



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 05:59 AM UTC

PDB ID : 6WDA / pdb_00006wda
EMDB ID : EMD-21629
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure III-C)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.80 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

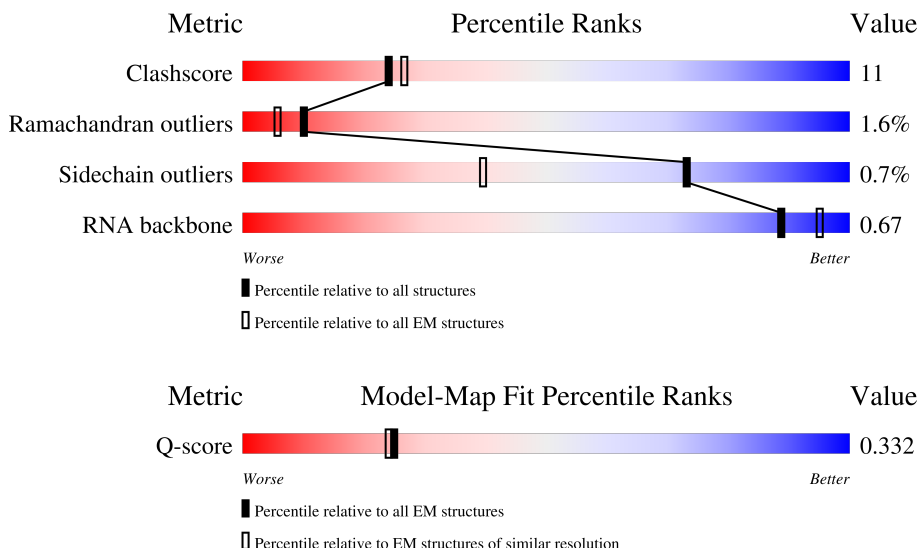
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.



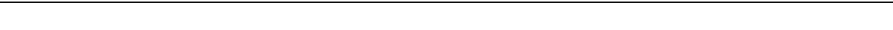
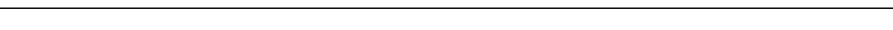
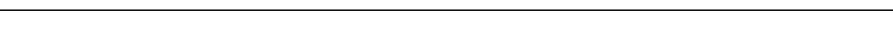
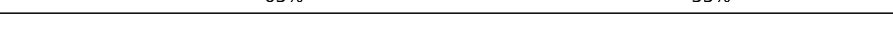
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	

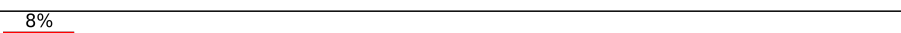
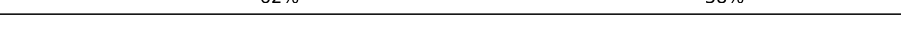
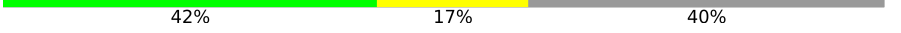
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Mol	Chain	Length	Quality of chain
4	e	177	 68% 31% .
5	f	176	 71% 27% ..
6	g	149	 26% 65% 34% .
7	h	131	 14% 52% 41% 5% .
8	i	141	 30% 67% 31% .
9	j	142	 78% 20% .
10	k	122	 68% 29% ..
11	l	143	 71% 26% ..
12	m	136	 60% 38% .
13	n	120	 70% 30%
14	o	116	 70% 28% .
15	p	114	 62% 38%
16	q	117	 77% 22% .
17	r	103	 63% 33% .
18	s	110	 71% 28% .
19	t	93	 76% 22% .
20	u	102	 61% 36% .
21	v	94	 69% 29% .
22	w	75	 81% 19%
23	x	77	 75% 23% .
24	y	63	 75% 25%
25	z	58	 67% 33%
26	B	56	 75% 25%
27	C	50	 76% 24%
28	D	46	 76% 24%

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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	51% 44% 5%
55	5	77	64% 32% •
55	6	77	5% 55% 39% 6%
56	4	18	6% 61% 39%
57	7	76	• 55% 38% 7%
58	8	400	20% 58% 28% • 13%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 152933 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
			917	574	179	163	1	0

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

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

- 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
			816	516	153	145	2	0

- 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
			857	532	166	156	3	0

- 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
			739	466	139	132	2	0

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

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

- 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 1036415628

- 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 1370526515

- 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	76	120	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		

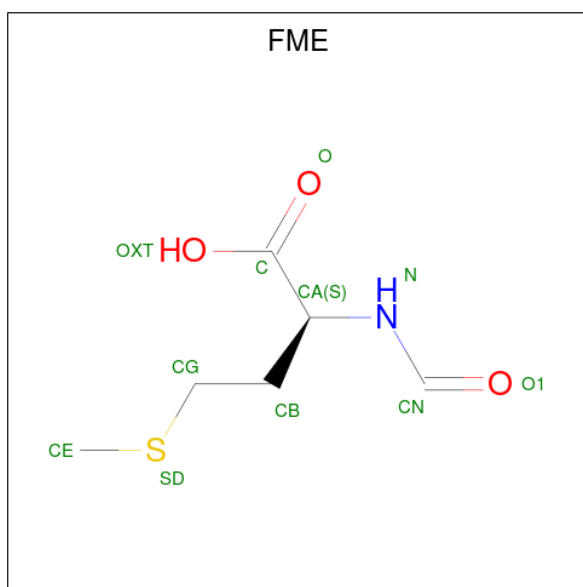
- Molecule 58 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	348	Total	C	N	O	S	0	0
			2683	1702	459	509	13		

There are 7 discrepancies between the modelled and reference sequences:

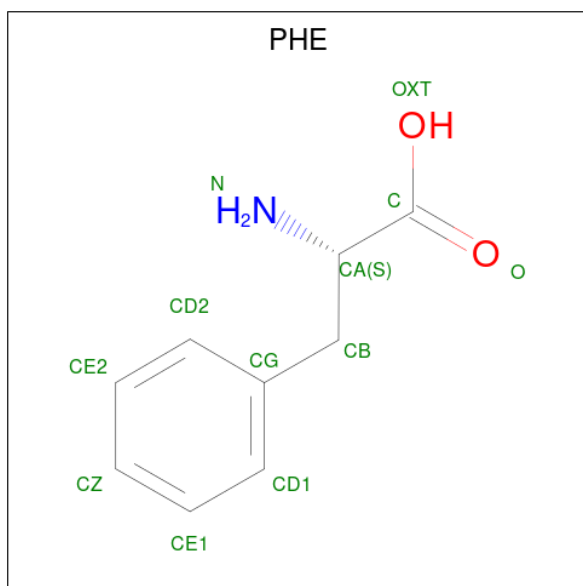
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag	UNP E2QFJ4

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



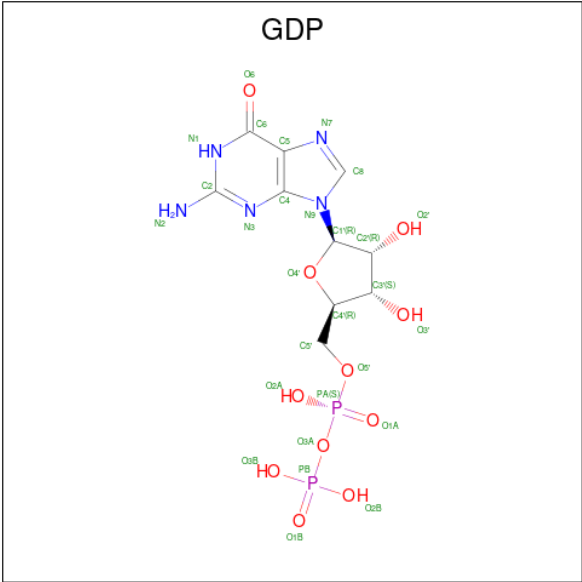
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 60 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms				AltConf
60	7	1	Total	C	N	O	0
			11	9	1	1	

- Molecule 61 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

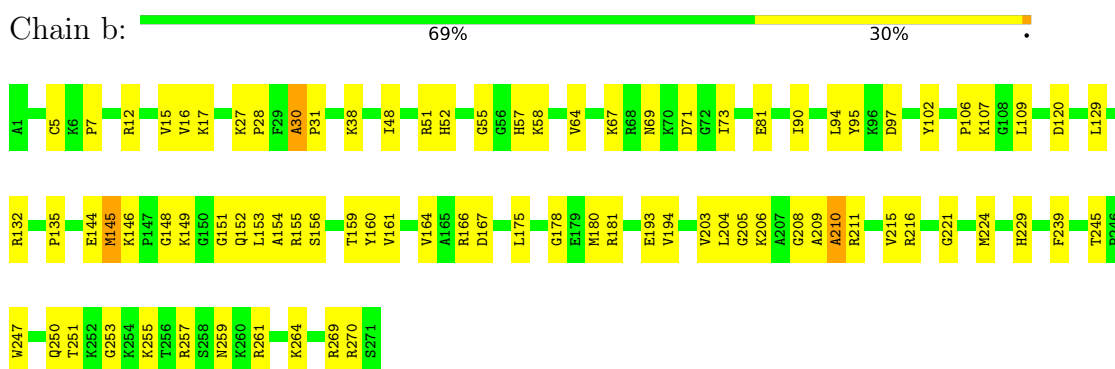


Mol	Chain	Residues	Atoms					AltConf
61	8	1	Total	C	N	O	P	0
			28	10	5	11	2	

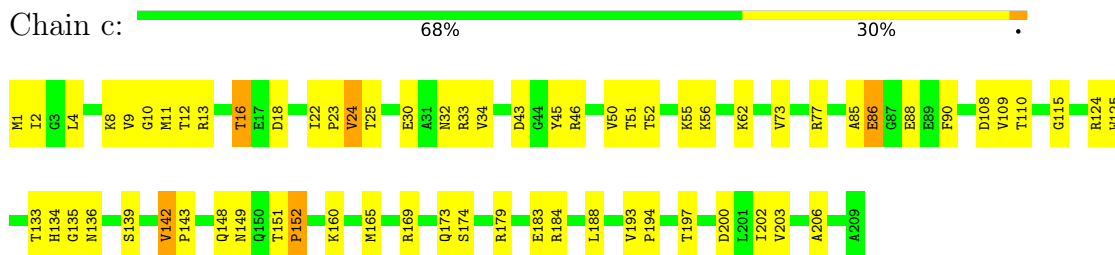
3 Residue-property plots [i](#)

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.

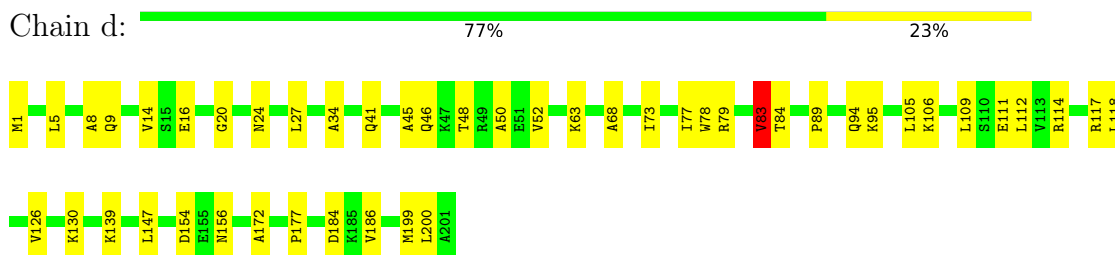
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

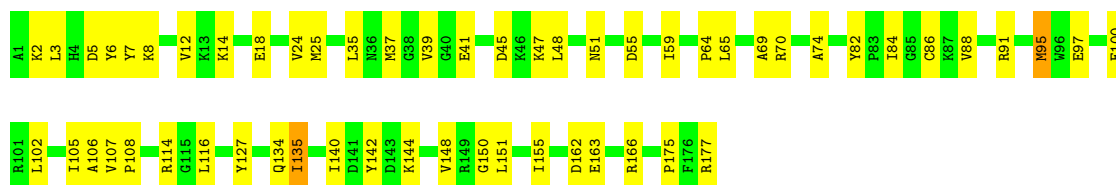


- Molecule 3: 50S ribosomal protein L4

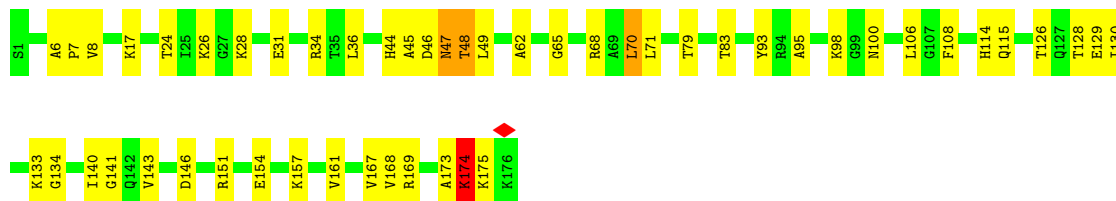


- Molecule 4: 50S ribosomal protein L5

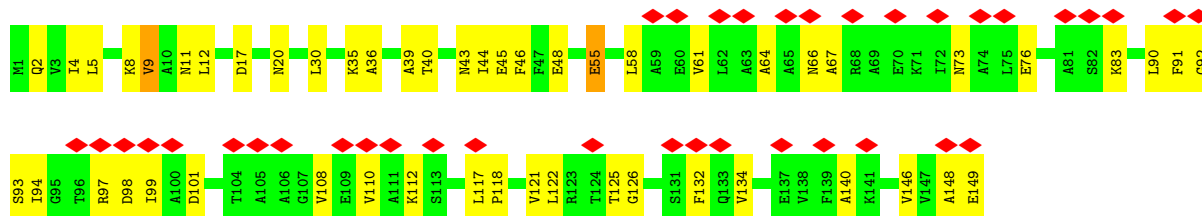




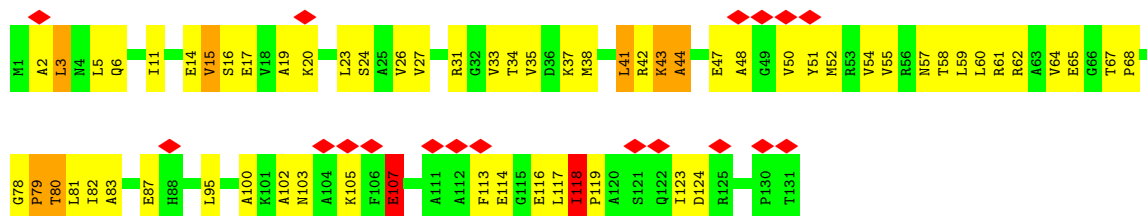
• Molecule 5: 50S ribosomal protein L6



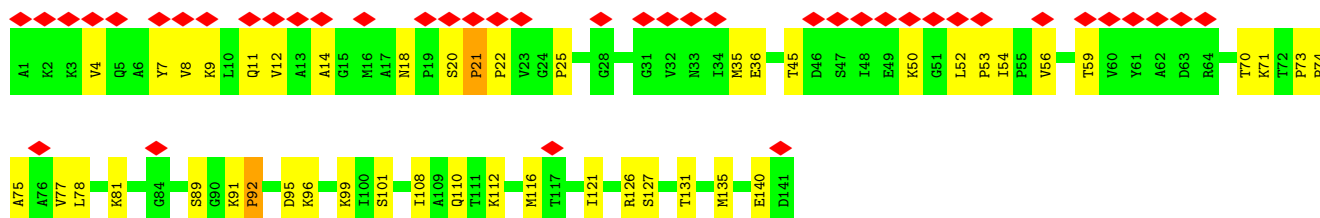
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L10

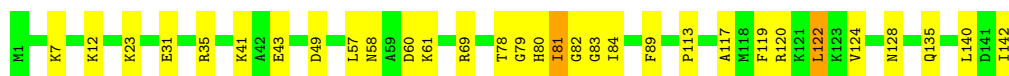


• Molecule 8: 50S ribosomal protein L11



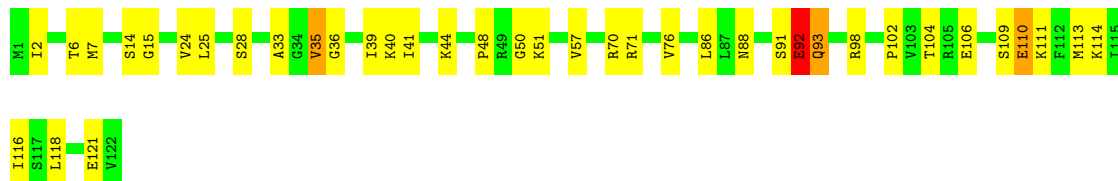
- Molecule 9: 50S ribosomal protein L13

Chain j:  78% 20%



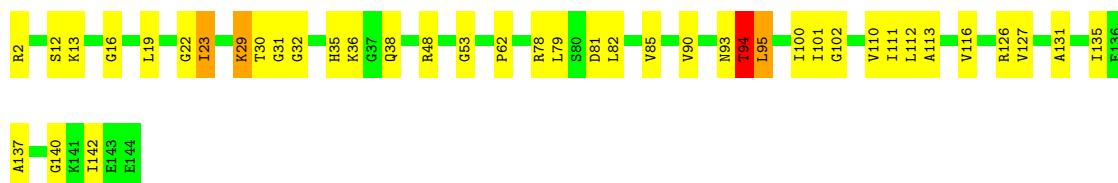
- Molecule 10: 50S ribosomal protein L14

Chain k:  68% 29%



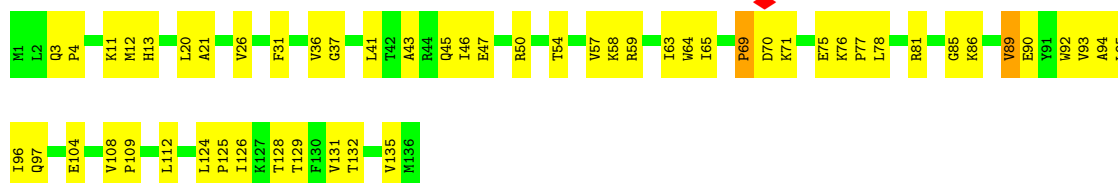
- Molecule 11: 50S ribosomal protein L15

Chain l:  71% 26%



- Molecule 12: 50S ribosomal protein L16

Chain m:  60% 38%



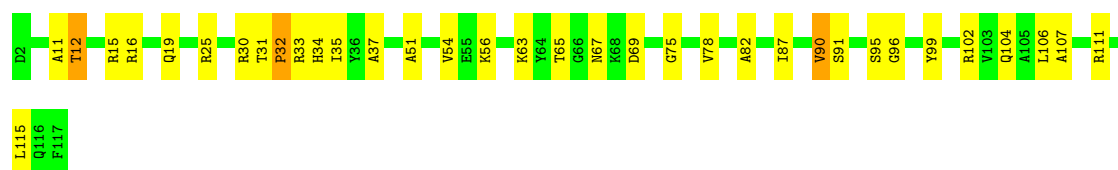
- Molecule 13: 50S ribosomal protein L17

Chain n:  70% 30%



- Molecule 14: 50S ribosomal protein L18

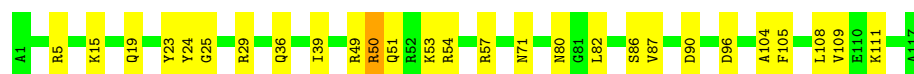
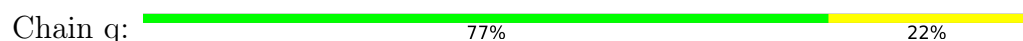
Chain o:  70% 28%



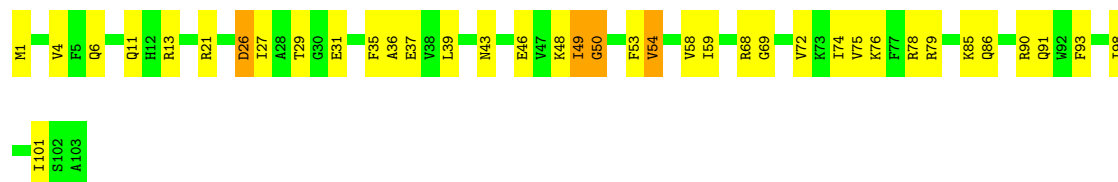
- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20



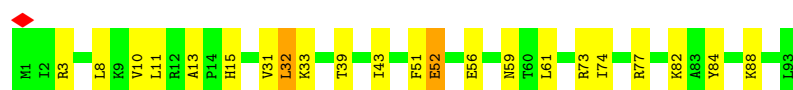
- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22

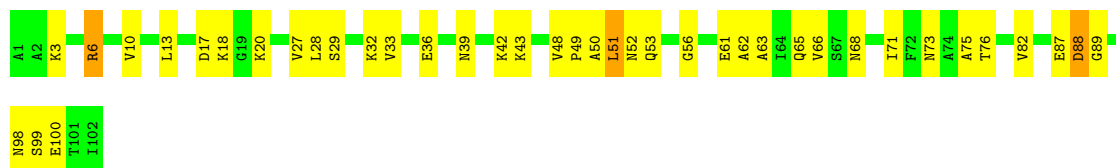


- Molecule 19: 50S ribosomal protein L23



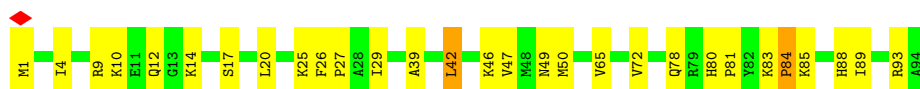
- Molecule 20: 50S ribosomal protein L24

Chain u:  61% 36%



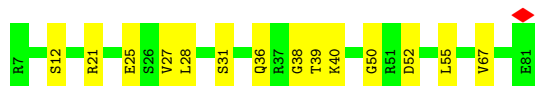
- Molecule 21: 50S ribosomal protein L25

Chain v:  69% 29%



- Molecule 22: 50S ribosomal protein L27

Chain w:  81% 19%



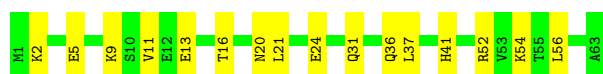
- Molecule 23: 50S ribosomal protein L28

Chain x:  75% 23%



- Molecule 24: 50S ribosomal protein L29

Chain y:  75% 25%



- Molecule 25: 50S ribosomal protein L30

Chain z:  67% 33%

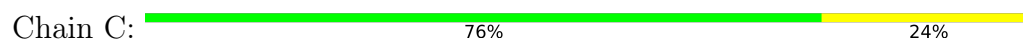


- Molecule 26: 50S ribosomal protein L32

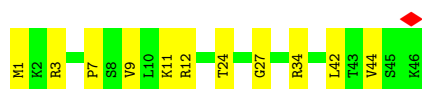
Chain B:  75% 25%



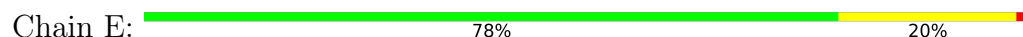
- Molecule 27: 50S ribosomal protein L33



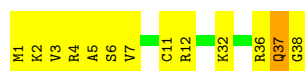
- Molecule 28: 50S ribosomal protein L34



- Molecule 29: 50S ribosomal protein L35



- Molecule 30: 50S ribosomal protein L36

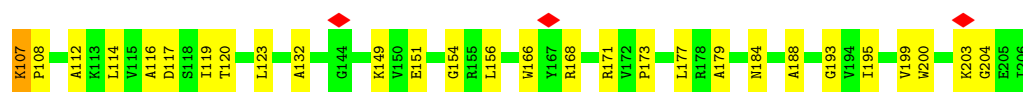


- Molecule 31: 30S ribosomal protein S2

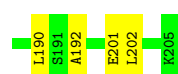
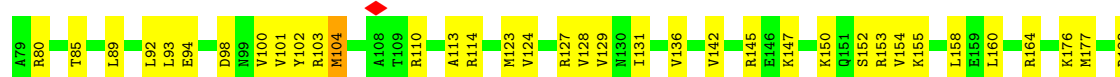


- Molecule 32: 30S ribosomal protein S3

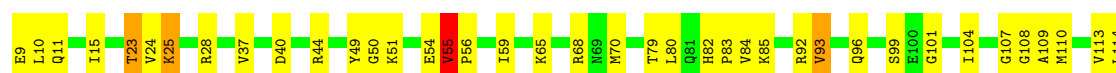




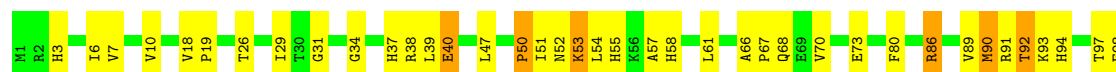
- Molecule 33: 30S ribosomal protein S4



- Molecule 34: 30S ribosomal protein S5



- Molecule 35: 30S ribosomal protein S6



- Molecule 36: 30S ribosomal protein S7



- Molecule 37: 30S ribosomal protein S8

Chain M:  67% 32% .



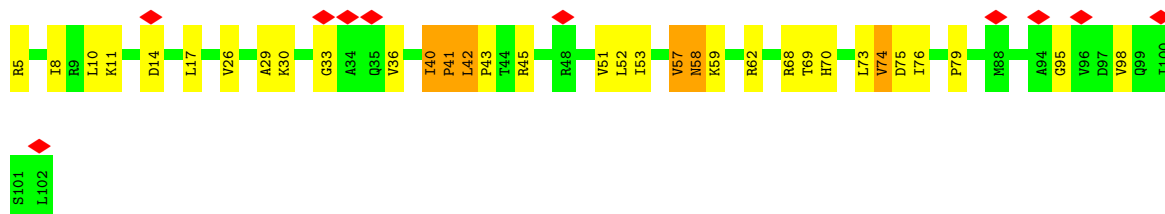
- Molecule 38: 30S ribosomal protein S9

Chain N:  62% 37% .



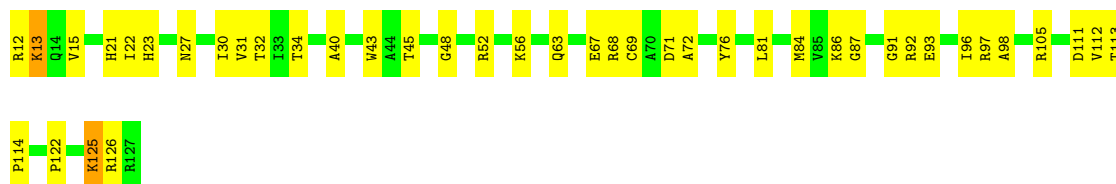
- Molecule 39: 30S ribosomal protein S10

Chain O:  10% 66% 28% 6%



- Molecule 40: 30S ribosomal protein S11

Chain P:  64% 34% .



- Molecule 41: 30S ribosomal protein S12

Chain Q:  64% 33% .





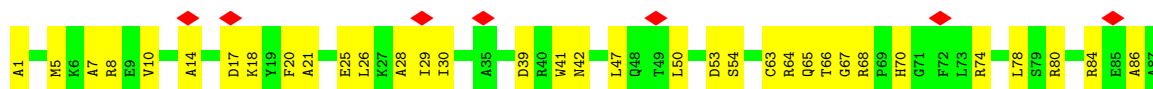
- Molecule 42: 30S ribosomal protein S13

Chain R: 59% 37% .



- Molecule 43: 30S ribosomal protein S14

Chain S: 8% 62% 38%



- Molecule 44: 30S ribosomal protein S15

Chain T: 76% 22% ..



- Molecule 45: 30S ribosomal protein S16

Chain U: 55% 40% 5%



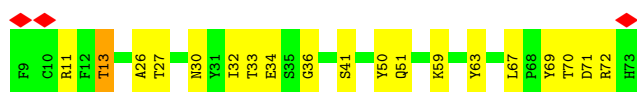
- Molecule 46: 30S ribosomal protein S17

Chain V: 70% 29% .



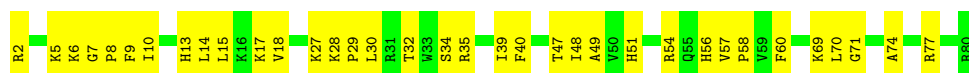
- Molecule 47: 30S ribosomal protein S18

Chain W: 5% 71% 28% .



- Molecule 48: 30S ribosomal protein S19

Chain X: 56% 44%



- Molecule 49: 30S ribosomal protein S20

Chain Y: 71% 28%



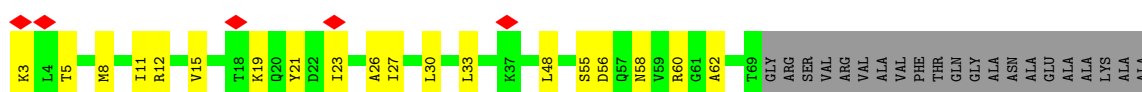
- Molecule 50: 30S ribosomal protein S21

Chain Z: 52% 35% 12%



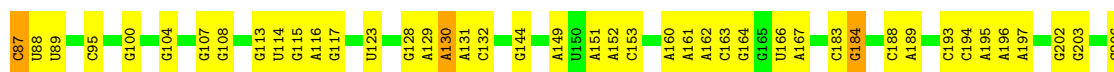
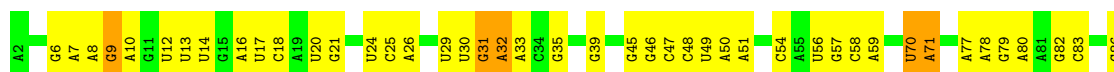
- Molecule 51: 50S ribosomal protein L1

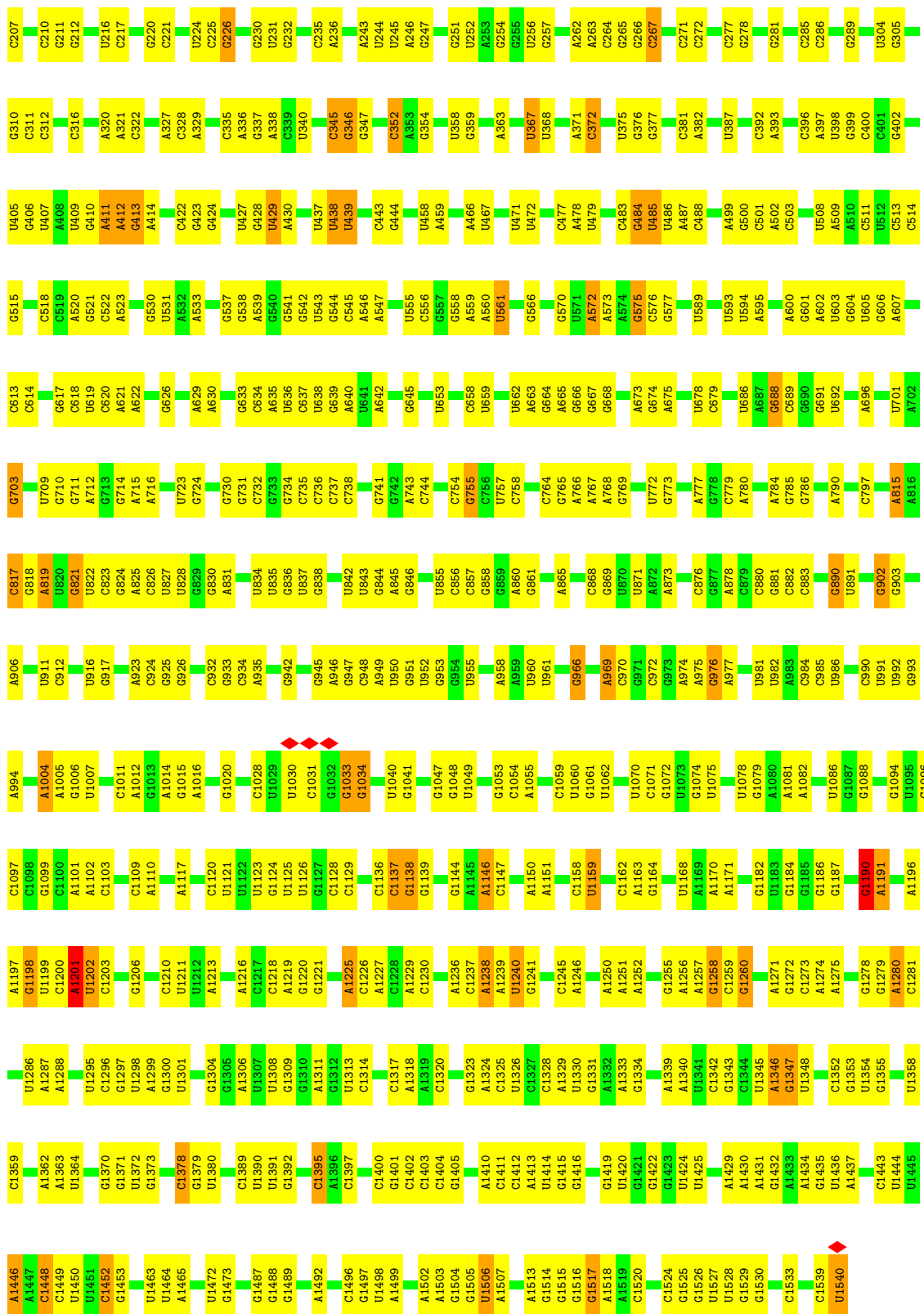
Chain a: 6% 42% 17% 40%



- Molecule 52: 16S ribosomal RNA

Chain 3: 55% 41%





• Molecule 53: 23S ribosomal RNA

Chain 1: 57% 39% 5%

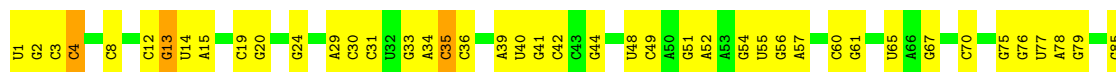
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A2762	U2763	U2726	U2449	G2620	U2528	U2449	U2359	G2276	U2210	U2123	G2046	C1956	C1852	U1796	U1688
G2764	U2765	U2727	U2450	G2621	U2529	U2450	U2360	G2277	U2211	U2124	G2047	C1957	C1853	C1797	G1689
U2766	U2767	U2728	U2451	G2622	U2530	U2451	U2361	G2278	U2212	U2125	G2048	C1958	C1854	C1894	G1690
C2768	U2769	U2729	U2452	G2623	U2531	U2452	U2362	G2279	U2213	U2126	G2049	C1959	C1855	U1798	G1691
A2770	U2771	U2730	U2453	G2624	U2532	U2453	U2363	G2280	U2214	U2127	G2050	C1960	C1856	U1799	U1692
G2772	U2773	U2731	U2454	G2625	U2533	U2454	U2364	G2281	U2215	U2128	G2051	C1961	C1857	C1799	G1693
C2774	U2775	U2732	U2455	G2626	U2534	U2455	U2365	G2282	U2216	U2129	G2052	C1962	C1858	U1799	U1694
G2776	U2777	U2733	U2456	G2627	U2535	U2456	U2366	G2283	U2217	U2130	G2053	C1963	C1859	C1799	U1695
U2778	U2779	U2734	U2457	G2628	U2536	U2457	U2367	G2284	U2218	U2131	G2054	C1964	C1860	U1799	G1696
C2780	U2781	U2735	U2458	G2629	U2537	U2458	U2368	G2285	U2219	U2132	G2055	C1965	C1861	C1799	U1697
A2782	U2783	U2736	U2459	G2630	U2538	U2459	U2369	G2286	U2220	U2133	G2056	C1966	C1862	C1894	G1698
G2784	U2785	U2737	U2460	G2631	U2539	U2460	U2370	G2287	U2221	U2134	G2057	C1967	C1863	U1799	U1699
U2786	U2787	U2738	U2461	G2632	U2540	U2461	U2371	G2288	U2222	U2135	G2058	C1968	C1864	U1799	G1699
C2788	U2789	U2739	U2462	G2633	U2541	U2462	U2372	G2289	U2223	U2136	G2059	C1969	C1865	U1799	G1699
G2790	U2791	U2740	U2463	G2634	U2542	U2463	U2373	G2290	U2224	U2137	G2060	C1970	C1866	U1799	G1699
U2792	U2793	U2741	U2464	G2635	U2543	U2464	U2374	G2291	U2225	U2138	G2061	C1971	C1867	U1799	G1699
C2794	U2795	U2742	U2465	G2636	U2544	U2465	U2375	G2292	U2226	U2139	G2062	C1972	C1868	U1799	G1699
U2796	U2797	U2743	U2466	G2637	U2545	U2466	U2376	G2293	U2227	U2140	G2063	C1973	C1869	U1799	G1699
G2798	U2799	U2744	U2467	G2638	U2546	U2467	U2377	G2294	U2228	U2141	G2064	C1974	C1870	U1799	G1699
A2800	U2801	U2745	U2468	G2639	U2547	U2468	U2378	G2295	U2229	U2142	G2065	C1975	C1871	U1799	G1699
C2802	U2803	U2746	U2469	G2640	U2548	U2469	U2379	G2296	U2230	U2143	G2066	C1976	C1872	U1799	G1699
U2804	U2805	U2747	U2470	G2641	U2549	U2470	U2380	G2297	U2231	U2144	G2067	C1977	C1873	U1799	G1699
G2806	U2807	U2748	U2471	G2642	U2550	U2471	U2381	G2298	U2232	U2145	G2068	C1978	C1874	U1799	G1699
C2808	U2809	U2749	U2472	G2643	U2551	U2472	U2382	G2299	U2233	U2146	G2069	C1979	C1875	U1799	G1699
U2810	U2811	U2750	U2473	G2644	U2552	U2473	U2383	G2300	U2234	U2147	G2070	C1980	C1876	U1799	G1699
G2812	U2813	U2751	U2474	G2645	U2553	U2474	U2384	G2301	U2235	U2148	G2071	C1981	C1877	U1799	G1699
A2814	U2815	U2752	U2475	G2646	U2554	U2475	U2385	G2302	U2236	U2149	G2072	C1982	C1878	U1799	G1699
C2816	U2817	U2753	U2476	G2647	U2555	U2476	U2386	G2303	U2237	U2150	G2073	C1983	C1879	U1799	G1699
U2818	U2819	U2754	U2477	G2648	U2556	U2477	U2387	G2304	U2238	U2151	G2074	C1984	C1880	U1799	G1699
G2820	U2821	U2755	U2478	G2649	U2557	U2478	U2388	G2305	U2239	U2152	G2075	C1985	C1881	U1799	G1699
C2822	U2823	U2756	U2479	G2650	U2558	U2479	U2389	G2306	U2240	U2153	G2076	C1986	C1882	U1799	G1699
U2824	U2825	U2757	U2480	G2651	U2559	U2480	U2390	G2307	U2241	U2154	G2077	C1987	C1883	U1799	G1699
G2826	U2827	U2758	U2481	G2652	U2560	U2481	U2391	G2308	U2242	U2155	G2078	C1988	C1884	U1799	G1699
A2828	U2829	U2759	U2482	G2653	U2561	U2482	U2392	G2309	U2243	U2156	G2079	C1989	C1885	U1799	G1699
C2830	U2831	U2760	U2483	G2654	U2562	U2483	U2393	G2310	U2244	U2157	G2080	C1990	C1886	U1799	G1699
U2832	U2833	U2761	U2484	G2655	U2563	U2484	U2394								



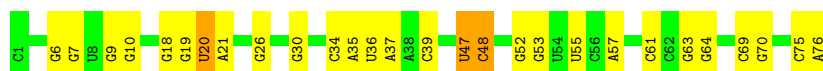
• Molecule 54: 5S ribosomal RNA

Chain 2: 51% 44% 5%



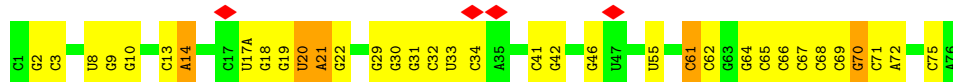
• Molecule 55: tRNA^{fMet}

Chain 5: 64% 32% 4%



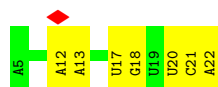
• Molecule 55: tRNA^{fMet}

Chain 6: 5% 55% 39% 6%



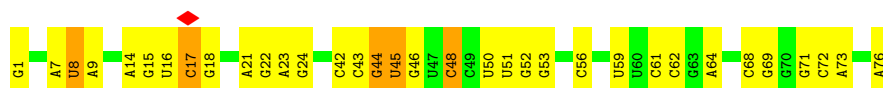
• Molecule 56: mRNA

Chain 4: 6% 61% 33%



• Molecule 57: tRNA^{Phe}

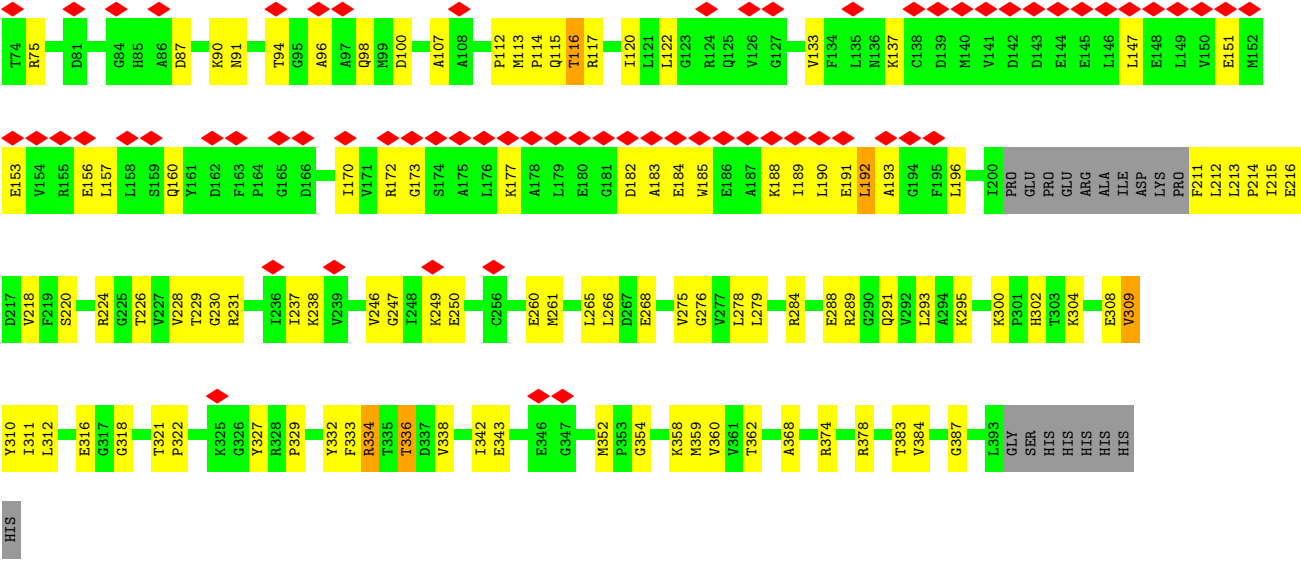
Chain 7: 55% 38% 7%



• Molecule 58: Elongation factor Tu

Chain 8: 20% 58% 28% 13%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	10215	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	17.183	Depositor
Minimum map value	-9.143	Depositor
Average map value	0.114	Depositor
Map value standard deviation	0.787	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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.28	0/2122	0.93	5/2852 (0.2%)
2	c	0.30	0/1586	0.86	2/2134 (0.1%)
3	d	0.29	0/1571	0.92	3/2113 (0.1%)
4	e	0.31	0/1435	0.85	4/1926 (0.2%)
5	f	0.30	0/1343	0.89	5/1816 (0.3%)
6	g	0.32	0/1122	0.94	3/1515 (0.2%)
7	h	0.36	0/1002	1.01	6/1350 (0.4%)
8	i	0.35	0/1046	0.95	2/1410 (0.1%)
9	j	0.29	0/1152	0.90	4/1551 (0.3%)
10	k	0.28	0/948	0.88	0/1268
11	l	0.30	0/1054	0.92	4/1403 (0.3%)
12	m	0.29	0/1093	0.87	0/1460
13	n	0.29	0/974	0.89	2/1301 (0.2%)
14	o	0.28	0/902	0.89	1/1209 (0.1%)
15	p	0.29	0/929	0.79	1/1242 (0.1%)
16	q	0.29	0/960	0.87	1/1278 (0.1%)
17	r	0.29	0/829	0.92	3/1107 (0.3%)
18	s	0.28	0/864	0.92	2/1156 (0.2%)
19	t	0.28	0/745	0.84	0/994
20	u	0.29	0/788	0.90	3/1051 (0.3%)
21	v	0.28	0/766	0.82	0/1025
22	w	0.27	0/582	0.84	1/769 (0.1%)
23	x	0.29	0/635	0.84	2/848 (0.2%)
24	y	0.27	0/510	0.91	1/677 (0.1%)
25	z	0.29	0/453	0.87	1/605 (0.2%)
26	B	0.27	0/450	0.88	1/599 (0.2%)
27	C	0.33	0/417	0.84	0/554
28	D	0.31	0/380	0.91	1/498 (0.2%)
29	E	0.29	0/513	0.95	2/676 (0.3%)
30	F	0.32	0/303	0.88	1/397 (0.3%)
31	G	0.29	0/1788	0.86	2/2408 (0.1%)
32	H	0.32	0/1652	0.87	5/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	0.92	8/2227 (0.4%)
34	J	0.35	1/1170 (0.1%)	0.92	2/1573 (0.1%)
35	K	0.32	0/836	0.93	5/1128 (0.4%)
36	L	0.29	0/1196	0.95	3/1602 (0.2%)
37	M	0.29	0/989	0.87	3/1326 (0.2%)
38	N	0.31	0/1034	0.96	3/1375 (0.2%)
39	O	0.31	0/797	0.87	3/1077 (0.3%)
40	P	0.33	0/886	0.89	3/1195 (0.3%)
41	Q	0.32	0/969	0.98	5/1300 (0.4%)
42	R	0.31	0/893	0.96	5/1193 (0.4%)
43	S	0.29	0/817	0.89	1/1088 (0.1%)
44	T	0.29	0/722	0.97	5/964 (0.5%)
45	U	0.32	0/659	0.99	4/884 (0.5%)
46	V	0.30	0/658	0.88	1/881 (0.1%)
47	W	0.31	0/545	0.86	1/731 (0.1%)
48	X	0.32	0/653	0.87	0/877
49	Y	0.30	0/671	0.94	2/888 (0.2%)
50	Z	0.34	0/551	1.04	2/728 (0.3%)
51	a	0.30	0/1034	0.83	1/1387 (0.1%)
52	3	0.41	0/36963	0.47	2/57662 (0.0%)
53	1	0.40	0/69796	0.48	2/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.40	0/1832	0.46	0/2855
55	6	0.40	0/1832	0.49	0/2855
56	4	0.41	0/436	0.47	0/679
57	7	0.40	0/1809	0.47	0/2819
58	8	0.33	0/2730	0.89	10/3693 (0.3%)
All	All	0.38	1/165929 (0.0%)	0.62	139/247771 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	J	55	VAL	CA-CB	5.54	1.56	1.54

The worst 5 of 139 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	e	148	VAL	N-CA-C	-8.57	102.86	111.77
33	I	46	ARG	N-CA-C	-8.36	102.86	113.23
58	8	100	ASP	N-CA-C	-8.23	102.96	113.16
49	Y	84	LYS	N-CA-C	-8.08	102.45	111.82
20	u	89	GLY	N-CA-C	-7.90	104.86	114.66

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	64	0
2	c	1565	0	1616	51	0
3	d	1552	0	1619	32	0
4	e	1411	0	1447	50	0
5	f	1323	0	1374	37	0
6	g	1111	0	1148	33	0
7	h	989	0	1025	56	0
8	i	1032	0	1088	30	0
9	j	1129	0	1162	23	0
10	k	939	0	1012	38	0
11	l	1045	0	1117	34	0
12	m	1074	0	1157	46	0
13	n	961	0	1000	26	0
14	o	892	0	923	28	0
15	p	917	0	965	34	0
16	q	947	0	1022	24	0
17	r	816	0	839	33	0
18	s	857	0	922	29	0
19	t	739	0	807	17	0
20	u	780	0	834	23	0
21	v	753	0	780	20	0
22	w	575	0	592	10	0
23	x	625	0	655	17	0
24	y	509	0	543	14	0
25	z	449	0	491	15	0
26	B	444	0	461	15	0
27	C	410	0	440	8	0
28	D	377	0	418	11	0
29	E	504	0	574	9	0
30	F	302	0	343	12	0
31	G	1757	0	1787	44	0
32	H	1625	0	1699	42	0
33	I	1643	0	1710	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	J	1157	0	1199	37	0
35	K	818	0	808	37	0
36	L	1182	0	1240	42	0
37	M	979	0	1034	34	0
38	N	1022	0	1070	42	0
39	O	787	0	828	32	0
40	P	870	0	878	34	0
41	Q	955	0	1019	37	0
42	R	884	0	944	40	0
43	S	805	0	847	29	0
44	T	714	0	737	15	0
45	U	649	0	666	31	0
46	V	649	0	691	23	0
47	W	536	0	552	14	0
48	X	638	0	665	29	0
49	Y	665	0	714	20	0
50	Z	545	0	579	28	0
51	a	1027	0	1092	31	0
52	3	33012	0	16618	575	0
53	1	62317	0	31346	896	0
54	2	2568	0	1303	55	0
55	5	1640	0	836	22	0
55	6	1640	0	837	25	0
56	4	388	0	196	5	0
57	7	1619	0	821	26	0
58	8	2683	0	2706	86	0
59	5	10	0	10	0	0
60	7	11	0	8	2	0
61	8	28	0	12	0	0
All	All	152933	0	103983	2784	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 11.

The worst 5 of 2784 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)
52:3:484:G:H4'	52:3:485:U:H5''	1.42	1.01
55:5:75:C:H2'	55:5:76:A:H5''	1.39	1.00
52:3:1259:C:H3'	52:3:1260:G:H5''	1.44	0.99
55:6:13:C:H2'	55:6:14:A:H5''	1.43	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:106:LEU:HD21	5:f:151:ARG:HB2	1.45	0.98

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	233 (87%)	32 (12%)	4 (2%)	8	36
2	c	207/209 (99%)	186 (90%)	20 (10%)	1 (0%)	24	57
3	d	199/201 (99%)	184 (92%)	14 (7%)	1 (0%)	24	57
4	e	175/177 (99%)	155 (89%)	20 (11%)	0	100	100
5	f	174/176 (99%)	149 (86%)	23 (13%)	2 (1%)	11	41
6	g	147/149 (99%)	130 (88%)	15 (10%)	2 (1%)	9	37
7	h	129/131 (98%)	96 (74%)	27 (21%)	6 (5%)	2	18
8	i	139/141 (99%)	126 (91%)	11 (8%)	2 (1%)	9	37
9	j	140/142 (99%)	128 (91%)	11 (8%)	1 (1%)	18	51
10	k	120/122 (98%)	93 (78%)	23 (19%)	4 (3%)	3	24
11	l	141/143 (99%)	109 (77%)	28 (20%)	4 (3%)	4	26
12	m	134/136 (98%)	117 (87%)	15 (11%)	2 (2%)	8	36
13	n	118/120 (98%)	103 (87%)	12 (10%)	3 (2%)	4	28
14	o	114/116 (98%)	104 (91%)	10 (9%)	0	100	100
15	p	112/114 (98%)	98 (88%)	12 (11%)	2 (2%)	6	33
16	q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
17	r	101/103 (98%)	83 (82%)	16 (16%)	2 (2%)	6	32
18	s	108/110 (98%)	100 (93%)	7 (6%)	1 (1%)	14	45
19	t	91/93 (98%)	82 (90%)	8 (9%)	1 (1%)	11	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	u	100/102 (98%)	82 (82%)	13 (13%)	5 (5%)	1	17
21	v	92/94 (98%)	83 (90%)	8 (9%)	1 (1%)	11	41
22	w	73/75 (97%)	66 (90%)	6 (8%)	1 (1%)	9	37
23	x	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
24	y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
25	z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
26	B	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
27	C	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
28	D	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
29	E	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	35
30	F	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	4	26
31	G	223/225 (99%)	208 (93%)	14 (6%)	1 (0%)	30	62
32	H	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
33	I	203/205 (99%)	180 (89%)	20 (10%)	3 (2%)	8	36
34	J	155/157 (99%)	126 (81%)	21 (14%)	8 (5%)	1	17
35	K	98/100 (98%)	77 (79%)	16 (16%)	5 (5%)	1	17
36	L	149/151 (99%)	136 (91%)	13 (9%)	0	100	100
37	M	127/129 (98%)	114 (90%)	13 (10%)	0	100	100
38	N	125/127 (98%)	101 (81%)	22 (18%)	2 (2%)	7	35
39	O	96/98 (98%)	80 (83%)	12 (12%)	4 (4%)	2	19
40	P	114/116 (98%)	95 (83%)	16 (14%)	3 (3%)	4	27
41	Q	121/123 (98%)	91 (75%)	25 (21%)	5 (4%)	2	20
42	R	112/114 (98%)	97 (87%)	10 (9%)	5 (4%)	2	18
43	S	98/100 (98%)	81 (83%)	17 (17%)	0	100	100
44	T	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	10	40
45	U	80/82 (98%)	70 (88%)	9 (11%)	1 (1%)	9	38
46	V	78/80 (98%)	62 (80%)	15 (19%)	1 (1%)	9	38
47	W	63/65 (97%)	55 (87%)	6 (10%)	2 (3%)	3	24
48	X	77/79 (98%)	72 (94%)	4 (5%)	1 (1%)	9	38
49	Y	83/85 (98%)	78 (94%)	4 (5%)	1 (1%)	10	40
50	Z	63/65 (97%)	42 (67%)	15 (24%)	6 (10%)	0	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	a	130/223 (58%)	122 (94%)	7 (5%)	1 (1%)	16	48
58	8	342/400 (86%)	321 (94%)	20 (6%)	1 (0%)	36	67
All	All	6261/6512 (96%)	5500 (88%)	663 (11%)	98 (2%)	10	35

5 of 98 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
5	f	45	ALA
5	f	174	LYS
7	h	80	THR
10	k	92	GLU

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	b	216/216 (100%)	216 (100%)	0	100	100
2	c	164/164 (100%)	161 (98%)	3 (2%)	51	67
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	147 (99%)	1 (1%)	76	77
5	f	137/137 (100%)	135 (98%)	2 (2%)	57	69
6	g	114/114 (100%)	114 (100%)	0	100	100
7	h	100/100 (100%)	97 (97%)	3 (3%)	36	57
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	74
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	74
11	l	102/102 (100%)	101 (99%)	1 (1%)	68	74
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	74
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	83 (96%)	3 (4%)	32	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	p	99/99 (100%)	99 (100%)	0	100	100
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	73
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	71
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	71
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%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	49 (96%)	2 (4%)	28	52
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	184 (99%)	2 (1%)	65	73
32	H	170/170 (100%)	170 (100%)	0	100	100
33	I	172/172 (100%)	170 (99%)	2 (1%)	63	72
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	76
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	73
36	L	124/124 (100%)	123 (99%)	1 (1%)	73	76
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	74
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	63
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	83 (100%)	0	100	100
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	63 (97%)	2 (3%)	35	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	V	74/74 (100%)	74 (100%)	0	100	100
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%)	53 (96%)	2 (4%)	31	54
51	a	110/174 (63%)	110 (100%)	0	100	100
58	8	290/332 (87%)	289 (100%)	1 (0%)	86	84
All	All	5198/5304 (98%)	5162 (99%)	36 (1%)	73	77

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	M	50	VAL
58	8	336	THR
39	O	14	ASP
45	U	77	GLU
12	m	89	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 116 such sidechains are listed below:

Mol	Chain	Res	Type
24	y	41	HIS
51	a	160	GLN
33	I	40	HIS
51	a	67	HIS
45	U	79	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	139 (9%)	4 (0%)
53	1	2902/2903 (99%)	323 (11%)	9 (0%)
54	2	119/120 (99%)	10 (8%)	1 (0%)
55	5	76/77 (98%)	7 (9%)	0
55	6	76/77 (98%)	14 (18%)	0
56	4	17/18 (94%)	2 (11%)	0
57	7	75/76 (98%)	10 (13%)	1 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4803/4810 (99%)	505 (10%)	15 (0%)

5 of 505 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	31	G
52	3	32	A
52	3	39	G

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	1130	U
54	2	88	C
53	1	1475	G
57	7	42	C
53	1	2326	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](#)

3 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
59	FME	5	101	55	8,9,10	0.50	0	8,9,11	0.88	0
60	PHE	7	101	57	10,11,12	0.69	0	8,13,15	0.24	0
61	GDP	8	501	-	29,30,30	1.40	5 (17%)	45,47,47	1.93	13 (28%)

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
59	FME	5	101	55	-	1/7/9/11	-
60	PHE	7	101	57	-	0/5/6/8	0/1/1/1
61	GDP	8	501	-	-	4/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GDP	PB-O1B	3.06	1.60	1.50
61	8	501	GDP	PA-O1A	2.75	1.60	1.50
61	8	501	GDP	PB-O3B	-2.54	1.45	1.54
61	8	501	GDP	O4'-C1'	2.45	1.47	1.42
61	8	501	GDP	PA-O3A	-2.08	1.57	1.59

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	C2-N3-C4	5.58	121.91	112.30
61	8	501	GDP	C5-C4-N3	-5.01	120.42	128.39
61	8	501	GDP	N9-C4-N3	3.54	133.03	125.95
61	8	501	GDP	O4'-C4'-C3'	3.24	111.58	105.15
61	8	501	GDP	C6-C5-N7	3.08	135.89	130.29

There are no chirality outliers.

All (5) torsion outliers are listed below:

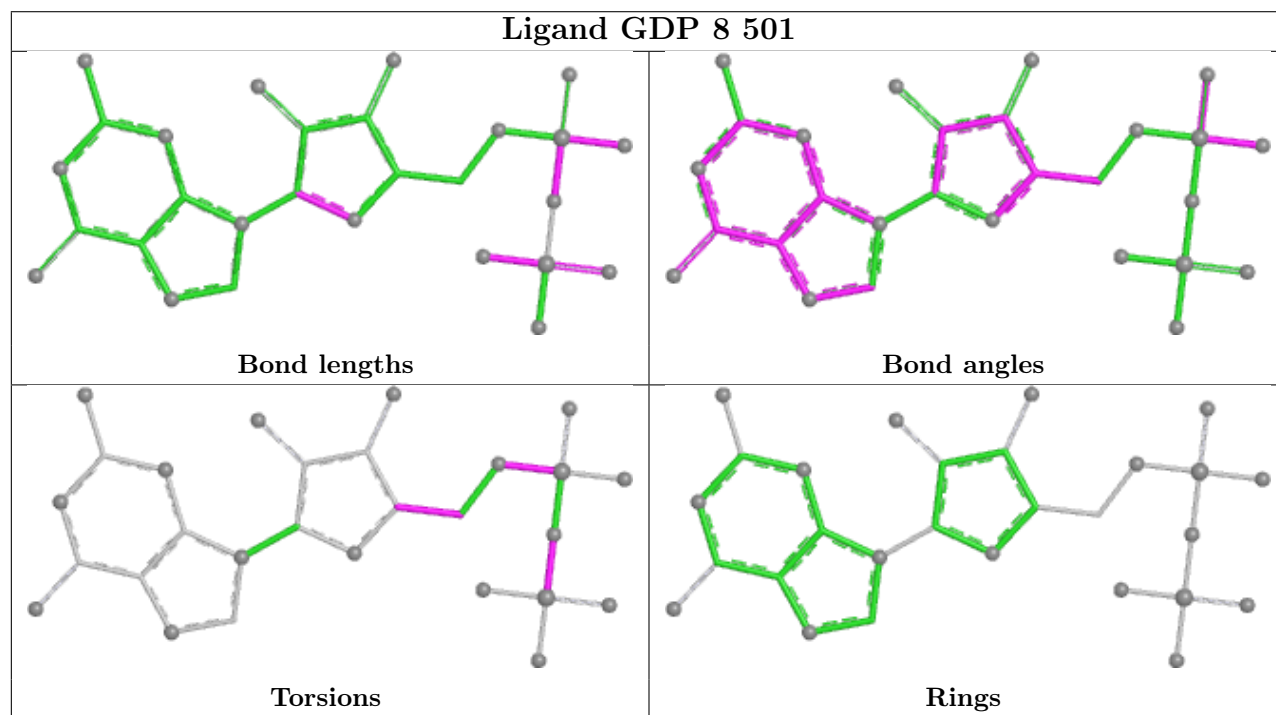
Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA
61	8	501	GDP	PA-O3A-PB-O3B
61	8	501	GDP	O4'-C4'-C5'-O5'
61	8	501	GDP	C3'-C4'-C5'-O5'
61	8	501	GDP	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	7	101	PHE	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

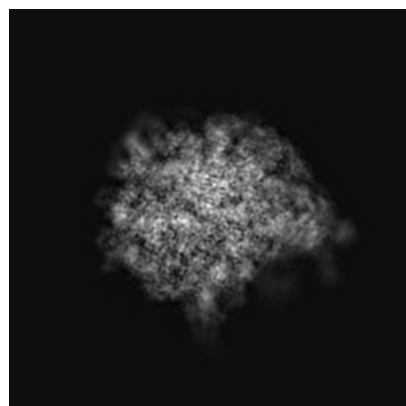
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21629. These allow visual inspection of the internal detail of the map and identification of artifacts.

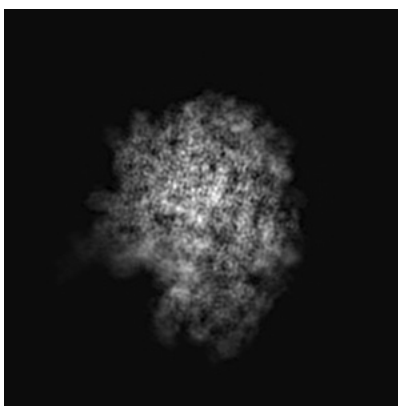
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

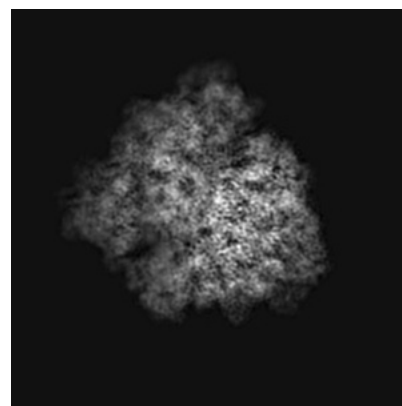
6.1.1 Primary map



X

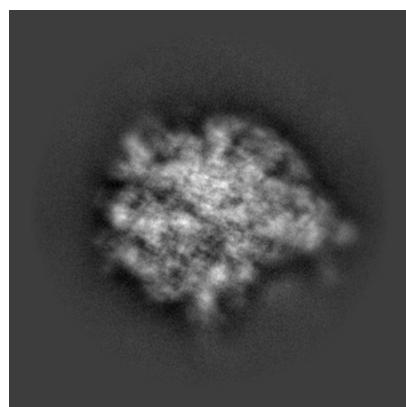


Y

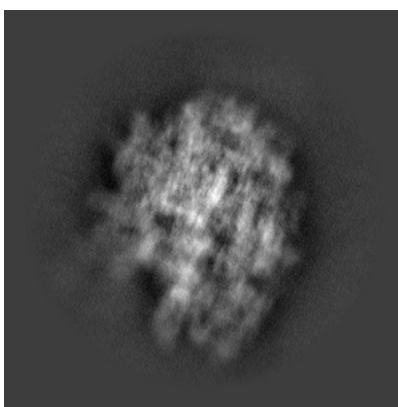


Z

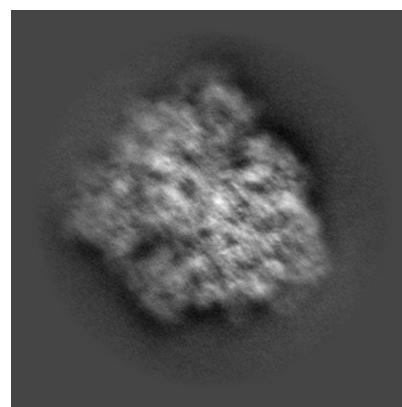
6.1.2 Raw map



X



Y

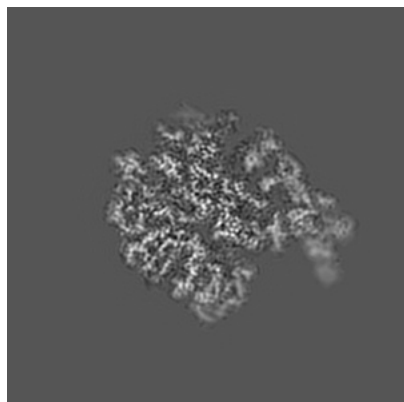


Z

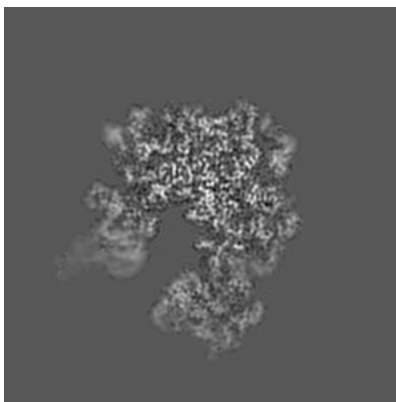
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

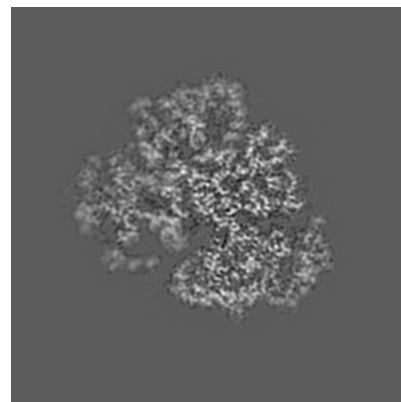
6.2.1 Primary map



X Index: 144

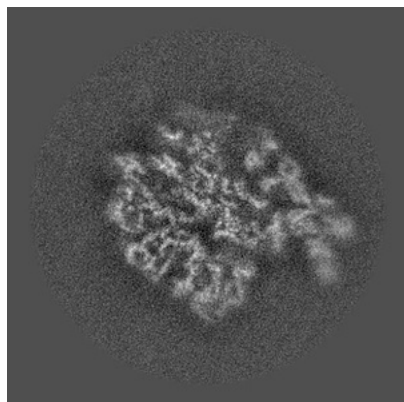


Y Index: 144

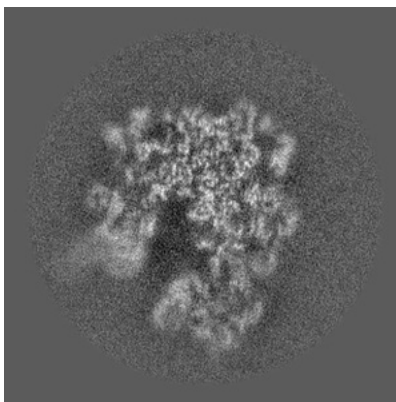


Z Index: 144

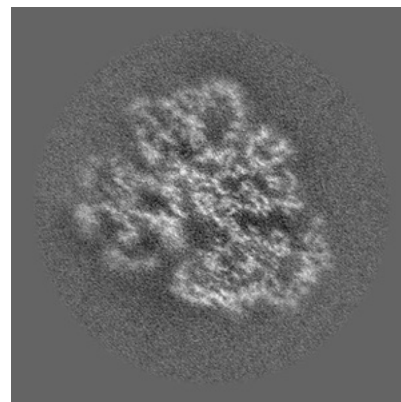
6.2.2 Raw map



X Index: 144



Y Index: 144

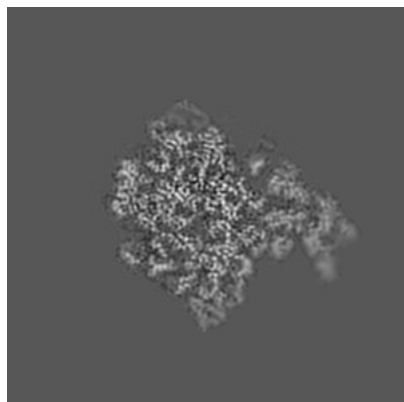


Z Index: 144

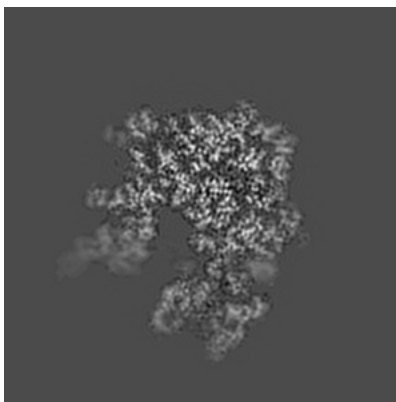
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

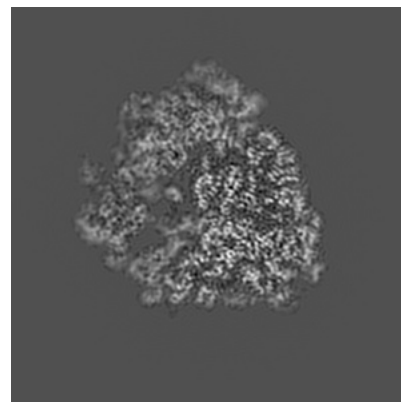
6.3.1 Primary map



X Index: 149

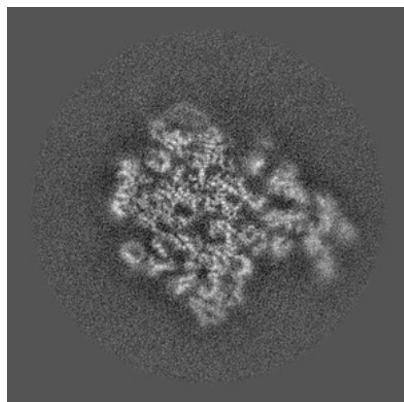


Y Index: 148

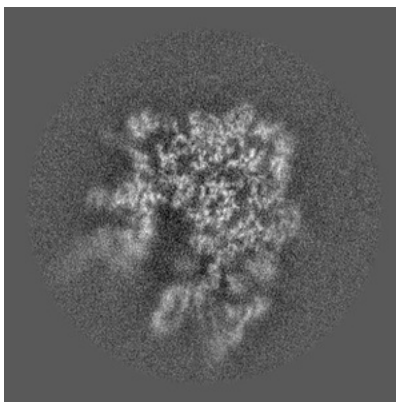


Z Index: 135

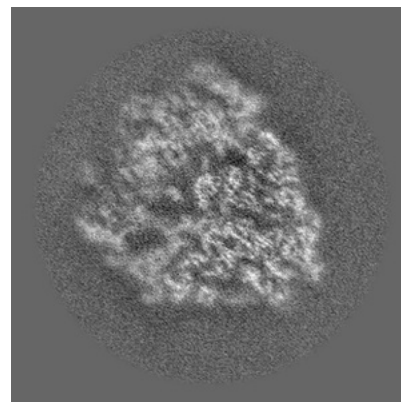
6.3.2 Raw map



X Index: 149



Y Index: 149

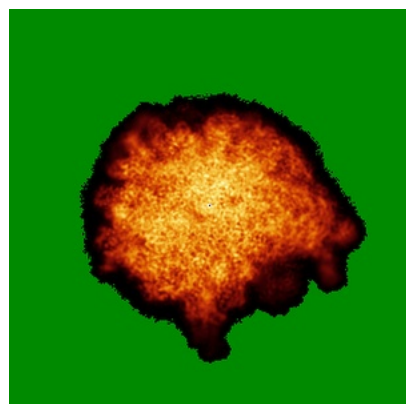


Z Index: 135

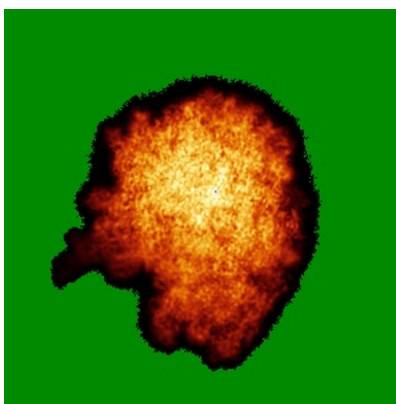
The images above show the largest variance slices of the map in three orthogonal directions.

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

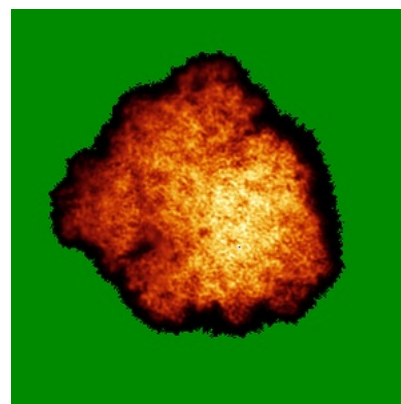
6.4.1 Primary map



X

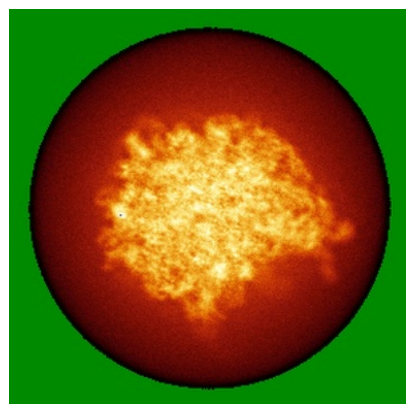


Y

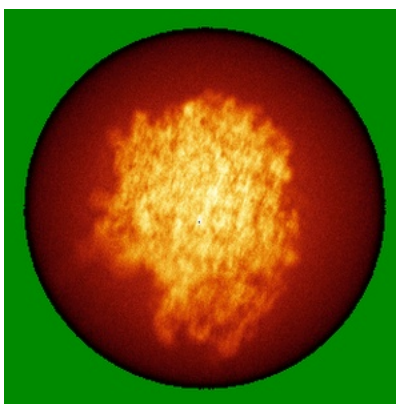


Z

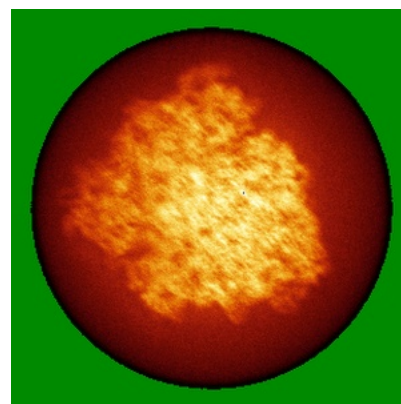
6.4.2 Raw map



X



Y

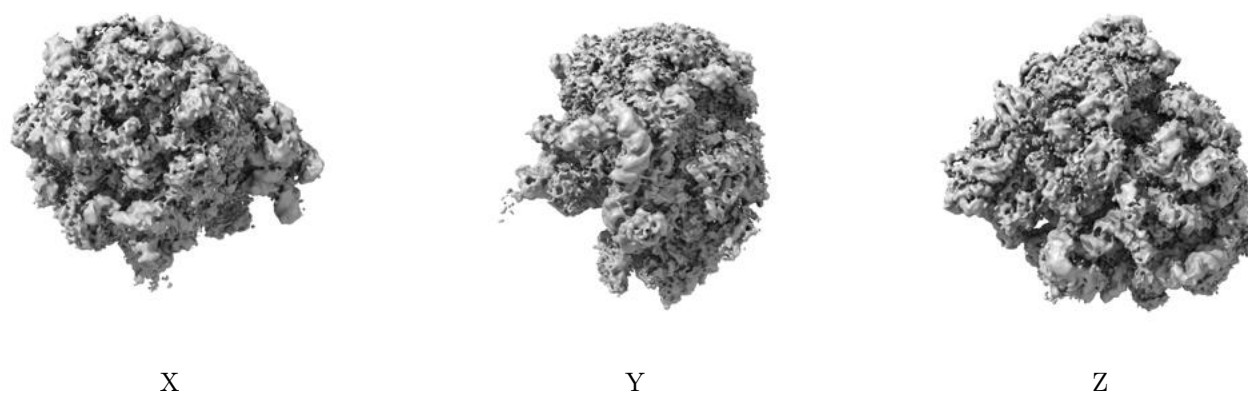


Z

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.

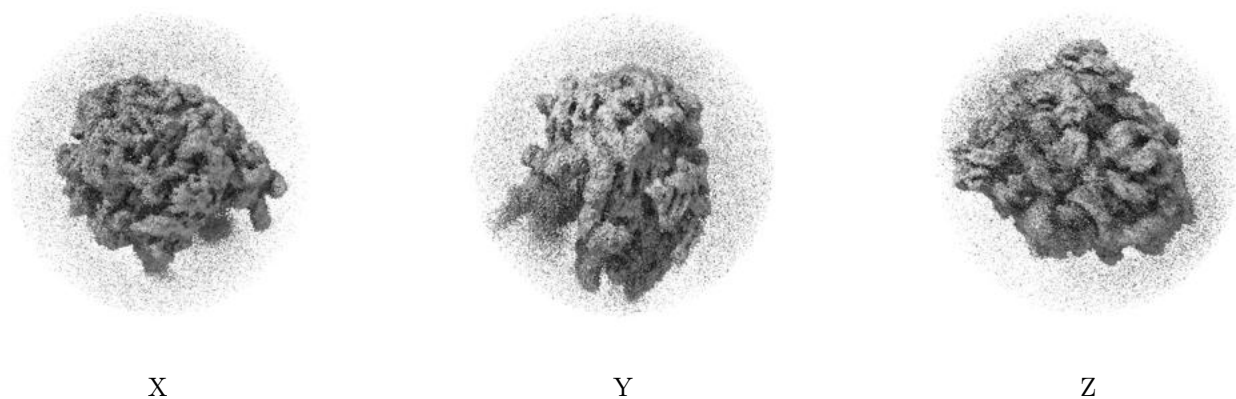
6.5 Orthogonal surface views [i](#)

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.

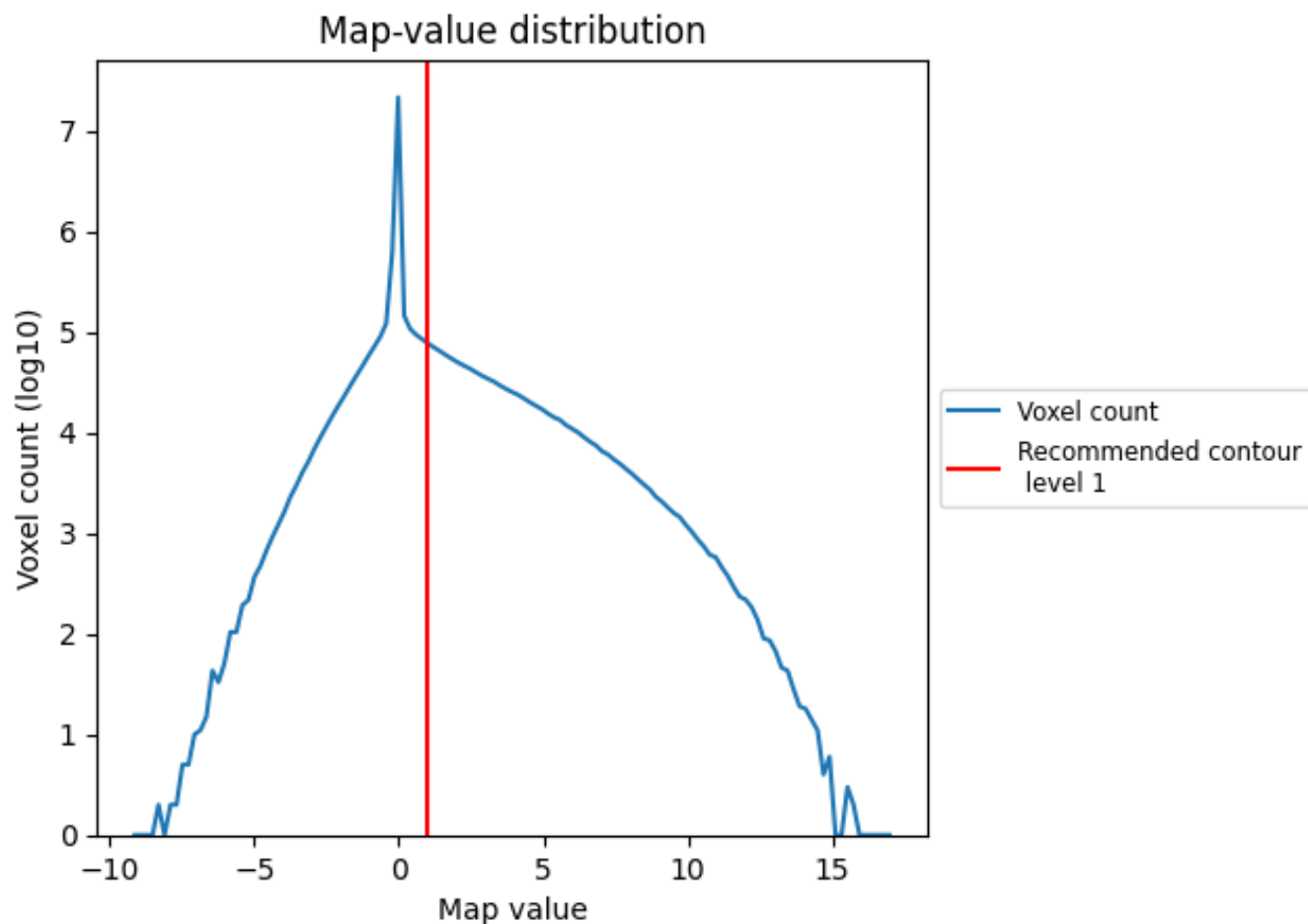
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

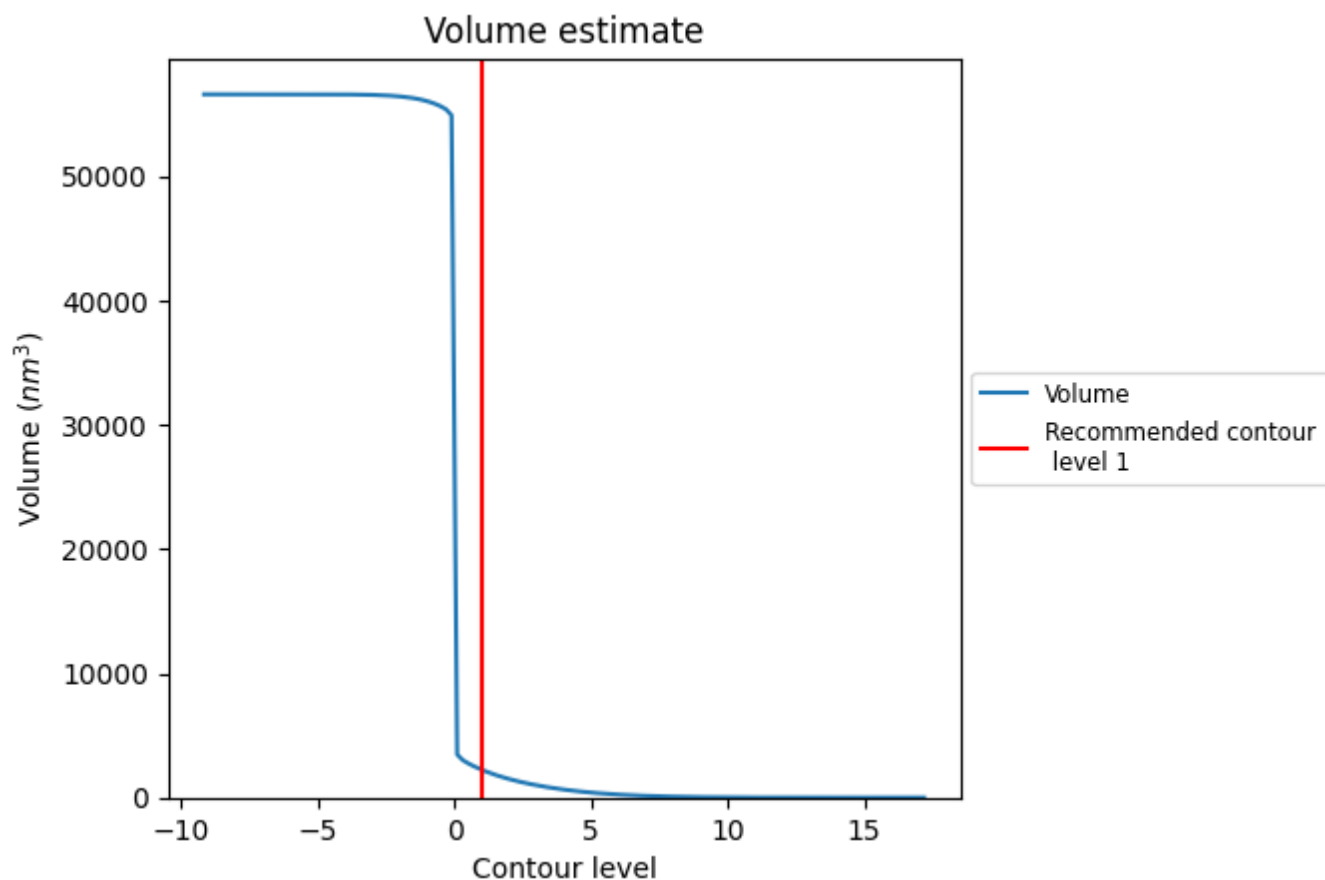
This section contains the results of statistical analysis of the map.

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.

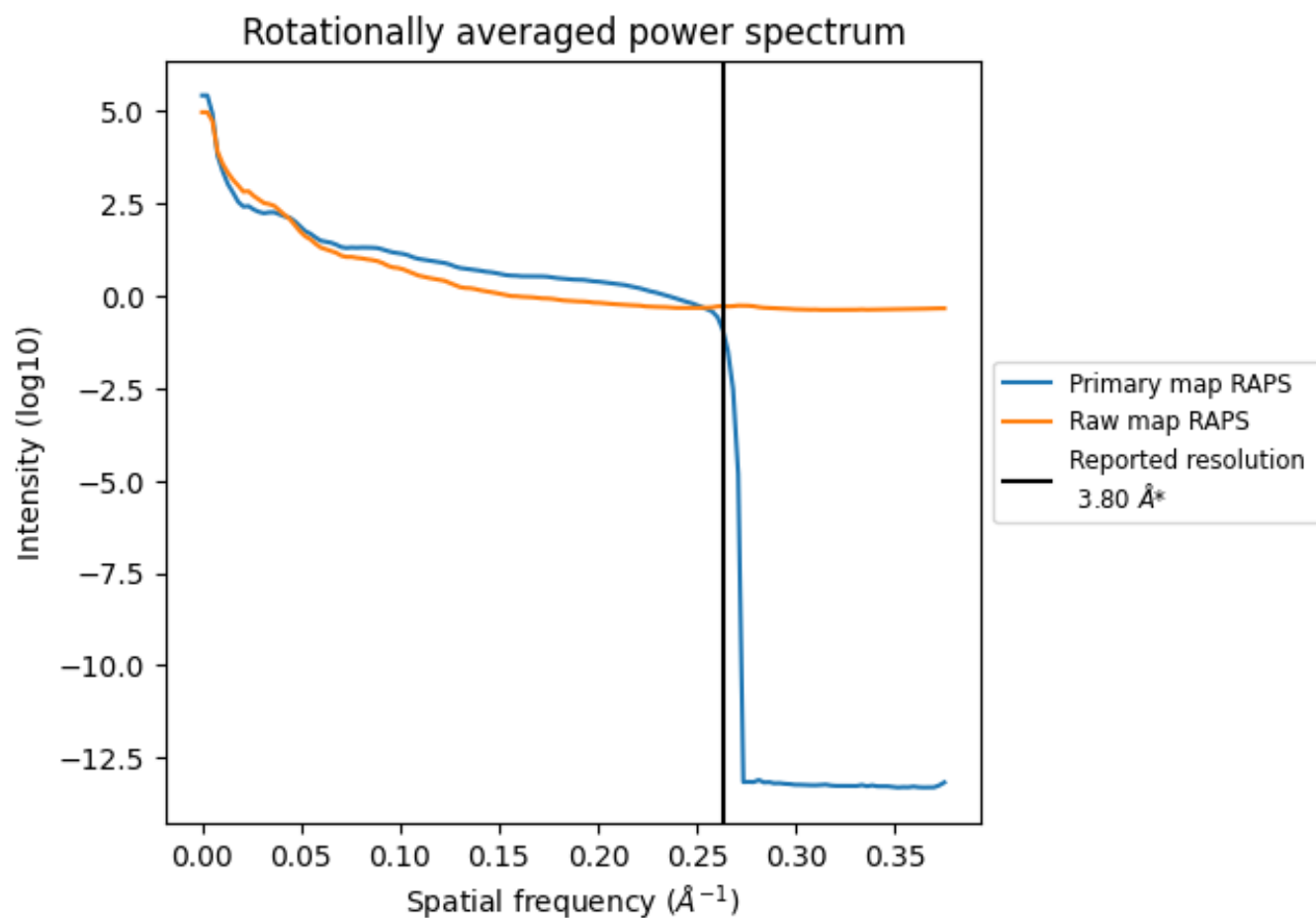
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2247 nm³; this corresponds to an approximate mass of 2030 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 ⓘ

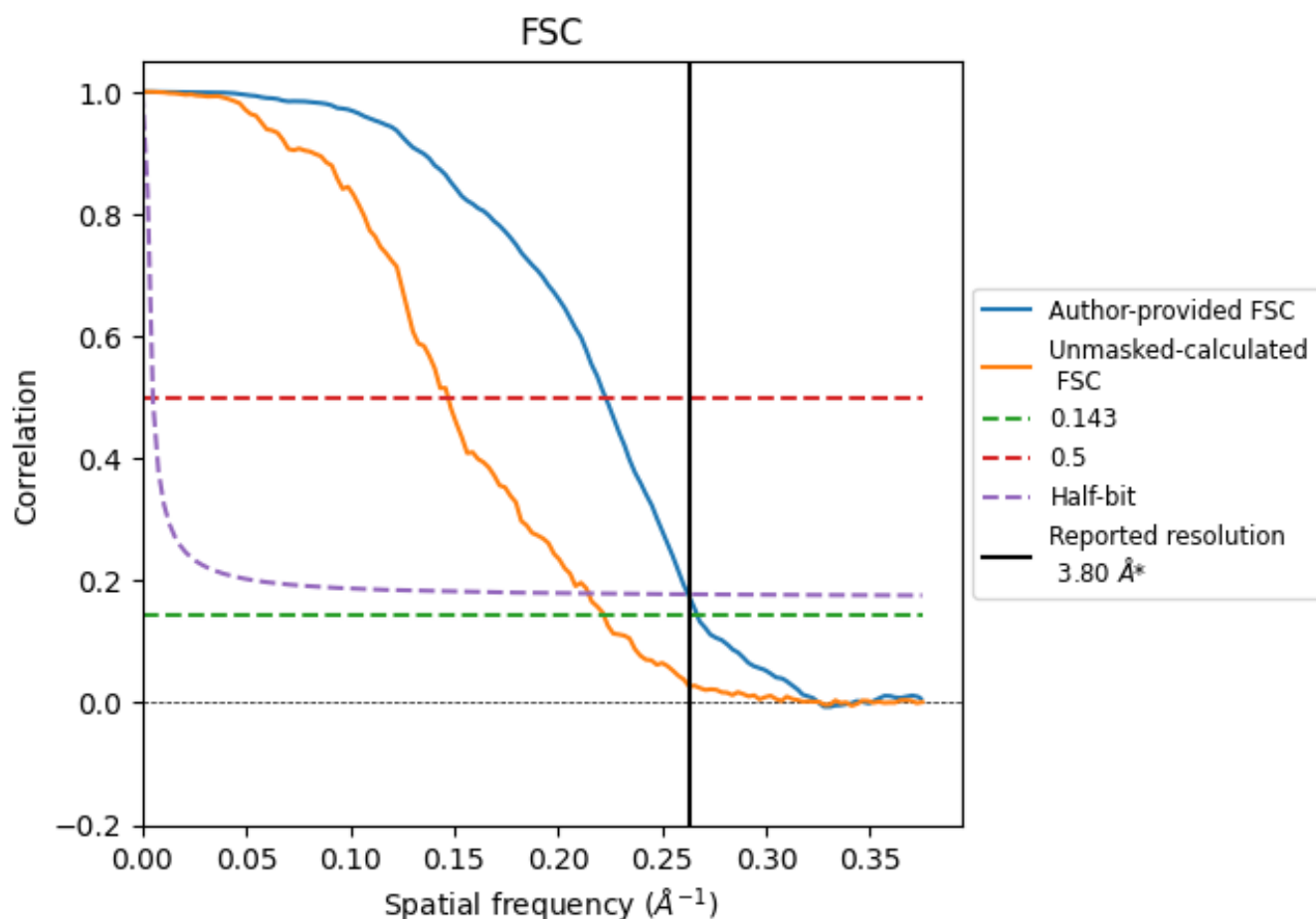


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 $0.263 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

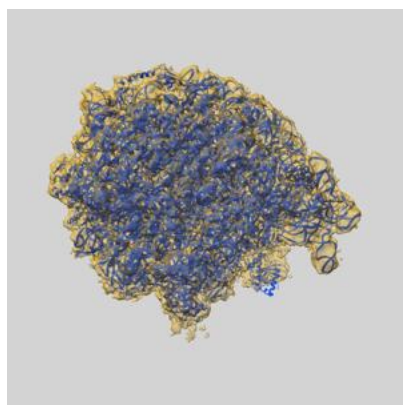
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.75	4.49	3.81
Unmasked-calculated*	4.50	6.80	4.66

*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 4.50 differs from the reported value 3.8 by more than 10 %

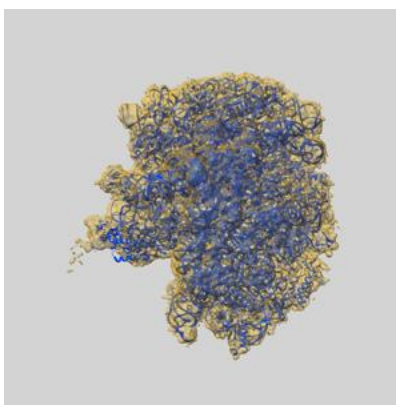
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21629 and PDB model 6WDA. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

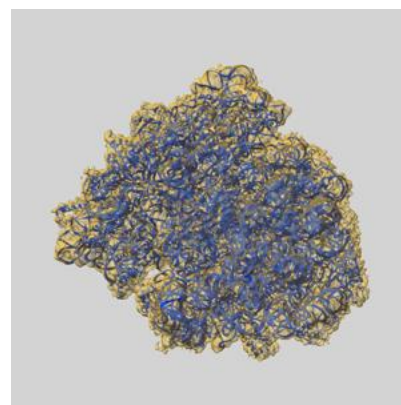
9.1 Map-model overlay [i](#)



X



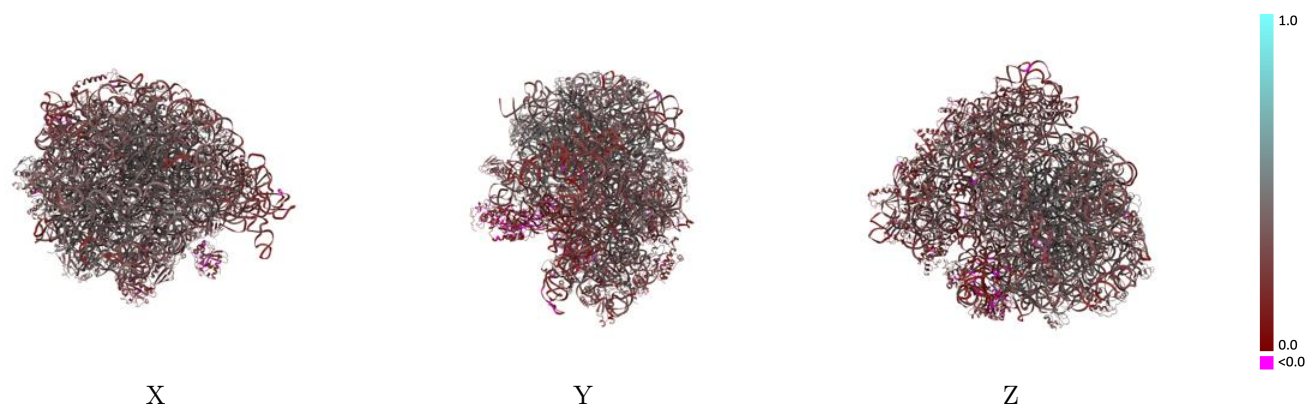
Y



Z

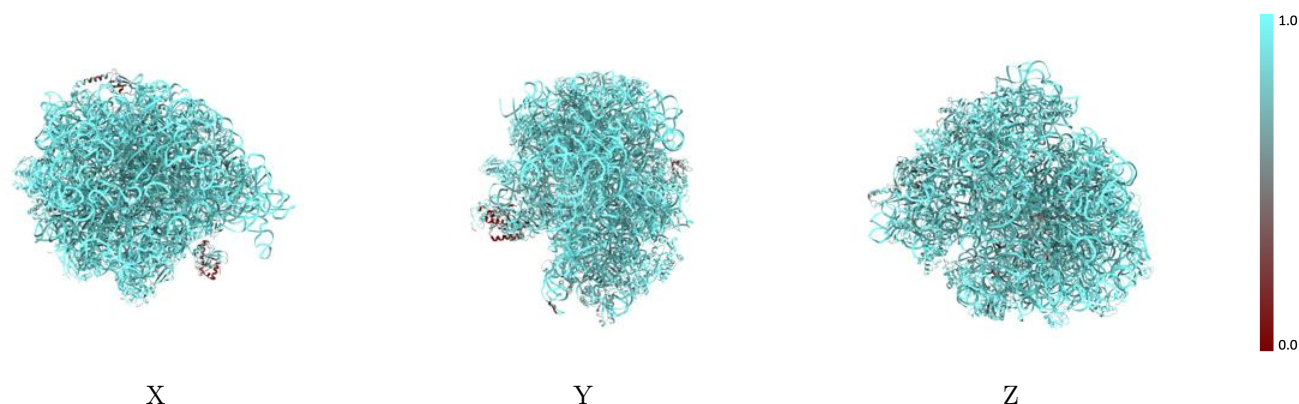
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



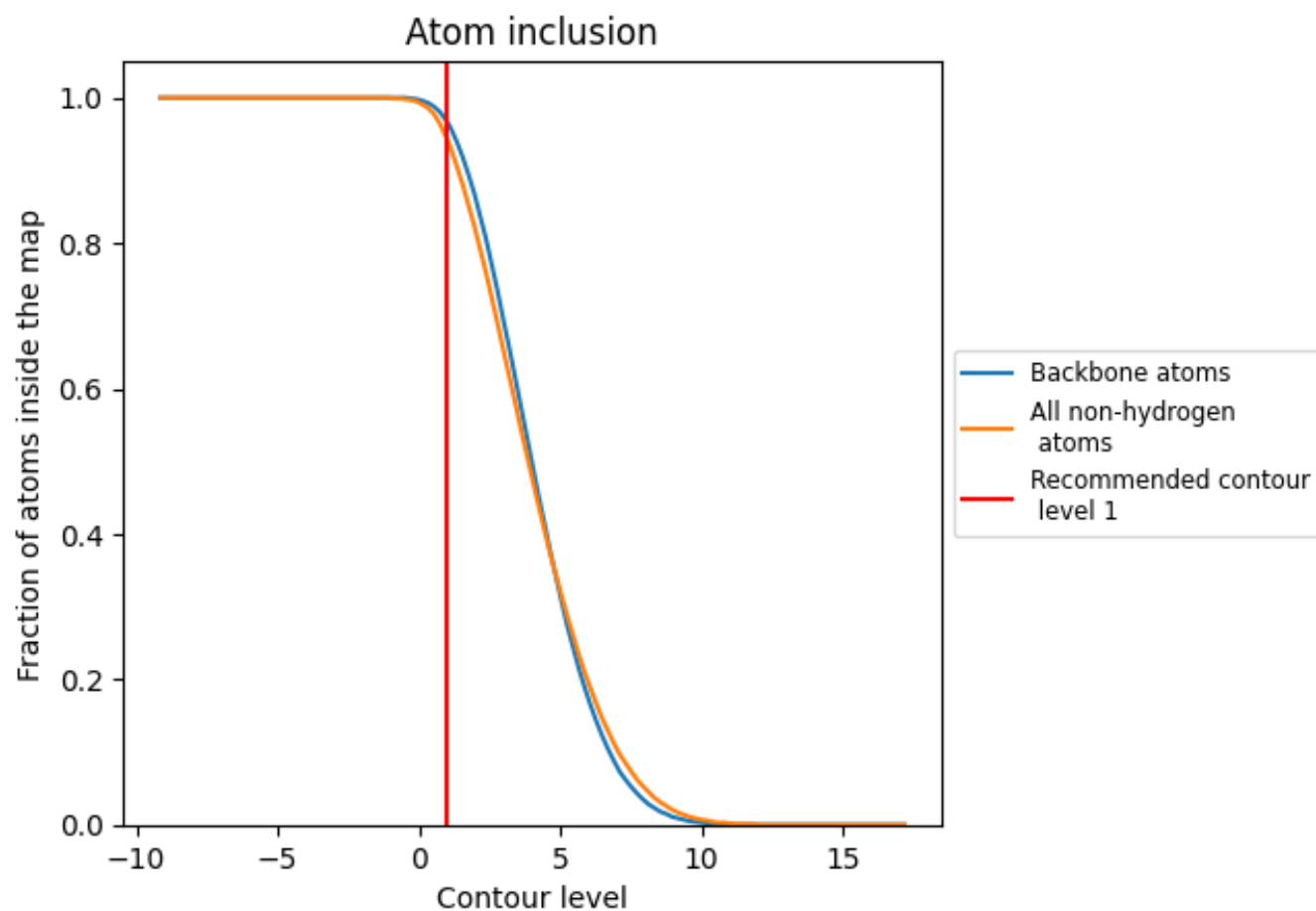
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 97% of all backbone atoms, 94% 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	 0.9430	 0.3320
1	 0.9810	 0.3610
2	 0.9820	 0.3160
3	 0.9750	 0.3080
4	 0.8790	 0.2360
5	 0.9690	 0.2890
6	 0.8190	 0.1350
7	 0.9280	 0.1450
8	 0.6980	 0.1460
B	 0.9390	 0.4060
C	 0.8280	 0.3600
D	 0.9270	 0.4330
E	 0.9180	 0.4380
F	 0.8250	 0.3670
G	 0.8690	 0.2920
H	 0.7740	 0.3050
I	 0.7720	 0.2170
J	 0.9150	 0.3650
K	 0.9320	 0.3550
L	 0.8990	 0.2690
M	 0.9250	 0.3560
N	 0.8620	 0.2830
O	 0.7180	 0.2840
P	 0.9270	 0.3480
Q	 0.9220	 0.3460
R	 0.9140	 0.2810
S	 0.7540	 0.2790
T	 0.9450	 0.3520
U	 0.8910	 0.3040
V	 0.9080	 0.3270
W	 0.8950	 0.3250
X	 0.9490	 0.2800
Y	 0.9340	 0.2880
Z	 0.8570	 0.2900
a	 0.7850	 0.1230



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Chain	Atom inclusion	Q-score
b	 0.9470	 0.4420
c	 0.9360	 0.4280
d	 0.9340	 0.3790
e	 0.9290	 0.2790
f	 0.9410	 0.3010
g	 0.6510	 0.2480
h	 0.7510	 0.1410
i	 0.6430	 0.1390
j	 0.9470	 0.4230
k	 0.9290	 0.4250
l	 0.9320	 0.4050
m	 0.9120	 0.4070
n	 0.9350	 0.4160
o	 0.9260	 0.3340
p	 0.9580	 0.4100
q	 0.9290	 0.4120
r	 0.9460	 0.3960
s	 0.9190	 0.4190
t	 0.9320	 0.4010
u	 0.9310	 0.3580
v	 0.9400	 0.3800
w	 0.9210	 0.4180
x	 0.9330	 0.4270
y	 0.9230	 0.3270
z	 0.9450	 0.4130