



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 11:17 AM UTC

PDB ID : 7JSZ / pdb_00007jsz
EMDB ID : EMD-22464
Title : ArfB Rescue of a 70S Ribosome stalled on truncated mRNA with a partial A-site codon (+2-IV)
Authors : Carbone, C.E.; Korostelev, A.A.
Deposited on : 2020-08-16
Resolution : 3.70 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

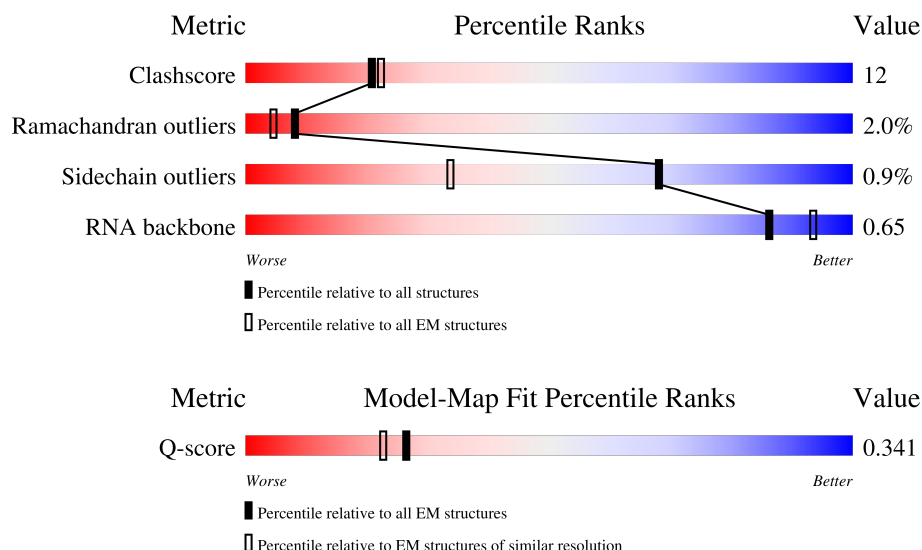
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



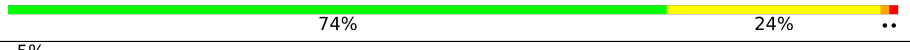
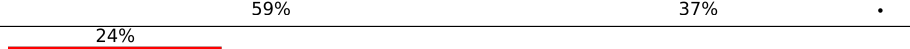
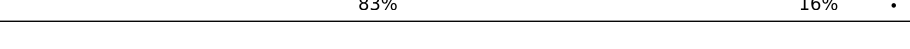
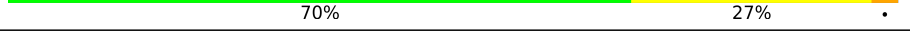
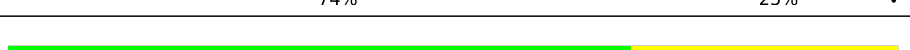
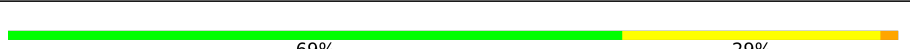
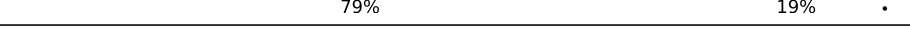
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	 72% 26%
2	c	209	 75% 24%
3	d	201	 76% 23%

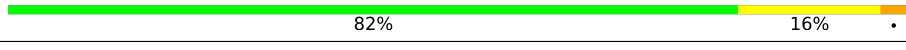
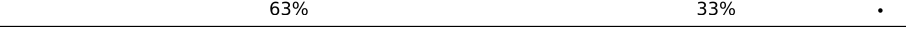
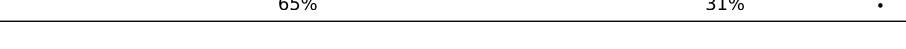
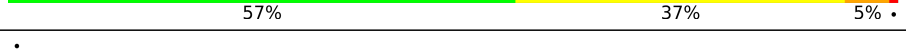
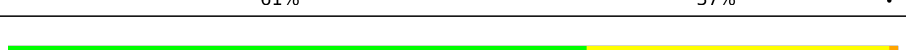
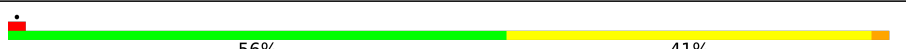
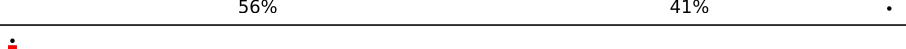
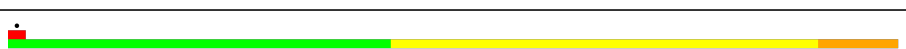
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	165	
8	i	142	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56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

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Mol	Chain	Length	Quality of chain
29	E	64	
30	F	38	
31	G	225	
32	H	206	
33	I	205	
34	J	157	
35	K	100	
36	L	151	
37	M	129	
38	N	127	
39	O	98	
40	P	116	
41	Q	123	
42	R	114	
43	S	100	
44	T	88	
45	U	82	
46	V	80	
47	W	65	
48	X	79	
49	Y	85	
50	Z	65	
51	a	234	
52	3	1539	
53	1	2903	

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Mol	Chain	Length	Quality of chain
54	2	120	47% 48% 6%
55	5	77	42% 52% 6%
56	4	16	25% 75%
57	8	132	45% 41% 6% 8%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 147860 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 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
			1026	645	186	193	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	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 53 is a RNA chain called 23S ribosomal RNA.

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 55 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	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	16	Total	C	N	O	P	0	0
			353	158	74	105	16		

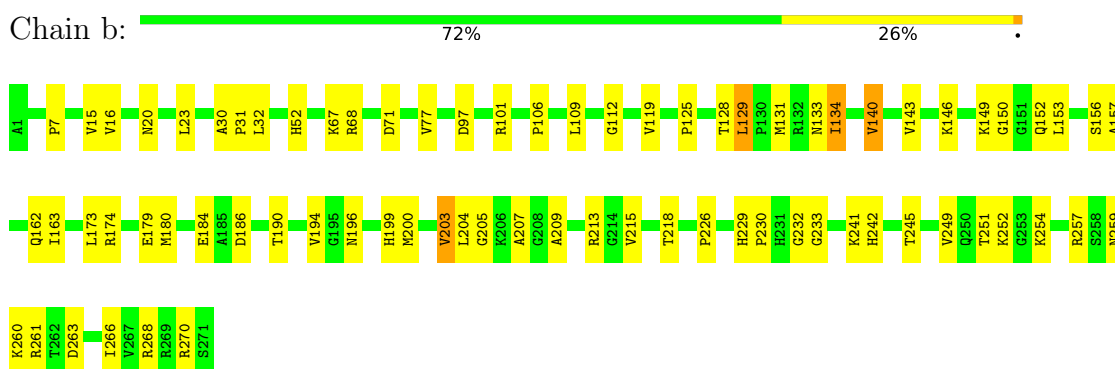
- Molecule 57 is a protein called Peptidyl-tRNA hydrolase ArfB.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	8	121	Total	C	N	O	S	0	0
			955	594	187	172	2		

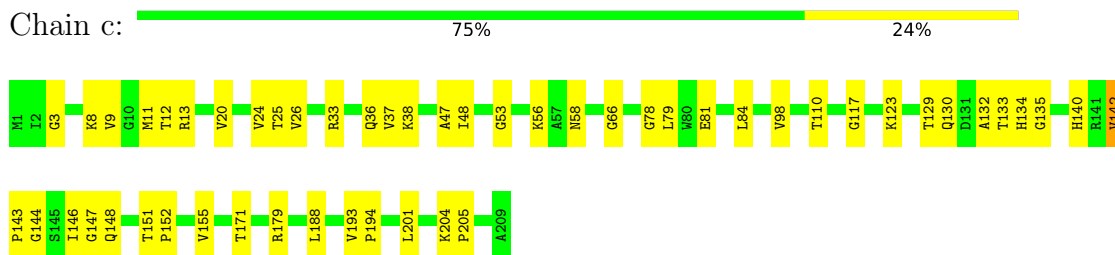
3 Residue-property plots

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.

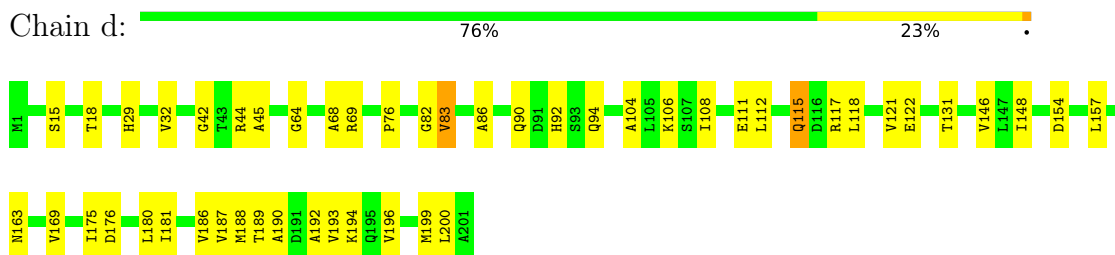
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

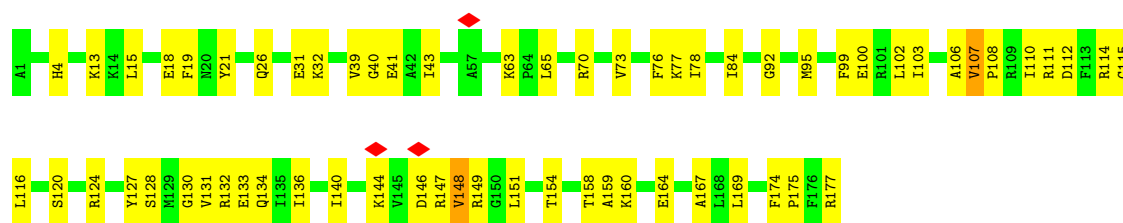


- Molecule 3: 50S ribosomal protein L4



- Molecule 4: 50S ribosomal protein L5





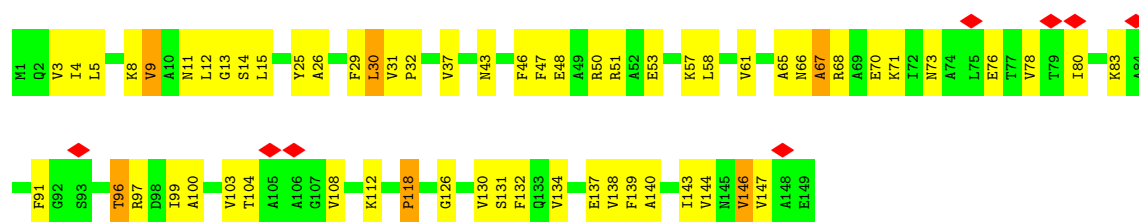
• Molecule 5: 50S ribosomal protein L6

Chain f: 74% 24% ..



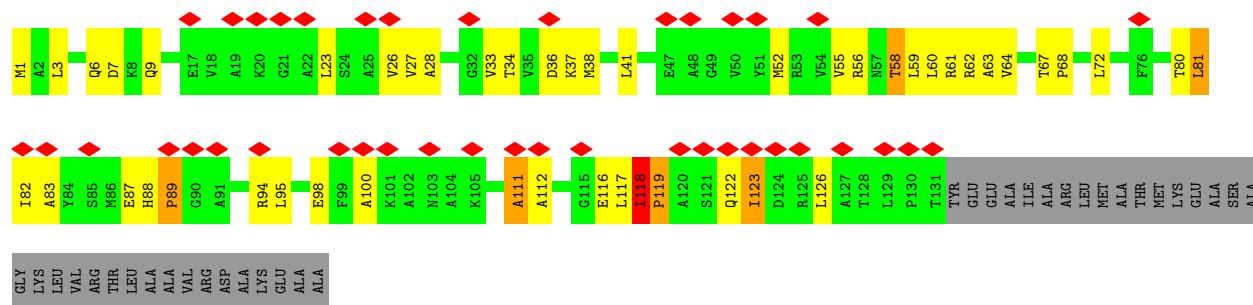
• Molecule 6: 50S ribosomal protein L9

Chain g: 5% 59% 37% .



• Molecule 7: 50S ribosomal protein L10

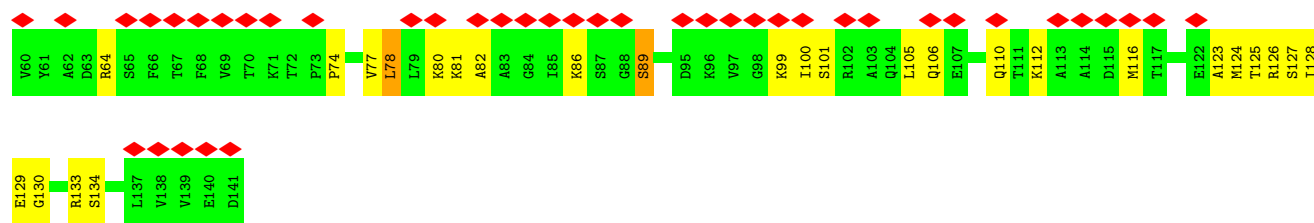
Chain h: 24% 50% 25% . 21%



• Molecule 8: 50S ribosomal protein L11

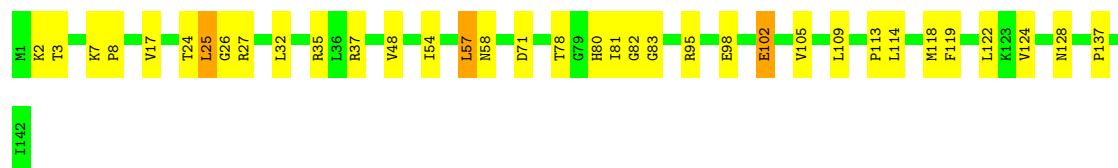
Chain i: 66% 68% 29% ..





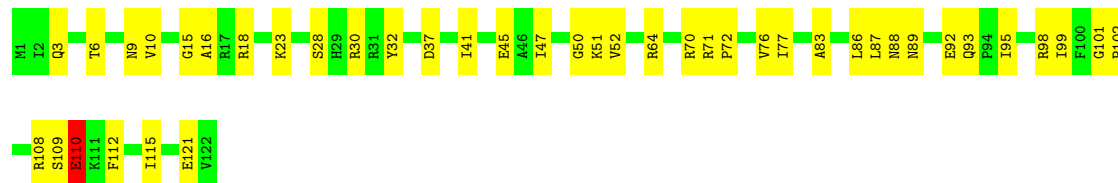
• Molecule 9: 50S ribosomal protein L13

Chain j: 75% 23%



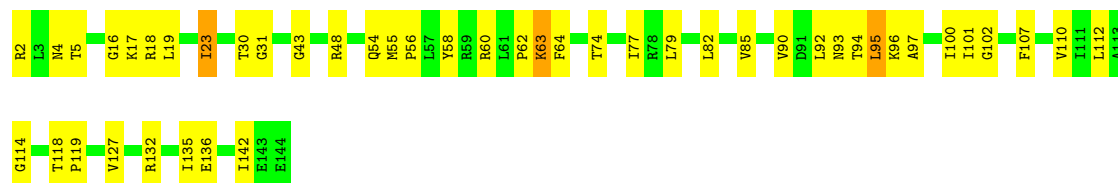
• Molecule 10: 50S ribosomal protein L14

Chain k: 66% 34%



• Molecule 11: 50S ribosomal protein L15

Chain l: 68% 30%



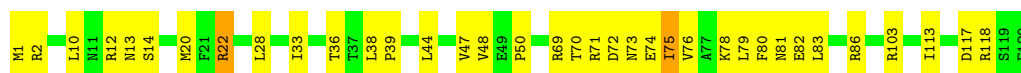
• Molecule 12: 50S ribosomal protein L16

Chain m: 83% 16%



• Molecule 13: 50S ribosomal protein L17

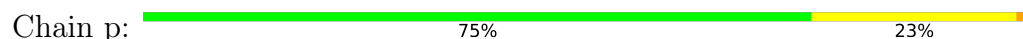
Chain n: 70% 28%



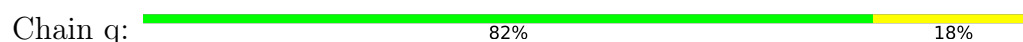
- Molecule 14: 50S ribosomal protein L18



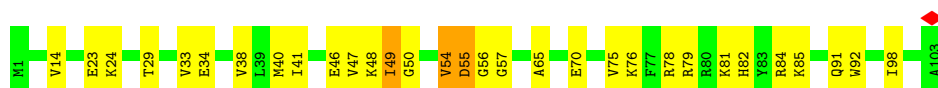
- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20



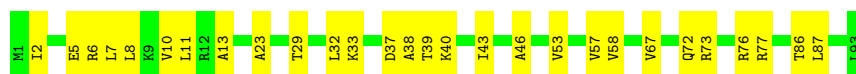
- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24





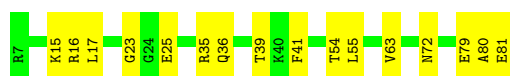
- Molecule 21: 50S ribosomal protein L25

Chain v: 83% 15%



- Molecule 22: 50S ribosomal protein L27

Chain w: 79% 21%



- Molecule 23: 50S ribosomal protein L28

Chain x: 79% 19%



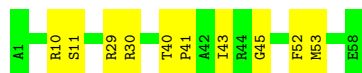
- Molecule 24: 50S ribosomal protein L29

Chain y: 67% 32%



- Molecule 25: 50S ribosomal protein L30

Chain z: 83% 17%



- Molecule 26: 50S ribosomal protein L32

Chain B: 84% 16%

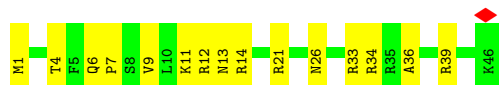


- Molecule 27: 50S ribosomal protein L33

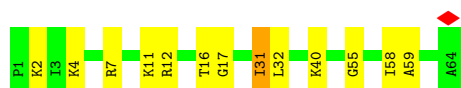
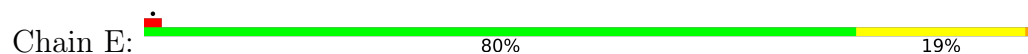
Chain C: 80% 18%



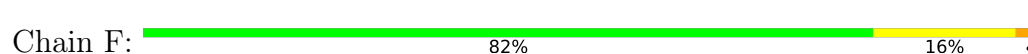
- Molecule 28: 50S ribosomal protein L34



- Molecule 29: 50S ribosomal protein L35



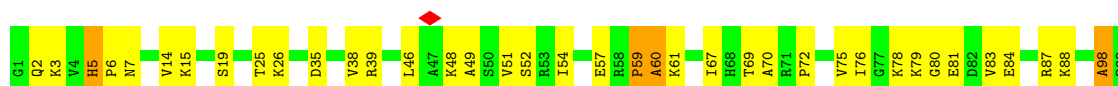
- Molecule 30: 50S ribosomal protein L36



- Molecule 31: 30S ribosomal protein S2



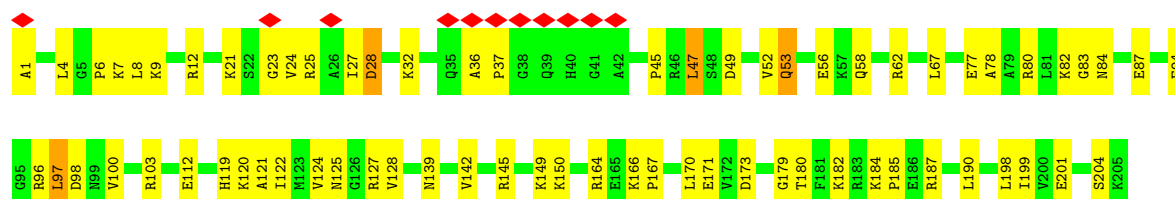
- Molecule 32: 30S ribosomal protein S3



I206

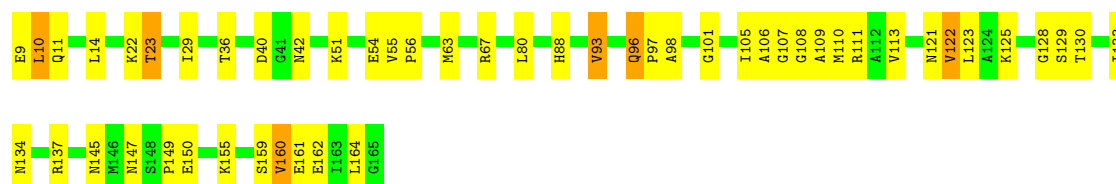
- Molecule 33: 30S ribosomal protein S4

Chain I:  5% 66% 32% .



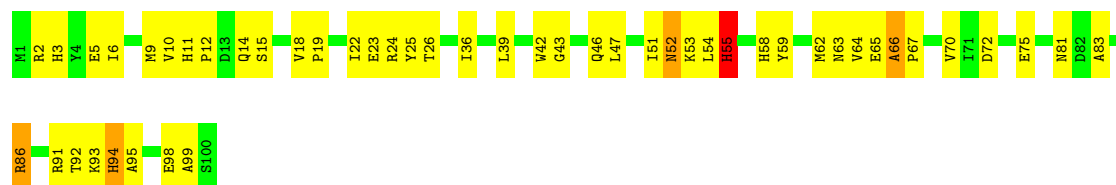
- Molecule 34: 30S ribosomal protein S5

Chain J:  68% 29% .



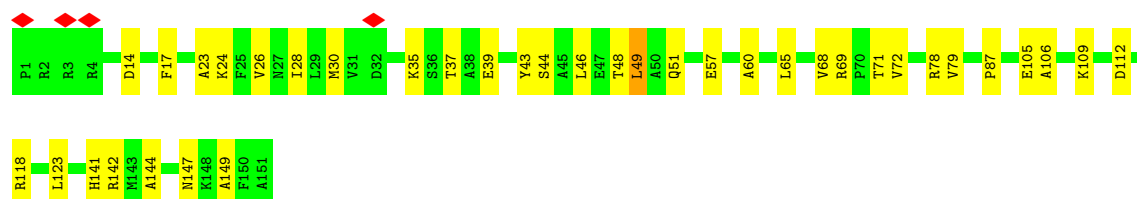
- Molecule 35: 30S ribosomal protein S6

Chain K:  51% 44% . .



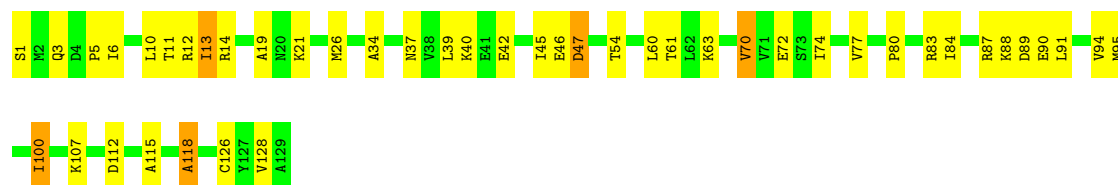
- Molecule 36: 30S ribosomal protein S7

Chain L:  75% 24% .

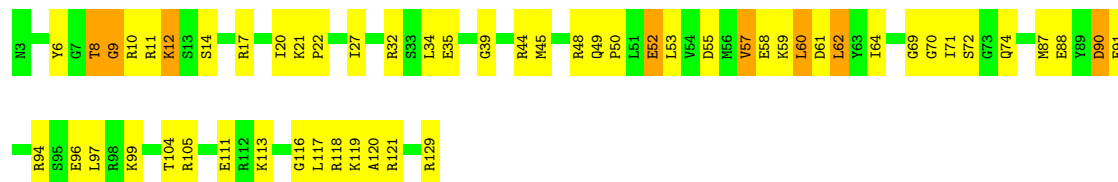


- Molecule 37: 30S ribosomal protein S8

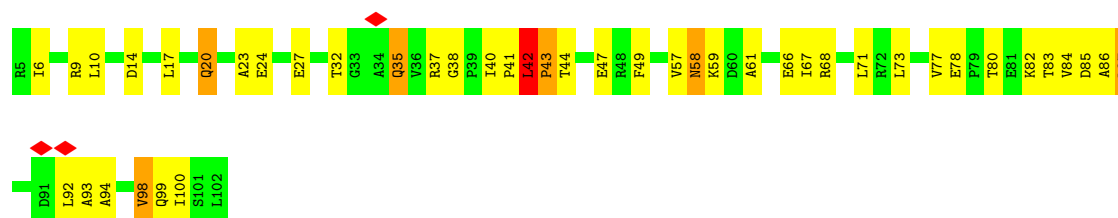
Chain M:  65% 31% .



- Molecule 38: 30S ribosomal protein S9



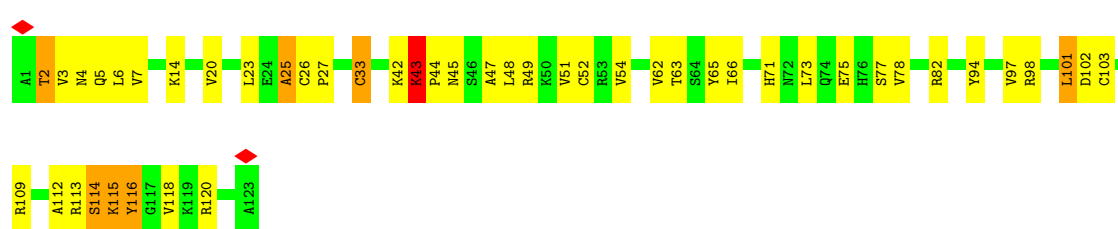
- Molecule 39: 30S ribosomal protein S10



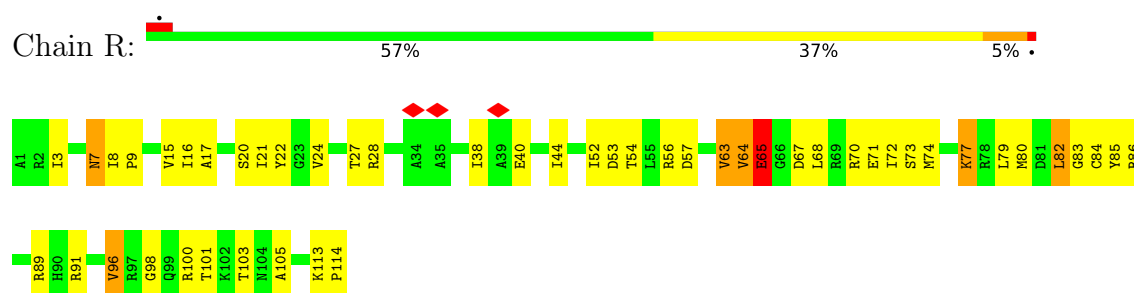
- Molecule 40: 30S ribosomal protein S11



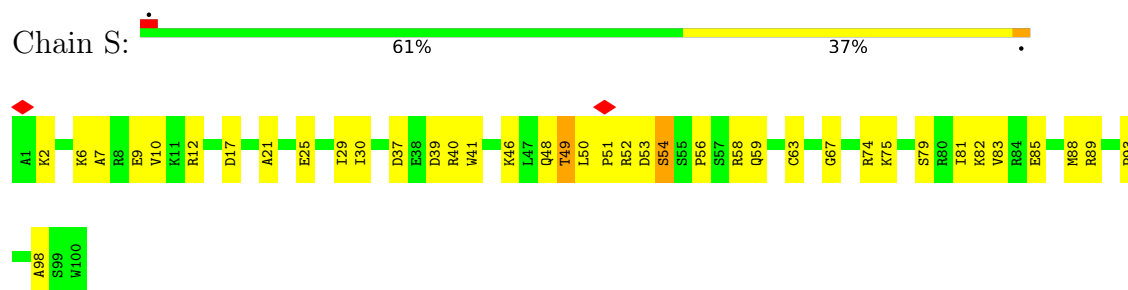
- Molecule 41: 30S ribosomal protein S12



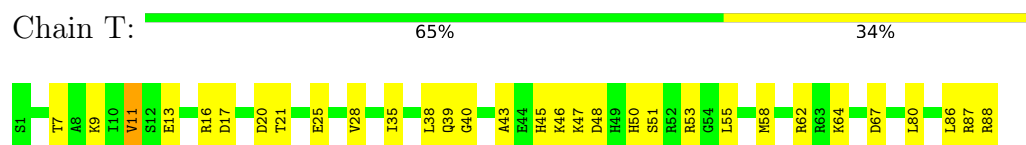
- Molecule 42: 30S ribosomal protein S13



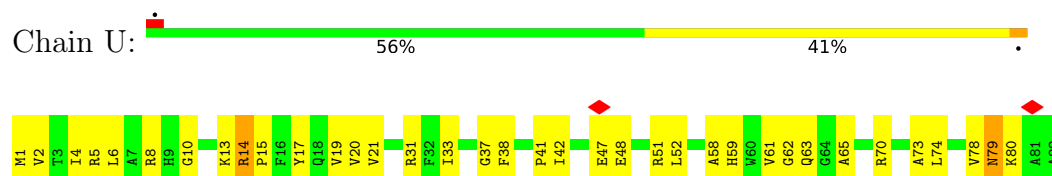
- Molecule 43: 30S ribosomal protein S14



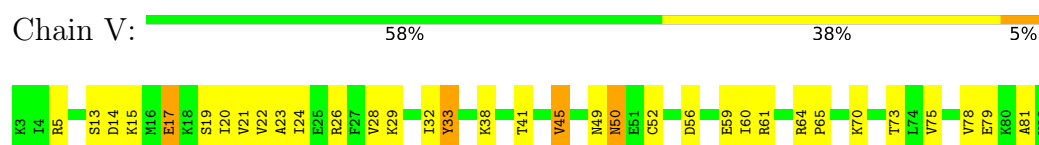
- Molecule 44: 30S ribosomal protein S15



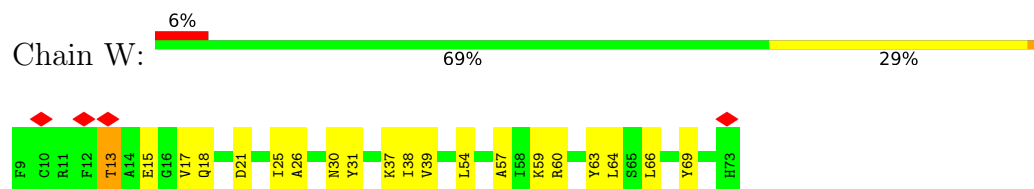
- Molecule 45: 30S ribosomal protein S16



- Molecule 46: 30S ribosomal protein S17

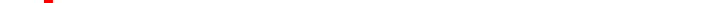


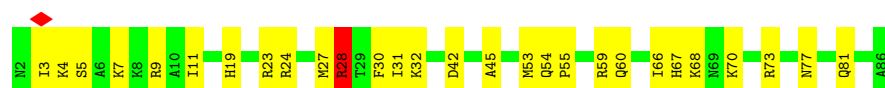
- Molecule 47: 30S ribosomal protein S18

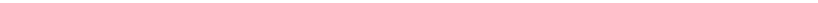


- Molecule 48: 30S ribosomal protein S19

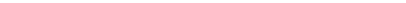


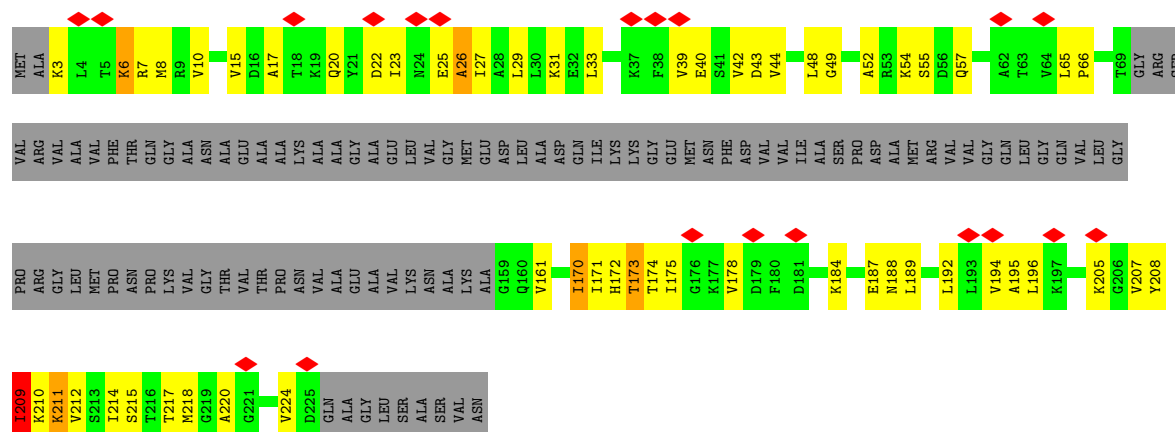
- Chain Y:  67% 32%



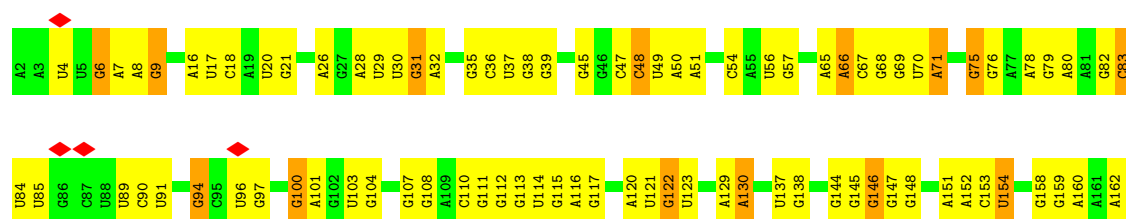
- Chain Z:  43% 48% 9%



- Chain a: 



- Chain 3: 48% 46% 6%

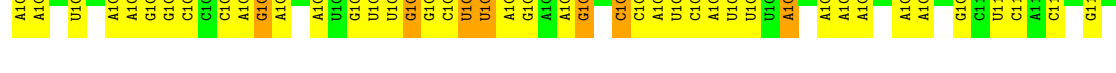
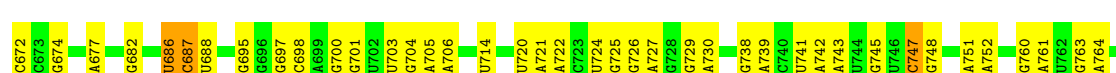
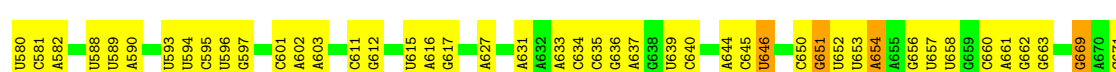
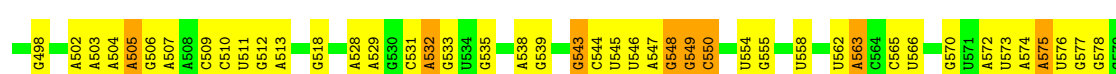
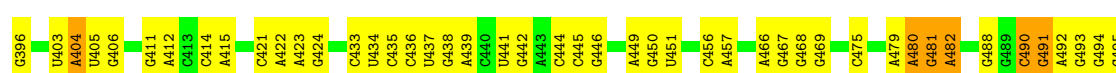
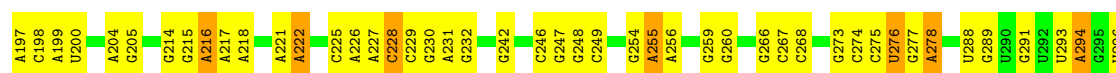
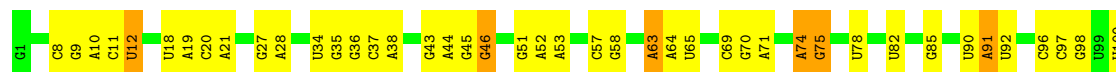


G1383	U1391	A1225	G1039	G969	G683	G577	U486	U420	G324	A243	U166
C1384	G1392	G1226	U1040	U870	U686	C578	A487	U421	C328	U244	U167
G1385	G1393	A1227	G1041	A871	A687	A579	C488	C422	C329	U245	G168
G1386	A1310	C1228	A1042	A872	G688	C580	C489	G423	A246	G247	G169
	A1311					G581	G491	G424			U170
	U1391	G1237	C1045	U875	U682	G585	A495	U425	G332	G251	U173
	G1316	A1238	G1048	C876	G693	C586		U426	U333	U252	U174
	C1317	A974		G877	G694	G587	A496	U427	C334	A253	A175
	A1318	A975		A878	A694	G588	C501	C428	C335	G254	C175
	A1155	G976		C879	A695	G589	A502	U429	A336	G255	C176
	U1052	A977		C880	A696		C503	A430	A337	U256	G177
	G1053					A596	C504	A431	A338	C178	C177
	C1054	U982					C505	A432	C339	G257	G179
	A1055	A983		C883	U701	A600	G506	G433	U340	G258	U180
				U884	A702	G601		U434	C341	G259	U181
		U986			G703		C514	A435	C342	A260	A182
		G987		G894	A704	G604	C515	U436	C343	U261	C183
		G988		C895	G705	U605	U516	U437	U344	A262	G184
					A706		G517	U438	C345	C264	
		U991		G902	U707	A621	C518	U439		G265	G187
		U992				A622			G350	G266	C188
		A994		A908	G710	C624	C528	G446	C351	C267	A189
		C995		A909	A711		G529	G447	C352		A190
				C910	G712		G530	A448	A353	C271	G191
				C912	G713	G628	G531	G449	G354	C272	C192
		C998			A715	A629	U531	G450		U273	C193
		C999		G917	A716	A630	A532	A451	U367	A274	A194
		A1000		A918	U717	A631	A533	A452		G275	A195
		C1001		A919	C821	U632	U534	G453	A371		A196
		G1002			A718	G633		G454	C372		A197
		G1003		G926	C720	C634	G537	G455		A279	
		A1004			G721	A635	G538	A456	U375	C280	
		A1005		G929	G722	U636	A539	A457	G376	G202	
		G1006		C930	U723		G540	U458	G377	G203	
		C1007		C931	G724	A642		A459		G204	
		U1008		C932		C643	G544	A460	A389	A205	
		U1009		C933	G730	U644	C545	A461	U390	C210	
		U1010		C934	G731	C651	A546	U462	G391	G211	
		C1011		A935	G732	U652	A547	U463	C392	G212	
		A1012		C936	G733	U653	A553	U464	A393	G213	
				A937	G734		U554	U465			
		G1015		A938	C735	C658	U555	A466	U398	U216	
				G939	G736		C556	U467	G399	G302	
		A1019			C737		G557	A468	C400	A303	
		G1020		G945		G664				U304	C221
		A1021		A946	G741	A685	G558	U471	U405	C222	
		U1022		G947	G742	G666	A559	U472	G406	A223	
		A1023		C948	A743	G667	A560	U473	A306	U224	
		G1024		A949		G668	U561	G474	U407	C307	
		U1025		A950	G750		U562	U475	A408	C225	
				G951	U751	U672	A563	U476	G410	G226	
		G1028		U952	G752	A673	C564	C477	A411	G227	
		U1029			A753	G674	U565	U478	A412	A228	
		C1030		U955	G754	A675	G566	U479	A413	U229	
		A1031			G755	A676		U480	G413	G230	
		G1032		A958		U677	A572	A481	A414	U231	
		G1033		A959	C758	U678	A573	A482	A415	G232	
		G1034		U960		C679	A574	A483	G417		
		A1035		G966	U762	G682	A575	G484	C418	G237	
					G763			U485	C419	A238	
		C1038									

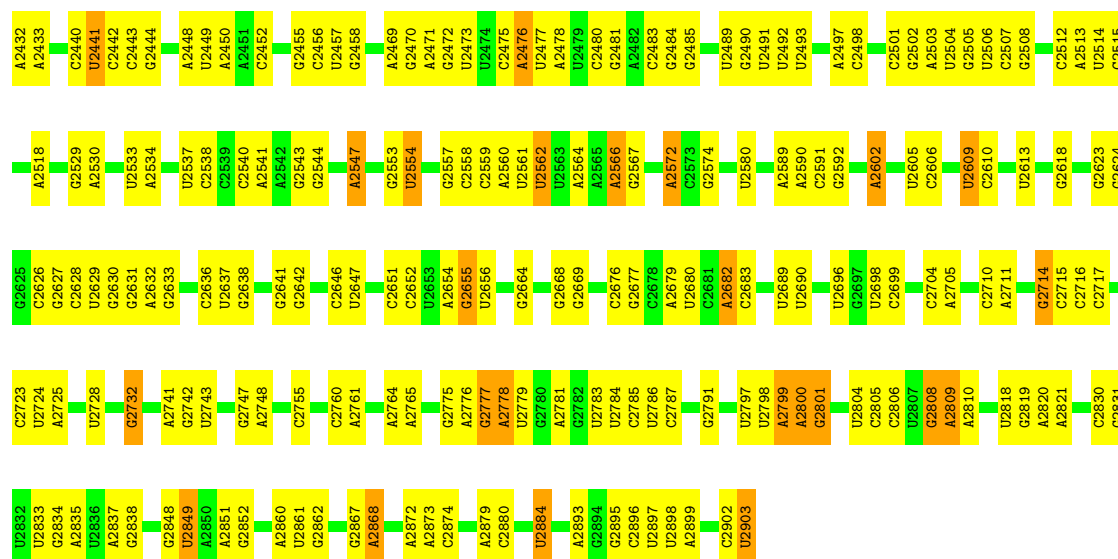


● Molecule 53: 23S ribosomal RNA

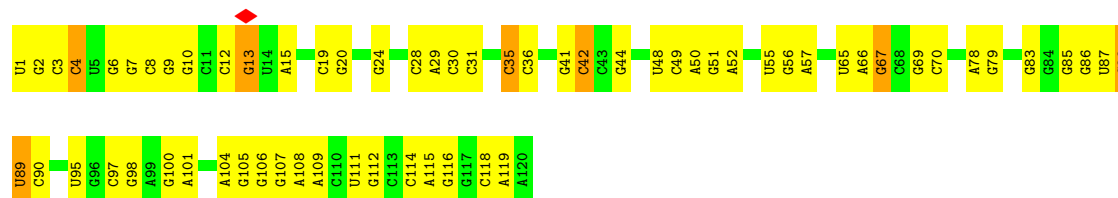
Chain 1: 52% 42% 6%



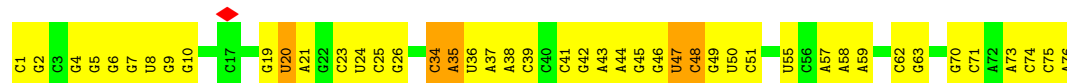




• Molecule 54: 5S ribosomal RNA



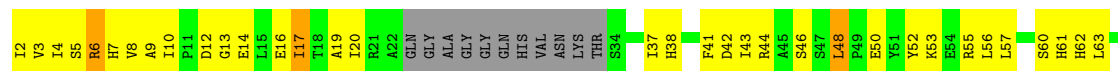
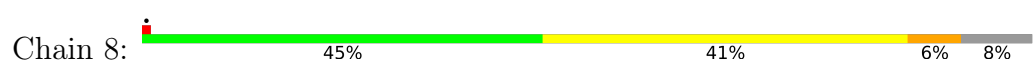
• Molecule 55: tRNA^{fMet}

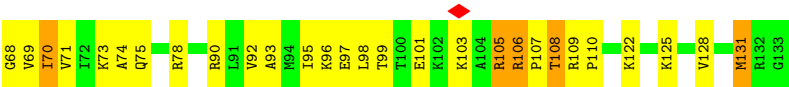


• Molecule 56: mRNA



• Molecule 57: 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	12528	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	11.938	Depositor
Minimum map value	-6.179	Depositor
Average map value	0.095	Depositor
Map value standard deviation	0.613	Depositor
Recommended contour level	0.8	Depositor
Map size ($\text{\AA}$)	389.76, 389.76, 389.76	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.87, 0.87, 0.87	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	0.28	0/2122	0.88	4/2852 (0.1%)
2	c	0.30	0/1586	0.88	2/2134 (0.1%)
3	d	0.28	0/1571	0.87	4/2113 (0.2%)
4	e	0.30	0/1435	0.91	5/1926 (0.3%)
5	f	0.31	0/1343	0.91	5/1816 (0.3%)
6	g	0.32	0/1122	0.95	3/1515 (0.2%)
7	h	0.32	0/1001	1.05	7/1350 (0.5%)
8	i	0.36	0/1046	0.95	3/1410 (0.2%)
9	j	0.30	0/1152	0.89	6/1551 (0.4%)
10	k	0.29	0/948	0.95	3/1268 (0.2%)
11	l	0.28	0/1054	1.00	7/1403 (0.5%)
12	m	0.28	0/1093	0.82	0/1460
13	n	0.29	0/974	0.91	5/1301 (0.4%)
14	o	0.29	0/902	0.92	6/1209 (0.5%)
15	p	0.29	0/929	0.86	4/1242 (0.3%)
16	q	0.30	0/960	0.88	2/1278 (0.2%)
17	r	0.30	0/829	1.02	7/1107 (0.6%)
18	s	0.28	0/864	0.86	0/1156
19	t	0.27	0/745	0.86	0/994
20	u	0.27	0/788	0.86	0/1051
21	v	0.28	0/766	0.86	2/1025 (0.2%)
22	w	0.27	0/582	0.83	0/769
23	x	0.27	0/635	0.87	1/848 (0.1%)
24	y	0.27	0/510	0.93	2/677 (0.3%)
25	z	0.27	0/453	0.77	0/605
26	B	0.27	0/450	0.67	0/599
27	C	0.29	0/417	0.75	0/554
28	D	0.30	0/380	1.01	4/498 (0.8%)
29	E	0.30	0/513	0.81	0/676
30	F	0.32	0/303	0.94	0/397
31	G	0.31	0/1788	0.95	9/2408 (0.4%)
32	H	0.30	0/1652	0.91	9/2225 (0.4%)
33	I	0.29	0/1665	0.97	6/2227 (0.3%)
34	J	0.31	0/1170	0.96	4/1573 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	K	0.32	0/836	1.00	3/1128 (0.3%)
36	L	0.29	0/1196	0.93	5/1602 (0.3%)
37	M	0.30	0/989	0.96	4/1326 (0.3%)
38	N	0.29	0/1034	1.04	11/1375 (0.8%)
39	O	0.32	0/797	1.08	9/1077 (0.8%)
40	P	0.32	0/886	0.98	7/1195 (0.6%)
41	Q	0.30	0/969	0.96	5/1300 (0.4%)
42	R	0.32	0/893	1.05	5/1193 (0.4%)
43	S	0.29	0/817	0.98	3/1088 (0.3%)
44	T	0.31	0/722	1.06	6/964 (0.6%)
45	U	0.32	0/659	1.03	4/884 (0.5%)
46	V	0.27	0/658	0.85	2/881 (0.2%)
47	W	0.31	0/545	0.87	3/731 (0.4%)
48	X	0.31	0/653	0.98	2/877 (0.2%)
49	Y	0.30	0/671	0.95	2/888 (0.2%)
50	Z	0.31	0/551	1.06	4/728 (0.5%)
51	a	0.31	0/1033	1.04	4/1387 (0.3%)
52	3	0.38	0/36963	0.47	0/57662
53	1	0.37	0/69796	0.48	2/108888 (0.0%)
54	2	0.38	0/2872	0.47	0/4479
55	5	0.38	0/1832	0.49	0/2855
56	4	0.44	0/398	0.64	0/620
57	8	0.33	0/965	1.10	7/1293 (0.5%)
All	All	0.35	0/160483	0.64	198/239638 (0.1%)

There are no bond length outliers.

The worst 5 of 198 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	T	43	ALA	N-CA-C	-11.19	98.31	113.30
57	8	13	GLY	N-CA-C	-9.09	102.58	114.85
45	U	33	ILE	N-CA-C	-8.95	103.17	111.67
50	Z	23	GLU	N-CA-C	8.77	121.77	109.31
33	I	204	SER	N-CA-C	-8.47	101.56	112.23

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	52	0
2	c	1565	0	1616	37	0
3	d	1552	0	1619	39	0
4	e	1411	0	1447	53	0
5	f	1323	0	1374	28	0
6	g	1111	0	1148	40	0
7	h	988	0	1025	34	0
8	i	1032	0	1088	50	0
9	j	1129	0	1162	27	0
10	k	939	0	1012	27	0
11	l	1045	0	1117	33	0
12	m	1074	0	1157	20	0
13	n	961	0	1000	28	0
14	o	892	0	923	27	0
15	p	917	0	965	20	0
16	q	947	0	1022	22	0
17	r	816	0	839	20	0
18	s	857	0	922	24	0
19	t	739	0	807	25	0
20	u	780	0	834	18	0
21	v	753	0	780	9	0
22	w	575	0	592	10	0
23	x	625	0	655	16	0
24	y	509	0	543	19	0
25	z	449	0	491	9	0
26	B	444	0	461	5	0
27	C	410	0	440	7	0
28	D	377	0	418	13	0
29	E	504	0	574	15	0
30	F	302	0	343	5	0
31	G	1757	0	1787	59	0
32	H	1625	0	1699	54	0
33	I	1643	0	1710	56	0
34	J	1157	0	1199	42	0
35	K	818	0	808	43	0
36	L	1182	0	1240	18	0
37	M	979	0	1034	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	40	0
39	O	787	0	828	36	0
40	P	870	0	878	47	0
41	Q	955	0	1019	37	0
42	R	884	0	944	48	0
43	S	805	0	847	28	0
44	T	714	0	737	18	0
45	U	649	0	666	34	0
46	V	649	0	691	27	0
47	W	536	0	552	14	0
48	X	638	0	665	28	0
49	Y	665	0	714	28	0
50	Z	545	0	579	35	0
51	a	1026	0	1092	45	0
52	3	33012	0	16619	673	0
53	1	62317	0	31346	1088	0
54	2	2568	0	1303	56	0
55	5	1640	0	837	34	0
56	4	353	0	175	12	0
57	8	955	0	1014	44	0
All	All	147860	0	100584	2968	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 2968 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)
52:3:1259:C:H3'	52:3:1260:G:H5''	1.26	1.13
50:Z:25:ALA:HB1	56:4:9:G:H4'	1.24	1.11
19:t:73:ARG:HH12	53:1:65:U:H1'	1.15	1.10
53:1:1300:G:H4'	53:1:1301:A:H5''	1.11	1.08
45:U:41:PRO:HB2	52:3:450:G:H4'	1.34	1.06

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	232 (86%)	34 (13%)	3 (1%)	11	42
2	c	207/209 (99%)	188 (91%)	17 (8%)	2 (1%)	12	43
3	d	199/201 (99%)	183 (92%)	13 (6%)	3 (2%)	8	36
4	e	175/177 (99%)	151 (86%)	23 (13%)	1 (1%)	21	52
5	f	174/176 (99%)	158 (91%)	15 (9%)	1 (1%)	21	52
6	g	147/149 (99%)	125 (85%)	18 (12%)	4 (3%)	4	27
7	h	129/165 (78%)	96 (74%)	27 (21%)	6 (5%)	2	18
8	i	139/142 (98%)	119 (86%)	18 (13%)	2 (1%)	9	37
9	j	140/142 (99%)	128 (91%)	11 (8%)	1 (1%)	18	50
10	k	120/122 (98%)	104 (87%)	14 (12%)	2 (2%)	7	34
11	l	141/143 (99%)	127 (90%)	14 (10%)	0	100	100
12	m	134/136 (98%)	122 (91%)	11 (8%)	1 (1%)	18	50
13	n	118/120 (98%)	99 (84%)	19 (16%)	0	100	100
14	o	114/116 (98%)	103 (90%)	9 (8%)	2 (2%)	6	34
15	p	112/114 (98%)	102 (91%)	9 (8%)	1 (1%)	14	45
16	q	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
17	r	101/103 (98%)	89 (88%)	10 (10%)	2 (2%)	6	32
18	s	108/110 (98%)	98 (91%)	8 (7%)	2 (2%)	6	33
19	t	91/93 (98%)	78 (86%)	12 (13%)	1 (1%)	11	42
20	u	100/102 (98%)	84 (84%)	12 (12%)	4 (4%)	2	21
21	v	92/94 (98%)	86 (94%)	5 (5%)	1 (1%)	11	42
22	w	73/75 (97%)	68 (93%)	4 (6%)	1 (1%)	9	37
23	x	75/77 (97%)	67 (89%)	7 (9%)	1 (1%)	9	38
24	y	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
25	z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
27	C	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
28	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
29	E	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	35
30	F	36/38 (95%)	32 (89%)	2 (6%)	2 (6%)	1	16
31	G	223/225 (99%)	185 (83%)	27 (12%)	11 (5%)	1	17
32	H	204/206 (99%)	186 (91%)	16 (8%)	2 (1%)	12	43
33	I	203/205 (99%)	172 (85%)	27 (13%)	4 (2%)	6	32
34	J	155/157 (99%)	125 (81%)	24 (16%)	6 (4%)	2	21
35	K	98/100 (98%)	78 (80%)	16 (16%)	4 (4%)	2	20
36	L	149/151 (99%)	132 (89%)	16 (11%)	1 (1%)	18	50
37	M	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	48
38	N	125/127 (98%)	108 (86%)	11 (9%)	6 (5%)	2	17
39	O	96/98 (98%)	81 (84%)	11 (12%)	4 (4%)	2	20
40	P	114/116 (98%)	91 (80%)	19 (17%)	4 (4%)	3	24
41	Q	121/123 (98%)	101 (84%)	14 (12%)	6 (5%)	1	17
42	R	112/114 (98%)	97 (87%)	12 (11%)	3 (3%)	4	27
43	S	98/100 (98%)	83 (85%)	15 (15%)	0	100	100
44	T	86/88 (98%)	72 (84%)	12 (14%)	2 (2%)	5	30
45	U	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	4	29
46	V	78/80 (98%)	61 (78%)	14 (18%)	3 (4%)	2	22
47	W	63/65 (97%)	55 (87%)	8 (13%)	0	100	100
48	X	77/79 (98%)	69 (90%)	7 (9%)	1 (1%)	9	38
49	Y	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
50	Z	63/65 (97%)	43 (68%)	17 (27%)	3 (5%)	2	17
51	a	130/234 (56%)	100 (77%)	24 (18%)	6 (5%)	2	18
57	8	117/132 (89%)	98 (84%)	12 (10%)	7 (6%)	1	15
All	All	6036/6290 (96%)	5254 (87%)	662 (11%)	120 (2%)	8	32

5 of 120 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY

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Mol	Chain	Res	Type
3	d	83	VAL
6	g	9	VAL
7	h	81	LEU
7	h	118	ILE

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%)	211 (98%)	5 (2%)	44	62
2	c	164/164 (100%)	162 (99%)	2 (1%)	63	72
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	68
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	75
7	h	100/123 (81%)	100 (100%)	0	100	100
8	i	109/110 (99%)	108 (99%)	1 (1%)	70	75
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	75
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	74
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	99 (99%)	1 (1%)	68	74
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	72
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%)	81 (96%)	3 (4%)	31	54
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	v	78/78 (100%)	76 (97%)	2 (3%)	40	60
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%)	43 (96%)	2 (4%)	25	50
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	184 (99%)	2 (1%)	65	73
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	79
33	I	172/172 (100%)	171 (99%)	1 (1%)	78	79
34	J	119/119 (100%)	117 (98%)	2 (2%)	53	67
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	73
36	L	124/124 (100%)	124 (100%)	0	100	100
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%)	86 (100%)	0	100	100
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%)	88 (96%)	4 (4%)	26	50
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%)	65 (100%)	0	100	100
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	54 (96%)	2 (4%)	31	54
48	X	70/70 (100%)	69 (99%)	1 (1%)	59	70
49	Y	65/65 (100%)	64 (98%)	1 (2%)	57	68
50	Z	55/55 (100%)	55 (100%)	0	100	100
51	a	110/181 (61%)	108 (98%)	2 (2%)	51	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
57	8	101/108 (94%)	98 (97%)	3 (3%)	36 57
All	All	5009/5111 (98%)	4965 (99%)	44 (1%)	68 75

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	J	130	THR
47	W	13	THR
35	K	55	HIS
42	R	65	GLU
48	X	23	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 137 such sidechains are listed below:

Mol	Chain	Res	Type
44	T	27	GLN
45	U	9	HIS
49	Y	51	ASN
15	p	14	GLN
15	p	11	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	170 (11%)	0
53	1	2902/2903 (99%)	341 (11%)	9 (0%)
54	2	119/120 (99%)	11 (9%)	0
55	5	76/77 (98%)	10 (13%)	0
56	4	15/16 (93%)	2 (13%)	0
All	All	4650/4655 (99%)	534 (11%)	9 (0%)

5 of 534 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	4	U
52	3	6	G
52	3	9	G
52	3	31	G
52	3	32	A

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	2326	C
53	1	2391	G
53	1	859	G
53	1	1020	A
53	1	1130	U

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](#)

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.

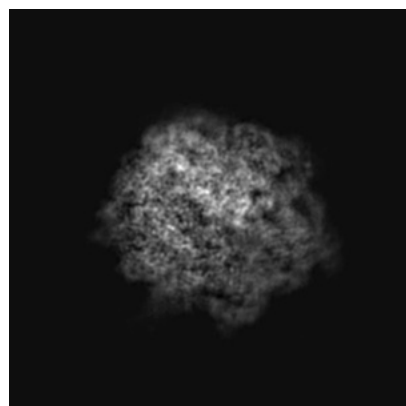
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22464. These allow visual inspection of the internal detail of the map and identification of artifacts.

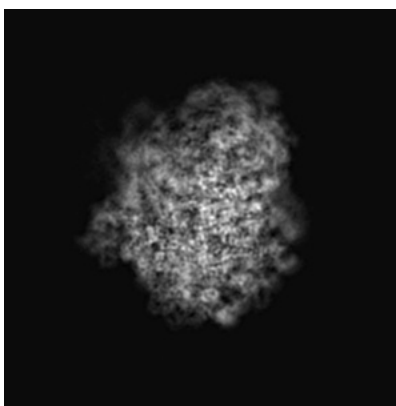
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

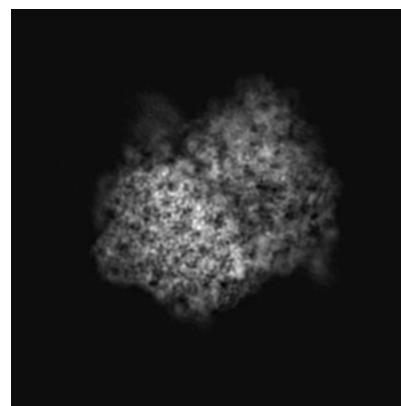
6.1.1 Primary map



X

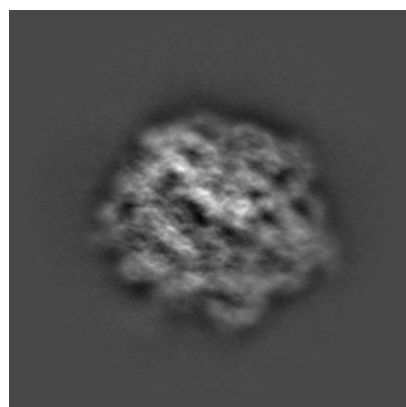


Y

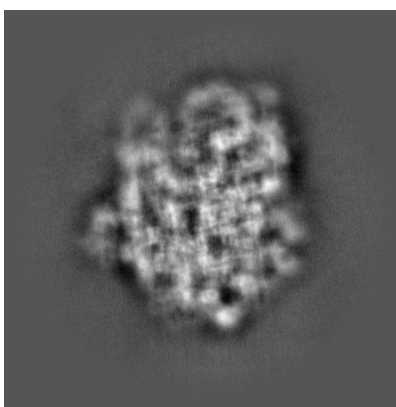


Z

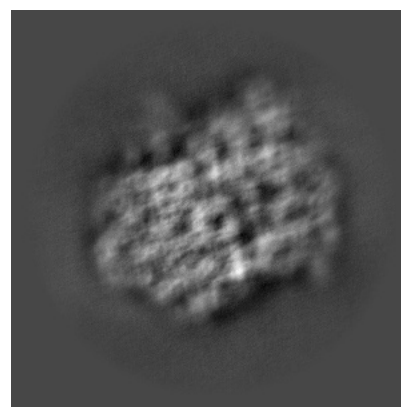
6.1.2 Raw map



X



Y

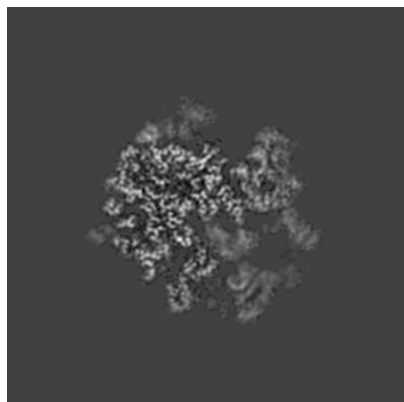


Z

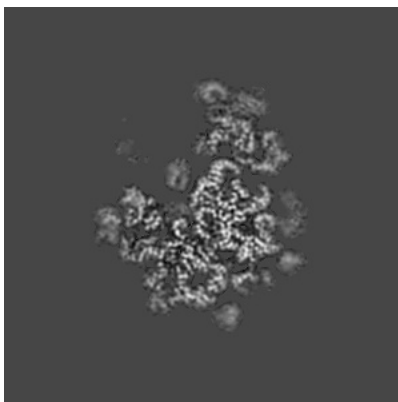
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

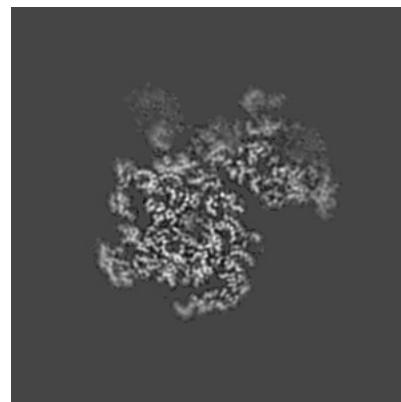
6.2.1 Primary map



X Index: 224

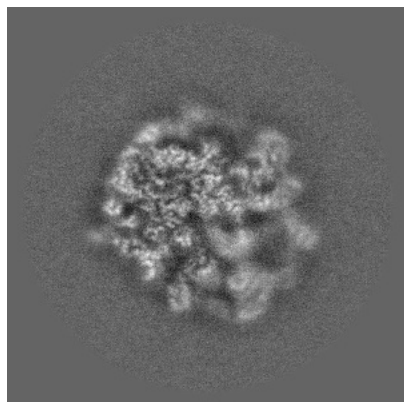


Y Index: 224

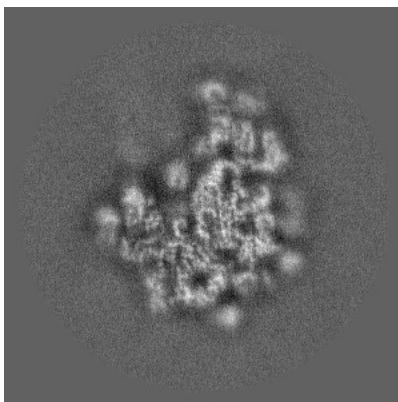


Z Index: 224

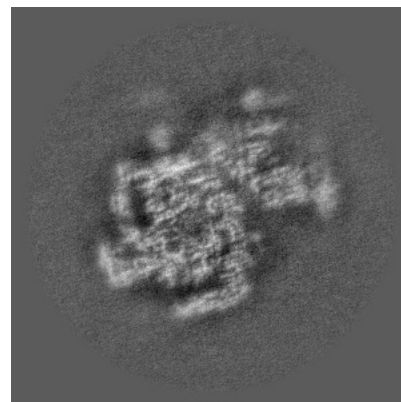
6.2.2 Raw map



X Index: 224



Y Index: 224

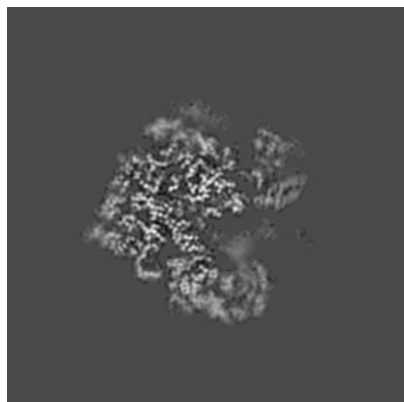


Z Index: 224

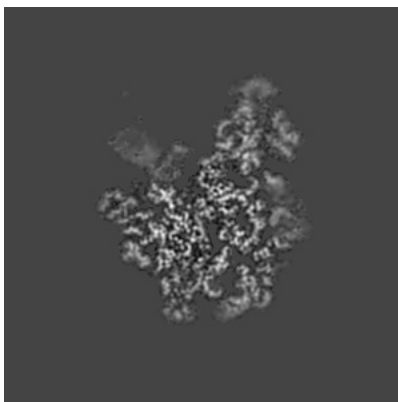
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

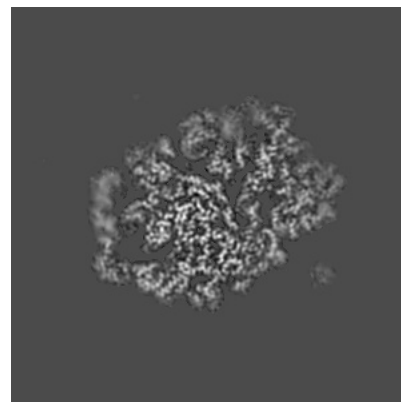
6.3.1 Primary map



X Index: 214

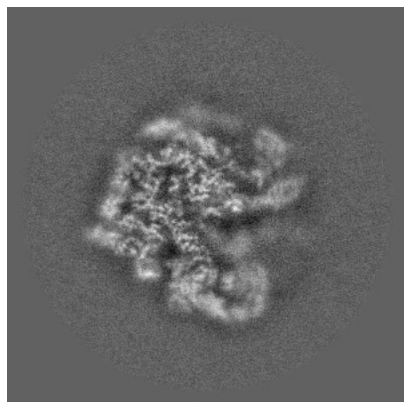


Y Index: 192

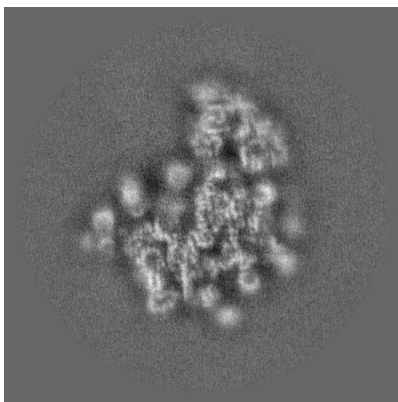


Z Index: 246

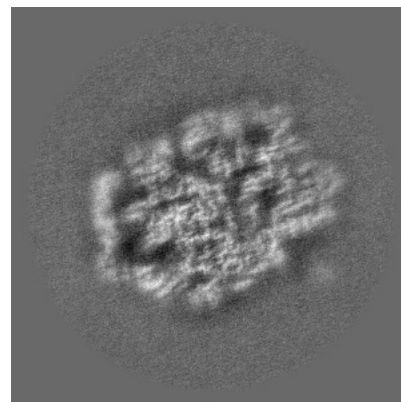
6.3.2 Raw map



X Index: 214



Y Index: 234

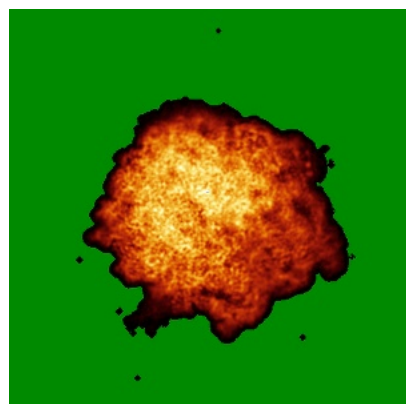


Z Index: 247

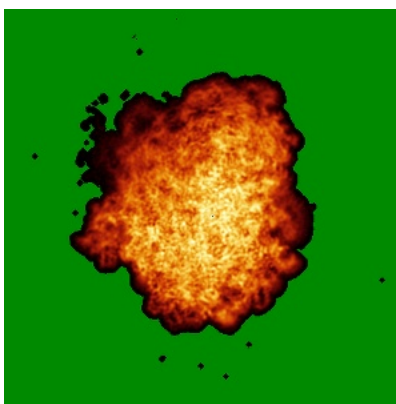
The images above show the largest variance slices of the map in three orthogonal directions.

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

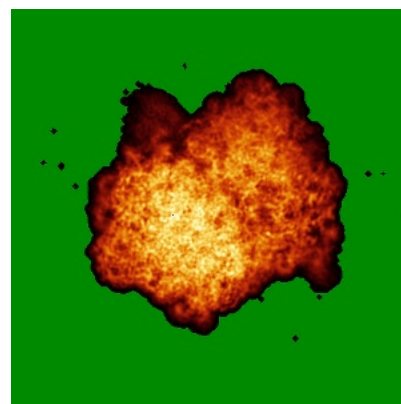
6.4.1 Primary map



X

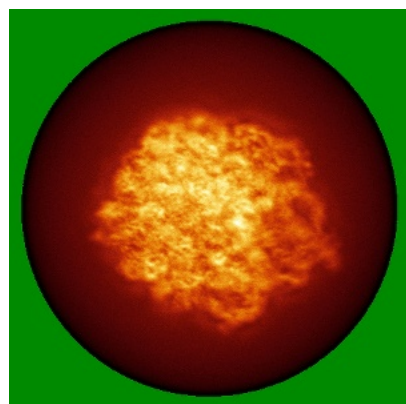


Y

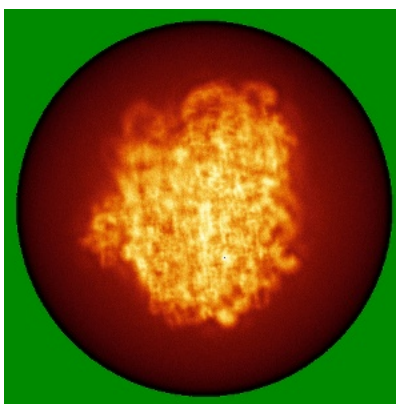


Z

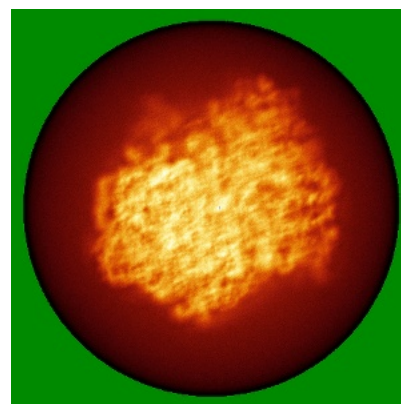
6.4.2 Raw map



X



Y

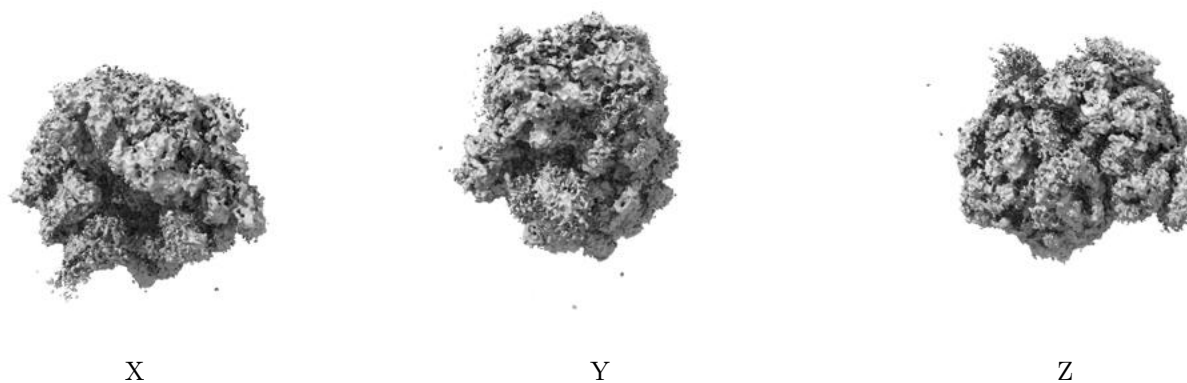


Z

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.

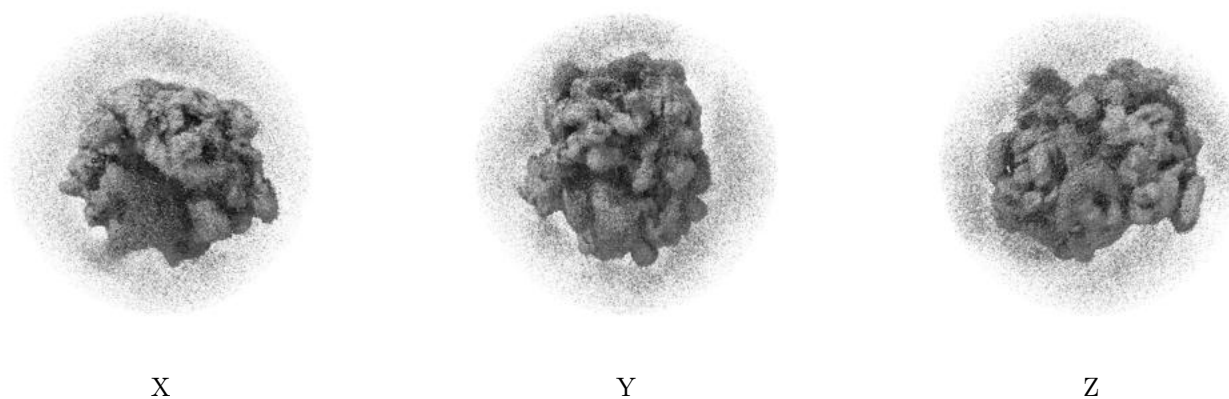
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.8. 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.

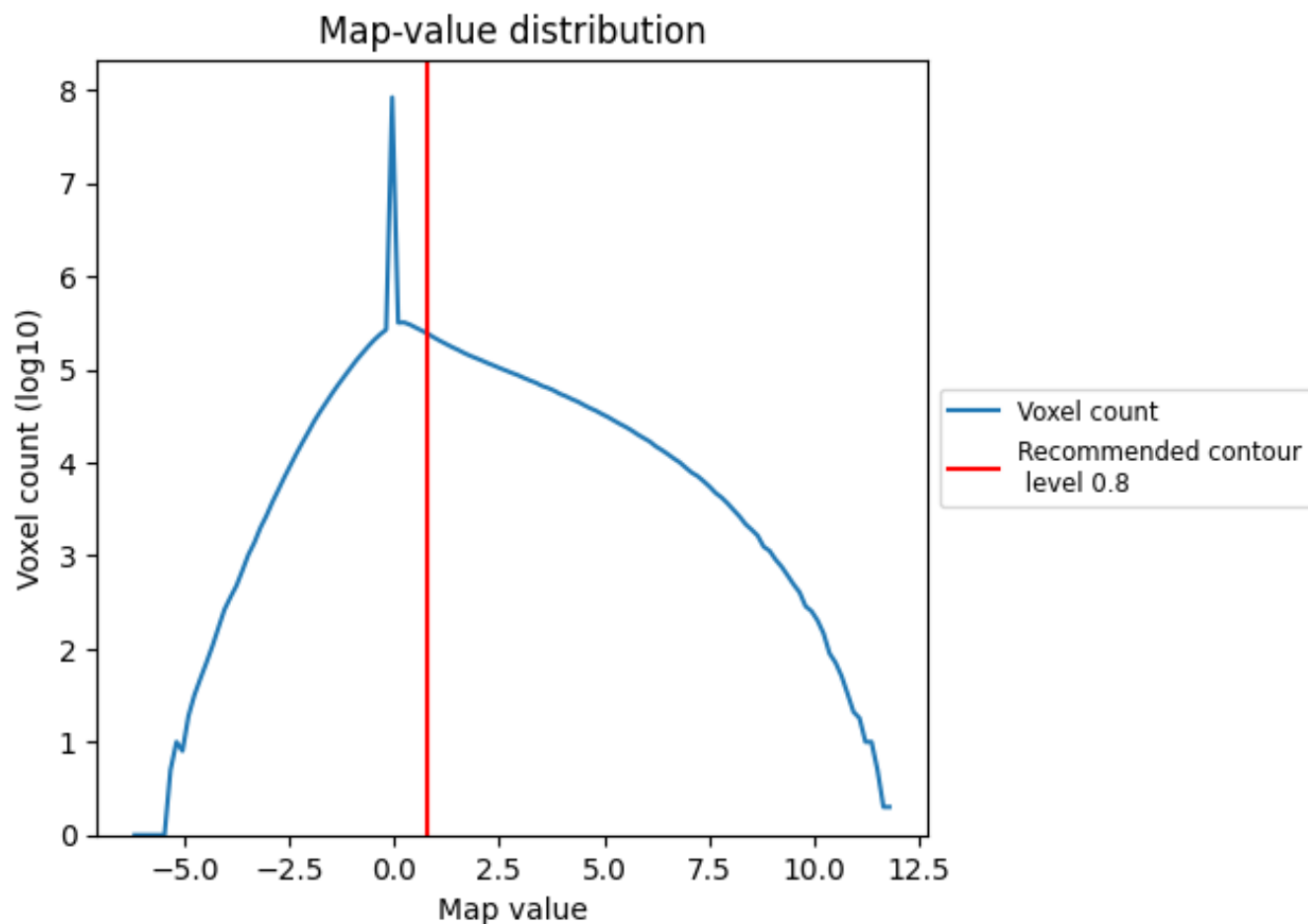
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

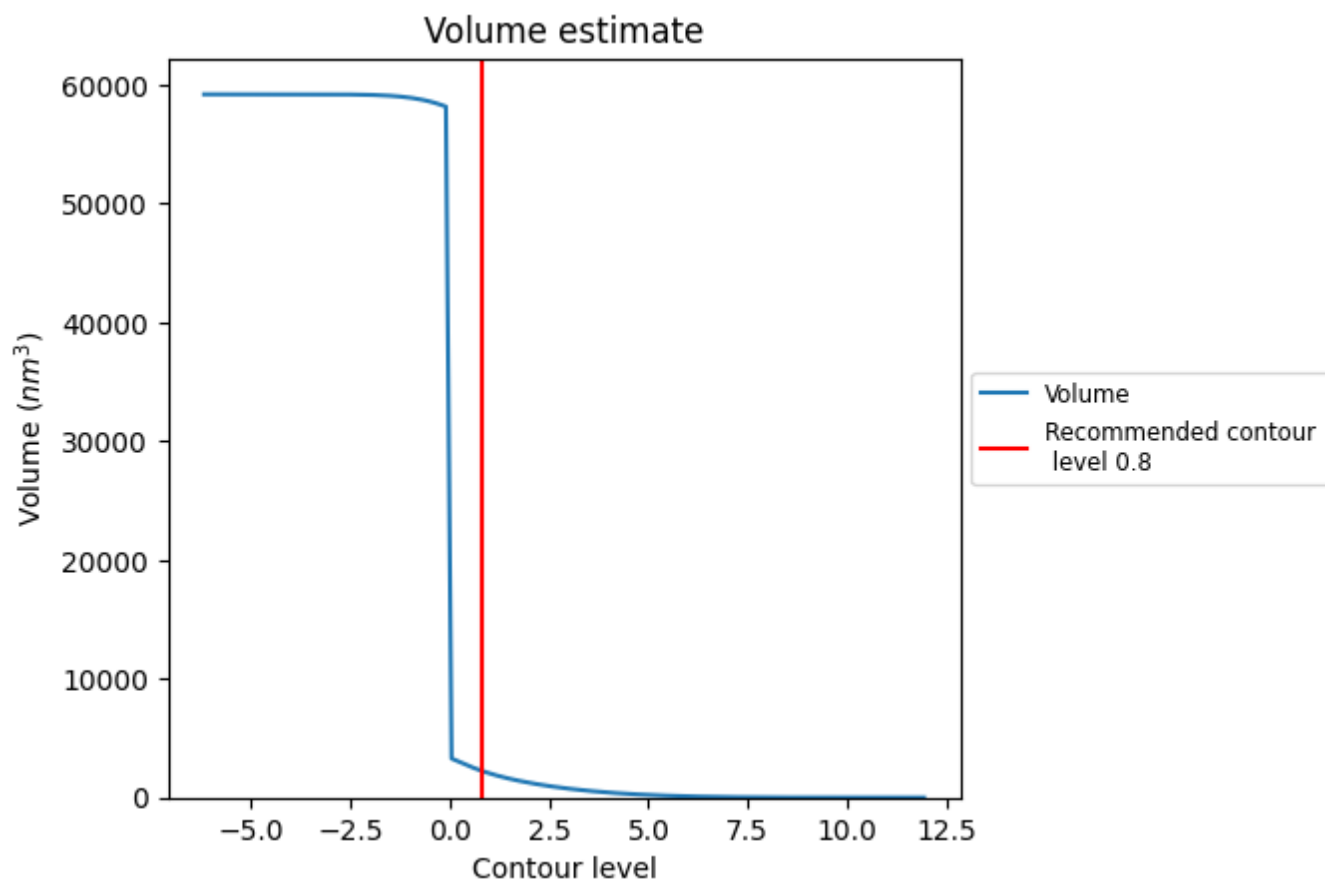
This section contains the results of statistical analysis of the map.

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.

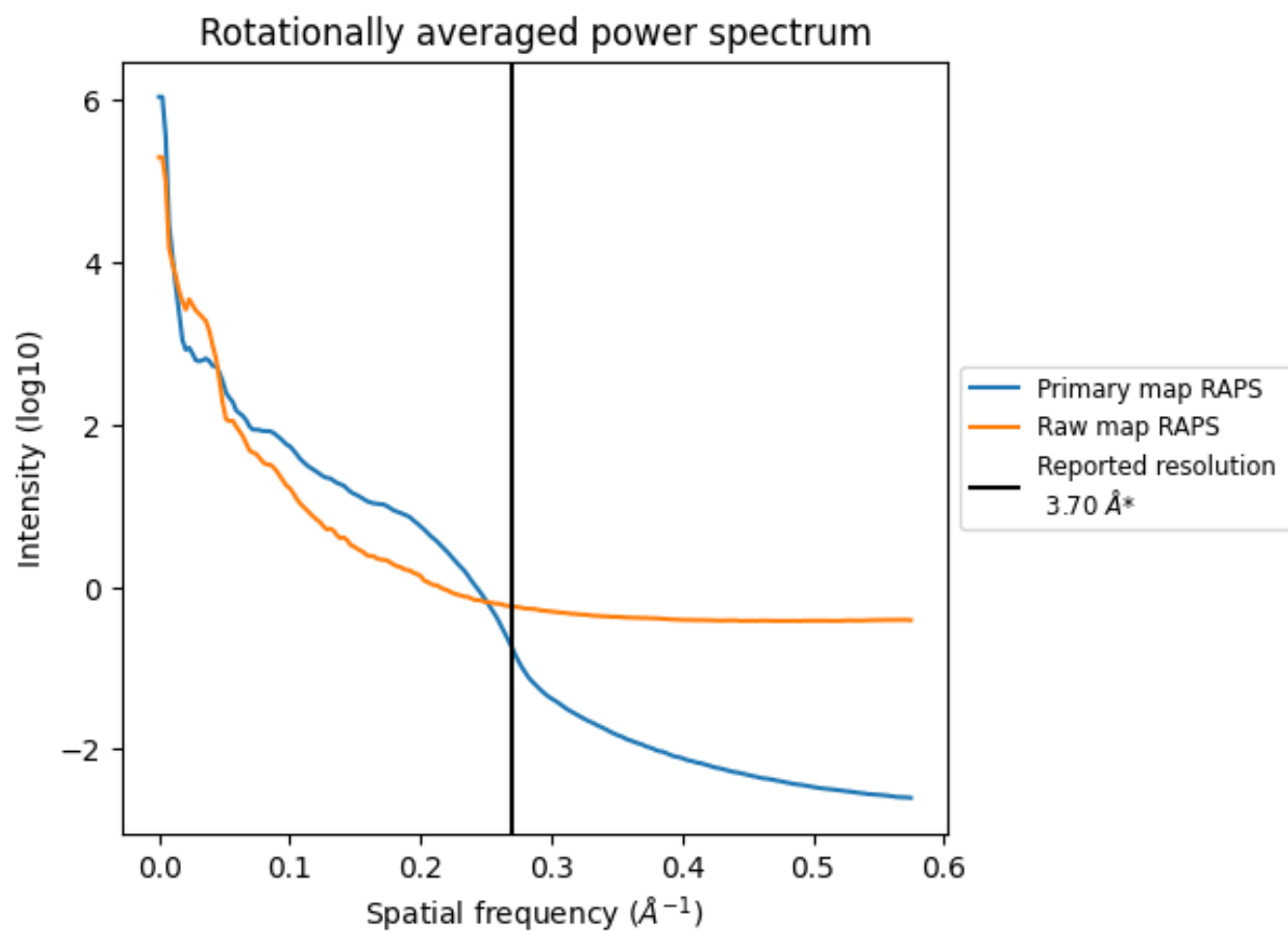
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2261 nm³; this corresponds to an approximate mass of 2042 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 ⓘ

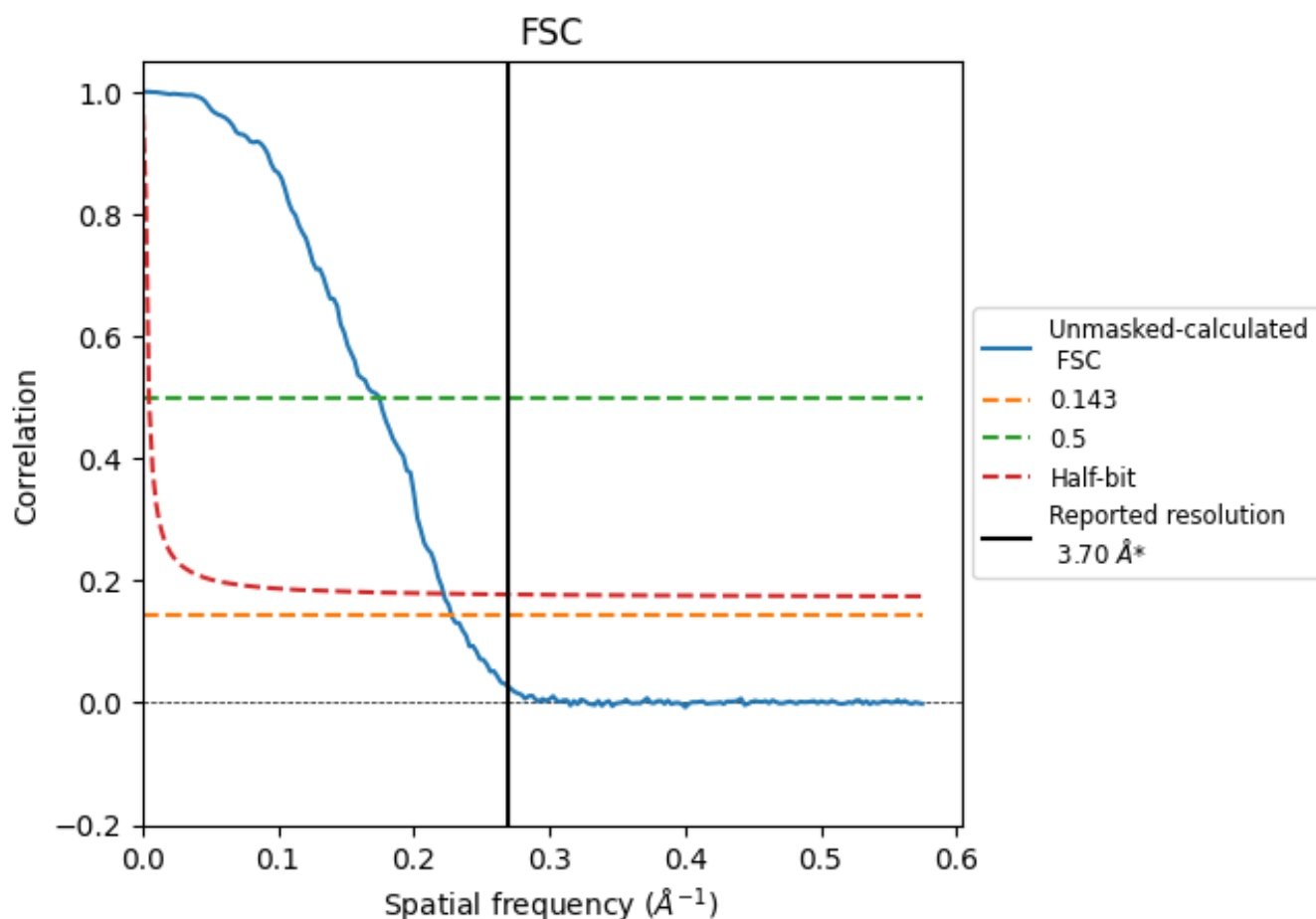


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

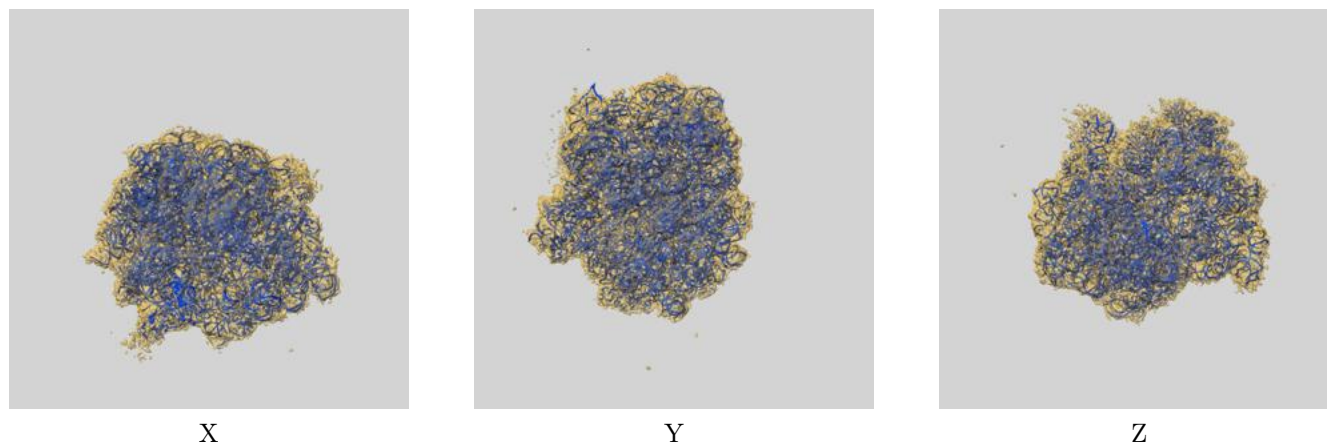
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.39	5.73	4.50

*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 4.39 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

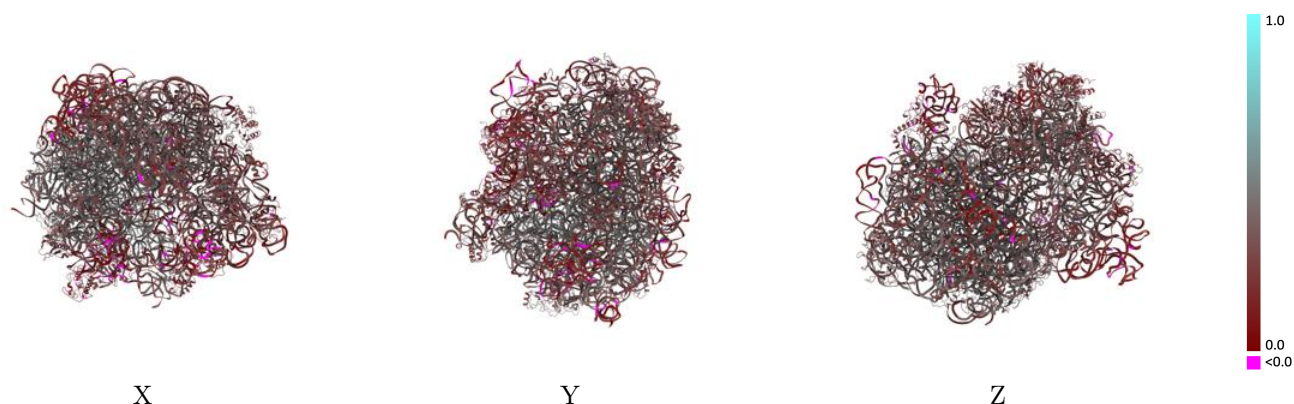
This section contains information regarding the fit between EMDB map EMD-22464 and PDB model 7JSZ. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



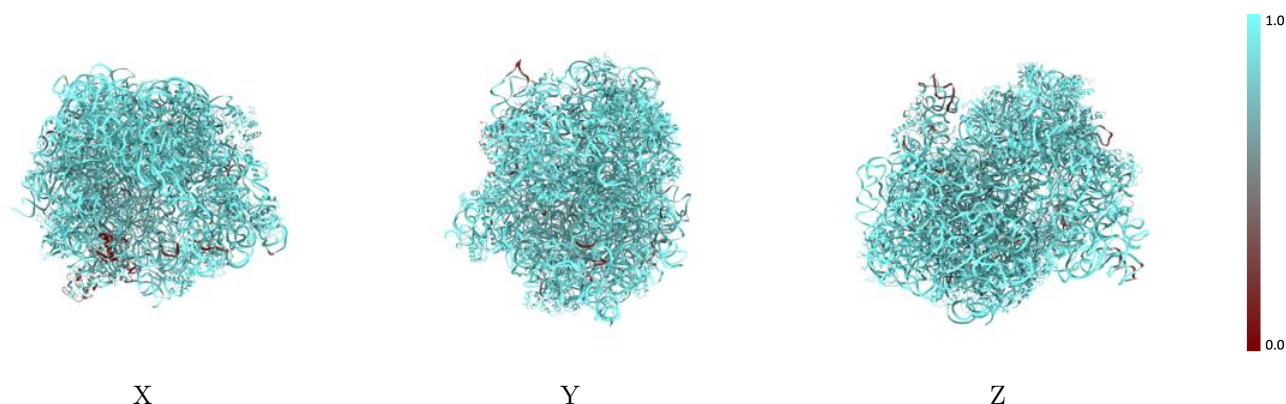
The images above show the 3D surface view of the map at the recommended contour level 0.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



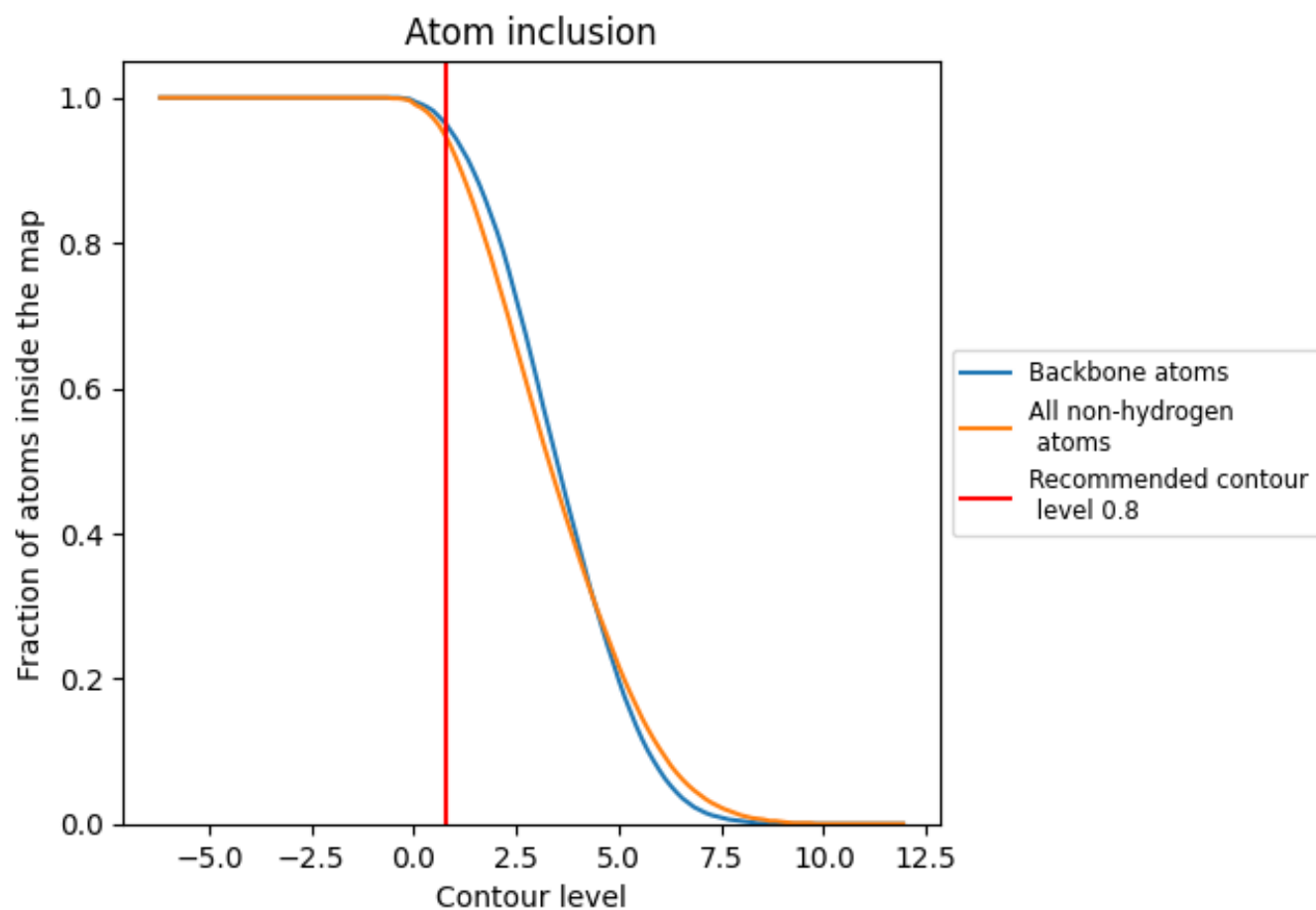
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% 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 (0.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9450	 0.3410
1	 0.9680	 0.3630
2	 0.9860	 0.3090
3	 0.9680	 0.3160
4	 0.9630	 0.2550
5	 0.9050	 0.1990
8	 0.9080	 0.2470
B	 0.9490	 0.4000
C	 0.9430	 0.3830
D	 0.9010	 0.4250
E	 0.9270	 0.4370
F	 0.9280	 0.3730
G	 0.9070	 0.3000
H	 0.9070	 0.3290
I	 0.8840	 0.2900
J	 0.9290	 0.3710
K	 0.9270	 0.2800
L	 0.9140	 0.2680
M	 0.9300	 0.3400
N	 0.9120	 0.2690
O	 0.8350	 0.2850
P	 0.9360	 0.3010
Q	 0.9370	 0.4060
R	 0.9170	 0.2470
S	 0.8720	 0.2770
T	 0.9330	 0.3020
U	 0.9250	 0.3340
V	 0.9590	 0.3650
W	 0.8620	 0.2680
X	 0.9660	 0.2220
Y	 0.9120	 0.3210
Z	 0.8780	 0.2710
a	 0.7280	 0.1850
b	 0.9400	 0.4240
c	 0.9370	 0.4270



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Chain	Atom inclusion	Q-score
d	 0.9300	 0.3850
e	 0.9260	 0.2220
f	 0.9370	 0.3190
g	 0.8220	 0.2840
h	 0.5640	 0.1770
i	 0.3000	 0.1280
j	 0.9460	 0.4160
k	 0.9230	 0.4290
l	 0.9350	 0.4110
m	 0.9380	 0.4150
n	 0.9330	 0.4220
o	 0.9300	 0.3220
p	 0.9530	 0.4210
q	 0.9320	 0.4060
r	 0.9460	 0.4180
s	 0.9310	 0.4210
t	 0.9350	 0.3830
u	 0.9560	 0.3690
v	 0.9500	 0.3750
w	 0.9320	 0.4320
x	 0.9570	 0.3870
y	 0.9280	 0.3060
z	 0.9410	 0.4110