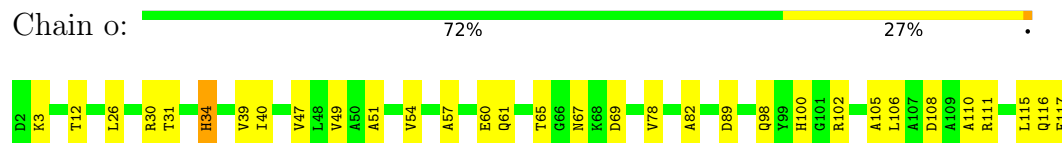
- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18

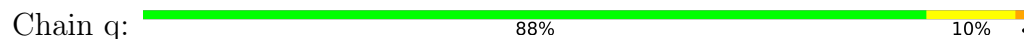


- Molecule 15: 50S ribosomal protein L19

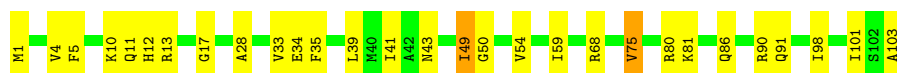




- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



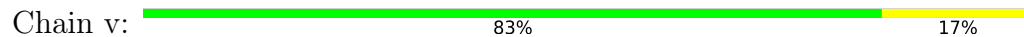
- Molecule 19: 50S ribosomal protein L23



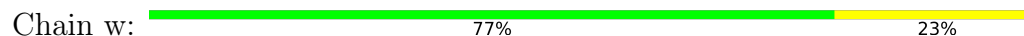
- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25



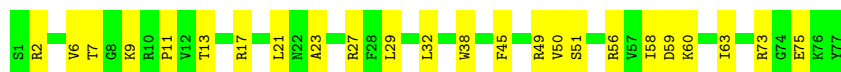
- Molecule 22: 50S ribosomal protein L27





- Molecule 23: 50S ribosomal protein L28

Chain x: 69% 31%



- Molecule 24: 50S ribosomal protein L29

Chain y: 76% 24%



- Molecule 25: 50S ribosomal protein L30

Chain z: 64% 36%



- Molecule 26: 50S ribosomal protein L32

Chain B: 70% 30%



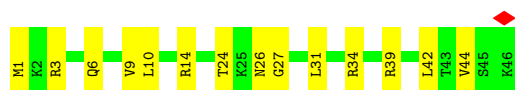
- Molecule 27: 50S ribosomal protein L33

Chain C: 84% 16%



- Molecule 28: 50S ribosomal protein L34

Chain D: 70% 30%

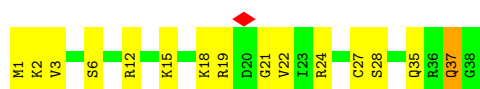


- Molecule 29: 50S ribosomal protein L35

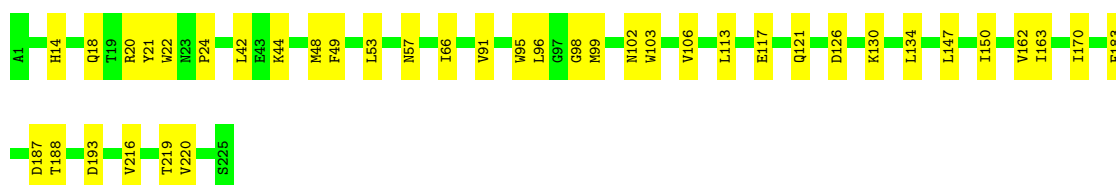
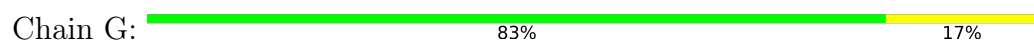
Chain E: 69% 31%



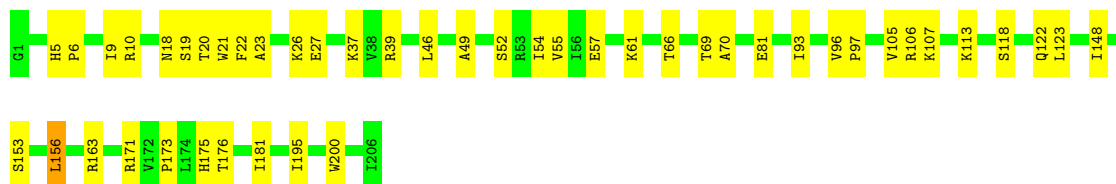
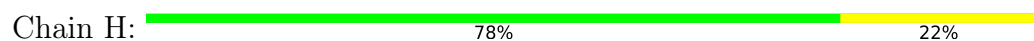
- Molecule 30: 50S ribosomal protein L36



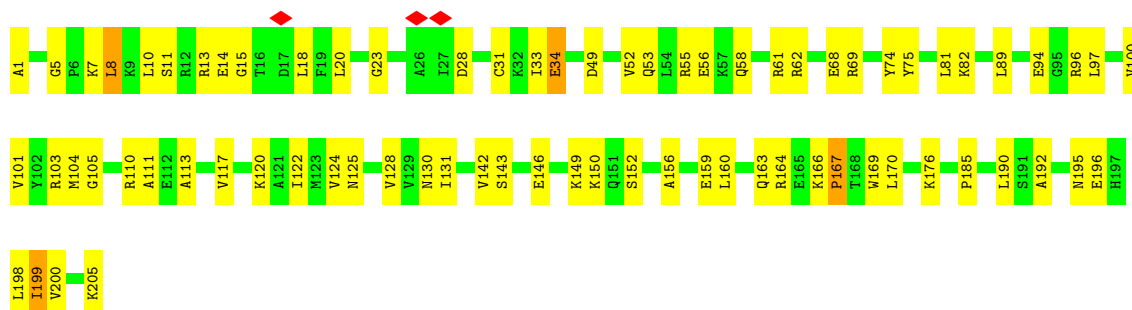
- Molecule 31: 30S ribosomal protein S2



- Molecule 32: 30S ribosomal protein S3

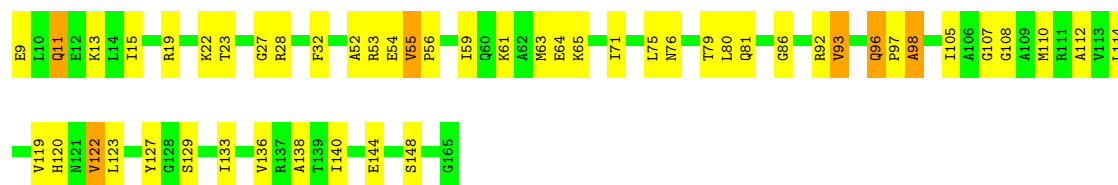


- Molecule 33: 30S ribosomal protein S4



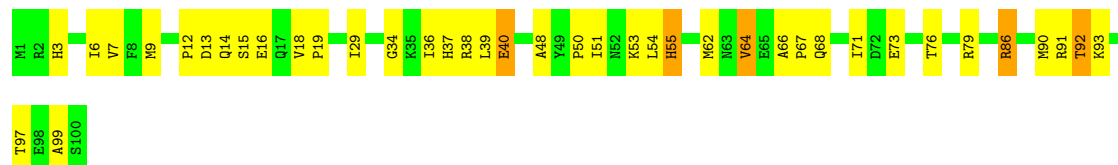
- Molecule 34: 30S ribosomal protein S5





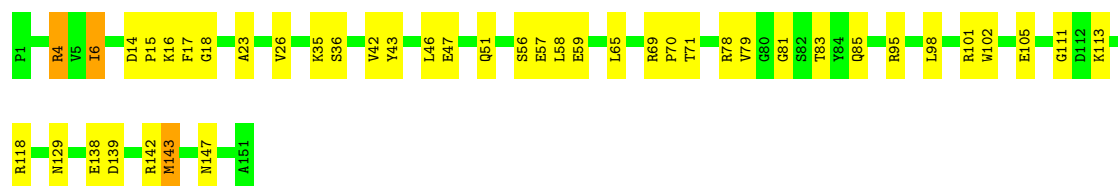
• Molecule 35: 30S ribosomal protein S6

Chain K: 60% 35% 5%



• Molecule 36: 30S ribosomal protein S7

Chain L: 72% 26% .



• Molecule 37: 30S ribosomal protein S8

Chain M: 72% 28%



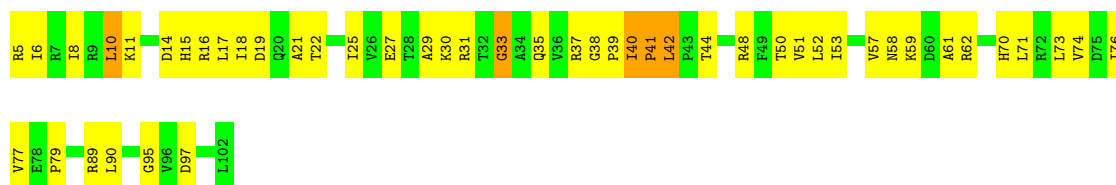
• Molecule 38: 30S ribosomal protein S9

Chain N: 63% 32% 5%



• Molecule 39: 30S ribosomal protein S10

Chain O: 51% 44% 5%



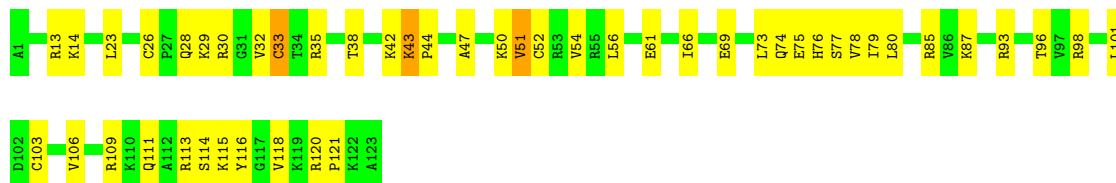
- Molecule 40: 30S ribosomal protein S11

Chain P: 69% 29%



- Molecule 41: 30S ribosomal protein S12

Chain Q: 61% 37%



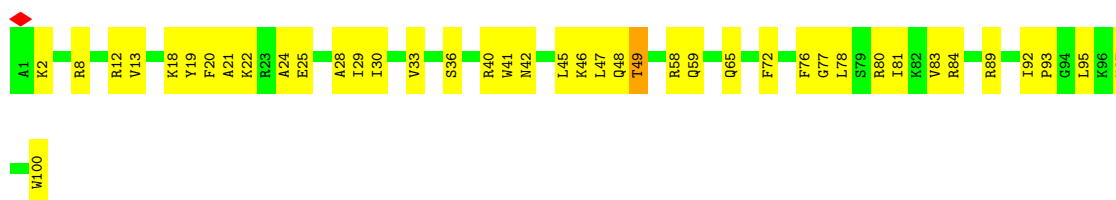
- Molecule 42: 30S ribosomal protein S13

Chain R: 69% 27%



- Molecule 43: 30S ribosomal protein S14

Chain S: 59% 40%

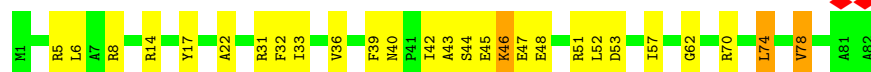


- Molecule 44: 30S ribosomal protein S15

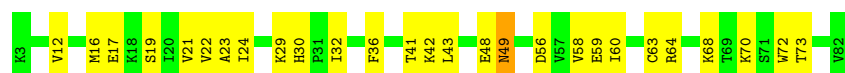
Chain T: 77% 23%



- Molecule 45: 30S ribosomal protein S16



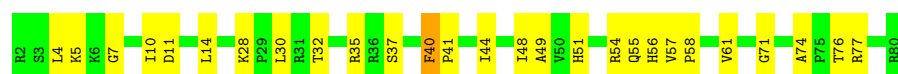
- Molecule 46: 30S ribosomal protein S17



- Molecule 47: 30S ribosomal protein S18



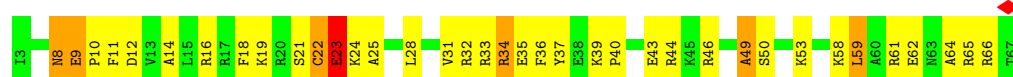
- Molecule 48: 30S ribosomal protein S19



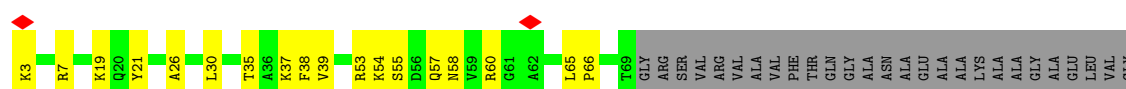
- Molecule 49: 30S ribosomal protein S20



- Molecule 50: 30S ribosomal protein S21



- Molecule 51: 50S ribosomal protein L1

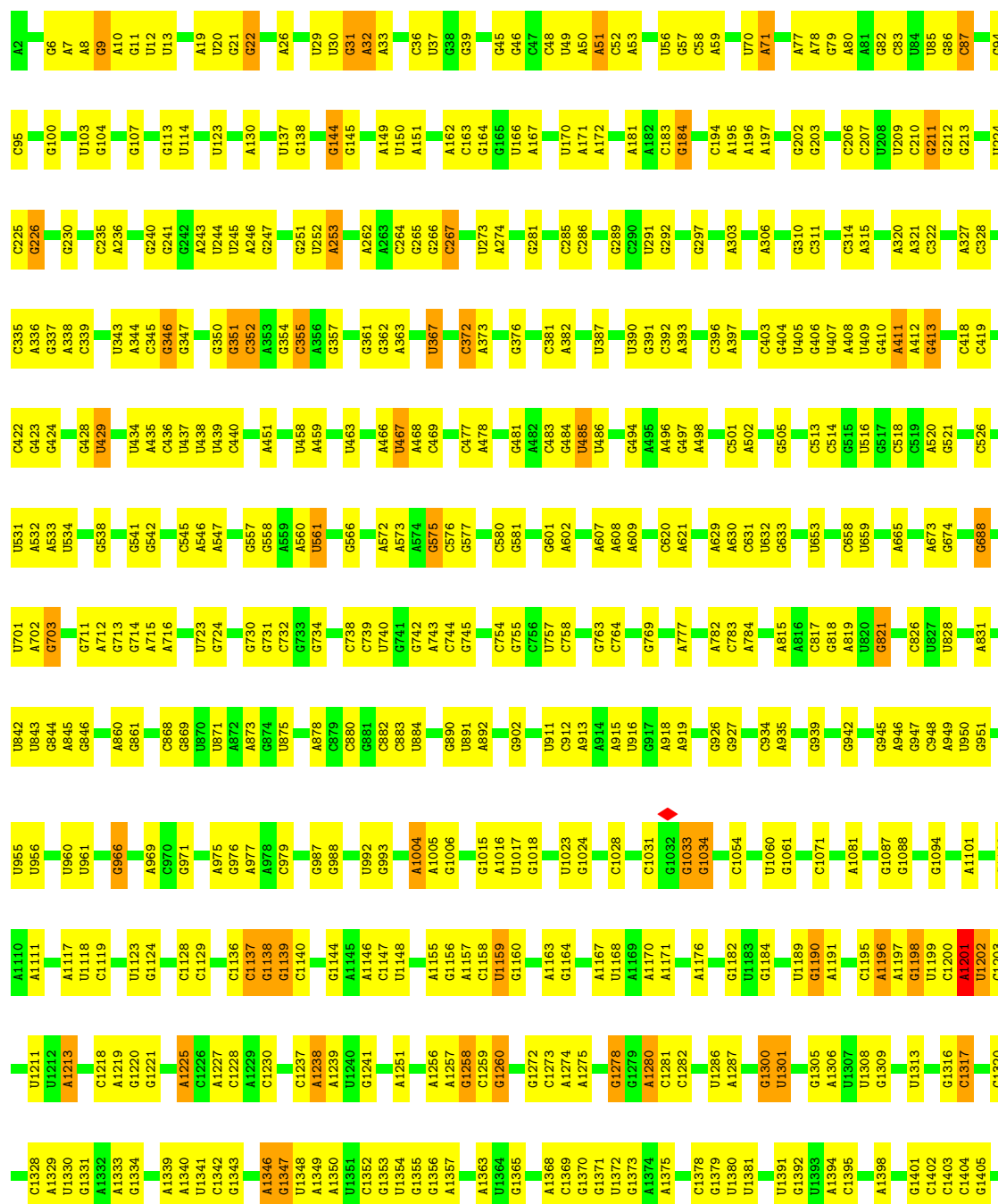


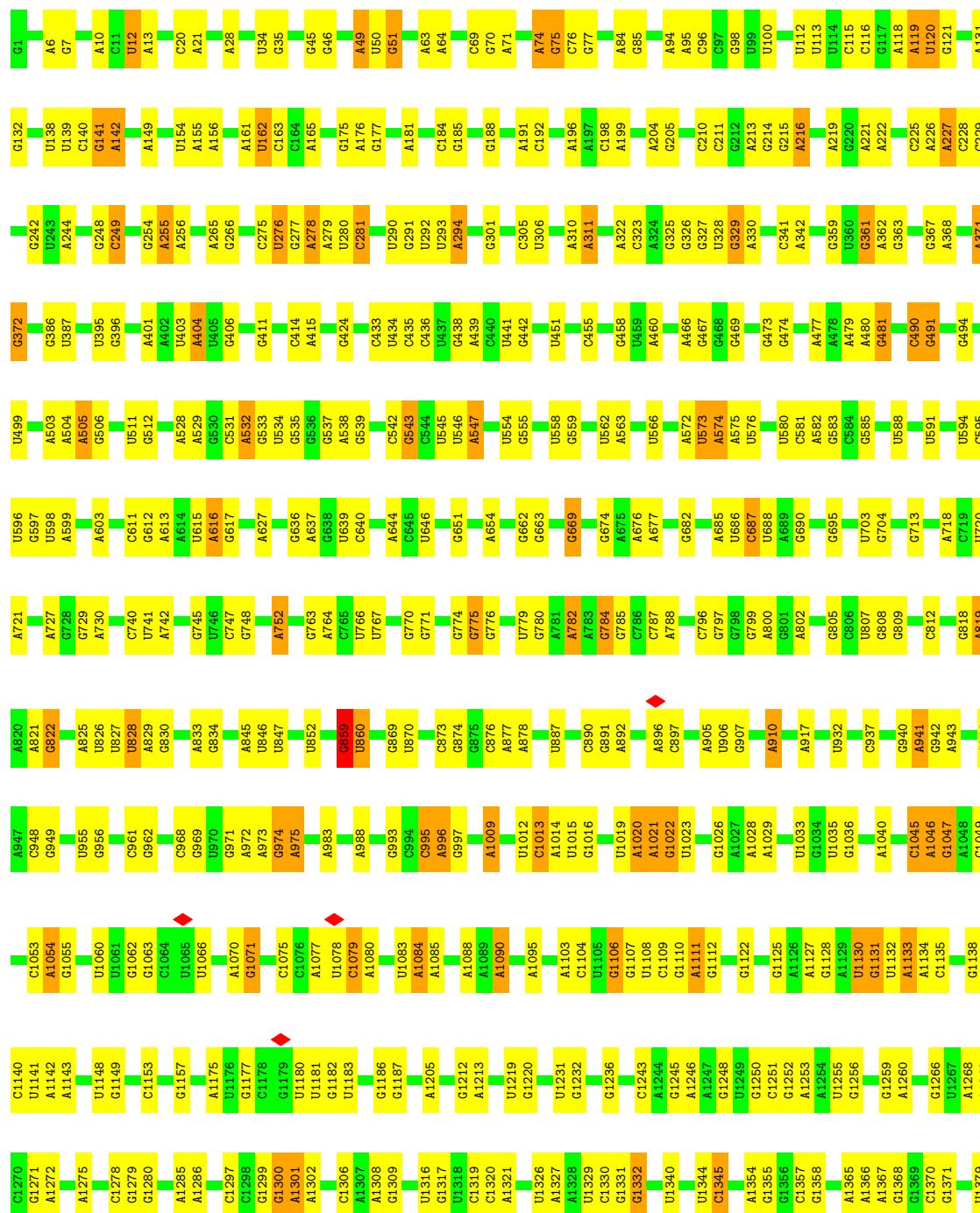
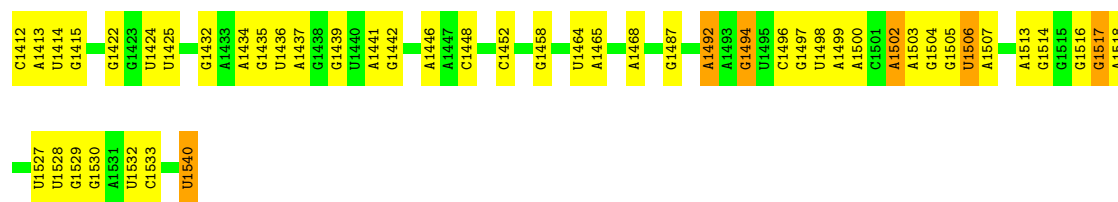
MET	GLU	ASP	LEU	ALA	ASP	GLN	ILE	LYS	LYS	GLY	GLU	MET	ASN	PHE	ASP	VAL	VAL	ILE	ALA	SER	PRO	ASP	ALA	MET	ARG	VAL	VAL	GLY	GLN	LEU	GLY	GLN	VAL	LEU	GLY	PRO	ARG	GLY	MET	PRO	ASN	PRO	LYS	VAL	GLY	THR	THR	PRO	ASN	VAL	ALA	GLU	ALA	VAL	LYS	ASN	ALA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



• Molecule 52: 16S ribosomal RNA

Chain 3: 64% 32%

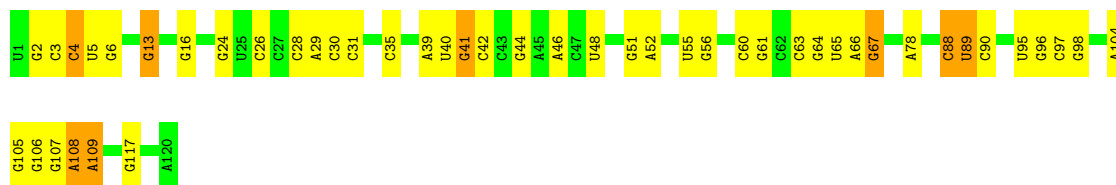




A2899	A2761	G2642	C2520	G2414	G2316	U2220	A2119	G2024	A1913	C1800	G1674	G1529	G1380
U2903	A2765	C2646	C2521	G2415	A2317	G2221	G2120	G2029	C1914	A1801	C1675	A1535	A1383
		U2647	G2529	U2419	G2318	G2222	U2121	A2030	U1917	G1807	A1676	C1536	C1386
	U2768	G2655	A2531	U2423	G2325	A2225	G2123	A2031	A1918	A1808	G1683	G1537	A1387
A2778			G2532	C2424	C2326	U2233	A2126	G2032	A1919	A1810	G1684	C1550	U1394
U2779		A2665	U2533	A2426	A2327	G2234	G2127	U2034	U1923	G1811	G1695	A1551	A1395
G2780		C2666	A2426	G2426	G2328	G2236	G2128	G2035	C1924	C1816	G1696	G1555	C1398
A2781		A2670	C2427	G2428	G2329	G2236	U2132	A2037	G1929	G1817	A1698	G1560	U1415
G2791		G2671	G2538	G2429	G2330	G2237	G2133	G2038	G1930	U1818	G1699		G1416
			C2539	A2430	G2331		G2139	U2039	U1931		C1706	A1566	A1419
C2796		A2679		U2431	U2384	A2241	G2140	G2040	A1936	U1825	C1706	G1567	A1420
U2797		A2682	G2542	A2432	G2337	G2242	G2141	U2041	A1937	G1826	G1715	G1568	G1421
U2798			G2544	A2435	G2338	U2243	A2142	A2042	A1938	U1827	G1715	A1569	G1422
A2799		U2687	C2339	U2440	G2339	U2244		C2043		G1828	U1720	G1581	G1423
A2800		G2688	U2546	G2441	A2340	U2245	C2145	G2048	U1943		G1721	U1584	G1424
G2801		U2689	A2547	U2441	U2344	G2246	U2149	C2055	G1954	C1843	U1729	C1585	G1425
G2802		G2691	G2549	G2447	G2345	A2247	U2151	C2056	U1955	C1844	G1730	A1590	
		G2692		A2448	G2346	U2249	G2155	A2060	U1956	G1845	C1732	A1591	
A2809			U2553		G2349	C2257	U2155	G2061	C1957	A1847	U1736	A1603	
A2813			U2554		C2350	C2258	G2156	A2062	U1963		G1737	C1606	
A2814			A2566		G2351		G2162		G1964	A1854	G1737	C1607	
A2820			G2567		G2360	U2265	G2162	C2066	C1965	U1855	G1738	A1608	
A2821			U2567		G2361	A2266	A2163	C2067	U1966	G1856	G1738	C1437	
G2822			A2572		G2362	A2267	C2164	U2068	C1967	G1857	G1753	C1438	
					G2364	G2268		G2069			U1757	C1464	
U2833			U2580		G2365	A2270	U2172	A2070	A1970	G1860	U1758	C1461	
G2834			G2581		C2368	G2271	A2173	A2071	U1971		C1759	C1462	
A2835			A2587		G2369	G2277	C2177	C2072	G1972	A1871	C1760	C1463	
					G2370	A2278	C2178	C2073		A1872	G1764	C1464	
G2841			C2591		G2371	G2279	A2183	U2074	A1978	G1873	U1765		
G2842			G2592		U2372	G2280	A2184		U1979	C1874	G1766		
U2845			A2602		A2381	A2281	U2189	U2086	U1991	G1884	A1772	U1474	
G2846			U2609		G2382	G2282	U2194	A2088	G1992		A1773	G1475	
U2849			C2610		U2384	C2283	G2193	G2093	U1993	G1888	C1774	U1476	
A2850			U2613		C2385	A2286	U2195				U1775	G1482	
C2853			G2618		G2389	A2288	C2196	C2096	C1996	C1892	G1776	A1490	
G2854					U2390	U2292	U2197	C2104	C1997	C1893	U1779	A1496	
					A2391	G2293	U2105	U2106	C1999	C1894	A1780	U1497	
G2867			G2623		A2392	G2293	A2198	U2107	C2000	A1899	U1781	C1498	
A2868			G2624		U2393	U2296	U2203	G2107	C2001	A1900	G1651	A1652	
					C2394	A2297	G2204	A2108		A1901	A1784	C1507	
A2872			C2628				A2205	U2109	A2009			G1653	
A2879			U2629		U2402	U2305	G2204	G2110	C2010	C1905	C1790	A1508	
C2880			G2630		A2406	A2309	U2111	U2111	U2011	G1906	A1791	A1509	
					A2407		A2212	G2112	G2012	G1907	G1792	G1510	
			C2636		A2407	U2312	U2213	U2113		C1908		A1515	
A2883			U2637		A2411	C2313	G2214	A2114	A2020	C1909	U1796	G1665	
U2884			G2638		A2412	A2314	C2215	A2117	U2022	G1910	G1797	A1668	
					U2518	G2216	G2161		U2021	A1912	U1798	G1524	
U2898			G2641		U2519	G2315		U2118	C2023		G1799	A1528	

• Molecule 54: 5S ribosomal RNA

Chain 2:  61% 32% 7%



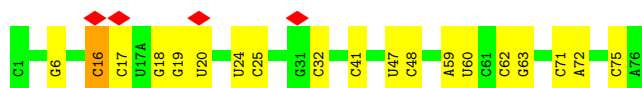
• Molecule 55: tRNAfMet

Chain 5:  78% 19% .



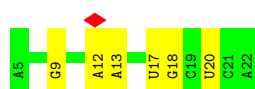
• Molecule 55: tRNAfMet

Chain 6:  5% 75% 23% .



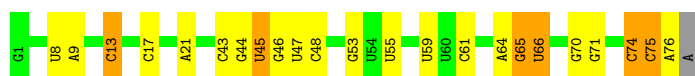
• Molecule 56: mRNA

Chain 4:  6% 67% 33% .



• Molecule 57: tRNAPhe

Chain 7:  69% 22% 8% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	12171	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 ($e^-/\text{\AA}^2$)	35	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	20.155	Depositor
Minimum map value	-11.482	Depositor
Average map value	0.121	Depositor
Map value standard deviation	0.992	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: FME

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	b	0.29	0/2122	0.92	5/2852 (0.2%)
2	c	0.29	0/1586	0.83	2/2134 (0.1%)
3	d	0.28	0/1571	0.88	4/2113 (0.2%)
4	e	0.30	0/1435	0.88	3/1926 (0.2%)
5	f	0.30	0/1343	0.88	2/1816 (0.1%)
6	g	0.32	0/1122	0.95	3/1515 (0.2%)
7	h	0.35	0/1002	1.05	9/1350 (0.7%)
8	i	0.35	0/1046	0.97	6/1410 (0.4%)
9	j	0.28	0/1152	0.87	2/1551 (0.1%)
10	k	0.28	0/948	0.84	2/1268 (0.2%)
11	l	0.30	0/1054	0.97	4/1403 (0.3%)
12	m	0.28	0/1093	0.85	1/1460 (0.1%)
13	n	0.30	0/974	0.86	4/1301 (0.3%)
14	o	0.29	0/902	0.84	1/1209 (0.1%)
15	p	0.28	0/929	0.76	0/1242
16	q	0.29	0/960	0.86	4/1278 (0.3%)
17	r	0.29	0/829	0.91	3/1107 (0.3%)
18	s	0.28	0/864	0.96	3/1156 (0.3%)
19	t	0.27	0/745	0.85	1/994 (0.1%)
20	u	0.30	0/788	0.87	2/1051 (0.2%)
21	v	0.27	0/766	0.80	1/1025 (0.1%)
22	w	0.28	0/582	0.82	0/769
23	x	0.28	0/635	0.78	0/848
24	y	0.29	0/510	0.91	2/677 (0.3%)
25	z	0.30	0/453	0.79	0/605
26	B	0.28	0/450	0.77	1/599 (0.2%)
27	C	0.32	0/417	0.78	0/554
28	D	0.34	0/380	0.89	2/498 (0.4%)
29	E	0.29	0/513	0.81	0/676
30	F	0.35	0/303	0.88	0/397
31	G	0.29	0/1788	0.87	5/2408 (0.2%)
32	H	0.29	0/1652	0.83	2/2225 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.29	0/1665	0.89	6/2227 (0.3%)
34	J	0.31	0/1170	0.99	4/1573 (0.3%)
35	K	0.30	0/836	0.93	5/1128 (0.4%)
36	L	0.29	0/1196	0.91	4/1602 (0.2%)
37	M	0.29	0/989	0.85	0/1326
38	N	0.30	0/1034	0.95	6/1375 (0.4%)
39	O	0.31	0/797	0.94	4/1077 (0.4%)
40	P	0.32	0/886	0.93	3/1195 (0.3%)
41	Q	0.30	0/969	0.94	5/1300 (0.4%)
42	R	0.30	0/893	0.87	2/1193 (0.2%)
43	S	0.29	0/817	0.92	1/1088 (0.1%)
44	T	0.27	0/722	0.88	3/964 (0.3%)
45	U	0.33	0/659	0.88	2/884 (0.2%)
46	V	0.27	0/658	0.90	3/881 (0.3%)
47	W	0.30	0/545	0.86	1/731 (0.1%)
48	X	0.31	0/653	0.94	2/877 (0.2%)
49	Y	0.29	0/671	0.93	1/888 (0.1%)
50	Z	0.32	0/551	1.00	4/728 (0.5%)
51	a	0.31	0/1034	0.82	1/1387 (0.1%)
52	3	0.40	0/36963	0.50	4/57662 (0.0%)
53	1	0.39	0/69796	0.50	3/108888 (0.0%)
54	2	0.40	0/2872	0.50	0/4479
55	5	0.40	0/1832	0.47	0/2855
55	6	0.41	0/1832	0.51	0/2855
56	4	0.40	0/436	0.49	0/679
57	7	0.40	0/1809	0.49	0/2819
All	All	0.37	0/163199	0.63	138/244078 (0.1%)

There are no bond length outliers.

The worst 5 of 138 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	r	50	GLY	N-CA-C	-9.58	100.90	112.49
18	s	66	ILE	N-CA-C	-7.99	103.39	113.22
34	J	120	HIS	N-CA-C	-7.98	100.55	111.56
41	Q	114	SER	N-CA-C	-7.97	102.67	111.36
7	h	117	LEU	N-CA-C	7.58	121.17	108.13

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	2083	0	2157	56	0
2	c	1565	0	1616	41	0
3	d	1552	0	1619	32	0
4	e	1411	0	1447	39	0
5	f	1323	0	1374	24	0
6	g	1111	0	1148	32	0
7	h	989	0	1025	41	0
8	i	1032	0	1088	42	0
9	j	1129	0	1162	28	0
10	k	939	0	1012	28	0
11	l	1045	0	1117	32	0
12	m	1074	0	1157	24	0
13	n	961	0	1000	24	0
14	o	892	0	923	23	0
15	p	917	0	965	24	0
16	q	947	0	1022	12	0
17	r	816	0	839	20	0
18	s	857	0	922	21	0
19	t	739	0	807	19	0
20	u	780	0	834	19	0
21	v	753	0	780	11	0
22	w	575	0	592	10	0
23	x	625	0	655	19	0
24	y	509	0	543	9	0
25	z	449	0	491	13	0
26	B	444	0	461	9	0
27	C	410	0	440	5	0
28	D	377	0	418	12	0
29	E	504	0	574	18	0
30	F	302	0	343	11	0
31	G	1757	0	1787	22	0
32	H	1625	0	1699	30	0
33	I	1643	0	1710	60	0
34	J	1157	0	1199	39	0
35	K	818	0	808	34	0
36	L	1182	0	1240	30	0
37	M	979	0	1034	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	32	0
39	O	787	0	828	39	0
40	P	870	0	878	22	0
41	Q	955	0	1019	39	0
42	R	884	0	944	25	0
43	S	805	0	847	33	0
44	T	714	0	737	11	0
45	U	649	0	666	26	0
46	V	649	0	691	18	0
47	W	536	0	552	15	0
48	X	638	0	665	18	0
49	Y	665	0	714	19	0
50	Z	545	0	579	33	0
51	a	1027	0	1092	34	0
52	3	33012	0	16618	378	0
53	1	62317	0	31346	664	0
54	2	2568	0	1303	52	0
55	5	1640	0	837	9	0
55	6	1640	0	837	12	0
56	4	388	0	197	4	0
57	7	1619	0	821	11	0
58	7	11	0	8	0	0
59	7	8	0	8	0	0
All	All	150220	0	101265	2120	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 2120 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:45:G:H5''	53:1:46:G:H5'	1.35	1.04
53:1:821:A:H5''	53:1:822:G:H5''	1.40	1.01
8:i:91:LYS:HE2	8:i:91:LYS:HA	1.43	0.99
9:j:100:VAL:HG13	9:j:101:ILE:HD12	1.45	0.99
39:O:57:VAL:HG22	39:O:58:ASN:H	1.30	0.97

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	241 (90%)	25 (9%)	3 (1%)	11	43
2	c	207/209 (99%)	186 (90%)	21 (10%)	0	100	100
3	d	199/201 (99%)	179 (90%)	18 (9%)	2 (1%)	12	45
4	e	175/177 (99%)	154 (88%)	19 (11%)	2 (1%)	11	43
5	f	174/176 (99%)	161 (92%)	12 (7%)	1 (1%)	21	54
6	g	147/149 (99%)	127 (86%)	16 (11%)	4 (3%)	4	27
7	h	129/131 (98%)	96 (74%)	28 (22%)	5 (4%)	2	20
8	i	139/141 (99%)	123 (88%)	11 (8%)	5 (4%)	2	22
9	j	140/142 (99%)	133 (95%)	4 (3%)	3 (2%)	5	31
10	k	120/122 (98%)	102 (85%)	17 (14%)	1 (1%)	16	49
11	l	141/143 (99%)	120 (85%)	16 (11%)	5 (4%)	3	23
12	m	134/136 (98%)	119 (89%)	12 (9%)	3 (2%)	5	30
13	n	118/120 (98%)	102 (86%)	15 (13%)	1 (1%)	16	49
14	o	114/116 (98%)	103 (90%)	10 (9%)	1 (1%)	14	46
15	p	112/114 (98%)	98 (88%)	14 (12%)	0	100	100
16	q	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
17	r	101/103 (98%)	94 (93%)	5 (5%)	2 (2%)	6	32
18	s	108/110 (98%)	96 (89%)	11 (10%)	1 (1%)	14	46
19	t	91/93 (98%)	78 (86%)	13 (14%)	0	100	100
20	u	100/102 (98%)	82 (82%)	14 (14%)	4 (4%)	2	20
21	v	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	w	73/75 (97%)	63 (86%)	10 (14%)	0	100	100
23	x	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
24	y	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
25	z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	47 (87%)	5 (9%)	2 (4%)	2	21
27	C	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
28	D	44/46 (96%)	36 (82%)	8 (18%)	0	100	100
29	E	62/64 (97%)	50 (81%)	11 (18%)	1 (2%)	7	36
30	F	36/38 (95%)	27 (75%)	8 (22%)	1 (3%)	4	26
31	G	223/225 (99%)	206 (92%)	17 (8%)	0	100	100
32	H	204/206 (99%)	192 (94%)	11 (5%)	1 (0%)	24	57
33	I	203/205 (99%)	180 (89%)	19 (9%)	4 (2%)	6	32
34	J	155/157 (99%)	128 (83%)	23 (15%)	4 (3%)	4	27
35	K	98/100 (98%)	84 (86%)	10 (10%)	4 (4%)	2	19
36	L	149/151 (99%)	136 (91%)	10 (7%)	3 (2%)	6	32
37	M	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	16	49
38	N	125/127 (98%)	105 (84%)	15 (12%)	5 (4%)	2	20
39	O	96/98 (98%)	81 (84%)	11 (12%)	4 (4%)	2	19
40	P	114/116 (98%)	94 (82%)	15 (13%)	5 (4%)	2	18
41	Q	121/123 (98%)	94 (78%)	23 (19%)	4 (3%)	3	24
42	R	112/114 (98%)	95 (85%)	12 (11%)	5 (4%)	2	17
43	S	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
44	T	86/88 (98%)	76 (88%)	9 (10%)	1 (1%)	10	41
45	U	80/82 (98%)	66 (82%)	13 (16%)	1 (1%)	9	39
46	V	78/80 (98%)	62 (80%)	14 (18%)	2 (3%)	4	27
47	W	63/65 (97%)	57 (90%)	5 (8%)	1 (2%)	7	36
48	X	77/79 (98%)	68 (88%)	7 (9%)	2 (3%)	4	27
49	Y	83/85 (98%)	78 (94%)	4 (5%)	1 (1%)	10	41
50	Z	63/65 (97%)	42 (67%)	15 (24%)	6 (10%)	0	6
51	a	130/223 (58%)	122 (94%)	8 (6%)	0	100	100
All	All	5919/6112 (97%)	5209 (88%)	609 (10%)	101 (2%)	9	35

5 of 101 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
5	f	45	ALA

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Mol	Chain	Res	Type
6	g	9	VAL
6	g	10	ALA
7	h	118	ILE

5.3.2 Protein sidechains [i](#)

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	b	216/216 (100%)	215 (100%)	1 (0%)	81	80
2	c	164/164 (100%)	162 (99%)	2 (1%)	63	73
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	147 (99%)	1 (1%)	76	78
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	114 (100%)	0	100	100
7	h	100/100 (100%)	99 (99%)	1 (1%)	68	75
8	i	109/109 (100%)	108 (99%)	1 (1%)	70	76
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	76
10	k	103/103 (100%)	103 (100%)	0	100	100
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	99 (99%)	1 (1%)	68	75
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	73
15	p	99/99 (100%)	99 (100%)	0	100	100
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	74
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	90 (97%)	3 (3%)	34	58
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	78 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	46 (98%)	1 (2%)	47	65
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	36 (95%)	2 (5%)	20	48
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	186 (100%)	0	100	100
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	79
33	I	172/172 (100%)	171 (99%)	1 (1%)	78	79
34	J	119/119 (100%)	117 (98%)	2 (2%)	53	69
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	74
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	104 (100%)	0	100	100
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	83 (96%)	3 (4%)	32	57
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	101 (98%)	2 (2%)	50	67
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	82 (99%)	1 (1%)	63	73
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	64 (98%)	1 (2%)	57	70
46	V	74/74 (100%)	73 (99%)	1 (1%)	59	71
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	54 (98%)	1 (2%)	51	68
51	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4908/4972 (99%)	4878 (99%)	30 (1%)	76	79

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	D	31	LEU
45	U	74	LEU
33	I	199	ILE
50	Z	23	GLU
41	Q	51	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 105 such sidechains are listed below:

Mol	Chain	Res	Type
25	z	33	HIS
33	I	130	ASN
49	Y	47	GLN
26	B	5	ASN
31	G	176	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	143 (9%)	2 (0%)
53	1	2902/2903 (99%)	329 (11%)	10 (0%)
54	2	119/120 (99%)	11 (9%)	1 (0%)
55	5	76/77 (98%)	8 (10%)	0
55	6	76/77 (98%)	7 (9%)	0
56	4	17/18 (94%)	2 (11%)	0
57	7	75/77 (97%)	13 (17%)	1 (1%)
All	All	4803/4811 (99%)	513 (10%)	14 (0%)

5 of 513 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	1475	G
53	1	2286	G
57	7	65	G
53	1	2391	G
54	2	88	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	PHE	7	101	59,57	10,11,12	0.70	0	8,13,15	0.33	0
59	FME	7	102	58	6,7,10	0.44	0	2,7,11	0.18	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	PHE	7	101	59,57	-	2/5/6/8	0/1/1/1
59	FME	7	102	58	-	0/5/6/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	7	101	PHE	CA-CB-CG-CD2
58	7	101	PHE	CA-CB-CG-CD1

There are no ring outliers.

No monomer is involved in short contacts.

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.

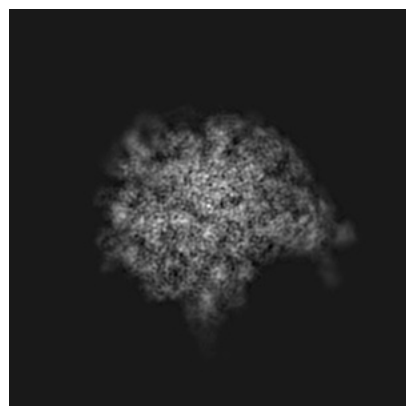
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21641. These allow visual inspection of the internal detail of the map and identification of artifacts.

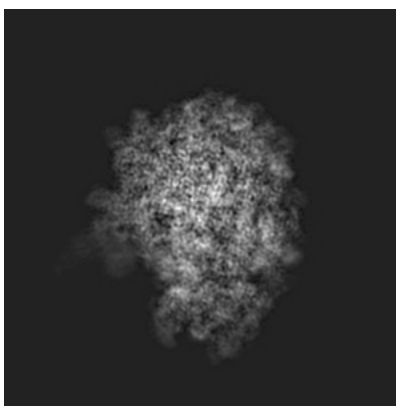
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

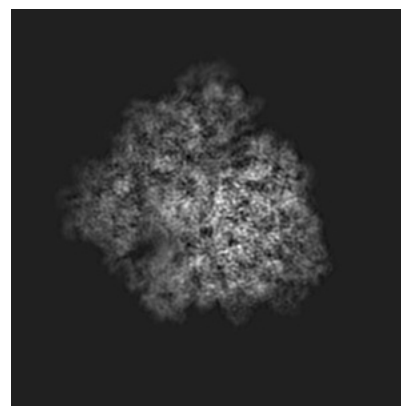
6.1.1 Primary map



X

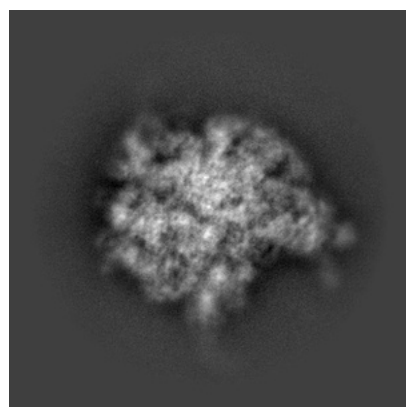


Y

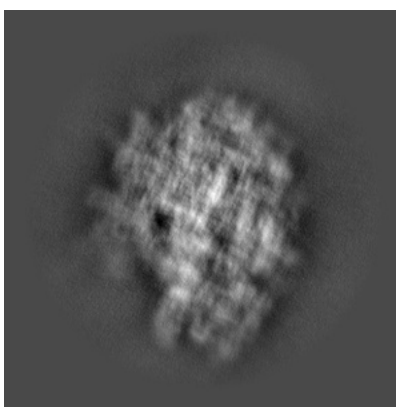


Z

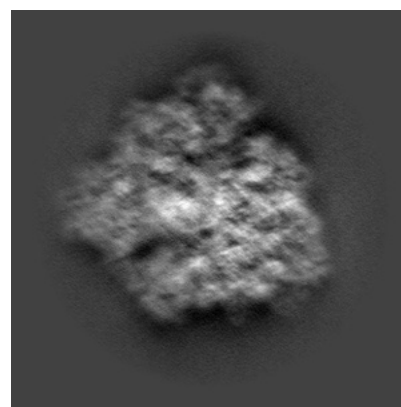
6.1.2 Raw map



X



Y

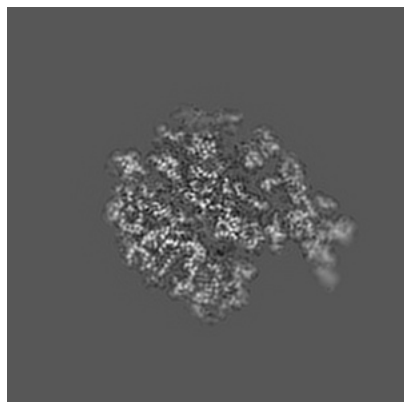


Z

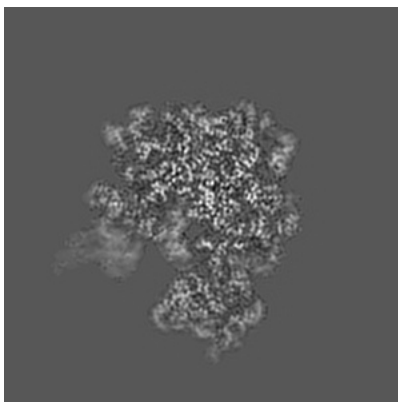
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

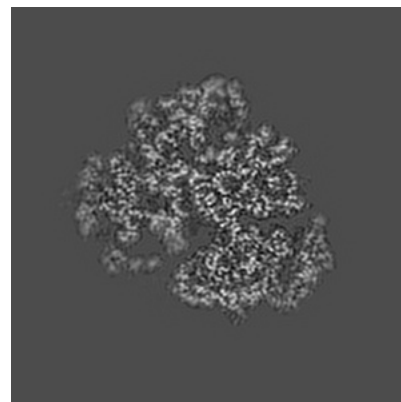
6.2.1 Primary map



X Index: 144

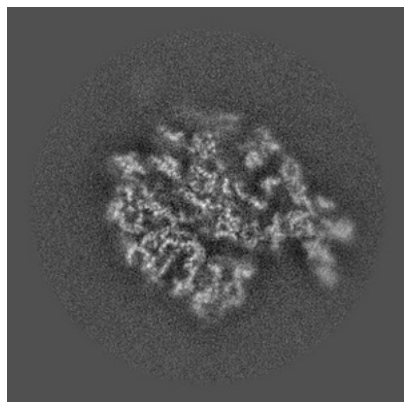


Y Index: 144

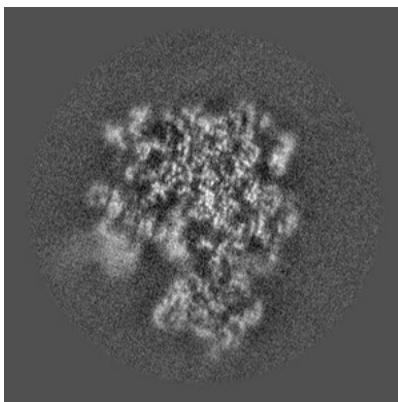


Z Index: 144

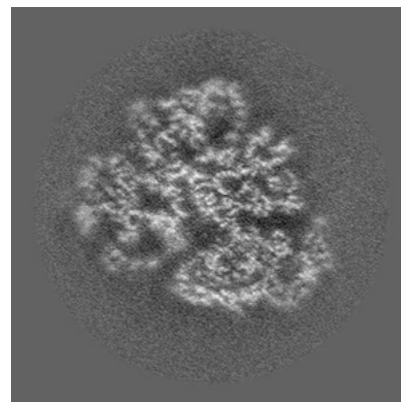
6.2.2 Raw map



X Index: 144



Y Index: 144

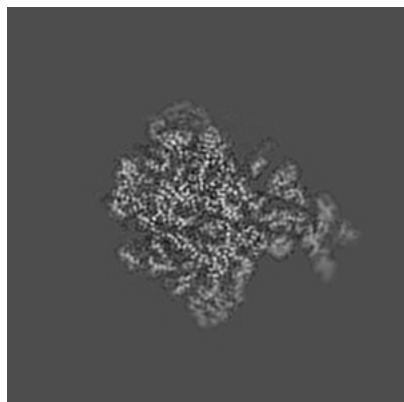


Z Index: 144

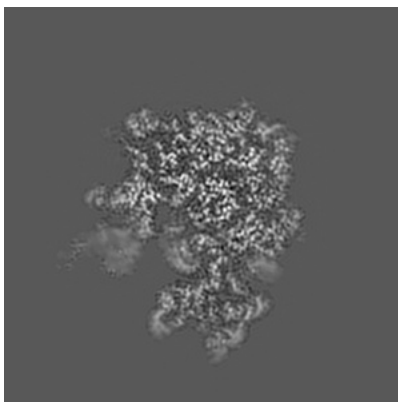
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

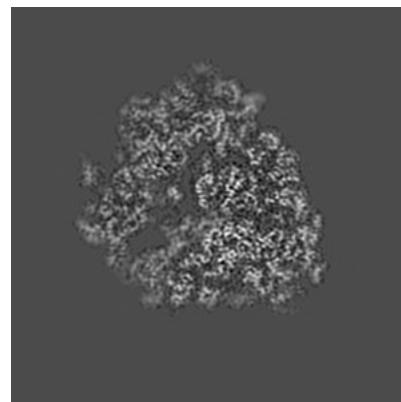
6.3.1 Primary map



X Index: 150

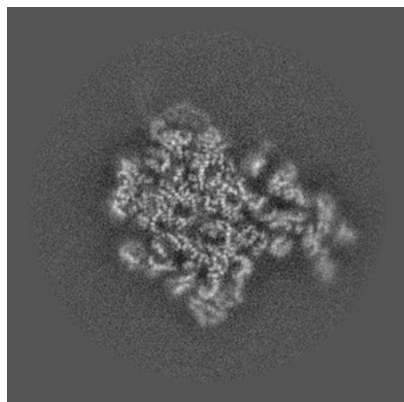


Y Index: 149

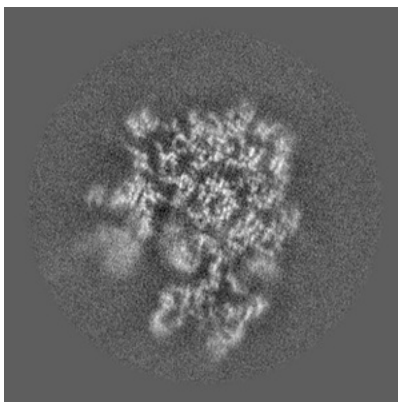


Z Index: 135

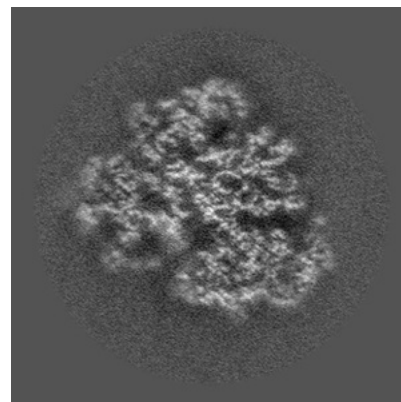
6.3.2 Raw map



X Index: 150



Y Index: 149

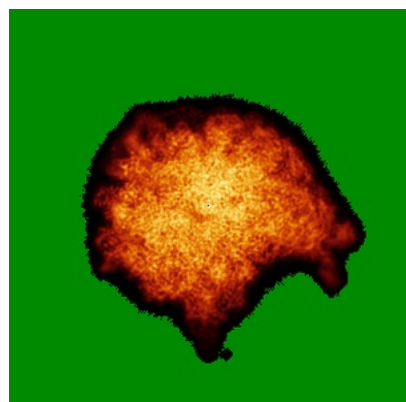


Z Index: 145

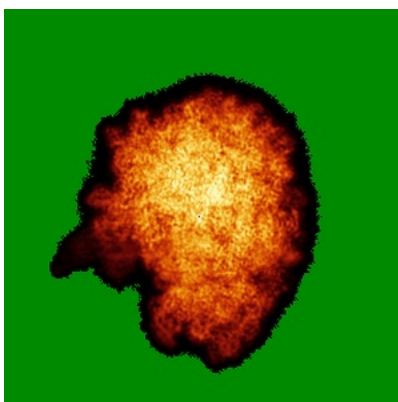
The images above show the largest variance slices of the map in three orthogonal directions.

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

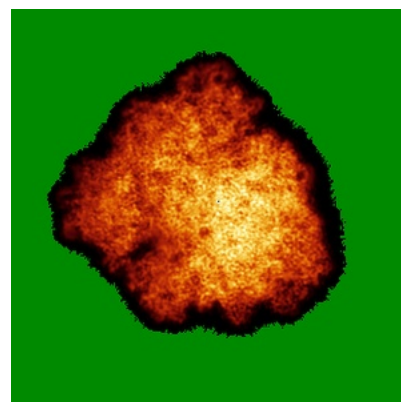
6.4.1 Primary map



X

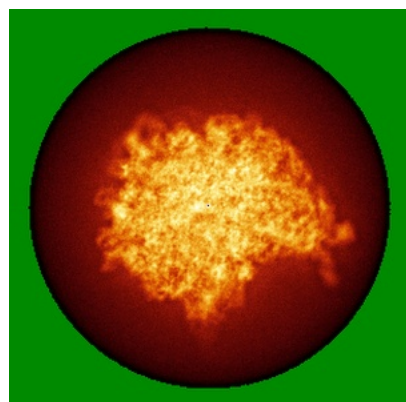


Y

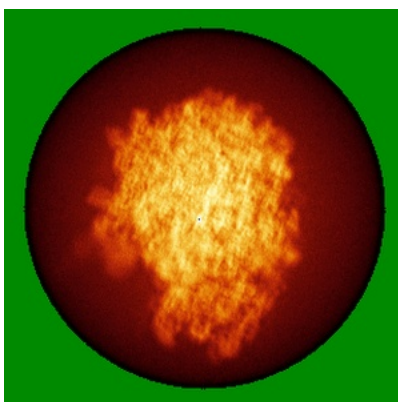


Z

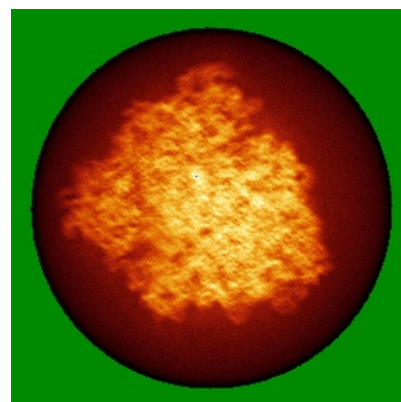
6.4.2 Raw map



X



Y

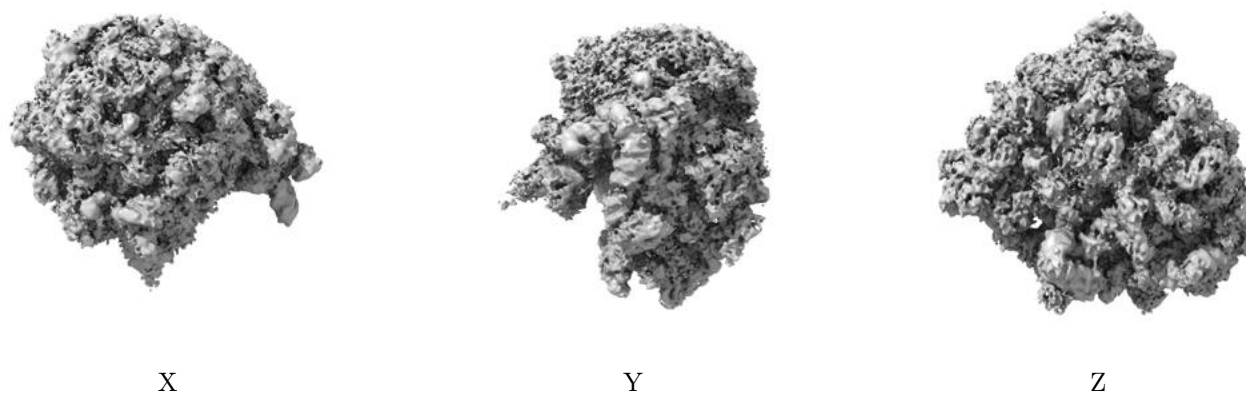


Z

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.

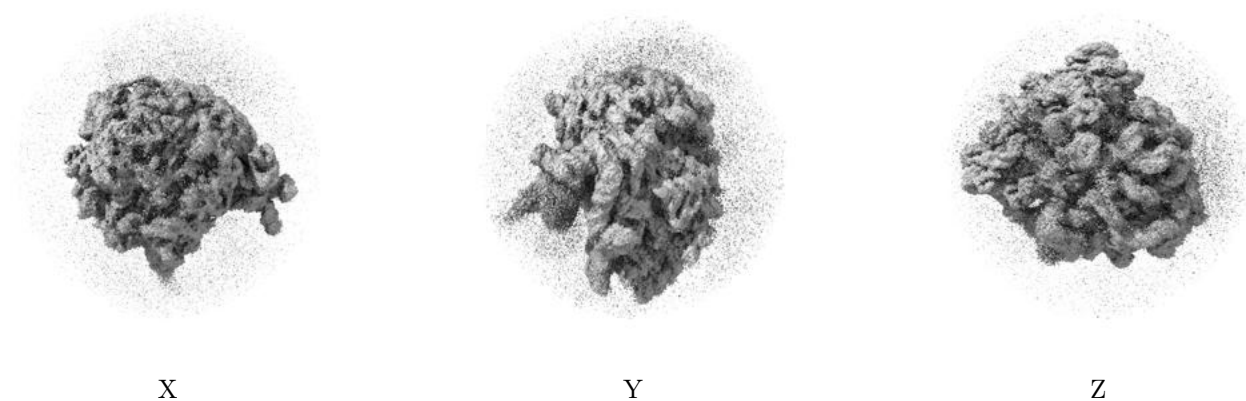
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. 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.

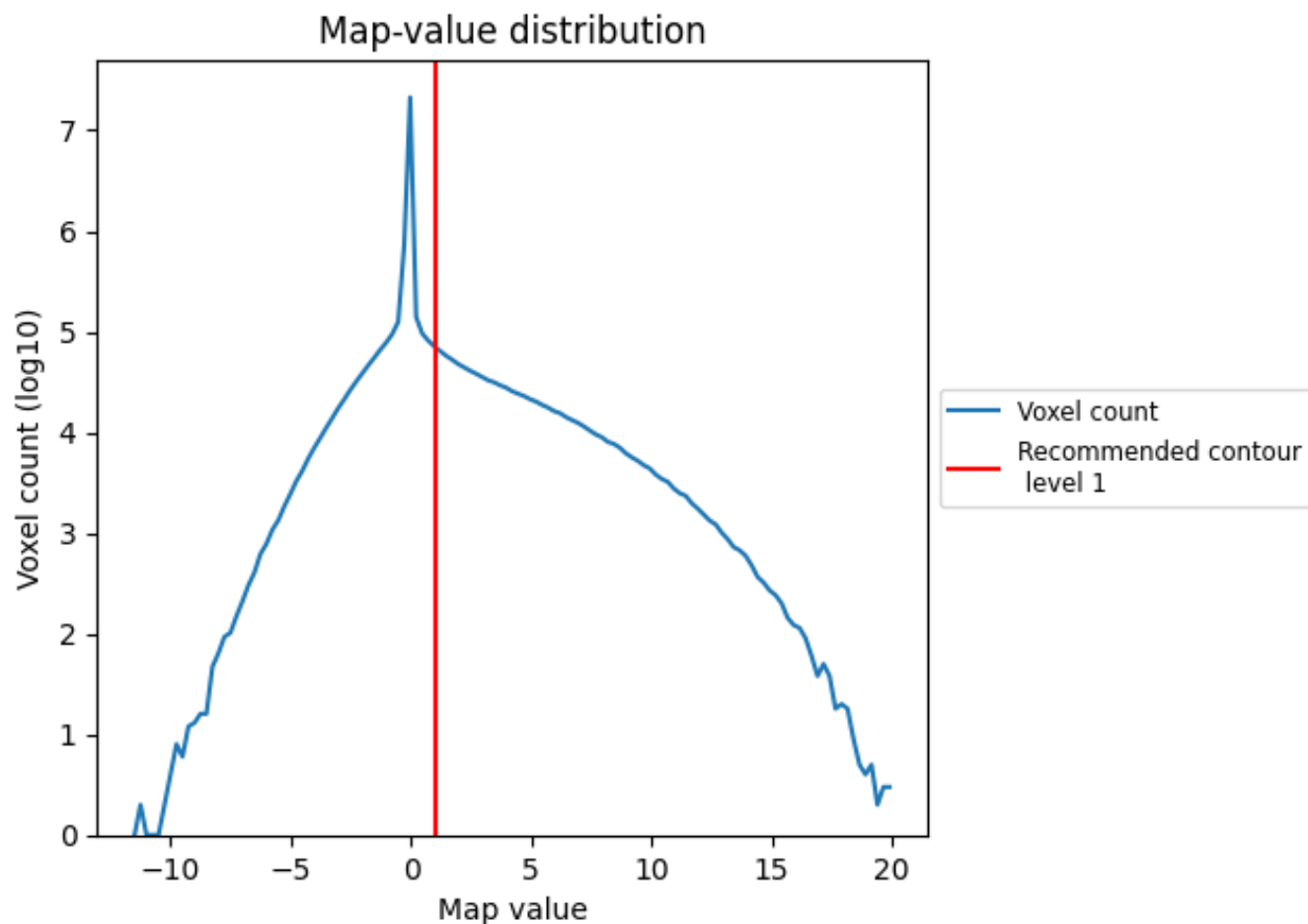
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

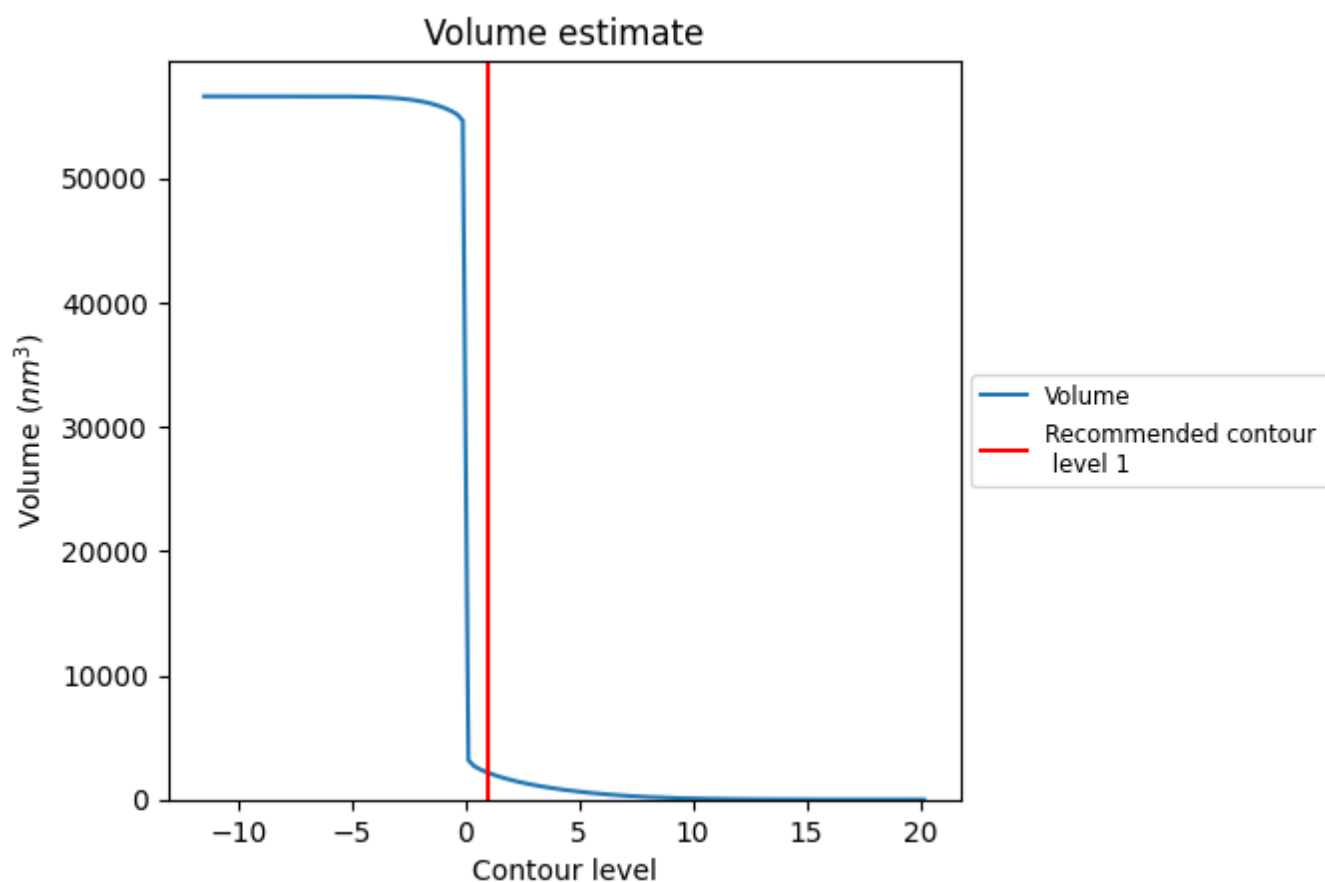
This section contains the results of statistical analysis of the map.

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.

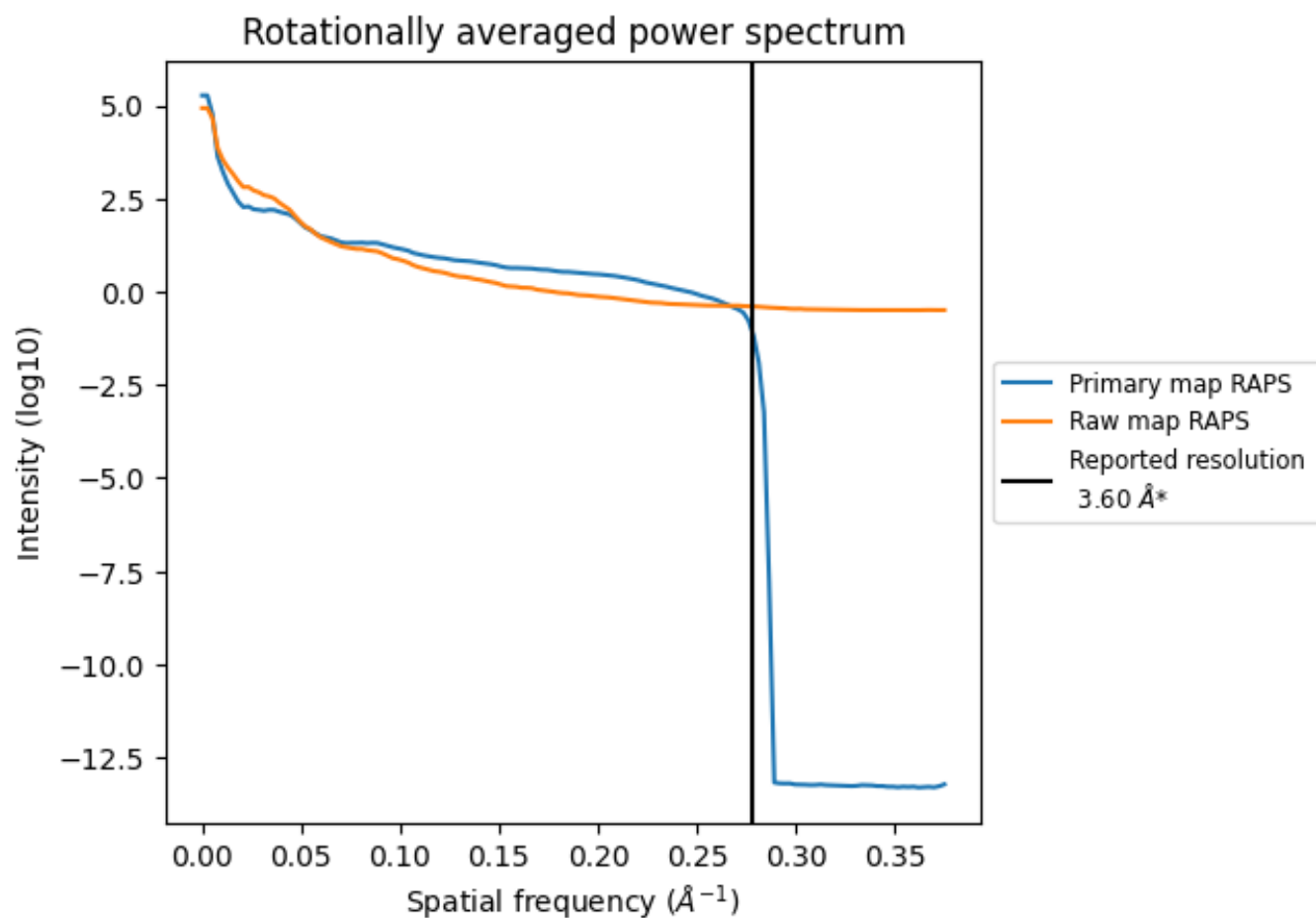
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2159 nm³; this corresponds to an approximate mass of 1951 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 ⓘ

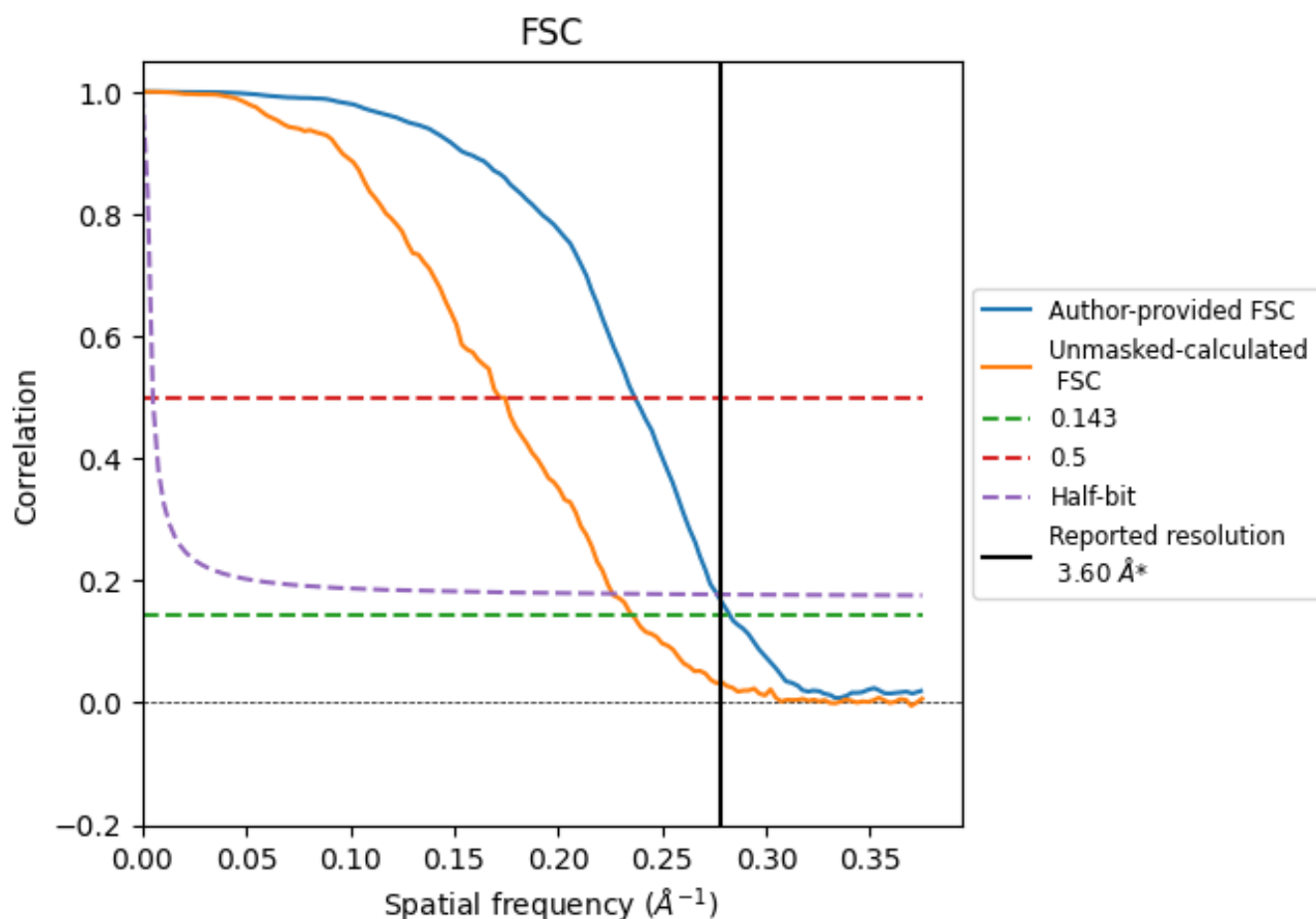


*Reported resolution corresponds to spatial frequency of $0.278 \text{ \AA}^{-1}$

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 $0.278 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

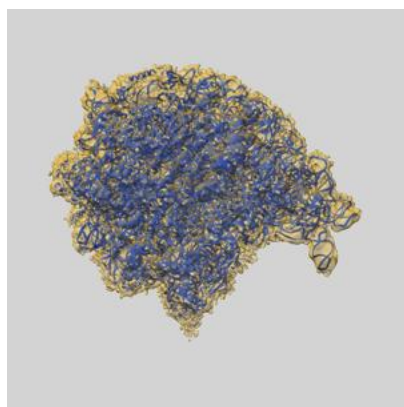
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.54	4.22	3.62
Unmasked-calculated*	4.24	5.82	4.42

*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 3.6 by more than 10 %

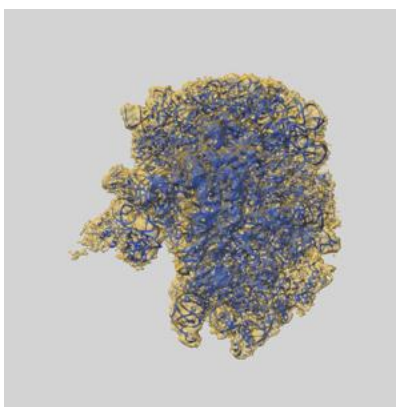
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21641 and PDB model 6WDM. Per-residue inclusion information can be found in section 3 on page 16.

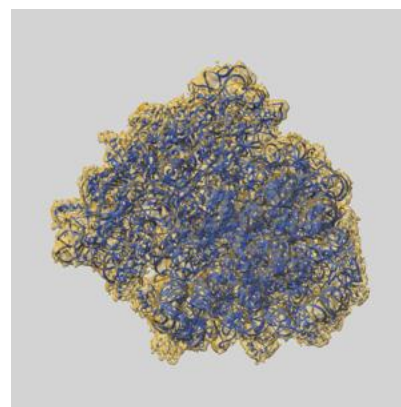
9.1 Map-model overlay [i](#)



X



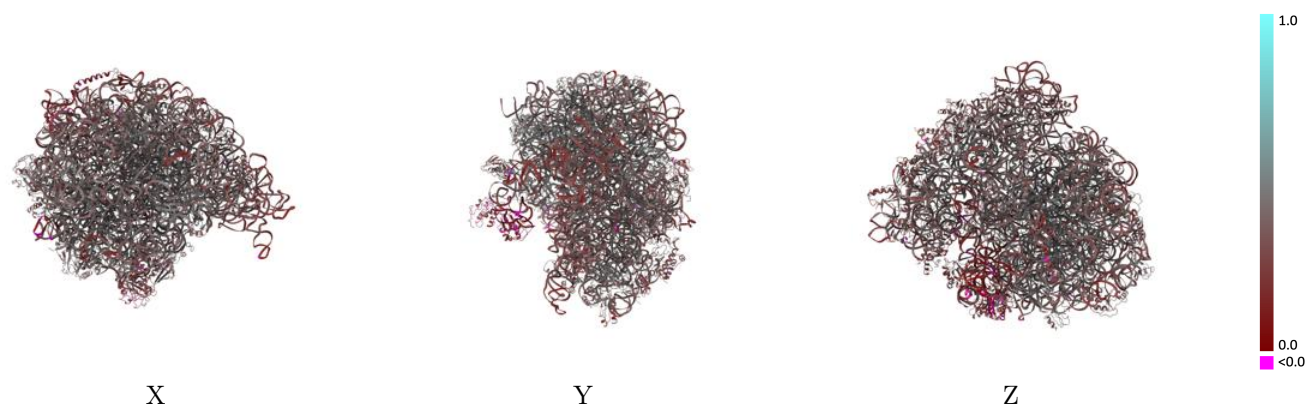
Y



Z

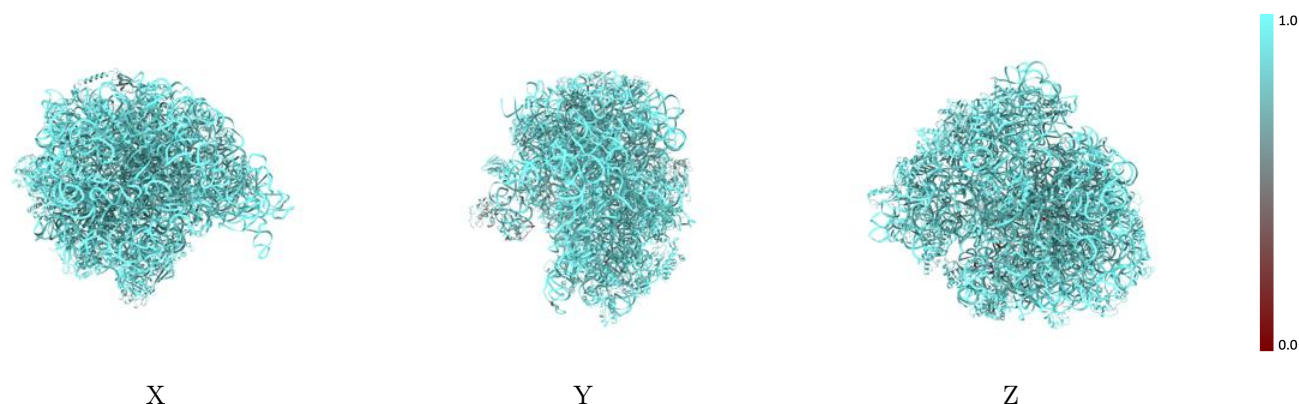
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



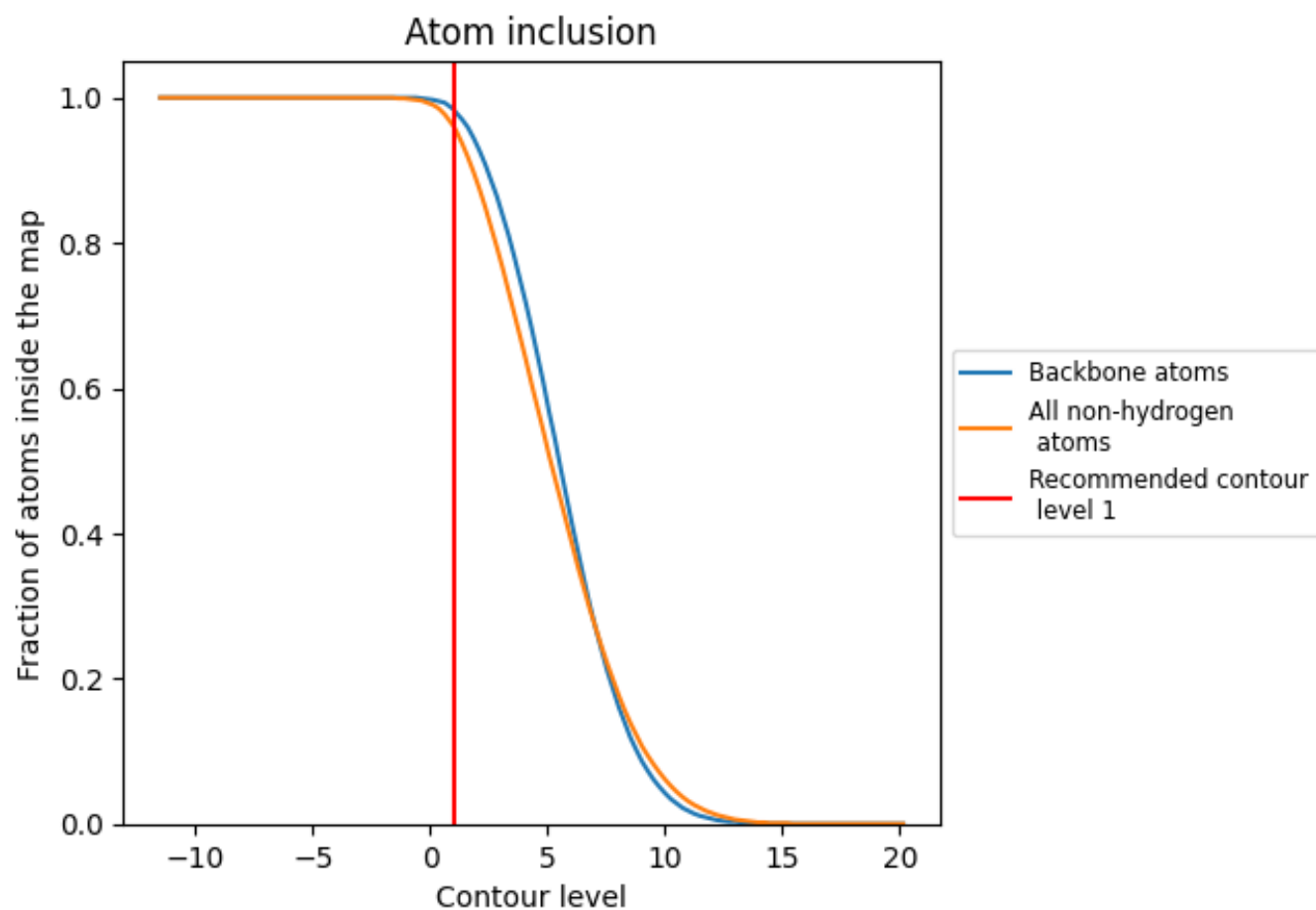
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9610	 0.3760
1	 0.9810	 0.3890
2	 0.9840	 0.3490
3	 0.9820	 0.3680
4	 0.9200	 0.3060
5	 0.9590	 0.3040
6	 0.8560	 0.1400
7	 0.9190	 0.2230
B	 0.9560	 0.4540
C	 0.9230	 0.4160
D	 0.9380	 0.4500
E	 0.9450	 0.4700
F	 0.9040	 0.4240
G	 0.9220	 0.3560
H	 0.9350	 0.4130
I	 0.9070	 0.3390
J	 0.9330	 0.4020
K	 0.9540	 0.3920
L	 0.9350	 0.3470
M	 0.9390	 0.4150
N	 0.9270	 0.3640
O	 0.8570	 0.3380
P	 0.9570	 0.4000
Q	 0.9340	 0.4330
R	 0.9470	 0.3320
S	 0.8940	 0.3680
T	 0.9480	 0.3900
U	 0.9380	 0.3860
V	 0.9370	 0.4050
W	 0.9300	 0.3770
X	 0.9700	 0.3740
Y	 0.8880	 0.3550
Z	 0.8630	 0.3040
a	 0.8800	 0.1610
b	 0.9500	 0.4630



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Chain	Atom inclusion	Q-score
c	 0.9470	 0.4530
d	 0.9530	 0.4140
e	 0.9470	 0.3170
f	 0.9630	 0.3640
g	 0.8200	 0.2770
h	 0.6720	 0.1330
i	 0.7100	 0.1100
j	 0.9480	 0.4550
k	 0.9480	 0.4590
l	 0.9440	 0.4340
m	 0.9310	 0.4480
n	 0.9450	 0.4430
o	 0.9480	 0.3730
p	 0.9430	 0.4380
q	 0.9380	 0.4440
r	 0.9540	 0.4350
s	 0.9190	 0.4390
t	 0.9280	 0.4240
u	 0.9450	 0.4090
v	 0.9580	 0.4200
w	 0.9450	 0.4590
x	 0.9620	 0.4470
y	 0.9400	 0.3550
z	 0.9500	 0.4370