



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 03:58 AM UTC

PDB ID : 7JT2 / pdb_00007jt2
EMDB ID : EMD-22469
Title : 70S ribosome stalled on long mRNA with ArfB bound in the A site
Authors : Carbone, C.E.; Korostelev, A.A.
Deposited on : 2020-08-16
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

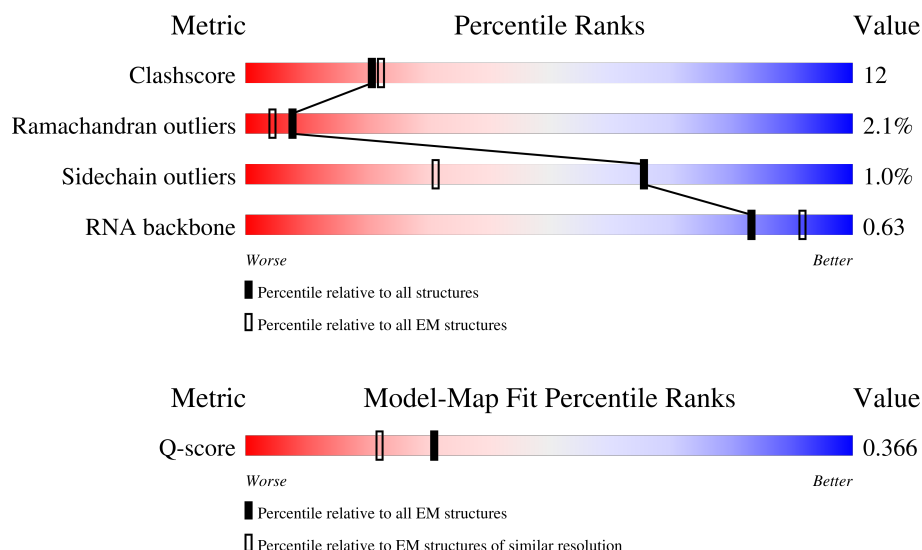
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



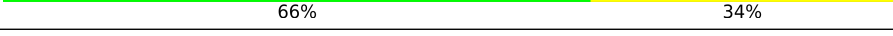
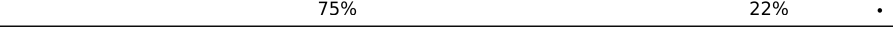
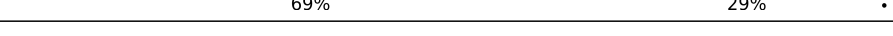
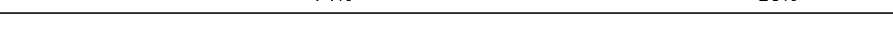
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	 68% 30% 2% 2%
2	c	209	 73% 25% 2% 2%
3	d	201	 71% 27% 2% 2%

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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	165	
8	j	142	
9	k	122	
10	l	143	
11	m	136	
12	n	120	
13	o	116	
14	p	114	
15	q	117	
16	r	103	
17	s	110	
18	t	93	
19	u	102	
20	v	94	
21	w	75	
22	x	77	
23	y	63	
24	z	58	
25	B	56	
26	C	50	
27	D	46	
28	E	64	

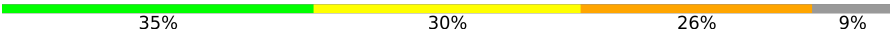
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Mol	Chain	Length	Quality of chain
29	F	38	
30	G	225	
31	H	206	
32	I	205	
33	J	157	
34	K	100	
35	L	151	
36	M	129	
37	N	127	
38	O	98	
39	P	116	
40	Q	123	
41	R	114	
42	S	100	
43	T	88	
44	U	82	
45	V	80	
46	W	65	
47	X	79	
48	Y	85	
49	Z	65	
50	3	1539	
51	1	2903	
52	2	120	
53	5	77	

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Mol	Chain	Length	Quality of chain
54	4	23	 35% 30% 26% 9%
55	8	132	 49% 39% 10% •

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 145984 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
			988	625	175	183	5		

- Molecule 8 is a protein called 50S ribosomal protein L13.

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

- Molecule 9 is a protein called 50S ribosomal protein L14.

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

- Molecule 10 is a protein called 50S ribosomal protein L15.

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

- Molecule 11 is a protein called 50S ribosomal protein L16.

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

- Molecule 12 is a protein called 50S ribosomal protein L17.

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

- Molecule 13 is a protein called 50S ribosomal protein L18.

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

- Molecule 14 is a protein called 50S ribosomal protein L19.

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

- Molecule 15 is a protein called 50S ribosomal protein L20.

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

- Molecule 16 is a protein called 50S ribosomal protein L21.

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

- Molecule 17 is a protein called 50S ribosomal protein L22.

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

- Molecule 18 is a protein called 50S ribosomal protein L23.

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

- Molecule 19 is a protein called 50S ribosomal protein L24.

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

- Molecule 20 is a protein called 50S ribosomal protein L25.

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

- Molecule 21 is a protein called 50S ribosomal protein L27.

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

- Molecule 22 is a protein called 50S ribosomal protein L28.

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

- Molecule 23 is a protein called 50S ribosomal protein L29.

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

- Molecule 24 is a protein called 50S ribosomal protein L30.

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

- Molecule 25 is a protein called 50S ribosomal protein L32.

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

- Molecule 26 is a protein called 50S ribosomal protein L33.

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

- Molecule 27 is a protein called 50S ribosomal protein L34.

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

- Molecule 28 is a protein called 50S ribosomal protein L35.

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

- Molecule 29 is a protein called 50S ribosomal protein L36.

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S3.

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

- Molecule 32 is a protein called 30S ribosomal protein S4.

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

- Molecule 33 is a protein called 30S ribosomal protein S5.

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

- Molecule 34 is a protein called 30S ribosomal protein S6.

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

- Molecule 35 is a protein called 30S ribosomal protein S7.

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

- Molecule 36 is a protein called 30S ribosomal protein S8.

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

- Molecule 37 is a protein called 30S ribosomal protein S9.

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

- Molecule 38 is a protein called 30S ribosomal protein S10.

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

- Molecule 39 is a protein called 30S ribosomal protein S11.

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

- Molecule 40 is a protein called 30S ribosomal protein S12.

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

- Molecule 41 is a protein called 30S ribosomal protein S13.

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

- Molecule 42 is a protein called 30S ribosomal protein S14.

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

- Molecule 43 is a protein called 30S ribosomal protein S15.

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

- Molecule 44 is a protein called 30S ribosomal protein S16.

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

- Molecule 45 is a protein called 30S ribosomal protein S17.

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

- Molecule 46 is a protein called 30S ribosomal protein S18.

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

- Molecule 47 is a protein called 30S ribosomal protein S19.

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

- Molecule 48 is a protein called 30S ribosomal protein S20.

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

- Molecule 49 is a protein called 30S ribosomal protein S21.

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

- Molecule 50 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	1539	Total	C	N	O	P	0	0
			33012	14725	6053	10696	1538		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	1490	C	U	conflict	GB 1789840096

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	2903	Total	C	N	O	P	0	0
			62315	27801	11468	20144	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 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	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 53 is a RNA chain called tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	21	Total	C	N	O	P	0	0
			461	207	96	137	21		

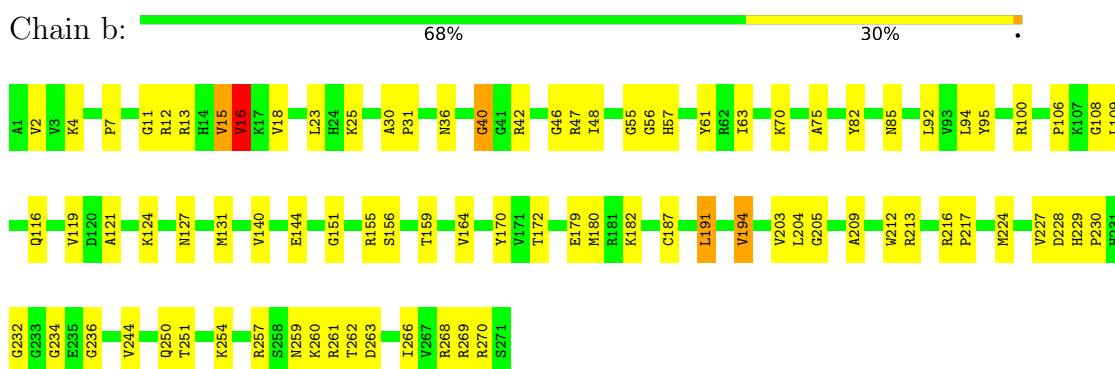
- Molecule 55 is a protein called Peptidyl-tRNA hydrolase ArfB.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	132	Total	C	N	O	S	0	0
			1031	638	204	187	2		

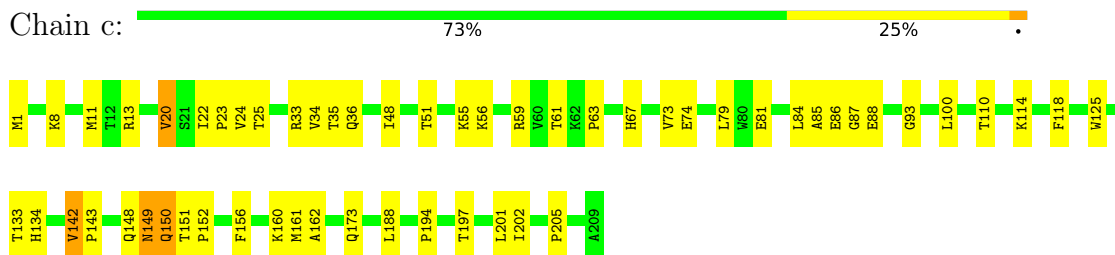
3 Residue-property plots

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.

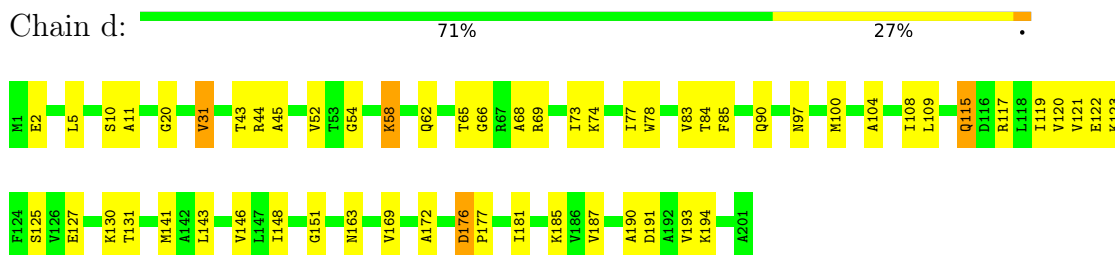
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3



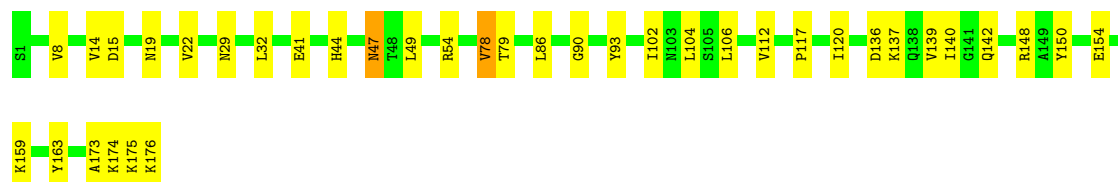
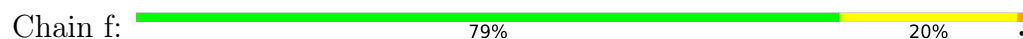
- Molecule 3: 50S ribosomal protein L4



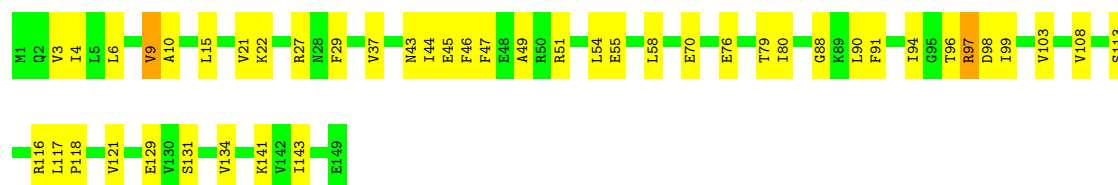
- Molecule 4: 50S ribosomal protein L5



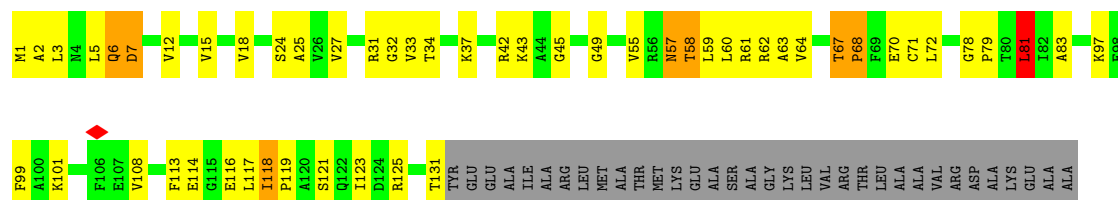
- Molecule 5: 50S ribosomal protein L6



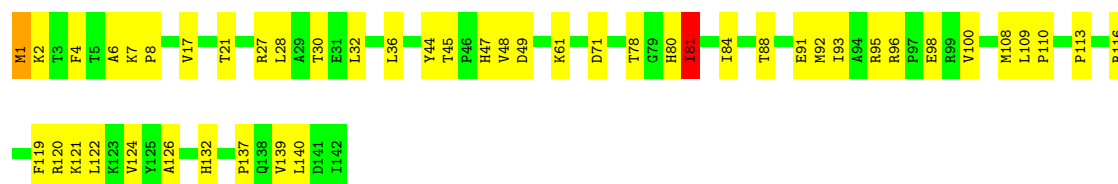
- Molecule 6: 50S ribosomal protein L9



- Molecule 7: 50S ribosomal protein L10

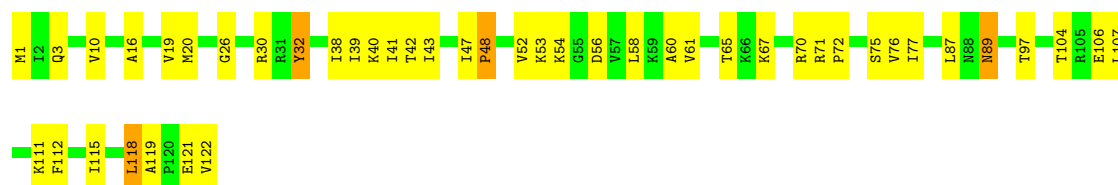


- Molecule 8: 50S ribosomal protein L13



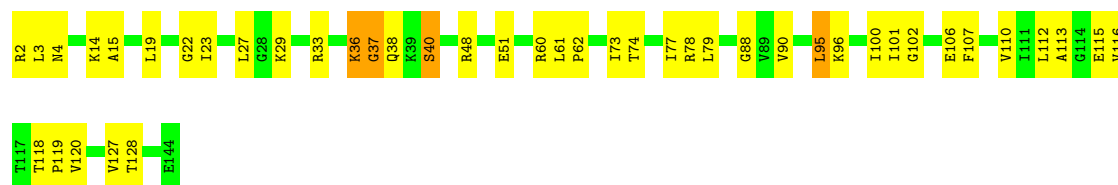
- Molecule 9: 50S ribosomal protein L14

Chain k:  63% 34%



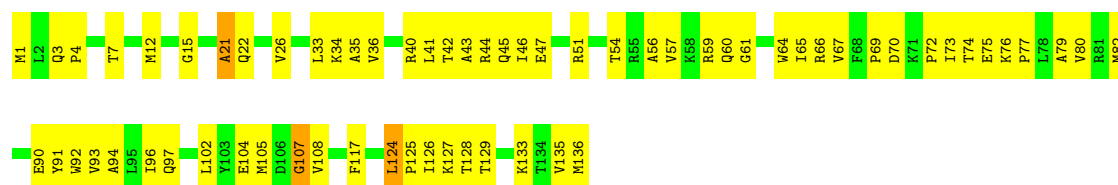
- Molecule 10: 50S ribosomal protein L15

Chain l:  69% 28%



- Molecule 11: 50S ribosomal protein L16

Chain m:  52% 46%



- Molecule 12: 50S ribosomal protein L17

Chain n:  66% 34%



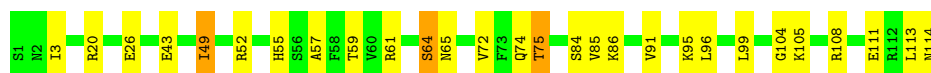
- Molecule 13: 50S ribosomal protein L18

Chain o:  73% 24%



- Molecule 14: 50S ribosomal protein L19

Chain p:  75% 22%



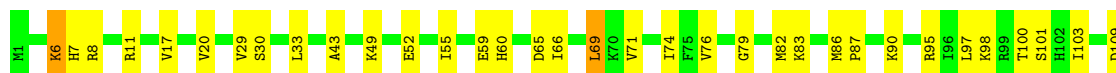
- Molecule 15: 50S ribosomal protein L20



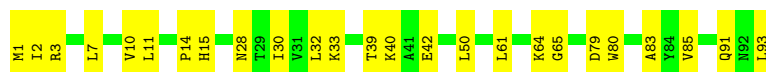
- Molecule 16: 50S ribosomal protein L21



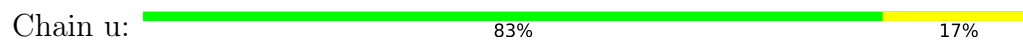
- Molecule 17: 50S ribosomal protein L22



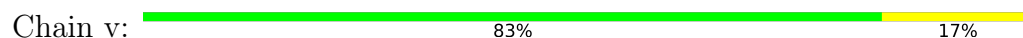
- Molecule 18: 50S ribosomal protein L23



- Molecule 19: 50S ribosomal protein L24



- Molecule 20: 50S ribosomal protein L25





- Molecule 21: 50S ribosomal protein L27

Chain w: 85% 13% .



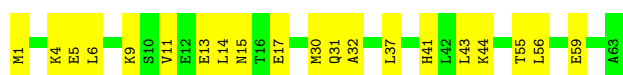
- Molecule 22: 50S ribosomal protein L28

Chain x: 74% 26%



- Molecule 23: 50S ribosomal protein L29

Chain y: 68% 32%



- Molecule 24: 50S ribosomal protein L30

Chain z: 83% 17%



- Molecule 25: 50S ribosomal protein L32

Chain B: 64% 34% .



- Molecule 26: 50S ribosomal protein L33

Chain C: 84% 16%



- Molecule 27: 50S ribosomal protein L34

Chain D: 74% 24% .



- Molecule 28: 50S ribosomal protein L35

Chain E: 69% 27% 5%



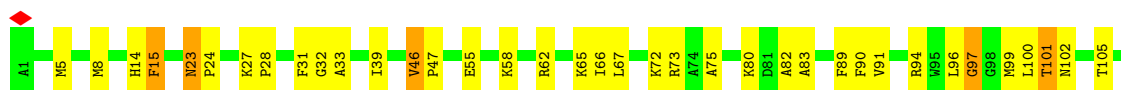
- Molecule 29: 50S ribosomal protein L36

Chain F: 66% 29% 5%



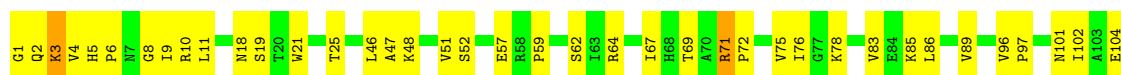
- Molecule 30: 30S ribosomal protein S2

Chain G: 70% 26% 5%



- Molecule 31: 30S ribosomal protein S3

Chain H: 69% 29% 5%



- Molecule 32: 30S ribosomal protein S4

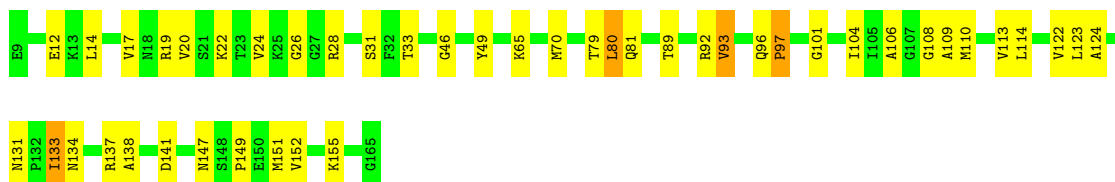
Chain I: 63% 33% 5%





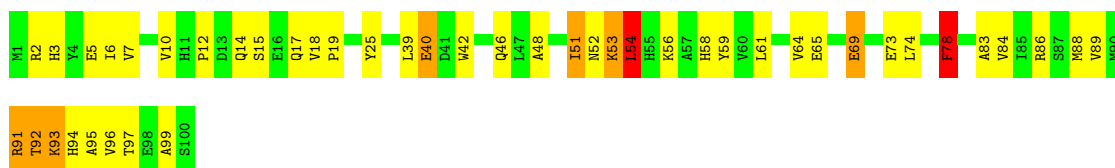
- Molecule 33: 30S ribosomal protein S5

Chain J: 71% 26% .



- Molecule 34: 30S ribosomal protein S6

Chain K: 55% 36% 7% .



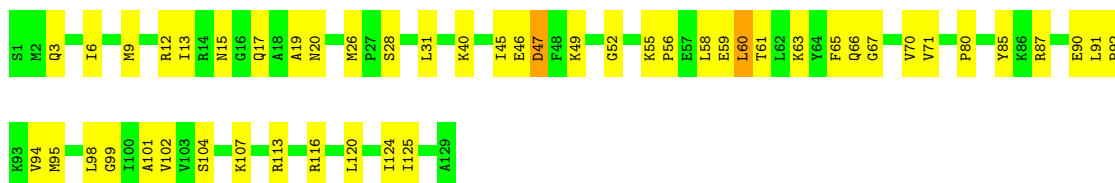
- Molecule 35: 30S ribosomal protein S7

Chain L: 79% 19% .



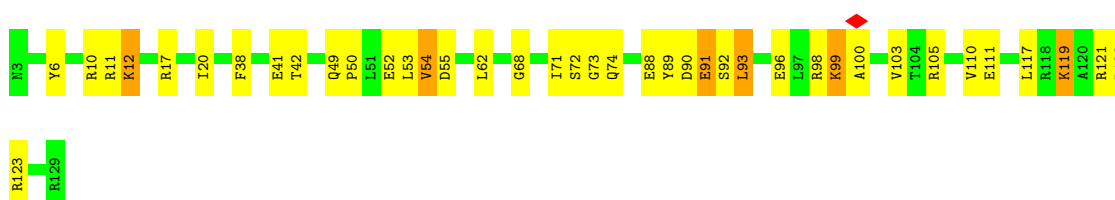
- Molecule 36: 30S ribosomal protein S8

Chain M: 62% 36% .



- Molecule 37: 30S ribosomal protein S9

Chain N: 69% 27% 5% .



- Molecule 38: 30S ribosomal protein S10

Chain O:  66% 29% ..



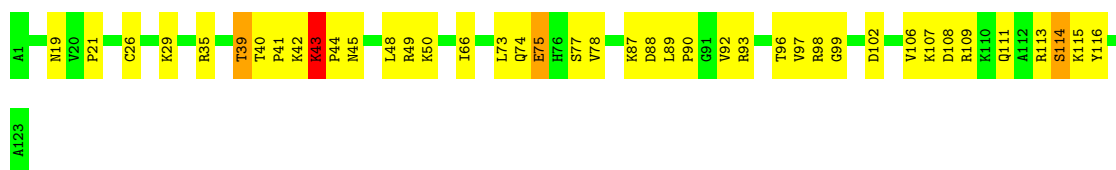
- Molecule 39: 30S ribosomal protein S11

Chain P:  72% 23% 5%



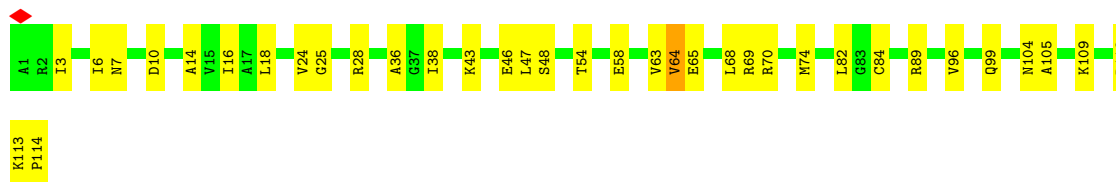
- Molecule 40: 30S ribosomal protein S12

Chain Q:  67% 30% ..



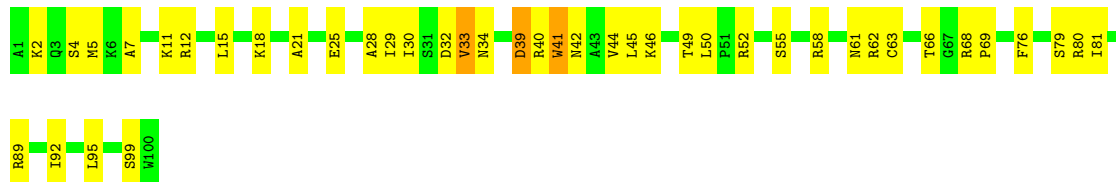
- Molecule 41: 30S ribosomal protein S13

Chain R:  68% 31% .



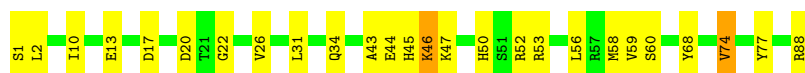
- Molecule 42: 30S ribosomal protein S14

Chain S:  58% 39% .



- Molecule 43: 30S ribosomal protein S15

Chain T:  70% 27% .



- Molecule 44: 30S ribosomal protein S16



- Molecule 45: 30S ribosomal protein S17



- Molecule 46: 30S ribosomal protein S18



- Molecule 47: 30S ribosomal protein S19



- Molecule 48: 30S ribosomal protein S20



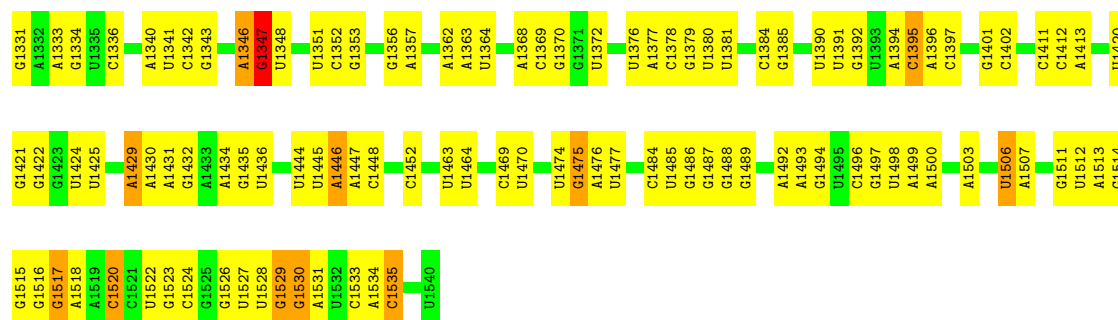
- Molecule 49: 30S ribosomal protein S21



- Molecule 50: 16S ribosomal RNA

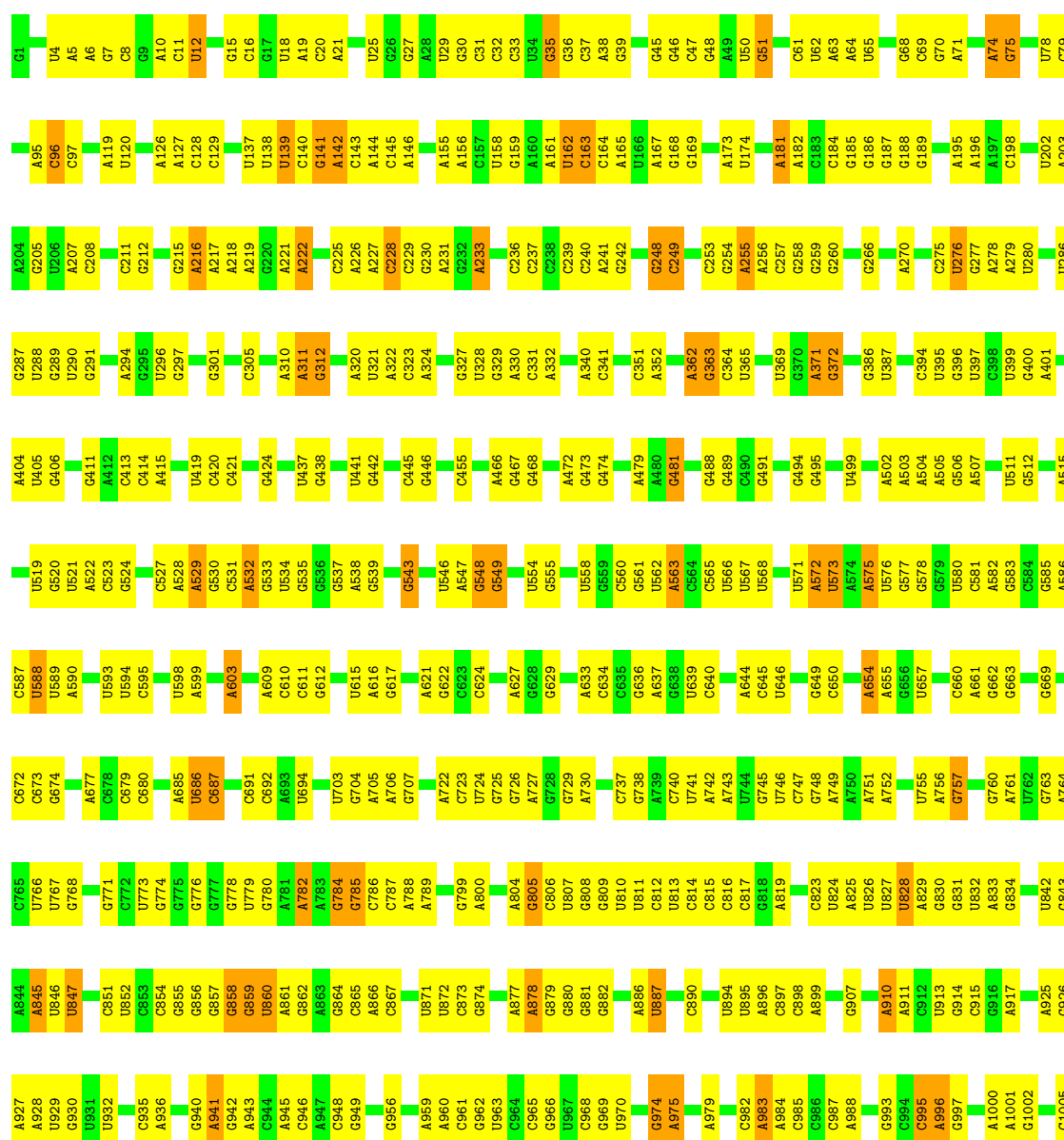


G1253	A1176	C1100	G830	C738	U652	U555	A451	A386	G281	A192	C90	A2
A1254	G1177	A1101	A831	C739	U652	C556	A452	U367	C284	C193	C90	
G1255	G1178	A1102	C833	U740	U662	G557		C372	C285	C194	U91	G6
A1257	G1182	C1103	C833	G741	A663	G558	A456	A373	C286	A195	C95	G9
G1258	U1183	A1104	U837	G742	A664	A559	A457	G376	G289	G201	G100	A10
C1259	G1184	A1105	C838	A743	A665	A560		G377		G202	G100	G11
G1260	G1185	A1106	C839	G744		U561	U463	U387	G297	G203	A109	A16
A1261	G1186	A1107	C839	G745	A673	C564	U469	U388	U304	G204	C110	U17
	U1264	A1111	U842	A746	A675	G566	C477	U389	G305	A205	G111	C18
A1271	G1272	C1112	U843	G747			A478	G391		U209	G112	A19
G1272		G1026	A845	A749	U678	G570	U479	C392	C308	C210	G113	U20
A1275		C1028	G846	C750	C879	U571	U480	A393	A309	G211	U114	G21
G1278	C1195	U1029	G847	G752	U680	A572		A397	A311	G212	G115	G22
U1279	A1196	A1117	C848	A753	A681	A573	C483	C396	C314	U216	U121	U29
G1280	A1197	U1118	C849	C754	G682	A574	G484	A402	C315	C217	G122	G31
A1281	G1198	A1119	U850	G755	G683	G575	U485	G403	A316	G220	U123	A32
U1282	U1199	C1120	G851		U684	C576	U486	C404	C316	C221		G35
C1283	C1200	G1124	U854	G763	G685	G577		G405	G319	C222	G128	C36
U1283	U1201	U1127	U855	A767	U686	C578	C490	U406	A320	U223	A129	U37
A1287	A1202	C1128	C856	A768	A687	C580	A493	U407	A321	A224	A130	G38
	A1204	C1129	G858	G769	G688	G581		A408	G322	C225		G39
G1206	U1205	A1130	C859		U692	G584	A496	U409	U323	G226	A143	C40
			U859	G775	G693	G585	G497	G410	A325	G230	G144	G41
U1211	U1212	U1135	C866	G776	A694	G592	C501	A411	A326	G235	G145	G42
G1296	U1213	C1136	G867	A777	A696	G593	A502	A412	A327	A236	G146	C47
U1297		G1138	C868	G778	U697	U594	C503	A413	C328		G147	C48
U1298		U1139	G869	C779	G700	A595	C504	A414	A329	A243	A151	U49
A1299	C1218	C1140	C870	A780	U701	A596	G505	A415	G332	U244	A152	A50
G1300	A1219	U1301	C879	A781	G702	U597	G506	G416	G335	U245	G159	A51
U1302	G1220	C1141	U870	A784	A703	C599	A509	C418	C336	A246	A162	C54
C1303		G1144	U871	G785	U709	A600		C419	A336	G247	A163	A55
G1304	A1225	A1145	A872	G800	G710	U603	C513	U420	U340	A250	U173	U56
C1226	C1226	C1146	A878	U801	G711	G604	C514	C422	C341	G251	A166	G57
A1227	A1227	C1147	C879	U804	G712	U605	C518	G423	G345	U252	A167	C58
G1306	C1228	A1151	C880	U804	G713	G606	C519	G424	C346	A253		A59
U1307	A1229	C1230	C881	C810	G714		A520	G425	G347	G254	U173	A66
U1308	C1230		C882	C811	A715	G620	G521	U426	G348	G255	G177	C67
G1309		A1157	C883	C811	U717	A621	C522	U427	A349	U256	C178	G68
G1310	C1234	C1158	U884	G812	A718	A622	A533	U428	G350	G257	A179	G69
		U1159	C885	A814		C623		A430	G351	G258	U180	A74
C1314	C1237	C1162	C886	U818	G721	G626	G537	C436	C352	G266	A181	G75
U1315	A1238	A1163	C887	U819	G722	G627	G538	U437	A353	C267	A182	G76
G1316	A1239	G1164	C888	U820	G723		A539	U438	G354	C183	C183	A80
A1317	U1240	U1165	C889	A819	G724	C631	G540	U439	C355	C272	G184	A81
A1318	G1241	G1166	U890	A819	G725	U632	G541	G542	U358	U273	U185	G82
A1319	G1242	U1085	U891	U818	G726	G633	G542	A441	U358	A274	G186	G83
		G1086	C890	C817	U727	C634	U543	A441	G359	G275	G187	U84
G1323	G1243	U1087	U891	U818	G728	A635	G544	G442	G362	G276	C188	
A1324	C1244	G1088	C892	U820	G729	U636	A545	G446	A279	G86	A189	U85
C1245	A1245	A1169	C893	U819	G730		A546	A448	C280		A190	G87
A1246		U1171	C894	A821	G731							
	C1249	C1172	C895	U822	G732							
C1328	A1250	U1096	C896	U823	G733							
A1251	A1251	C1097	C897	G824	G734							
U1330	A1252	G1002	C897	A825	G735							
		A1004	G902	C826								
				G829								

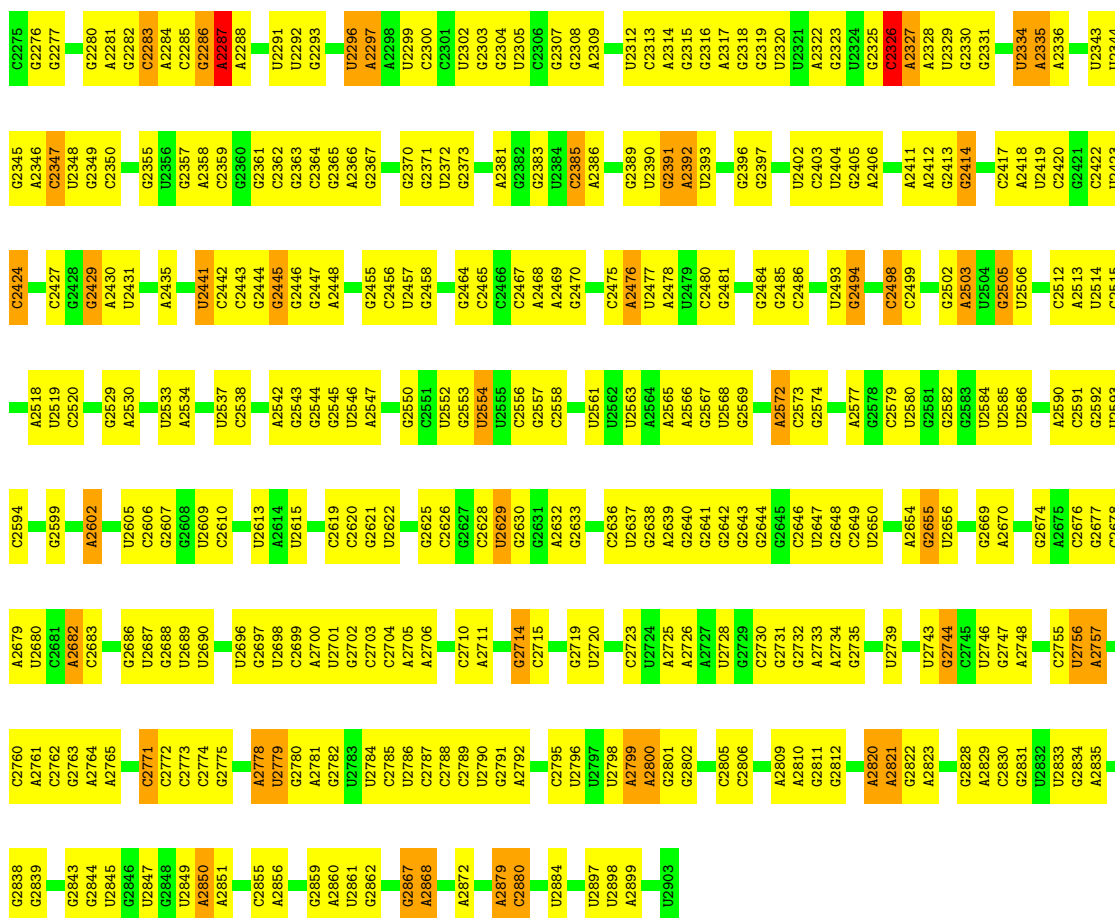


• Molecule 51: 23S ribosomal RNA

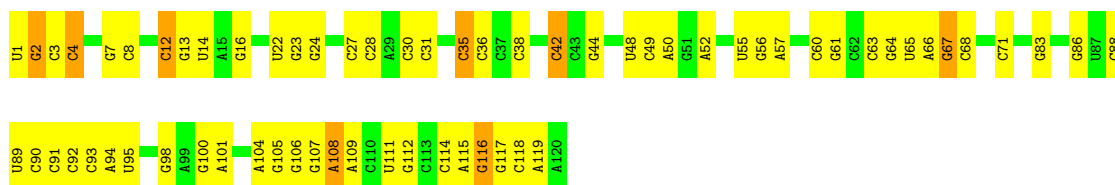
Chain 1: 48% 45% 7%



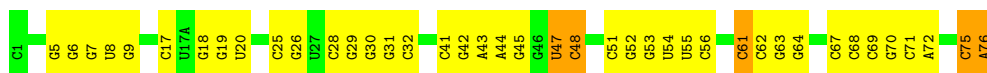
C2196	C2197	A2126	G2052	U1963	C1874	C1790	A1713	A1616	A1528	A1438	C1351	U1174	C1006
U2197	A2198	G2127	G2053	G1964	G1875	A1791	U1714	A1616	G1529	U1440	U1352	A1175	U1012
A2199	C2199	C2054	C2055	C1965	C1965	A1794	G1715	G1623	A1535	U1441	A1353	U1176	C1013
C2200	G2056	C2056	C1967	C1967	U1882	U1795	G1725	C1625	A1536	U1442	G1355	C1100	C1101
G2201	A2059	U1230	A1970	U1883	U1883	U1796	G1726	C1625	G1537	U1443	G1356	C1178	A1020
U2202	A2060	U1231	G1970	G1884	G1797	G1797	C1727	A1626	G1538	U1444	C1357	U1180	A1021
G2203	G2061	G2133	U1971	A1885	U1798	G1798	C1728	A1635	U1539	C1447	G1358	U1181	U1022
C2204	A2134	A2134	U1886	C1887	G1799	G1799	U1729	U1636	G1540	U1448	C1360	U1182	G1023
A2135	A2062	A2062	C1887	U1979	C1800	C1800	C1730	U1636	C1541	G1448	G1360	U1183	U1023
G2136			U1888	A1901	A1901	A1901			U1542	C1454	G1361	U1184	G1026
C2207	C2065	G2140	G1980	A1889	A1802	A1802	U1735	C1639	G1543	U1458	A1365	G1185	A1027
C2208	C2066	G2141	A1981	A1890	A1803	A1803	U1736	A1640		U1459	A1366	G1186	A1028
C2209	G2067	G2142	U1982	G1891			G1737		A1549	G1459	A1367	G1187	U1033
U2210	U2068	C2143	G1983		G1807	G1807	G1738	C1645	C1550	U1460	G1368	C1117	
U2213	C2069	C2143	U1899	A1900	A1808	A1808	U1739	C1646	C1551	U1461	A1369	C1118	
C2214	A2070	G2144	A1901	A1901	A1901	A1901	G1740	U1647	A1552	G1461	G1370	U1189	C1045
G2215	C2071	C2145	U1991	A1901	A1901	A1901	C1741	U1648	U1554	G1464	C1371	U1198	A1046
C2216	C2072	C2146	G1992	G1908	U1811	U1811	U1742	A1652	G1555	G1465		U1199	
G2217	U2075	A2147	U1993	G1904	U1812	U1812	G1743	A1652	G1555				C1052
U2220	C2078	G2148	U1994	C1905	G1813	G1813	U1744	G1653	C1558	U1468	A1378	U1203	C1053
G2221	U2079	U2149	U1995	G1906	A1814	A1814	A1745	A1654	C1559	U1469	U1379	G1210	A1054
U2222	C1997	C2150	C1997	G1907	A1815	A1815	U1746	A1655	U1559	A1470	A1301	G1211	G1055
G2224	A2080	U2151	A1998	C1909	G1817	G1817	U1747	U1659	G1560	G1476	A1383	U1209	G1056
A2225				G1910	U1818	U1818	G1748	C1658	C1561	A1477	A1387	G1210	U1057
C2226	U2086	A2154	U2011	G1911	U1819	U1819	A1749	G1659	U1562	A1477	G1388	G1211	U1058
A2227	G2087	U2155	G2012	A1912	A1821	A1821	G1750	G1660	U1563	G1478	G1389	C1212	G1059
G2230	C2088	G2157	C1913	A1913	C1822	C1822	G1753	U1661	C1564	U1479	U1394	G1212	U1060
U2233	A2090	U2159	U1914	A1914	G1823	G1823	A1754	U1662	C1565	C1480	U1394	A1213	U1061
G2234			U1915	A1915	G1824	G1824	G1755	A1669	G1566	U1481	C1398	U1219	G1063
U2235	C2093	C2160	A1916	A1916	U1827	U1827	G1756	A1672	C1568	G1482	C1404	G1220	C1064
G2236	C2096	C2161	U1917	A1917	G1828	G1828	A1757	G1673	U1569	A1490	U1405	G1223	U1065
C2237	A2097	C2165	U1918	A1918	A1829	A1829	U1758	G1674	A1571	U1497	U1406	U1224	U1066
G2238	U2098	U2166	C1920	C1920	A1833	A1833	A1762	G1681	A1572	G1501	U1409	G1229	G1068
C2239	U2099	U2167	G1929	G1929	U1834	U1834	C1764	G1682	A1583	A1502	G1410	A1230	A1069
U2240	G2100	G2168	U1930	U1930	C1837	C1837	U1765	U1683	U1584	A1503	A1411	A1231	A1070
A2241	A2101	A2169	A1931	A1931	C1837	C1837	G1766	G1684	C1585	A1504	U1412	G1236	G1071
G2242	C2102	C2170	A1932	A1932	G1942	G1942	G1767	C1685		A1505	A1413	U1239	C1072
U2243	C2103	U2171	G1933	G1933	C1843	C1843	C1768	C1686	U1589	U1506	G1416	U1240	A1073
U2244	C2104	U2172	G1934	G1934	C1843	C1843	U1769	A1690	A1590	C1507	C1417	U1241	G1074
	U2105	A2173	A1935	A1935	G1846	G1846	G1770	C1691	A1591	A1508	G1418	C1243	C1075
C2248	G2035	C2174	A1936	A1936	A1847	A1847		U1692	C1592	A1509	G1418	U1244	A1077
U2249	C2107	A2175	A1937	A1937	A1947	A1947	A1773	U1693	U1593	G1510	A1419	A1246	U1078
G2250	U2110	C2179	U2037	U2037	U1856	U1856	G1774	C1694	U1594	C1512	A1420	U1247	C1161
U2259	G2111	U2180	G2038	G2038	G1857	G1857	U1775	G1695	C1595	U1513	G1423	G1248	G1162
U2262	U2040	A2183	G2039	G2039	A1858	A1858	U1776	A1698	A1598	G1514	G1424	U1249	U1083
C2263	U2041	U2184	U1944	U1944	U1859	U1859	U1777			U1515	G1424	U1250	A1084
G2264	A2042	C2284	G1945	G1945	G1860	G1860	U1778	U1701	G1601	G1516	G1430	G1251	A1085
U2265	C2043	U2185	U1946	U1946	G1861	G1861	U1779	U1702	U1602	G1517	A1431	C1252	A1086
G2266	G2044	G2186	C2044	C2044	G1861	G1861	U1780	G1703	A1603	G1521	G1432	U1253	G1167
A2267	C2045	U2187	G2045	G2045	A1866	A1866	U1781	G1703	U1603	A1522	A1433	G1254	A1087
A2268	G2046	U2188	G2046	G2046	A1867	A1867	U1782	G1703	C1607	U1523	A1434	U1255	A1088
	U2118	U2188	U2188	U2188	C1868	C1868	A1783	U1709	G1608	G1524	G1435	U1256	A1089
A2273	U2193	G2193	U2188	U2188	G1869	G1869	A1784	G1710	A1609	A1525	G1436	G1256	A1090
U2274	U2194	U2195	G2193	G2193	C1870	C1870	A1785	U1711	A1610	C1526	G1437	U1268	C1091
					U1786	U1786		U1712	C1611	C1527	U1438	A1269	C1092
													G1093



• Molecule 52: 5S ribosomal RNA



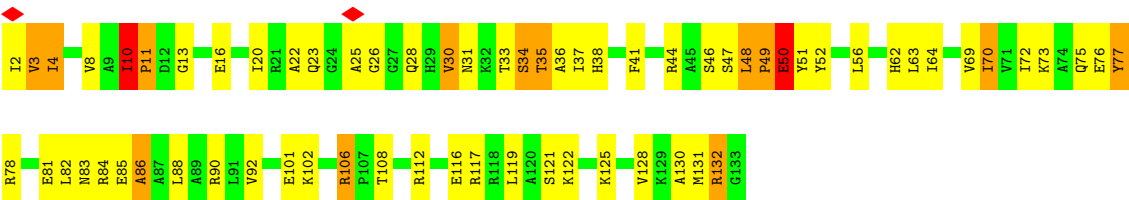
• Molecule 53: tRNA^{fMet}



• Molecule 54: mRNA



● Molecule 55: Peptidyl-tRNA hydrolase ArfB



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8184	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.6	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	11.966	Depositor
Minimum map value	-5.215	Depositor
Average map value	0.097	Depositor
Map value standard deviation	0.602	Depositor
Recommended contour level	0.43	Depositor
Map size ($\text{\AA}$)	375.12003, 375.12003, 375.12003	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.042, 1.042, 1.042	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.35	0/2122	0.94	9/2852 (0.3%)
2	c	0.35	0/1586	0.89	3/2134 (0.1%)
3	d	0.32	0/1571	0.93	7/2113 (0.3%)
4	e	0.36	0/1435	1.03	11/1926 (0.6%)
5	f	0.35	0/1343	0.86	1/1816 (0.1%)
6	g	0.36	0/1122	1.04	7/1515 (0.5%)
7	h	0.40	0/1001	1.10	8/1350 (0.6%)
8	j	0.35	0/1152	0.97	7/1551 (0.5%)
9	k	0.37	0/948	1.02	3/1268 (0.2%)
10	l	0.35	0/1054	0.99	6/1403 (0.4%)
11	m	0.35	0/1093	0.97	10/1460 (0.7%)
12	n	0.35	0/974	0.90	4/1301 (0.3%)
13	o	0.31	0/902	0.88	3/1209 (0.2%)
14	p	0.34	0/929	0.83	1/1242 (0.1%)
15	q	0.33	0/960	0.94	4/1278 (0.3%)
16	r	0.34	0/829	0.93	4/1107 (0.4%)
17	s	0.35	0/864	0.95	2/1156 (0.2%)
18	t	0.32	0/745	0.88	2/994 (0.2%)
19	u	0.33	0/788	0.92	3/1051 (0.3%)
20	v	0.32	0/766	0.98	2/1025 (0.2%)
21	w	0.32	0/582	0.89	2/769 (0.3%)
22	x	0.32	0/635	0.84	1/848 (0.1%)
23	y	0.30	0/510	0.89	1/677 (0.1%)
24	z	0.34	0/453	0.89	1/605 (0.2%)
25	B	0.35	0/450	0.85	1/599 (0.2%)
26	C	0.34	0/417	0.79	0/554
27	D	0.39	0/380	0.96	2/498 (0.4%)
28	E	0.33	0/513	0.86	0/676
29	F	0.34	0/303	0.95	1/397 (0.3%)
30	G	0.34	0/1788	0.96	8/2408 (0.3%)
31	H	0.34	0/1652	0.96	9/2225 (0.4%)
32	I	0.35	0/1665	1.07	12/2227 (0.5%)
33	J	0.33	0/1170	0.96	4/1573 (0.3%)
34	K	0.36	0/836	1.05	5/1128 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	L	0.34	0/1196	0.95	1/1602 (0.1%)
36	M	0.33	0/989	0.94	2/1326 (0.2%)
37	N	0.36	0/1034	1.00	7/1375 (0.5%)
38	O	0.37	0/797	1.01	5/1077 (0.5%)
39	P	0.35	0/886	1.01	6/1195 (0.5%)
40	Q	0.33	0/969	0.98	4/1300 (0.3%)
41	R	0.36	0/893	0.88	2/1193 (0.2%)
42	S	0.33	0/817	1.00	5/1088 (0.5%)
43	T	0.31	0/722	1.03	6/964 (0.6%)
44	U	0.36	0/659	0.89	1/884 (0.1%)
45	V	0.37	0/658	0.89	2/881 (0.2%)
46	W	0.38	0/545	1.05	4/731 (0.5%)
47	X	0.38	0/653	0.95	3/877 (0.3%)
48	Y	0.31	0/671	1.01	4/888 (0.5%)
49	Z	0.36	0/551	1.08	5/728 (0.7%)
50	3	0.43	0/36963	0.49	4/57662 (0.0%)
51	1	0.44	0/69794	0.50	7/108883 (0.0%)
52	2	0.44	0/2872	0.49	0/4479
53	5	0.43	0/1832	0.48	0/2855
54	4	0.50	0/520	0.66	0/810
55	8	0.37	0/1043	1.22	17/1399 (1.2%)
All	All	0.41	0/158602	0.65	229/237132 (0.1%)

There are no bond length outliers.

The worst 5 of 229 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	8	106	ARG	N-CA-C	-9.76	98.90	110.13
31	H	204	GLY	N-CA-C	9.37	124.22	112.14
3	d	73	ILE	N-CA-C	-8.87	104.05	112.83
4	e	106	ALA	N-CA-C	8.37	120.03	111.07
55	8	47	SER	N-CA-C	8.37	122.85	112.47

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	72	0
2	c	1565	0	1616	42	0
3	d	1552	0	1619	42	0
4	e	1411	0	1447	45	0
5	f	1323	0	1374	22	0
6	g	1111	0	1148	23	0
7	h	988	0	1025	37	0
8	j	1129	0	1162	39	0
9	k	939	0	1012	37	0
10	l	1045	0	1117	36	0
11	m	1074	0	1157	43	0
12	n	961	0	1000	27	0
13	o	892	0	923	26	0
14	p	917	0	965	24	0
15	q	947	0	1022	36	0
16	r	816	0	839	25	0
17	s	857	0	922	23	0
18	t	739	0	807	20	0
19	u	780	0	834	8	0
20	v	753	0	780	12	0
21	w	575	0	592	14	0
22	x	625	0	655	20	0
23	y	509	0	543	14	0
24	z	449	0	491	6	0
25	B	444	0	461	16	0
26	C	410	0	440	4	0
27	D	377	0	418	9	0
28	E	504	0	574	16	0
29	F	302	0	343	11	0
30	G	1757	0	1787	42	0
31	H	1625	0	1699	41	0
32	I	1643	0	1710	64	0
33	J	1157	0	1199	35	0
34	K	818	0	808	35	0
35	L	1182	0	1240	22	0
36	M	979	0	1034	37	0
37	N	1022	0	1070	36	0
38	O	787	0	828	21	0
39	P	870	0	878	24	0
40	Q	955	0	1019	29	0
41	R	884	0	944	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	S	805	0	847	37	0
43	T	714	0	737	13	0
44	U	649	0	666	23	0
45	V	649	0	691	27	0
46	W	536	0	552	15	0
47	X	638	0	665	31	0
48	Y	665	0	714	13	0
49	Z	545	0	579	30	0
50	3	33012	0	16619	652	0
51	1	62315	0	31346	1173	0
52	2	2568	0	1303	58	0
53	5	1640	0	837	31	0
54	4	461	0	229	11	0
55	8	1031	0	1087	57	0
All	All	145984	0	98531	2942	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 12.

The worst 5 of 2942 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:J:110:MET:HE1	50:3:9:G:H5'	1.34	1.10
21:w:39:THR:H	51:1:2331:G:H4'	1.19	1.06
20:v:9:ARG:HG2	20:v:41:GLU:HG3	1.37	1.05
51:1:45:G:H5''	51:1:46:G:H5'	1.30	1.05
2:c:173:GLN:HE21	51:1:2731:G:H4'	1.20	1.03

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%)	236 (88%)	29 (11%)	4 (2%)	8	37
2	c	207/209 (99%)	180 (87%)	23 (11%)	4 (2%)	6	33
3	d	199/201 (99%)	181 (91%)	16 (8%)	2 (1%)	12	44
4	e	175/177 (99%)	155 (89%)	15 (9%)	5 (3%)	3	26
5	f	174/176 (99%)	161 (92%)	11 (6%)	2 (1%)	11	43
6	g	147/149 (99%)	123 (84%)	20 (14%)	4 (3%)	4	27
7	h	129/165 (78%)	99 (77%)	24 (19%)	6 (5%)	2	17
8	j	140/142 (99%)	129 (92%)	9 (6%)	2 (1%)	9	38
9	k	120/122 (98%)	103 (86%)	13 (11%)	4 (3%)	3	23
10	l	141/143 (99%)	119 (84%)	20 (14%)	2 (1%)	9	38
11	m	134/136 (98%)	125 (93%)	7 (5%)	2 (2%)	8	37
12	n	118/120 (98%)	95 (80%)	21 (18%)	2 (2%)	7	35
13	o	114/116 (98%)	104 (91%)	8 (7%)	2 (2%)	6	34
14	p	112/114 (98%)	101 (90%)	9 (8%)	2 (2%)	6	34
15	q	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
16	r	101/103 (98%)	83 (82%)	17 (17%)	1 (1%)	12	44
17	s	108/110 (98%)	93 (86%)	14 (13%)	1 (1%)	14	47
18	t	91/93 (98%)	80 (88%)	11 (12%)	0	100	100
19	u	100/102 (98%)	86 (86%)	13 (13%)	1 (1%)	12	44
20	v	92/94 (98%)	83 (90%)	9 (10%)	0	100	100
21	w	73/75 (97%)	66 (90%)	7 (10%)	0	100	100
22	x	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
23	y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
24	z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
25	B	54/56 (96%)	49 (91%)	4 (7%)	1 (2%)	6	33
26	C	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
27	D	44/46 (96%)	39 (89%)	4 (9%)	1 (2%)	5	30
28	E	62/64 (97%)	49 (79%)	10 (16%)	3 (5%)	2	16
29	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	26
30	G	223/225 (99%)	192 (86%)	26 (12%)	5 (2%)	5	30
31	H	204/206 (99%)	188 (92%)	14 (7%)	2 (1%)	12	44
32	I	203/205 (99%)	173 (85%)	29 (14%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	J	155/157 (99%)	122 (79%)	29 (19%)	4 (3%)	4	27
34	K	98/100 (98%)	77 (79%)	15 (15%)	6 (6%)	1	12
35	L	149/151 (99%)	133 (89%)	15 (10%)	1 (1%)	18	51
36	M	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	7	36
37	N	125/127 (98%)	101 (81%)	21 (17%)	3 (2%)	4	29
38	O	96/98 (98%)	78 (81%)	16 (17%)	2 (2%)	5	31
39	P	114/116 (98%)	86 (75%)	23 (20%)	5 (4%)	2	17
40	Q	121/123 (98%)	98 (81%)	20 (16%)	3 (2%)	4	28
41	R	112/114 (98%)	96 (86%)	16 (14%)	0	100	100
42	S	98/100 (98%)	87 (89%)	9 (9%)	2 (2%)	6	32
43	T	86/88 (98%)	78 (91%)	7 (8%)	1 (1%)	10	41
44	U	80/82 (98%)	70 (88%)	9 (11%)	1 (1%)	9	39
45	V	78/80 (98%)	63 (81%)	10 (13%)	5 (6%)	1	11
46	W	63/65 (97%)	56 (89%)	3 (5%)	4 (6%)	1	12
47	X	77/79 (98%)	66 (86%)	10 (13%)	1 (1%)	9	39
48	Y	83/85 (98%)	78 (94%)	4 (5%)	1 (1%)	10	41
49	Z	63/65 (97%)	48 (76%)	8 (13%)	7 (11%)	0	5
55	8	130/132 (98%)	99 (76%)	20 (15%)	11 (8%)	0	7
All	All	5780/5914 (98%)	5000 (86%)	661 (11%)	119 (2%)	8	31

5 of 119 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	e	173	ASP
5	f	47	ASN
5	f	117	PRO
6	g	9	VAL
7	h	81	LEU

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%)	215 (100%)	1 (0%)	81	80
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	79
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	146 (99%)	2 (1%)	59	71
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	78
6	g	114/114 (100%)	112 (98%)	2 (2%)	51	69
7	h	100/123 (81%)	97 (97%)	3 (3%)	36	60
8	j	116/116 (100%)	114 (98%)	2 (2%)	53	70
9	k	103/103 (100%)	101 (98%)	2 (2%)	50	68
10	l	102/102 (100%)	102 (100%)	0	100	100
11	m	109/109 (100%)	108 (99%)	1 (1%)	70	76
12	n	100/100 (100%)	100 (100%)	0	100	100
13	o	86/86 (100%)	85 (99%)	1 (1%)	63	73
14	p	99/99 (100%)	98 (99%)	1 (1%)	68	75
15	q	89/89 (100%)	89 (100%)	0	100	100
16	r	84/84 (100%)	84 (100%)	0	100	100
17	s	93/93 (100%)	93 (100%)	0	100	100
18	t	80/80 (100%)	80 (100%)	0	100	100
19	u	83/83 (100%)	82 (99%)	1 (1%)	63	73
20	v	78/78 (100%)	76 (97%)	2 (3%)	40	62
21	w	57/57 (100%)	56 (98%)	1 (2%)	51	69
22	x	67/67 (100%)	67 (100%)	0	100	100
23	y	55/55 (100%)	55 (100%)	0	100	100
24	z	48/48 (100%)	47 (98%)	1 (2%)	47	66
25	B	47/47 (100%)	46 (98%)	1 (2%)	47	66
26	C	45/45 (100%)	45 (100%)	0	100	100
27	D	38/38 (100%)	38 (100%)	0	100	100
28	E	51/51 (100%)	51 (100%)	0	100	100
29	F	34/34 (100%)	33 (97%)	1 (3%)	37	60
30	G	186/186 (100%)	185 (100%)	1 (0%)	81	80
31	H	170/170 (100%)	168 (99%)	2 (1%)	63	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	I	172/172 (100%)	172 (100%)	0	100	100
33	J	119/119 (100%)	119 (100%)	0	100	100
34	K	87/87 (100%)	83 (95%)	4 (5%)	24	50
35	L	124/124 (100%)	122 (98%)	2 (2%)	55	70
36	M	104/104 (100%)	103 (99%)	1 (1%)	68	75
37	N	105/105 (100%)	105 (100%)	0	100	100
38	O	86/86 (100%)	84 (98%)	2 (2%)	44	64
39	P	89/89 (100%)	88 (99%)	1 (1%)	65	74
40	Q	103/103 (100%)	99 (96%)	4 (4%)	28	54
41	R	92/92 (100%)	91 (99%)	1 (1%)	65	74
42	S	83/83 (100%)	83 (100%)	0	100	100
43	T	76/76 (100%)	76 (100%)	0	100	100
44	U	65/65 (100%)	65 (100%)	0	100	100
45	V	74/74 (100%)	73 (99%)	1 (1%)	59	71
46	W	56/56 (100%)	56 (100%)	0	100	100
47	X	70/70 (100%)	69 (99%)	1 (1%)	59	71
48	Y	65/65 (100%)	65 (100%)	0	100	100
49	Z	55/55 (100%)	54 (98%)	1 (2%)	51	69
55	8	108/108 (100%)	106 (98%)	2 (2%)	50	68
All	All	4797/4820 (100%)	4750 (99%)	47 (1%)	65	75

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	K	54	LEU
38	O	57	VAL
34	K	78	PHE
35	L	14	ASP
40	Q	39	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 123 such sidechains are listed below:

Mol	Chain	Res	Type
20	v	44	HIS

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Mol	Chain	Res	Type
42	S	70	HIS
30	G	23	ASN
42	S	65	GLN
45	V	46	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	1538/1539 (99%)	157 (10%)	2 (0%)
51	1	2902/2903 (99%)	365 (12%)	9 (0%)
52	2	119/120 (99%)	14 (11%)	0
53	5	76/77 (98%)	8 (10%)	0
54	4	20/23 (86%)	6 (30%)	2 (10%)
All	All	4655/4662 (99%)	550 (11%)	13 (0%)

5 of 550 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	6	G
50	3	9	G
50	3	22	G
50	3	31	G
50	3	32	A

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	2296	U
51	1	2326	C
54	4	24	A
51	1	2756	U
54	4	22	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

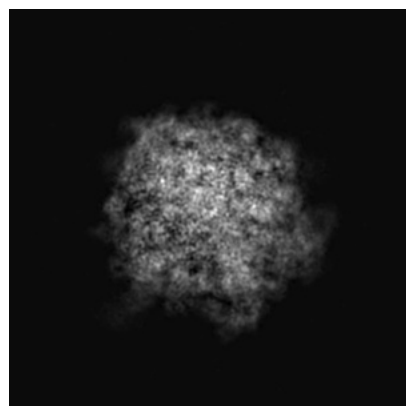
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22469. These allow visual inspection of the internal detail of the map and identification of artifacts.

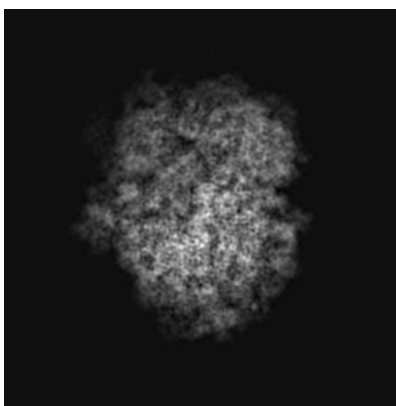
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

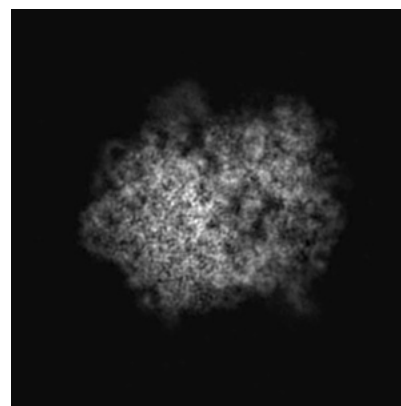
6.1.1 Primary map



X

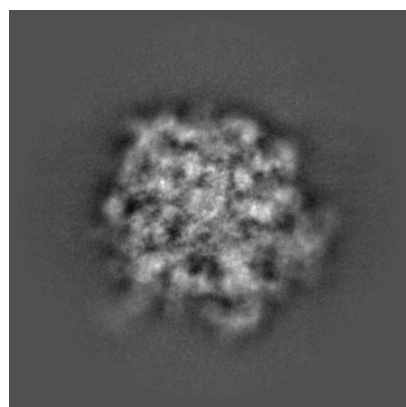


Y

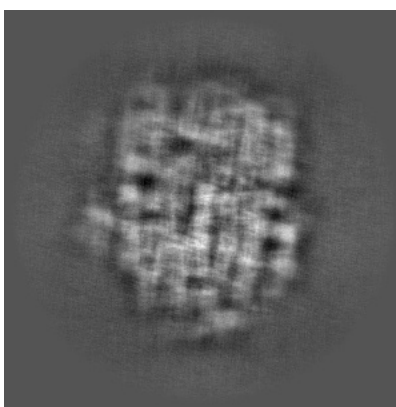


Z

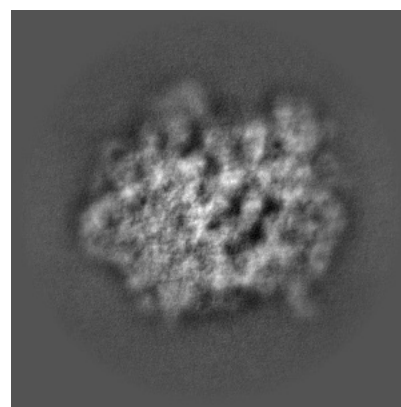
6.1.2 Raw map



X



Y

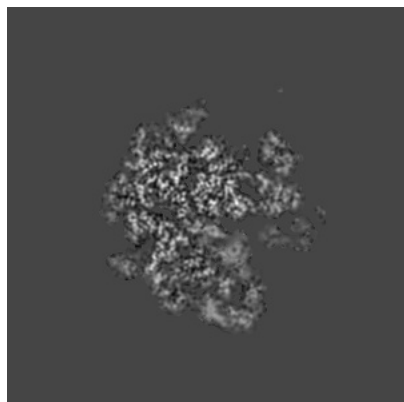


Z

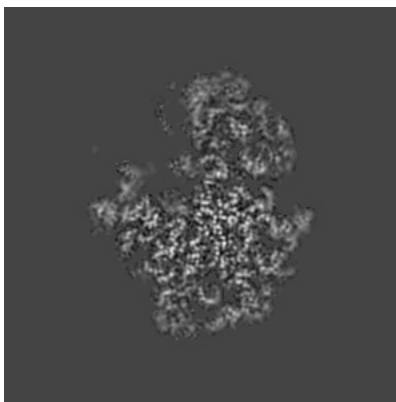
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

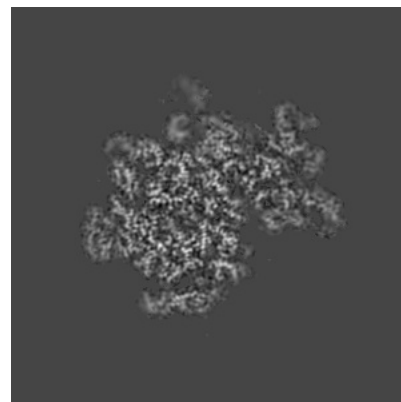
6.2.1 Primary map



X Index: 180

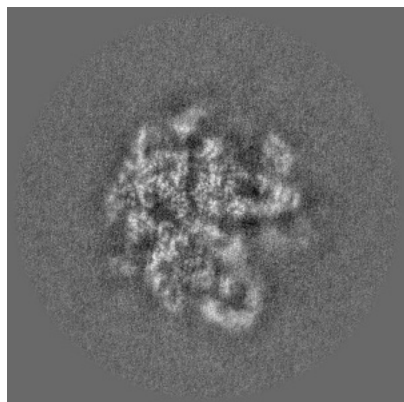


Y Index: 180

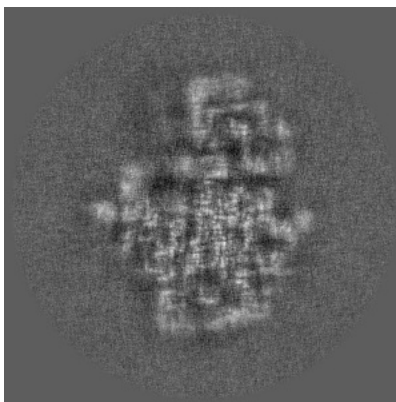


Z Index: 180

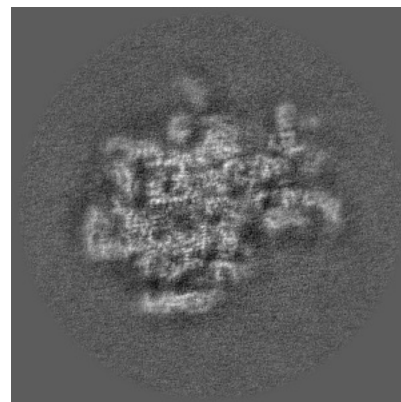
6.2.2 Raw map



X Index: 180



Y Index: 180

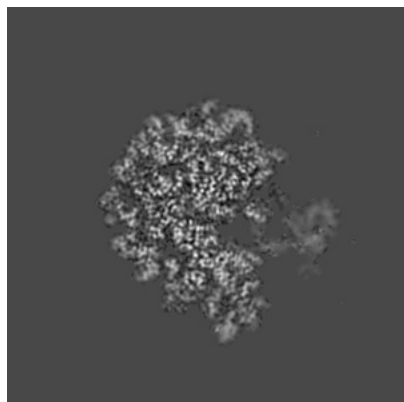


Z Index: 180

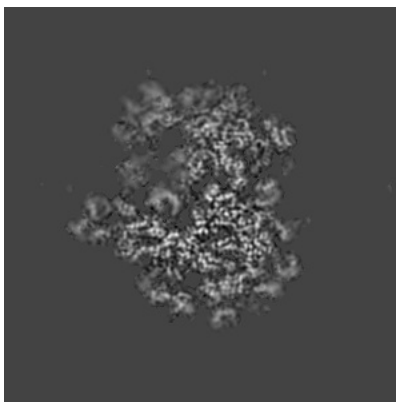
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

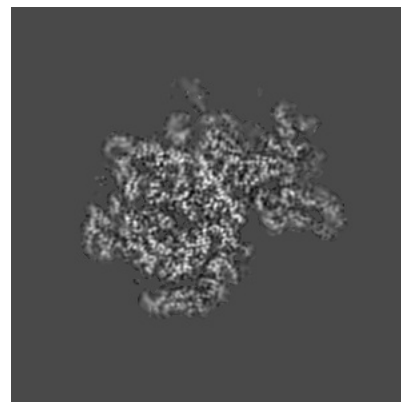
6.3.1 Primary map



X Index: 163

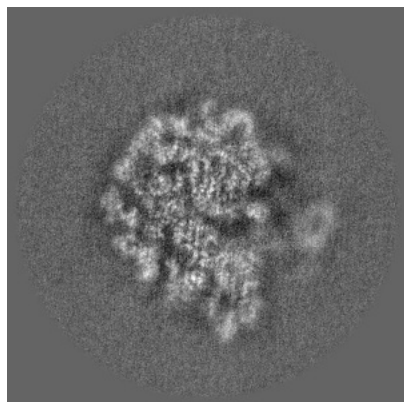


Y Index: 192

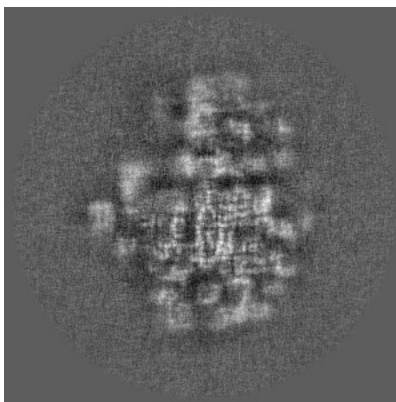


Z Index: 182

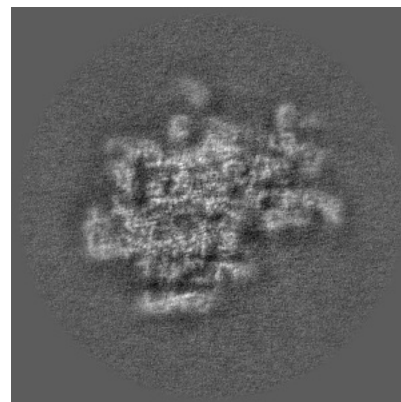
6.3.2 Raw map



X Index: 163



Y Index: 183

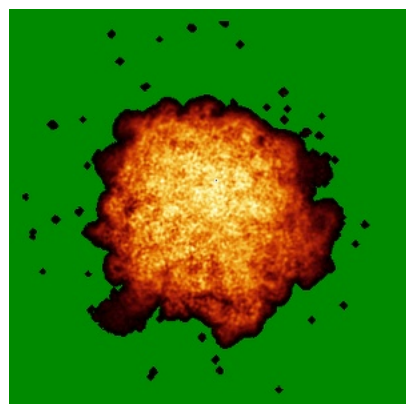


Z Index: 179

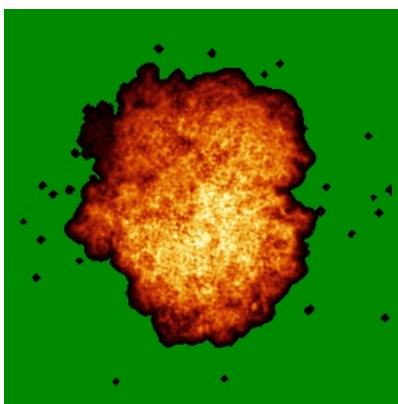
The images above show the largest variance slices of the map in three orthogonal directions.

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

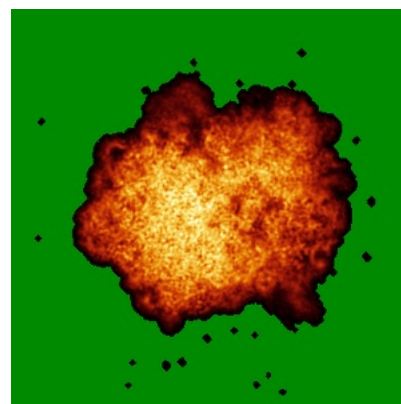
6.4.1 Primary map



X

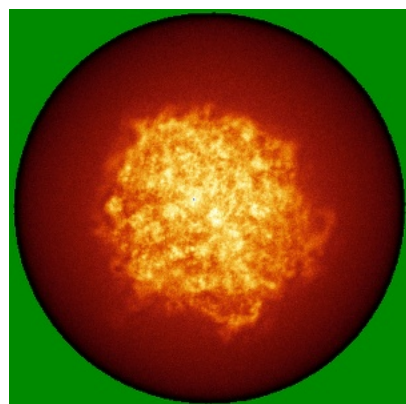


Y

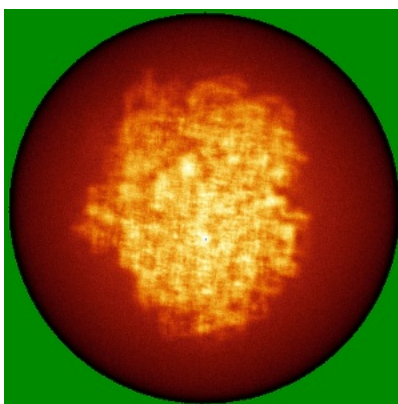


Z

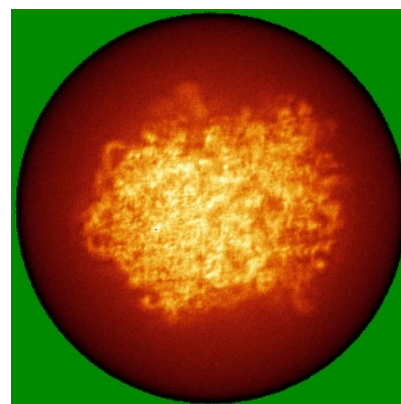
6.4.2 Raw map



X



Y

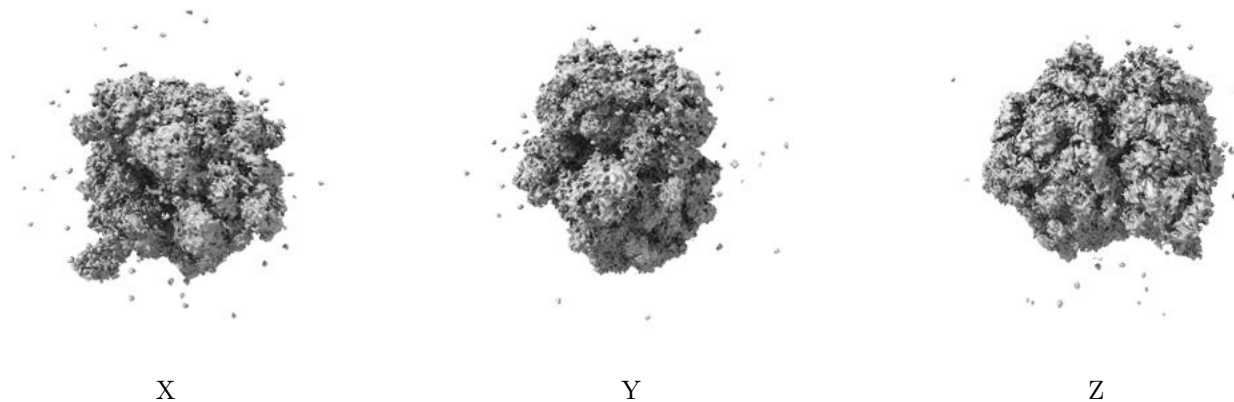


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

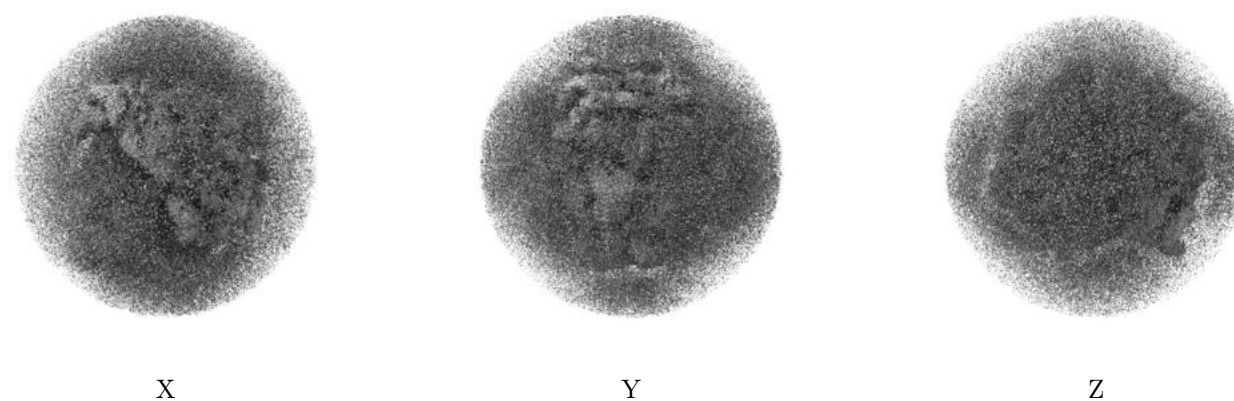
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.43. 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.

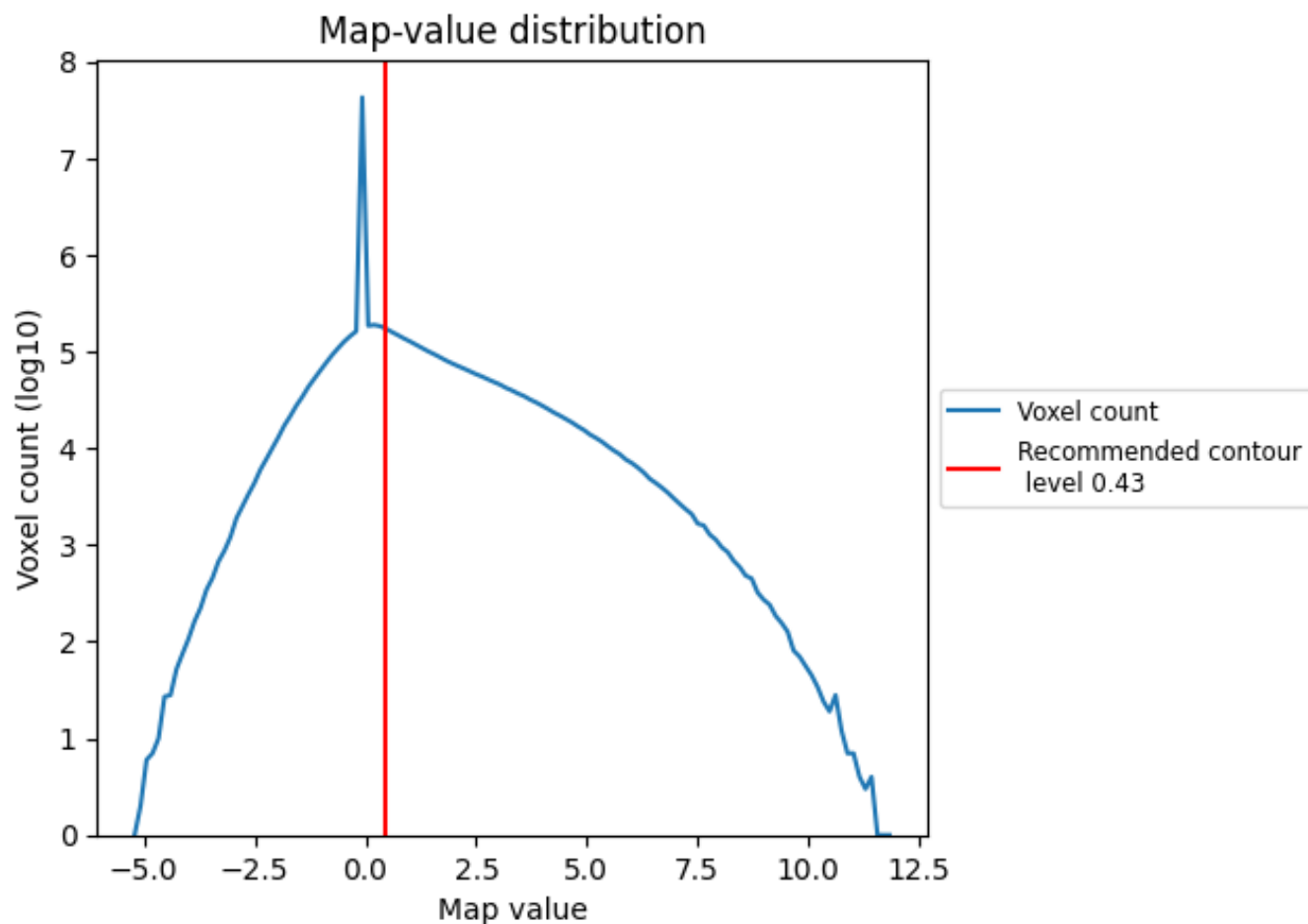
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

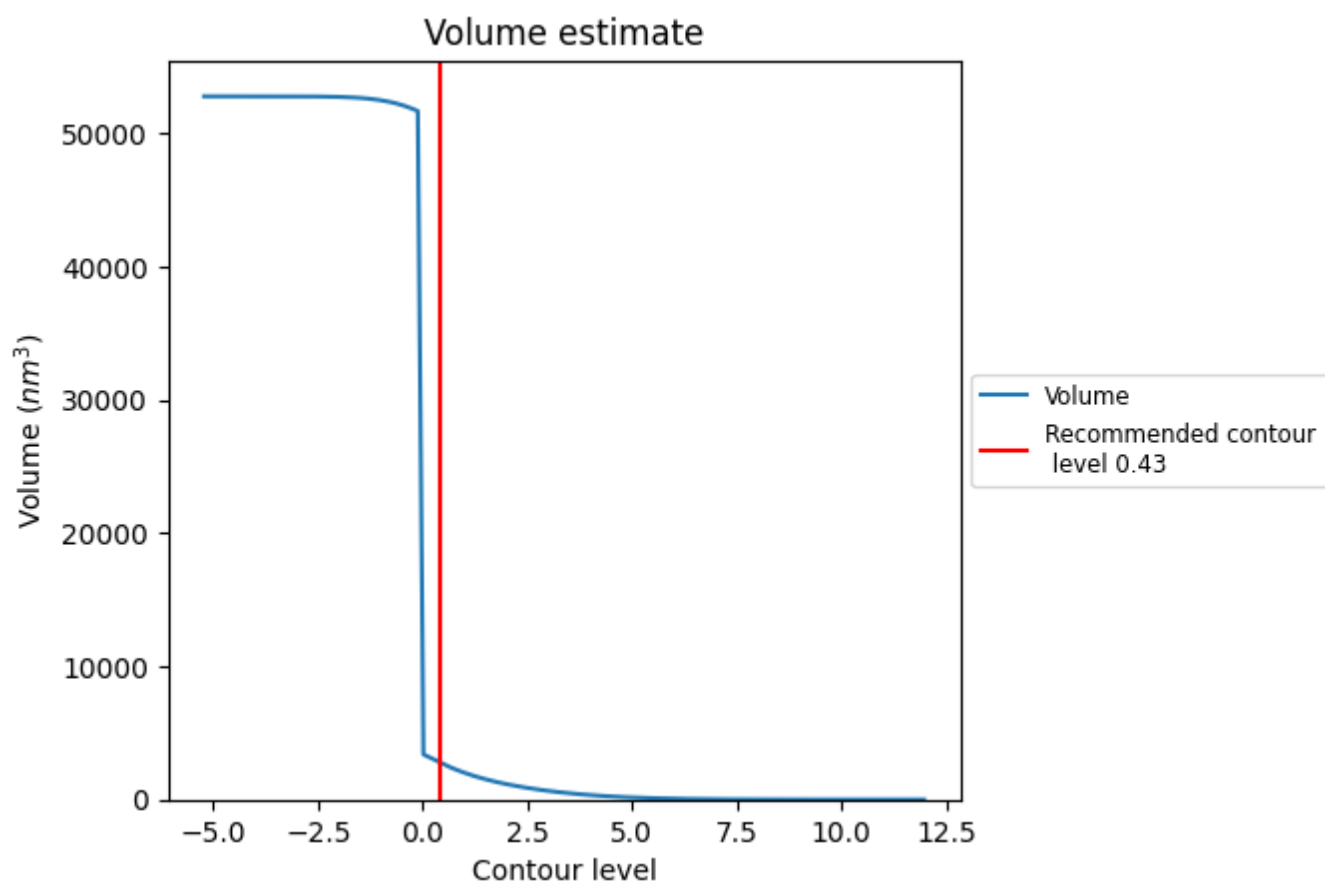
This section contains the results of statistical analysis of the map.

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.

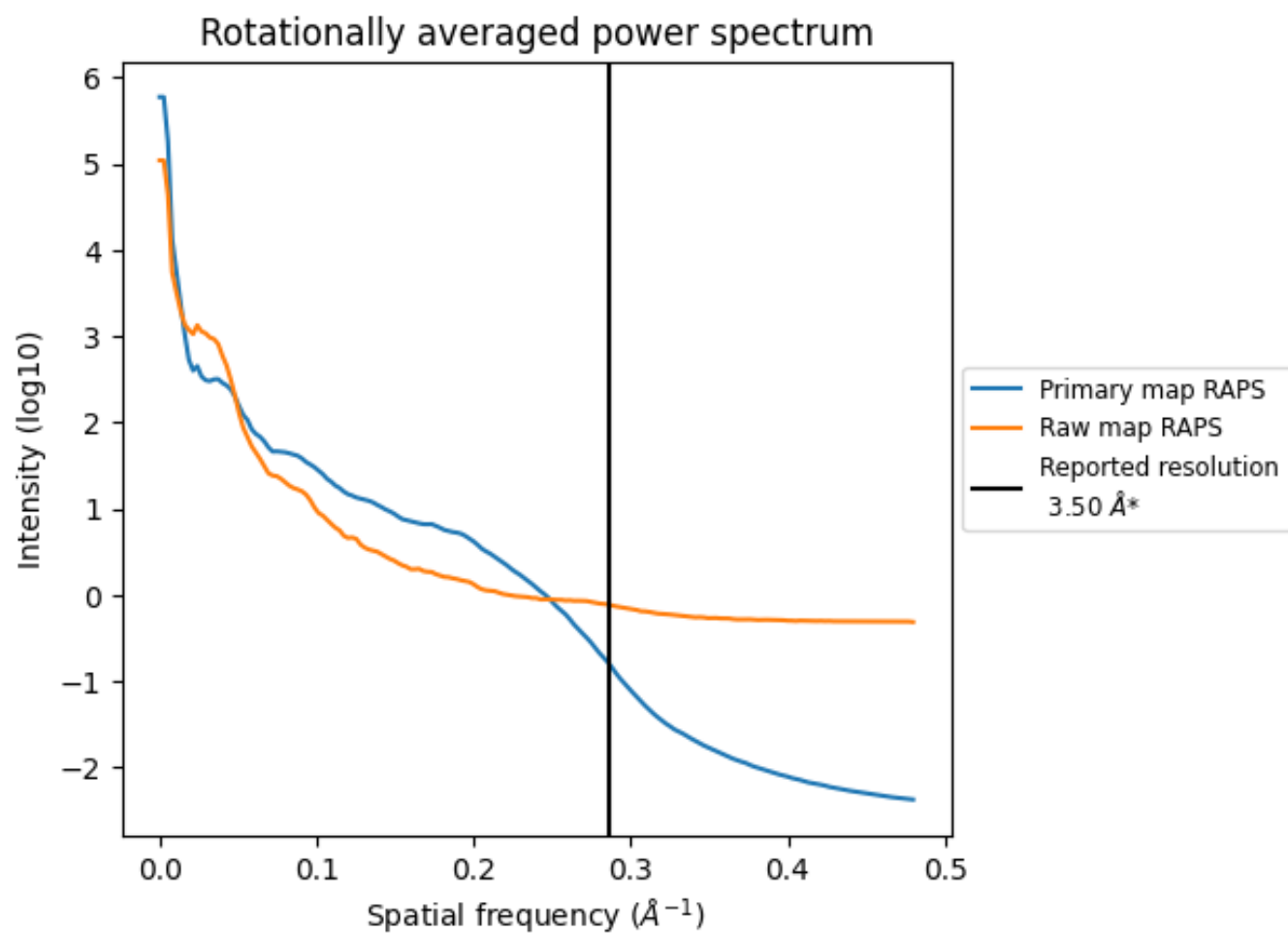
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2750 nm³; this corresponds to an approximate mass of 2484 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 ⓘ

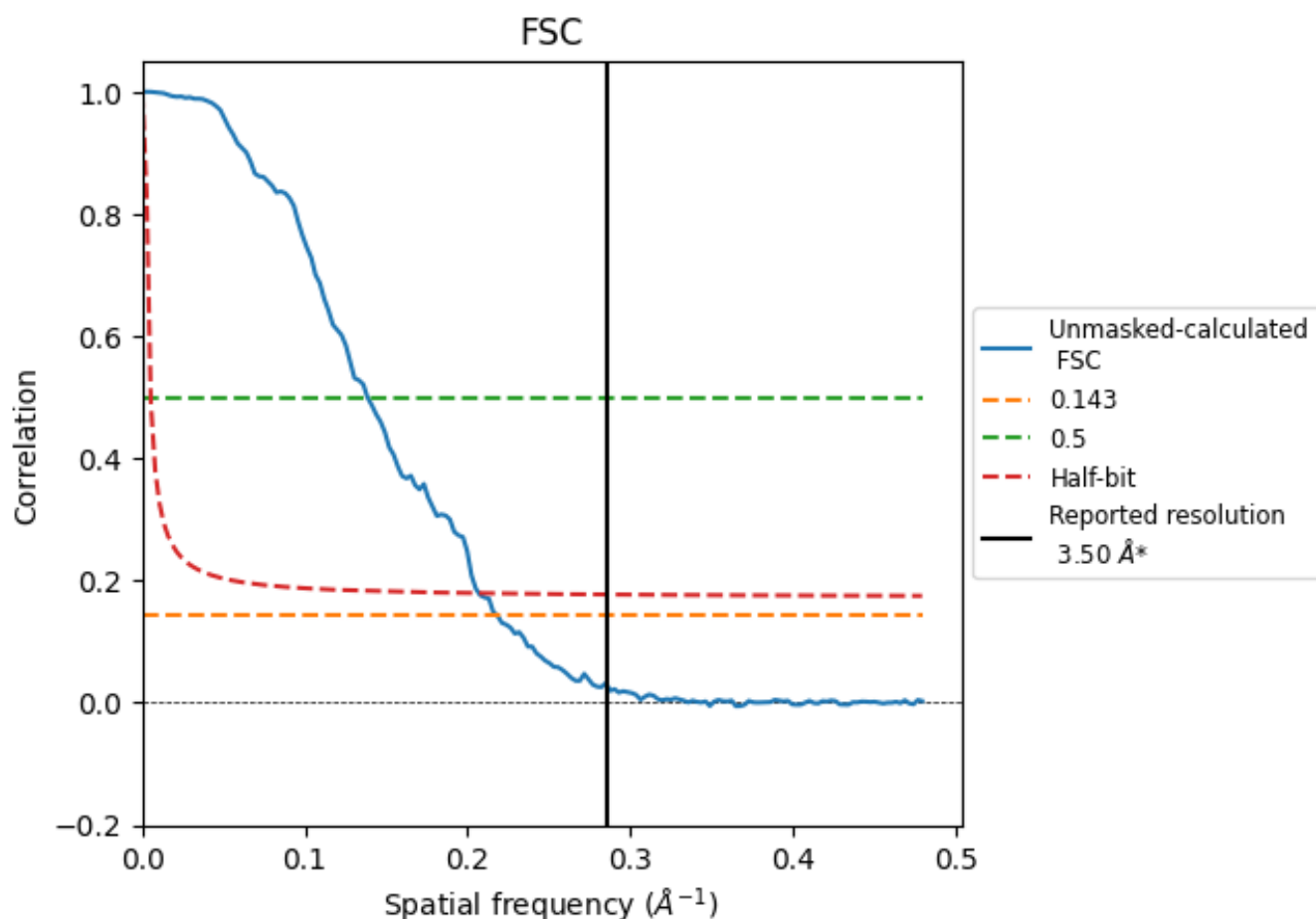


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

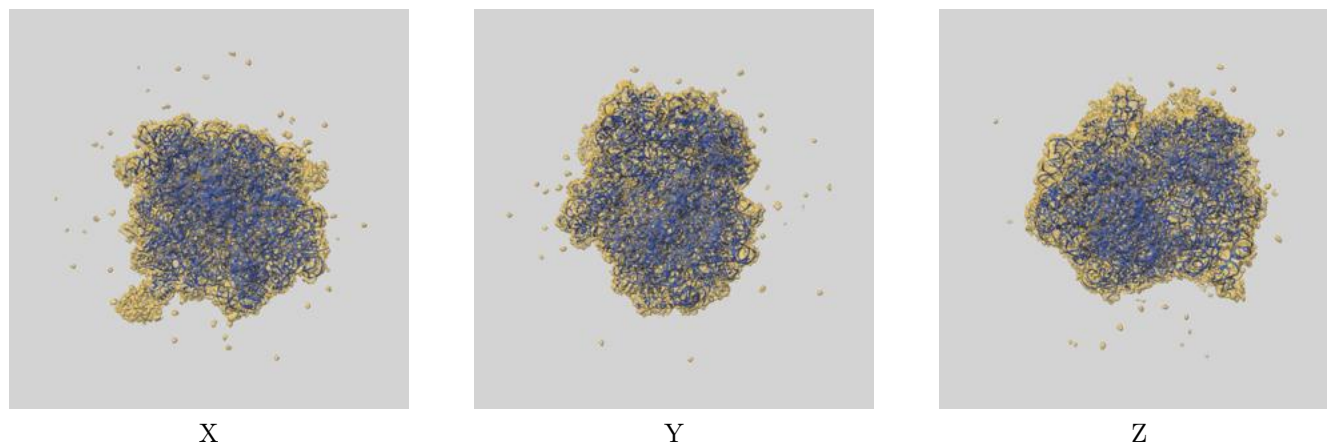
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.58	7.22	4.83

*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 4.58 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

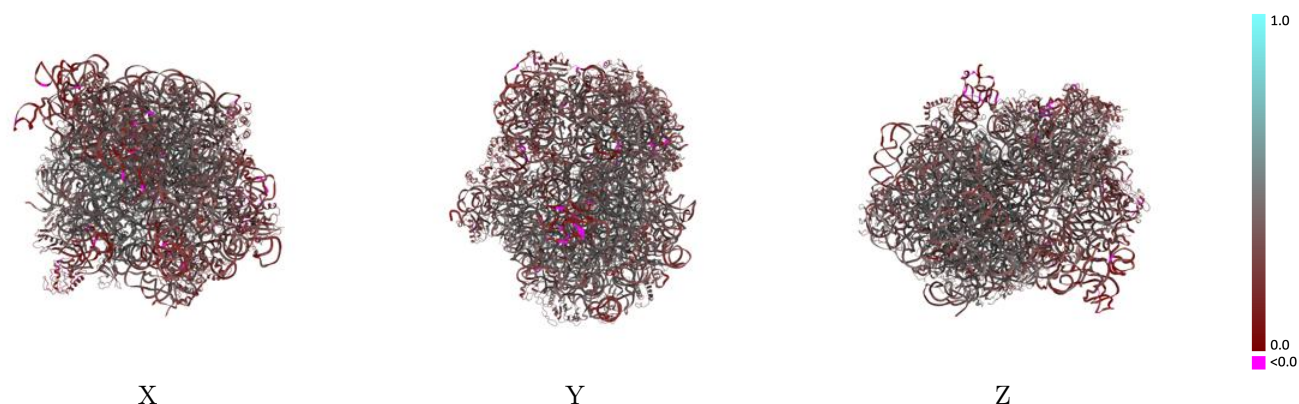
This section contains information regarding the fit between EMDB map EMD-22469 and PDB model 7JT2. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



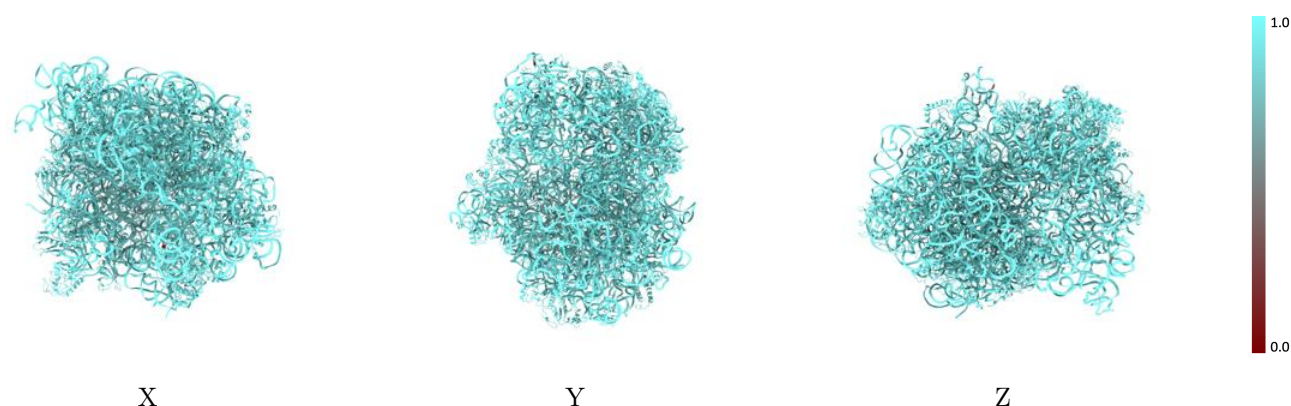
The images above show the 3D surface view of the map at the recommended contour level 0.43 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



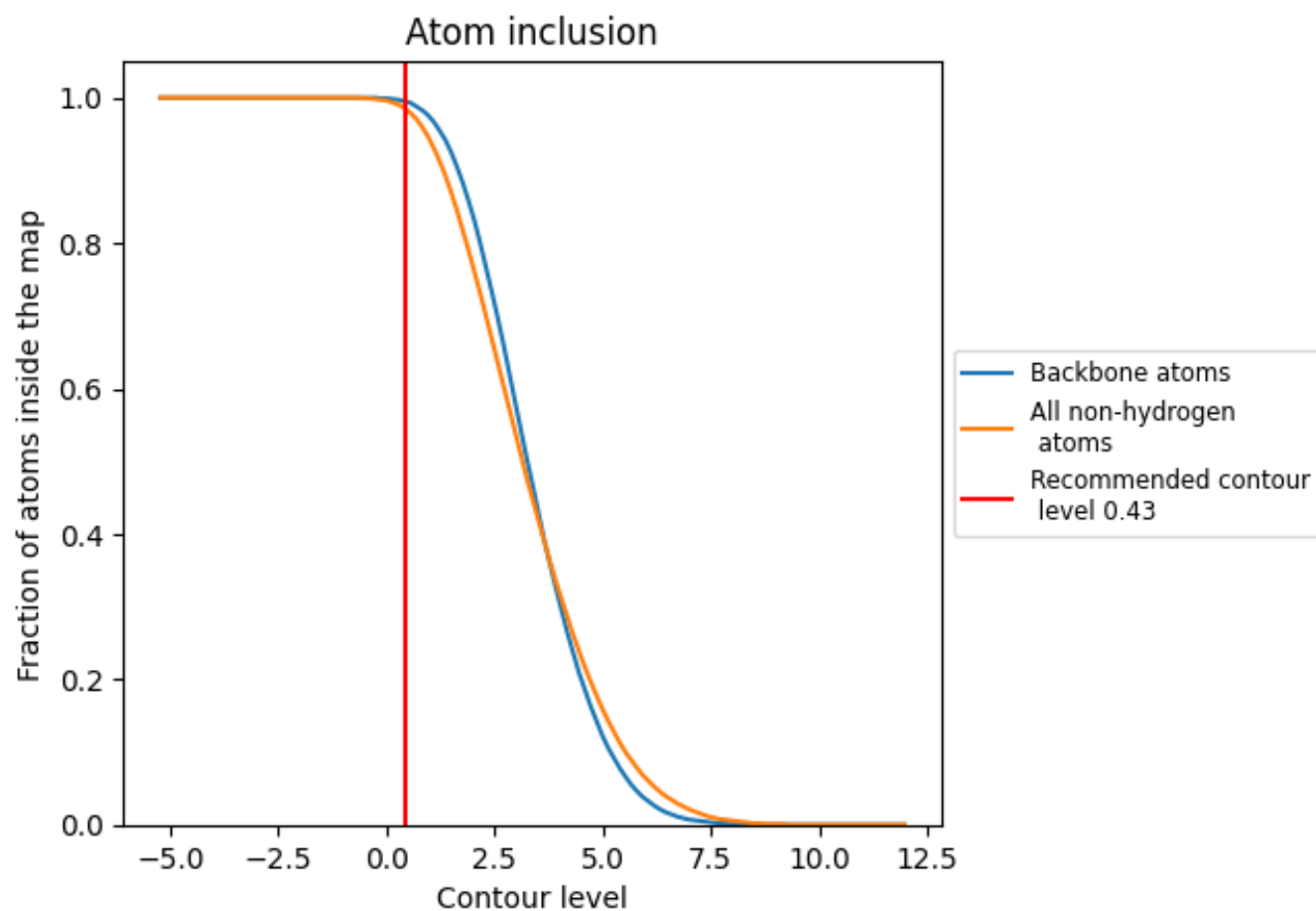
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.43).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.43) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9850	 0.3660
1	 0.9930	 0.3880
2	 0.9950	 0.3270
3	 0.9910	 0.3380
4	 0.9720	 0.2130
5	 0.9870	 0.2890
8	 0.9400	 0.3190
B	 0.9700	 0.4110
C	 0.9750	 0.3730
D	 0.9750	 0.4490
E	 0.9780	 0.4270
F	 0.9760	 0.4220
G	 0.9620	 0.3140
H	 0.9680	 0.3520
I	 0.9470	 0.2780
J	 0.9740	 0.3840
K	 0.9760	 0.3470
L	 0.9750	 0.3080
M	 0.9650	 0.3540
N	 0.9610	 0.3130
O	 0.9210	 0.3180
P	 0.9800	 0.3610
Q	 0.9740	 0.3570
R	 0.9670	 0.3140
S	 0.9420	 0.3180
T	 0.9780	 0.3580
U	 0.9510	 0.3430
V	 0.9870	 0.3610
W	 0.9630	 0.3730
X	 0.9870	 0.2990
Y	 0.9540	 0.2790
Z	 0.9300	 0.3250
b	 0.9780	 0.4510
c	 0.9730	 0.4310
d	 0.9770	 0.3940



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Chain	Atom inclusion	Q-score
e	 0.9810	 0.3000
f	 0.9880	 0.3550
g	 0.9830	 0.3060
h	 0.9380	 0.1850
j	 0.9740	 0.4160
k	 0.9800	 0.4170
l	 0.9650	 0.3970
m	 0.9700	 0.4190
n	 0.9630	 0.4180
o	 0.9660	 0.3400
p	 0.9850	 0.4160
q	 0.9750	 0.4230
r	 0.9700	 0.3960
s	 0.9740	 0.4190
t	 0.9680	 0.4020
u	 0.9870	 0.3720
v	 0.9780	 0.3910
w	 0.9710	 0.4300
x	 0.9930	 0.4340
y	 0.9700	 0.3330
z	 0.9860	 0.4030