



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 05:16 AM UTC

PDB ID : 6WDF / pdb_00006wdf
EMDB ID : EMD-21634
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure VI-A)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

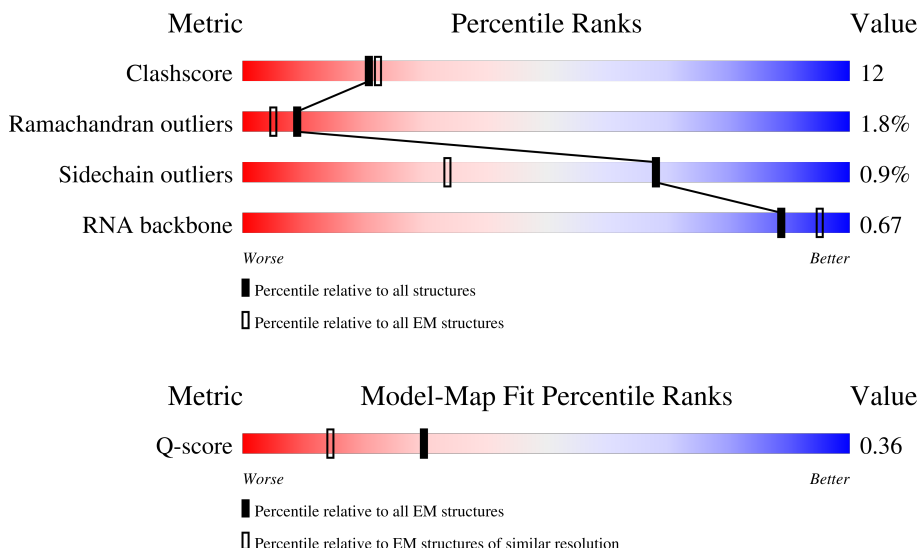
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.



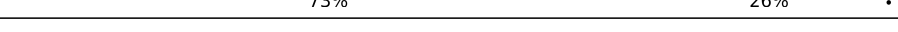
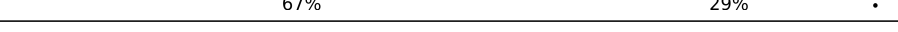
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	b	271	
2	c	209	
3	d	201	

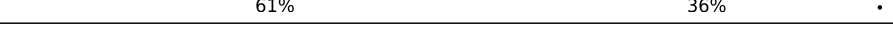
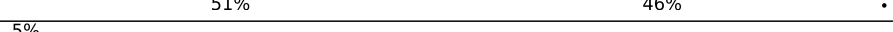
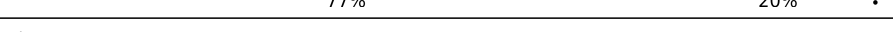
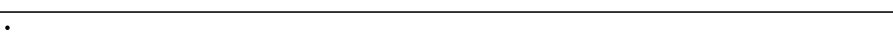
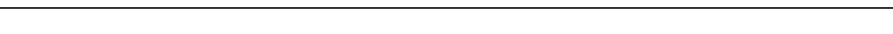
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Mol	Chain	Length	Quality of chain
4	e	177	 55% 45% .
5	f	176	 78% 22% .
6	g	149	 20% 62% 38% .
7	h	131	 14% 49% 42% 8% .
8	i	141	 16% 64% 31% 5% .
9	j	142	 77% 22% .
10	k	122	 67% 30% . .
11	l	143	 64% 31% 5% .
12	m	136	 67% 32% .
13	n	120	 75% 23% .
14	o	116	 72% 28% .
15	p	114	 67% 33% .
16	q	117	 71% 28% .
17	r	103	 70% 27% .
18	s	110	 78% 19% .
19	t	93	 73% 26% .
20	u	102	 67% 29% .
21	v	94	 61% 37% .
22	w	75	 63% 36% .
23	x	77	 79% 21% .
24	y	63	 68% 32% .
25	z	58	 66% 34% .
26	B	56	 62% 38% .
27	C	50	 70% 28% .
28	D	46	 72% 26% .

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

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Mol	Chain	Length	Quality of chain
54	2	120	56% 38% 6%
55	5	77	32% 47% 19%
56	4	18	11% 50% 44% 6%
57	7	76	39% 51% 9%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 148582 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L2.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

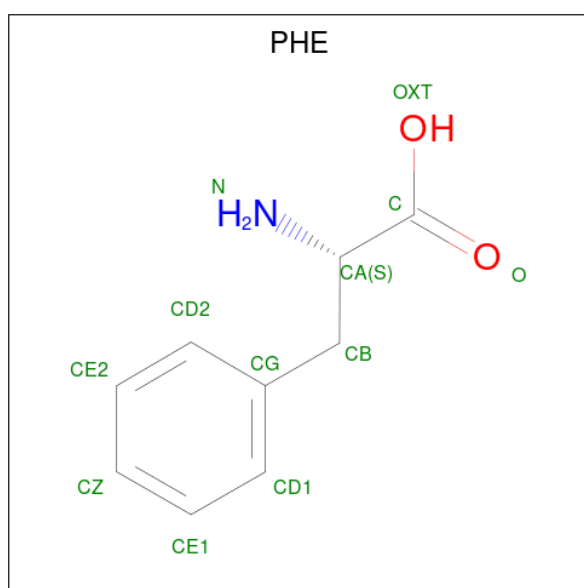
- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 57 is a RNA chain called tRNAPhe.

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

- Molecule 58 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



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

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$).

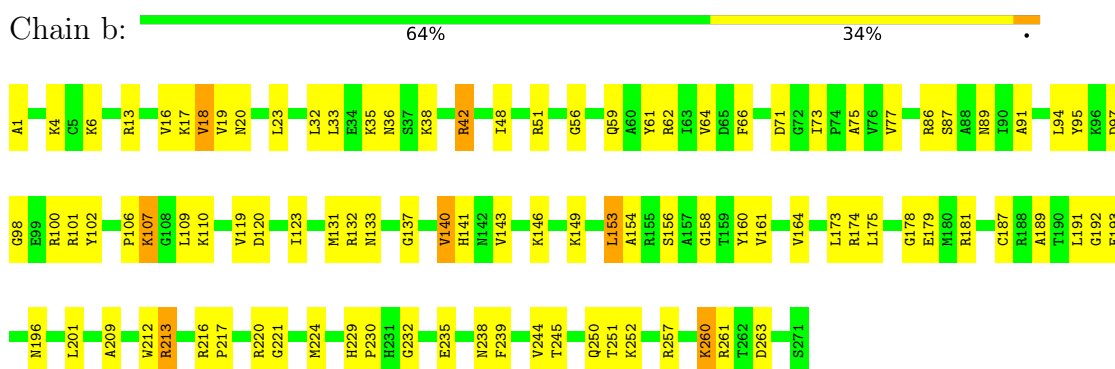


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
59	7	1	10	6	1	2	1	0

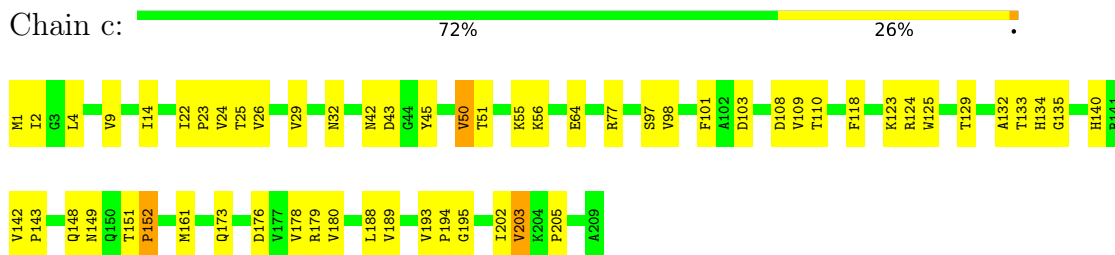
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

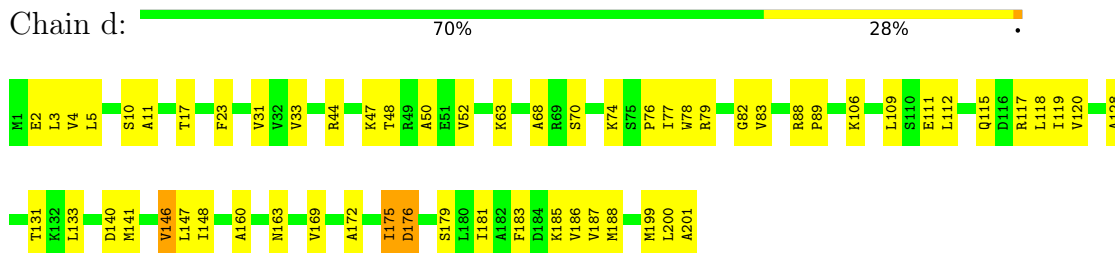
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3



- Molecule 3: 50S ribosomal protein L4



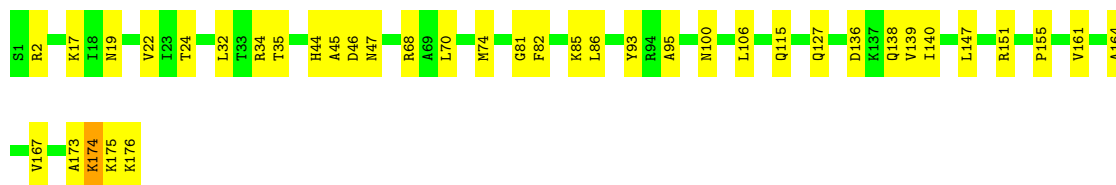
- Molecule 4: 50S ribosomal protein L5





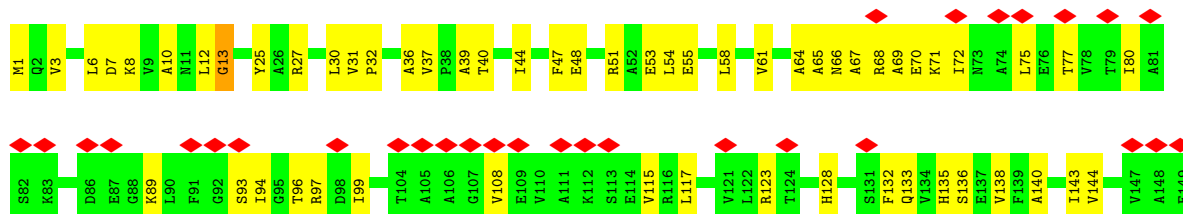
- Molecule 5: 50S ribosomal protein L6

Chain f: 78% 22% .



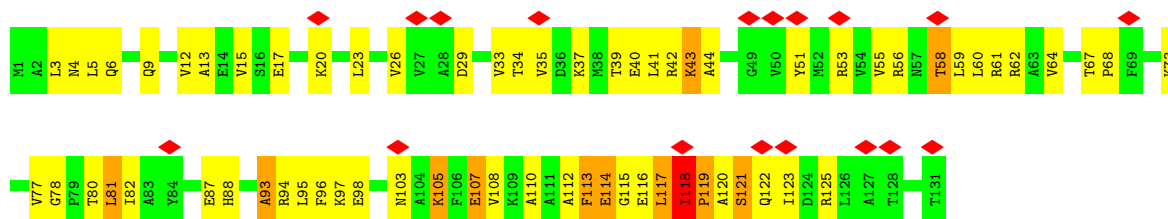
- Molecule 6: 50S ribosomal protein L9

Chain g: 20% 62% 38% .



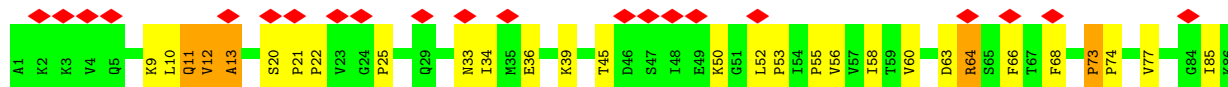
- Molecule 7: 50S ribosomal protein L10

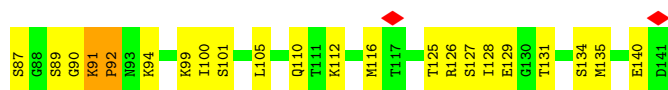
Chain h: 14% 49% 42% 8% .



- Molecule 8: 50S ribosomal protein L11

Chain i: 16% 64% 31% 5% .





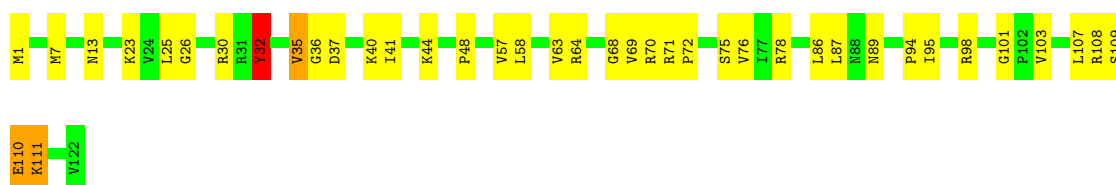
- Molecule 9: 50S ribosomal protein L13

Chain j: 77% 22%



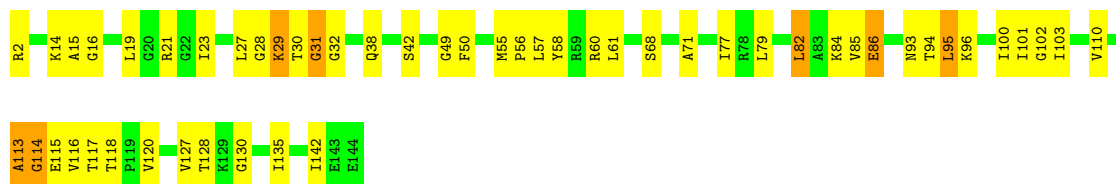
- Molecule 10: 50S ribosomal protein L14

Chain k: 67% 30%



- Molecule 11: 50S ribosomal protein L15

Chain l: 64% 31% 5%



- Molecule 12: 50S ribosomal protein L16

Chain m: 67% 32%



- Molecule 13: 50S ribosomal protein L17

Chain n: 75% 23%



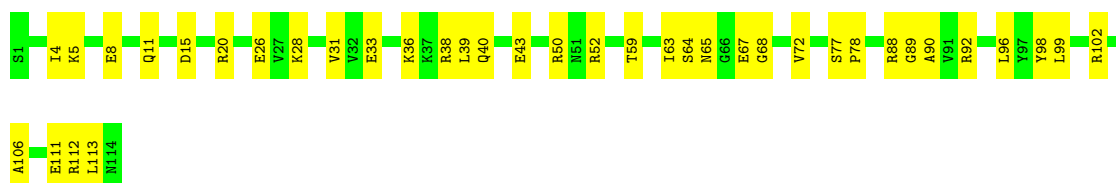
- Molecule 14: 50S ribosomal protein L18

Chain o:  72% 28%



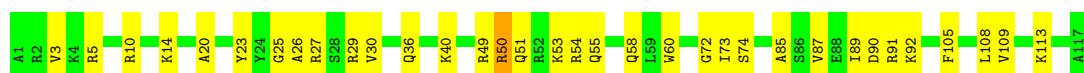
- Molecule 15: 50S ribosomal protein L19

Chain p:  67% 33%



- Molecule 16: 50S ribosomal protein L20

Chain q:  71% 28%



- Molecule 17: 50S ribosomal protein L21

Chain r:  70% 27%



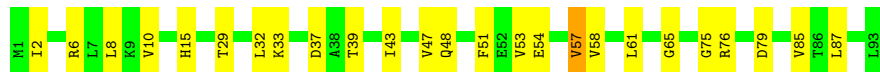
- Molecule 18: 50S ribosomal protein L22

Chain s:  78% 19%



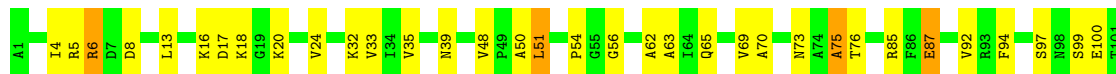
- Molecule 19: 50S ribosomal protein L23

Chain t:  73% 26%



- Molecule 20: 50S ribosomal protein L24

Chain u:  67% 29%



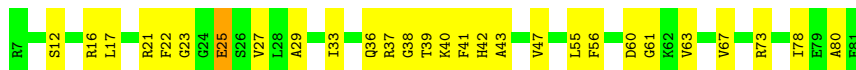
I102

- Molecule 21: 50S ribosomal protein L25

Chain v:  61% 37%


A94

- Molecule 22: 50S ribosomal protein L27

Chain w:  63% 36%


- Molecule 23: 50S ribosomal protein L28

Chain x:  79% 21%


- Molecule 24: 50S ribosomal protein L29

Chain y:  68% 32%


- Molecule 25: 50S ribosomal protein L30

Chain z:  66% 34%


- Molecule 26: 50S ribosomal protein L32

Chain B:  62% 38%


- Molecule 27: 50S ribosomal protein L33

Chain C:  70% 28% .



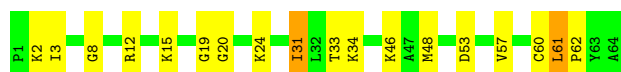
- Molecule 28: 50S ribosomal protein L34

Chain D:  72% 26% .



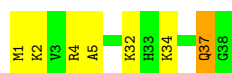
- Molecule 29: 50S ribosomal protein L35

Chain E:  72% 25% .



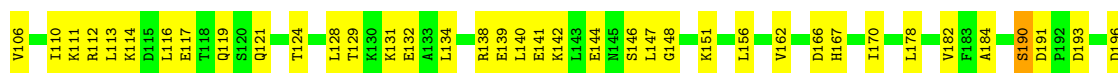
- Molecule 30: 50S ribosomal protein L36

Chain F:  82% 16% .



- Molecule 31: 30S ribosomal protein S2

Chain G:  62% 36% .



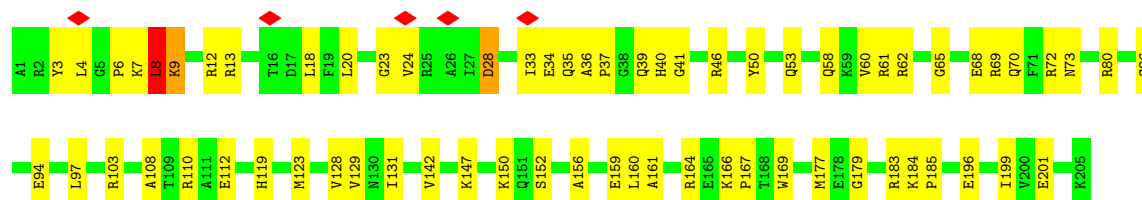
- Molecule 32: 30S ribosomal protein S3

Chain H:  73% 25% .

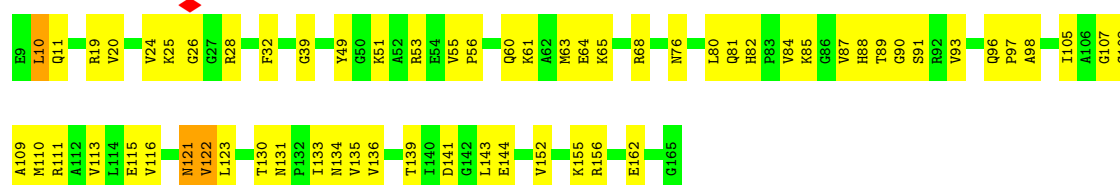




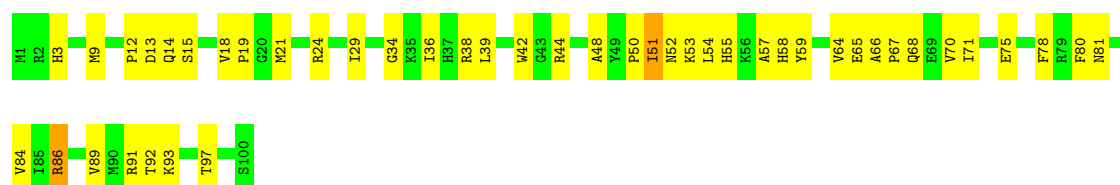
- Molecule 33: 30S ribosomal protein S4



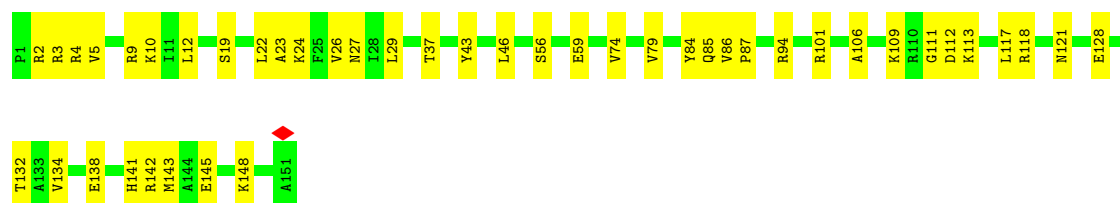
- Molecule 34: 30S ribosomal protein S5



- Molecule 35: 30S ribosomal protein S6

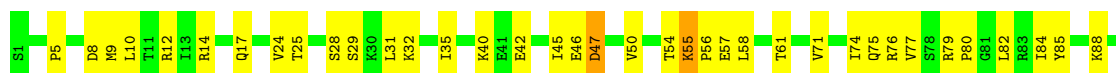


- Molecule 36: 30S ribosomal protein S7

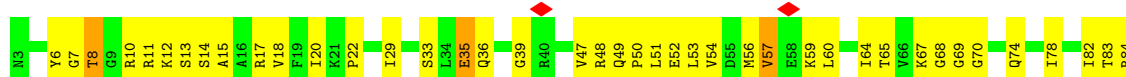


- Molecule 37: 30S ribosomal protein S8





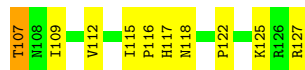
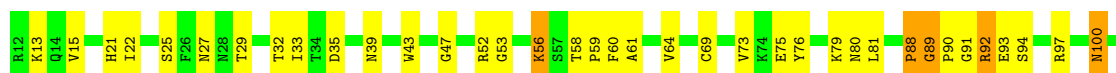
- Molecule 38: 30S ribosomal protein S9



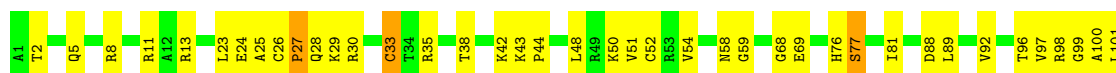
- Molecule 39: 30S ribosomal protein S10



- Molecule 40: 30S ribosomal protein S11

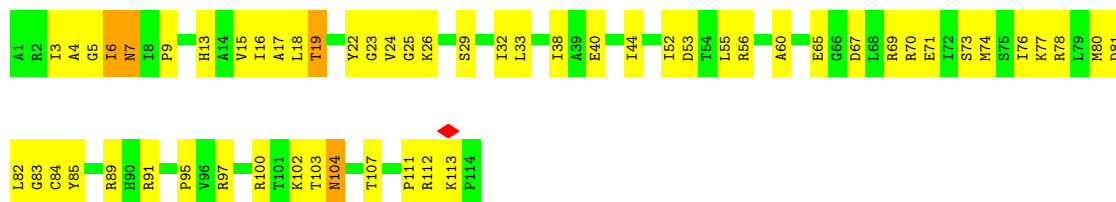


- Molecule 41: 30S ribosomal protein S12



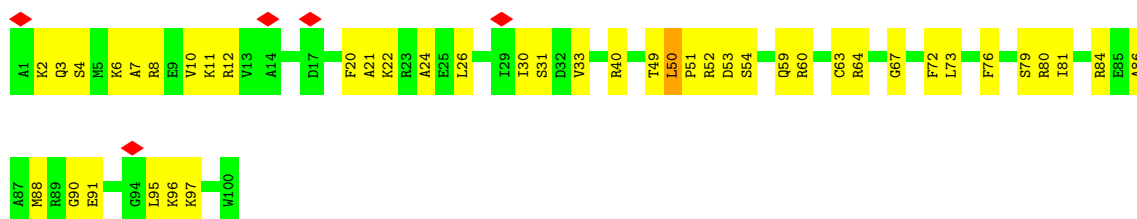
- Molecule 42: 30S ribosomal protein S13

Chain R:  51% 46%



- Molecule 43: 30S ribosomal protein S14

Chain S:  5% 57% 42%



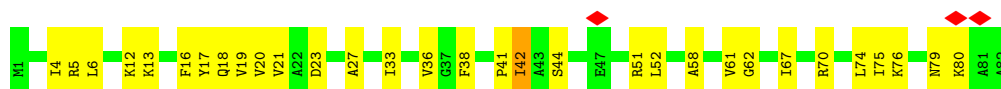
- Molecule 44: 30S ribosomal protein S15

Chain T:  77% 20%

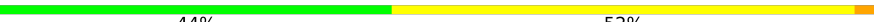


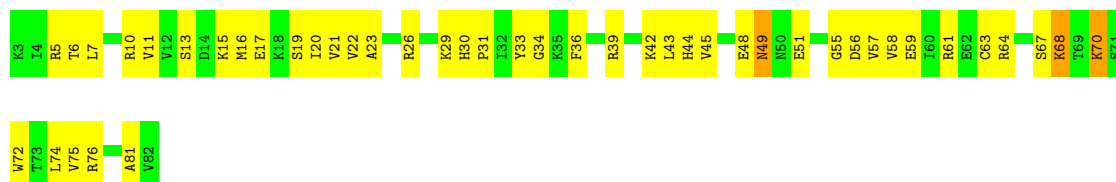
- Molecule 45: 30S ribosomal protein S16

Chain U:  62% 37%



- Molecule 46: 30S ribosomal protein S17

Chain V:  44% 52%



- Molecule 47: 30S ribosomal protein S18

Chain W:  57% 43%

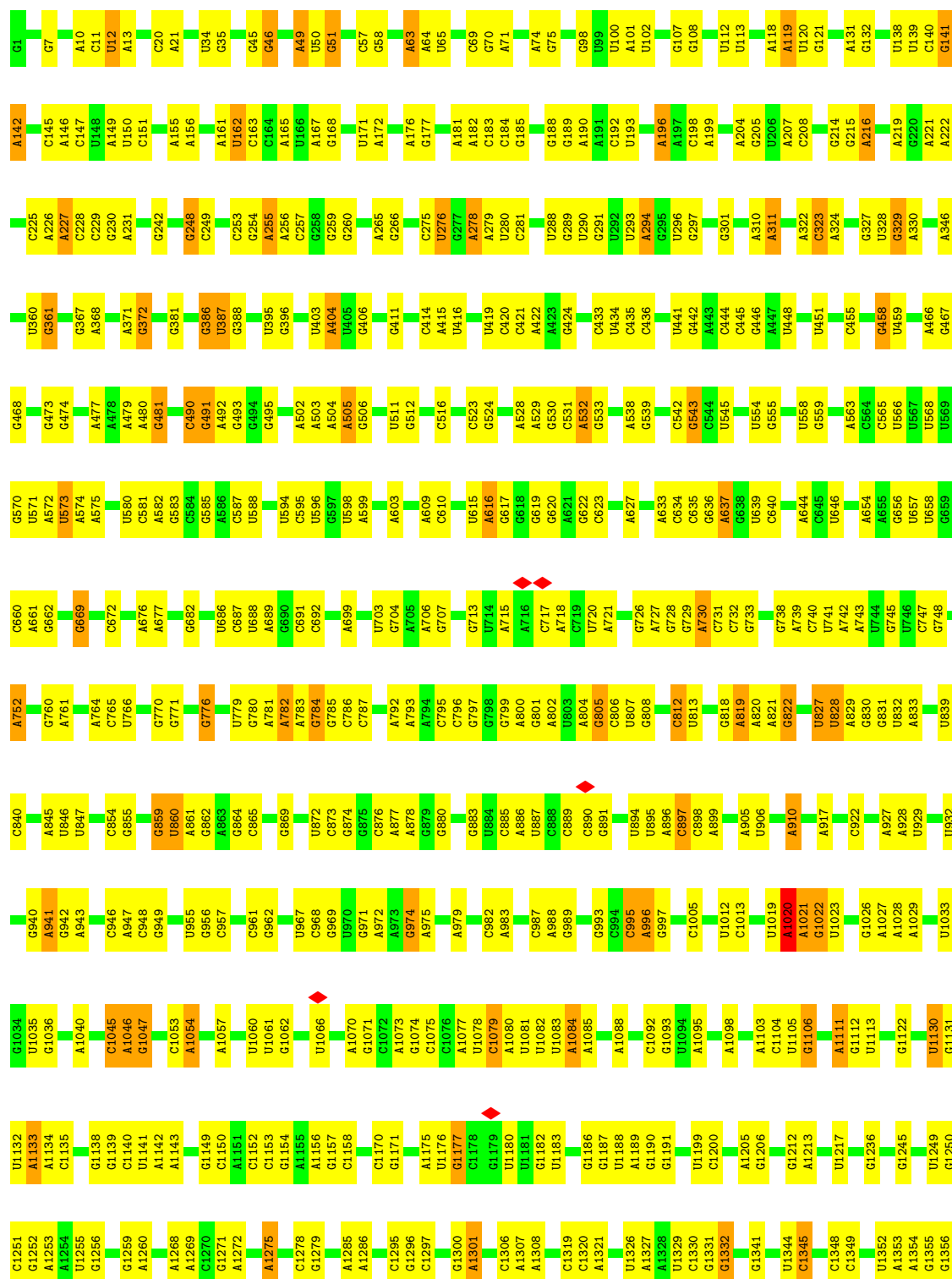


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U1451	A1374	G1304	G1221	C1140	C1031	G944	A743	G664	G557	A466	U367	G286	G184
C1452	A1375	G1305	G1222		G1032	G945	G744	A665	G560	U467	G289	G289	
G1453	U1376	A1306	C1223	G1144	G1033	A946	G745	G666	A561	A468	C371	U291	C193
A1456	G1378	U1308	U1224	G1145	G1034	G947	C754	G667	U562	G474	C372	G292	C194
G1457	G1379	G1309	C1225	A1146	U1047	C948	G755	G668	A563		G376		A197
G1458	U1380	G1310	C1226	A1147	G1048	A949	C756	G669	C564	C483	G377	C295	
U1381	A1311	A1227	U1148	U1049	U1049	U950	U757	A673	U585	G484	G378	U296	
C1460	G1312	A1229	U1049		G951	G951	C758	G674	U485	G485	C379	G297	
G1385	U1313	C1230	A1150		U952	U952			U571	U486	U367		C206
G1386	C1314				G953	G953	G763	C680	A572		U387	A300	C207
G1387	U1315	G1233	A1157		C1054	G954	C764	A681	A573	G494	G301	U208	
C1388	G1316	C1234	C1158		U955	U955	G765	U686	A574	A495	U390	G209	
	U1391	U1235	U1159		C1059	U956	A766	C575	A496	G391	A303	C210	
	C1467	A1236	U1060		U1060	U957	A767	A687	C576	G392	U304	G211	
A1468	G1392	A1318	C1237	G1161	G1061	U958	A768	G688	G577	A498	A393	G305	G212
	U1393	A1238	C1162		C1066	A959	G769	G689	C578	A506	A306	G213	
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G1473	C1395	U1240	A1167		A1067	U961	G771	G691	C580	A502	A397	C308	G226
	A1396	G1241	U1168		U1070	G966	U772	G692	C581	C503	C401	G310	
C1484	C1397	G1242	U1169		C1071	C967	G773	G693	C582	C504	G402	A311	C235
U1485	U1327	C1243	A1170		G1072	A968	A777	A694	G583	G505	G405	C312	A236
G1486	C1328	C1245	A1171		U1073	A969		A695	U594	A509	U405	A313	G237
G1487	G1401	U1246	A1176		G1074	C970	A784	A696	U594	A510	U407	C314	A238
C1402	U1330		G885		U1075	G971	G785	U697	A595				
G1488	G1331	A1250					G786			C514	A408	A321	A243
G1489	C1332	A1251	G1177		G1079	A974		A702	U598	C322	U409	C322	U244
	A1333	A1252	G1178		A1080	A975	G791	G703	C599	G515	G410	U323	U245
G1405		G1253	U1182		U1088	G976		U709	U616	U516	A411	A246	
	G1338	A1254	G1183		G1088	A977	G800	G710	G601	G517	A412	A327	G247
C1409	A1410	G1255	U1184		A1092	A978	U801	G711		C518	G413	C328	
U1495	C1411	A1256	G1185		C979	U978	A802	A712		C519	A414		A250
G1496	C1412	A1257	U1186		U1093	C979	U901	G713	G604	A520	A415	G331	G251
U1498	A1413	G1258	G1186		C980	A908	A908	G714	G605	G521	G416	G332	U252
A1499	U1414	C1259	G1187		U1094	U981	C805	A715	G606	C522	G417	A253	
G1415	U1345	G1260	U1095		U1095	U982		A716	A607	A823	C418	A336	
A1500	U1346	A1261	C1096		C912	A983	C810				C419		U256
G1416	G1347		A1191		A913		C811	G717	C613	G530	G337	G337	C257
	A1502		U1191			U986	G812	A718	C614	U531	A338	C339	G258
G1419	U1348	G1270	C1192		G917	C990	A815	C719	U619	C422	G423		G259
	A1349	A1271	G1193		A918	U991	A918	G720	A532	G423	G424	U343	G260
G1422	G1352	G1272	U1194		U991	U991	A816	G721	A533	G424	G425	A344	U261
G1423	G1353	C1273	C1195		U992	U992	C817	G722	A621	A534	G425	A344	U261
U1424	U1354	A1274	A1196		U993	U993	G818	U723	A622	C345	U426	A262	
U1425	G1355	G1275	A1197		C1112		A819	G724	G629	G536	U427	G346	A263
	G1356	U1276	U1198		C1112		U820	G725	A629	G537	G428	G347	C264
G1432	G1356	C1277	U1199		A923		U821	C726	A630	G538	U429	G265	
A1433	U1357	G1278	C1200		A1004		G821		C631	A539	A430		G266
G1434	A1362	U1279	U1201		G1006		U822	A729	U632	G540	G351	C267	
G1435	A1363	A1280	U1202		U1123		C823	G730	G633		U434	C352	U268
U1436	U1364	C1281	C1203		G1124		G824	G731	A634	A435	U435	A353	U273
A1437	C1282	C1282	U1204		U1125		A825	C732	G544	C436	G354	G354	G274
G1438	U1205	U1205	U1205		U1126		C930	G733	C545	U437	U438	A356	
	C1366	U1286	G1127		G931		U827	G734	C643	A546	U438		
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			C1128		C932		G832	C736	U553	G450	G450	G361	G281
			C1129		C933		G833	C737	G654	A451		G362	
			A1130		C934				A553				C284
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			C1028		U1029		G836	G741					

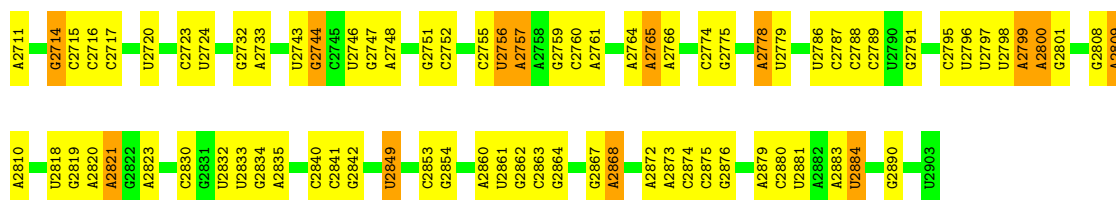


• Molecule 53: 23S ribosomal RNA

Chain 1: 58% 37% 5%

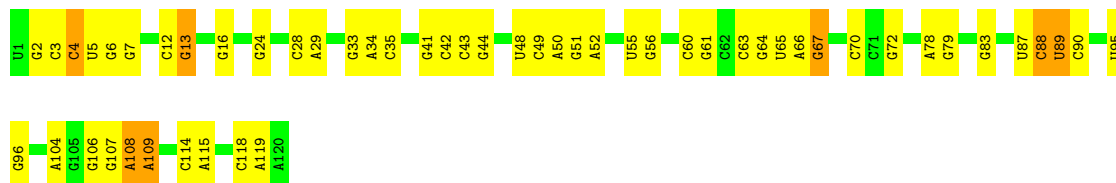


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G2627	G2628	G2629	U2629	G2443	G2444	A2534	U2291	U2441	G2365	U2291	A2198	U2111	C2023	U1926	U1818	C1694	G1567	G1473	G1358
			U2629	G2444	G2445	U2537	U2292	U2442	G2371	U2292	A2199	G2112	G2024	G1930	A1819	G1695	G1568	U1474	G1360
			U2629	G2445	G2446	U2538	U2293	U2443	G2372	U2293	A2119	U2113		G1930	A1820	G1696	G1570	G1475	G1361
A2632	G2633			G2446	G2447	U2547	U2296	U2444	U2203	U2296	A2114	A2114	G2029	C1934	U1827	G1697	A1571	U1476	A1365
				G2447	G2448	U2548	U2297	U2445	G2204	U2297	A2117	A2030	A2031	G1935	G1828	G1479	A1572		A1366
C2636	U2637	G2638	A2639	G2452	A2453	U2553	U2298	U2446	C2208	U2298	A2118	A2032	G2033	A1936	G1829	C1480	G1573		A1367
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G2641	G2642	G2643		G2454		U2555	U2300	U2448	G2210	U2300	A2120	G2035	G2036	A1938	G1831	G1721	G1581		G1369
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				G2481		U2582	U2327	U2475	G2238	U2327	U2151		G2067	C1980	G1886	G1648	G1648		A1433
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				G2493		U2594	U2339	U2487	G2250	U2339	U2163		G2079	C1992	G1898	G1542	G1542		G1436
				G2494		U2595	U2340	U2488	G2251	U2340	U2164		G2080	C1993	G1899	G1543	G1543		U1437
				G2495		U2596	U2341	U2489	G2252	U2341	U2165		G2081	C1994	G1900	C1547	C1547		U1438
				G2496		U2597	U2342	U2490	G2253	U2342	U2166		G2082	C1995	G1901	A1548	A1548		G1444
				G2497		U2598	U2343	U2491	G2254	U2343	U2167		G2083	C1996	G1902	C1549	C1549		G1445
				G2498		U2599	U2344	U2492	G2255	U2344	U2168		G2084	C1997	G1903	G1550	G1550		C1446
				G2499		U2600	U2345	U2493	G2256	U2345	U2169		G2085	C2001	G1904	G1551	G1551		G1447
				G2500		U2601	U2346	U2494	G2257	U2346	U2170		G2086	C2002	G1905	G1552	G1552		C1448
				G2501		U2602	U2347	U2495	G2258	U2347	U2171		G2087	C2003	G1906	G1553	G1553		G1449
				G2502		U2603	U2348	U2496	G2259	U2348	U2172		G2088	C2004	G1907	G1554	G1554		G1450
				G2503		U2604	U2349	U2497	G2260	U2349	U2173		G2089	C2005	G1908	G1555	G1555		U1451
				G2504		U2605	U2350	U2498	G2261	U2350	U2174		G2090	C2006	G1909	G1556	G1556		
				G2505		U2606	U2351	U2499	G2262	U2351	U2175		G2091	C2007	G1910	G1557	G1557		
				G2506		U2607	U2352	U2500	G2263	U2352	U2176		G2092	C2008	G1911	G1558	G1558		
				G2507		U2608	U2353	U2501	G2264	U2353	U2177		G2093	C2009	G1912	G1559	G1559		
				G2508		U2609	U2354	U2502	G2265	U2354	U2178		G2094	C2010	G1913	G1560	G1560		
				G2509		U2610	U2355	U2503	G2266	U2355	U2179		G2095	C2011	G1914	G1561	G1561		
				G2510		U2611	U2356	U2504	G2267	U2356	U2180		G2096	C2012	G1915	G1562	G1562		
				G2511		U2612	U2357	U2505	G2268	U2357	U2181		G2097	C2013	G1916	G1563	G1563		
				G2512		U2613	U2358	U2506	G2269	U2358	U2182		G2098	C2014	G1917	G1564	G1564		
				G2513		U2614	U2359	U2507	G2270	U2359	U2183		G2099	C2015	G1918	G1565	G1565		
				G2514		U2615	U2360	U2508	G2271	U2360	U2184		G2100	C2016	G1919	G1566	G1566		
				G2515		U2616	U2361	U2509	G2272	U2361	U2185		G2101	C2017	G1920	G1567	G1567		
				G2516		U2617	U2362	U2510	G2273	U2362	U2186		G2102	C2018	G1921	G1568	G1568		
				G2517		U2618	U2363	U2511	G2274	U2363	U2187		G2103	C2019	G1922	G1569	G1569		
				G2518		U2619	U2364	U2512	G2275	U2364	U2188		G2104	C2020	G1923	G1570	G1570		
				G2519		U2620	U2365	U2513	G2276	U2365	U2189		G2105	C2021	G1924	G1571	G1571		
				G2520		U2621	U2366	U2514	G2277	U2366	U2190		G2106	C2022	G1925	G1572	G1572		
				G2521		U2622	U2367	U2515	G2278	U2367	U2191		G2107	C2023	G1926	G1573	G1573		
				G2522		U2623	U2368	U2516	G2279	U2368	U2192		G2108	C2024	G1927	G1574	G1574		
				G2523		U2624	U2369	U2517	G2280	U2369	U2193		G2109	C2025	G1928	G1575	G1575		
				G2524		U2625	U2370	U2518	G2281	U2370	U2194		G2110	C2026	G1929				



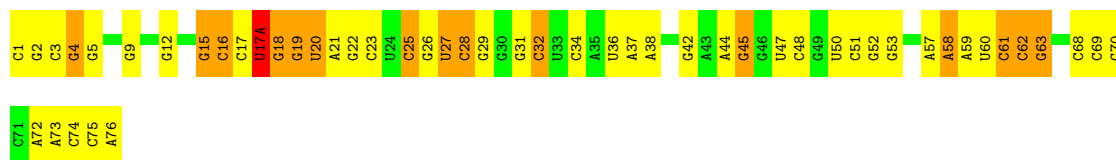
- Molecule 54: 5S ribosomal RNA

Chain 2: 56% 38% 6%



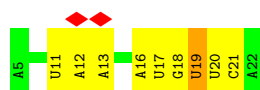
- Molecule 55: tRNA^{fMet}

Chain 5: 32% 47% 19%



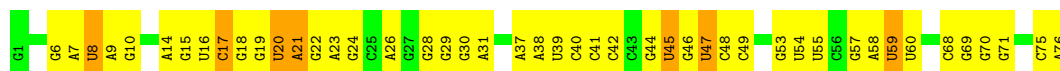
- Molecule 56: mRNA

Chain 4: 11% 50% 44% 6%



- Molecule 57: tRNA^{Phe}

Chain 7: 39% 51% 9%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18925	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	23.785	Depositor
Minimum map value	-12.967	Depositor
Average map value	0.117	Depositor
Map value standard deviation	0.971	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	b	0.29	0/2122	0.96	8/2852 (0.3%)
2	c	0.30	0/1586	0.87	4/2134 (0.2%)
3	d	0.28	0/1571	0.88	5/2113 (0.2%)
4	e	0.31	0/1435	0.92	7/1926 (0.4%)
5	f	0.30	0/1343	0.87	3/1816 (0.2%)
6	g	0.32	0/1122	1.01	10/1515 (0.7%)
7	h	0.35	0/1002	1.11	12/1350 (0.9%)
8	i	0.38	0/1046	0.98	6/1410 (0.4%)
9	j	0.29	0/1152	0.89	2/1551 (0.1%)
10	k	0.29	0/948	0.94	2/1268 (0.2%)
11	l	0.30	0/1054	0.98	6/1403 (0.4%)
12	m	0.29	0/1093	0.88	2/1460 (0.1%)
13	n	0.29	0/974	0.90	3/1301 (0.2%)
14	o	0.29	0/902	0.90	1/1209 (0.1%)
15	p	0.29	0/929	0.82	0/1242
16	q	0.28	0/960	0.95	4/1278 (0.3%)
17	r	0.29	0/829	0.90	2/1107 (0.2%)
18	s	0.28	0/864	0.86	2/1156 (0.2%)
19	t	0.28	0/745	0.81	0/994
20	u	0.30	0/788	0.94	3/1051 (0.3%)
21	v	0.29	0/766	0.99	5/1025 (0.5%)
22	w	0.28	0/582	0.81	0/769
23	x	0.28	0/635	0.93	1/848 (0.1%)
24	y	0.27	0/510	0.92	2/677 (0.3%)
25	z	0.28	0/453	0.88	2/605 (0.3%)
26	B	0.30	0/450	0.84	0/599
27	C	0.32	0/417	0.84	3/554 (0.5%)
28	D	0.32	0/380	0.86	1/498 (0.2%)
29	E	0.28	0/513	0.86	2/676 (0.3%)
30	F	0.30	0/303	0.87	0/397
31	G	0.30	0/1788	0.92	6/2408 (0.2%)
32	H	0.33	0/1652	0.93	6/2225 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.32	0/1665	0.96	9/2227 (0.4%)
34	J	0.33	0/1170	0.90	1/1573 (0.1%)
35	K	0.31	0/836	0.96	4/1128 (0.4%)
36	L	0.31	0/1196	0.93	4/1602 (0.2%)
37	M	0.31	0/989	0.96	2/1326 (0.2%)
38	N	0.33	0/1034	0.95	3/1375 (0.2%)
39	O	0.34	0/797	0.94	6/1077 (0.6%)
40	P	0.33	0/886	0.97	8/1195 (0.7%)
41	Q	0.33	0/969	0.97	3/1300 (0.2%)
42	R	0.32	0/893	0.94	4/1193 (0.3%)
43	S	0.32	0/817	0.94	5/1088 (0.5%)
44	T	0.29	0/722	0.97	3/964 (0.3%)
45	U	0.32	0/659	0.95	2/884 (0.2%)
46	V	0.31	0/658	0.89	1/881 (0.1%)
47	W	0.31	0/545	0.81	1/731 (0.1%)
48	X	0.34	0/653	0.86	0/877
49	Y	0.29	0/671	0.92	1/888 (0.1%)
50	Z	0.34	0/551	1.08	3/728 (0.4%)
51	a	0.32	0/1034	0.86	3/1387 (0.2%)
52	3	0.42	0/36963	0.47	2/57662 (0.0%)
53	1	0.40	0/69796	0.47	4/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.65	0/1832	0.57	1/2855 (0.0%)
56	4	0.49	0/436	0.48	0/679
57	7	0.64	0/1809	0.59	0/2819
All	All	0.39	0/161367	0.63	180/241223 (0.1%)

There are no bond length outliers.

The worst 5 of 180 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	Z	59	LEU	N-CA-C	-10.43	99.42	112.88
44	T	49	HIS	N-CA-C	9.38	121.11	111.07
1	b	87	SER	N-CA-C	-8.21	103.78	113.88
1	b	213	ARG	N-CA-C	-8.08	101.54	111.40
43	S	49	THR	N-CA-C	-7.91	102.65	111.82

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	81	0
2	c	1565	0	1616	45	0
3	d	1552	0	1619	48	0
4	e	1411	0	1447	71	0
5	f	1323	0	1374	27	0
6	g	1111	0	1148	39	0
7	h	989	0	1025	61	0
8	i	1032	0	1088	39	0
9	j	1129	0	1162	32	0
10	k	939	0	1012	33	0
11	l	1045	0	1117	42	0
12	m	1074	0	1157	35	0
13	n	961	0	1000	23	0
14	o	892	0	923	24	0
15	p	917	0	965	35	0
16	q	947	0	1022	35	0
17	r	816	0	839	31	0
18	s	857	0	922	16	0
19	t	739	0	807	19	0
20	u	780	0	834	20	0
21	v	753	0	780	23	0
22	w	575	0	592	20	0
23	x	625	0	655	12	0
24	y	509	0	543	12	0
25	z	449	0	491	13	0
26	B	444	0	461	20	0
27	C	410	0	440	8	0
28	D	377	0	418	9	0
29	E	504	0	574	17	0
30	F	302	0	343	11	0
31	G	1757	0	1787	59	0
32	H	1625	0	1699	40	0
33	I	1643	0	1710	56	0
34	J	1157	0	1199	55	0
35	K	818	0	808	30	0
36	L	1182	0	1240	40	0
37	M	979	0	1034	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	59	0
39	O	787	0	828	32	0
40	P	870	0	878	35	0
41	Q	955	0	1019	42	0
42	R	884	0	944	47	0
43	S	805	0	847	45	0
44	T	714	0	737	19	0
45	U	649	0	666	22	0
46	V	649	0	691	33	0
47	W	536	0	552	23	0
48	X	638	0	665	29	0
49	Y	665	0	714	38	0
50	Z	545	0	579	32	0
51	a	1027	0	1092	33	0
52	3	33012	0	16618	701	0
53	1	62317	0	31346	918	0
54	2	2568	0	1303	44	0
55	5	1640	0	837	54	0
56	4	388	0	196	10	0
57	7	1619	0	821	33	0
58	7	11	0	8	0	0
59	7	10	0	10	0	0
All	All	148582	0	100429	2979	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 2979 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:45:G:H5''	53:1:46:G:H5'	1.27	1.17
43:S:3:GLN:HA	43:S:6:LYS:HE2	1.39	1.00
42:R:111:PRO:HB2	42:R:113:LYS:HE2	1.45	0.99
53:1:2048:G:H2'	53:1:2049:G:H5''	1.45	0.96
53:1:2277:G:H2'	53:1:2278:A:H5''	1.50	0.93

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%)	230 (86%)	36 (13%)	3 (1%)	11	39
2	c	207/209 (99%)	185 (89%)	22 (11%)	0	100	100
3	d	199/201 (99%)	183 (92%)	14 (7%)	2 (1%)	12	40
4	e	175/177 (99%)	156 (89%)	19 (11%)	0	100	100
5	f	174/176 (99%)	153 (88%)	19 (11%)	2 (1%)	11	39
6	g	147/149 (99%)	124 (84%)	22 (15%)	1 (1%)	18	49
7	h	129/131 (98%)	92 (71%)	31 (24%)	6 (5%)	2	12
8	i	139/141 (99%)	119 (86%)	14 (10%)	6 (4%)	2	14
9	j	140/142 (99%)	123 (88%)	17 (12%)	0	100	100
10	k	120/122 (98%)	98 (82%)	16 (13%)	6 (5%)	1	11
11	l	141/143 (99%)	116 (82%)	19 (14%)	6 (4%)	2	14
12	m	134/136 (98%)	111 (83%)	19 (14%)	4 (3%)	3	20
13	n	118/120 (98%)	99 (84%)	18 (15%)	1 (1%)	16	45
14	o	114/116 (98%)	107 (94%)	6 (5%)	1 (1%)	14	43
15	p	112/114 (98%)	94 (84%)	17 (15%)	1 (1%)	14	43
16	q	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
17	r	101/103 (98%)	86 (85%)	13 (13%)	2 (2%)	6	27
18	s	108/110 (98%)	96 (89%)	9 (8%)	3 (3%)	4	21
19	t	91/93 (98%)	83 (91%)	8 (9%)	0	100	100
20	u	100/102 (98%)	85 (85%)	9 (9%)	6 (6%)	1	9
21	v	92/94 (98%)	82 (89%)	9 (10%)	1 (1%)	11	39
22	w	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
23	x	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
24	y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
25	z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	46 (85%)	8 (15%)	0	100	100
27	C	48/50 (96%)	40 (83%)	7 (15%)	1 (2%)	5	26
28	D	44/46 (96%)	38 (86%)	6 (14%)	0	100	100
29	E	62/64 (97%)	52 (84%)	9 (14%)	1 (2%)	7	31
30	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	21
31	G	223/225 (99%)	205 (92%)	16 (7%)	2 (1%)	14	43
32	H	204/206 (99%)	186 (91%)	17 (8%)	1 (0%)	24	55
33	I	203/205 (99%)	179 (88%)	22 (11%)	2 (1%)	12	40
34	J	155/157 (99%)	128 (83%)	21 (14%)	6 (4%)	2	16
35	K	98/100 (98%)	80 (82%)	16 (16%)	2 (2%)	6	27
36	L	149/151 (99%)	134 (90%)	15 (10%)	0	100	100
37	M	127/129 (98%)	115 (91%)	11 (9%)	1 (1%)	16	45
38	N	125/127 (98%)	104 (83%)	17 (14%)	4 (3%)	3	19
39	O	96/98 (98%)	78 (81%)	13 (14%)	5 (5%)	1	11
40	P	114/116 (98%)	92 (81%)	18 (16%)	4 (4%)	3	18
41	Q	121/123 (98%)	91 (75%)	25 (21%)	5 (4%)	2	15
42	R	112/114 (98%)	96 (86%)	10 (9%)	6 (5%)	1	10
43	S	98/100 (98%)	79 (81%)	19 (19%)	0	100	100
44	T	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	37
45	U	80/82 (98%)	68 (85%)	9 (11%)	3 (4%)	2	16
46	V	78/80 (98%)	61 (78%)	13 (17%)	4 (5%)	1	11
47	W	63/65 (97%)	57 (90%)	5 (8%)	1 (2%)	7	31
48	X	77/79 (98%)	65 (84%)	12 (16%)	0	100	100
49	Y	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
50	Z	63/65 (97%)	42 (67%)	15 (24%)	6 (10%)	0	3
51	a	130/223 (58%)	123 (95%)	6 (5%)	1 (1%)	16	45
All	All	5919/6112 (97%)	5125 (87%)	686 (12%)	108 (2%)	9	29

5 of 108 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
3	d	83	VAL

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Mol	Chain	Res	Type
5	f	45	ALA
7	h	107	GLU
7	h	108	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	212 (98%)	4 (2%)	50	68
2	c	164/164 (100%)	160 (98%)	4 (2%)	43	65
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	81
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	78
7	h	100/100 (100%)	98 (98%)	2 (2%)	48	68
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	114 (98%)	2 (2%)	53	71
10	k	103/103 (100%)	99 (96%)	4 (4%)	28	56
11	l	102/102 (100%)	101 (99%)	1 (1%)	68	76
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	86 (100%)	0	100	100
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	76
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	76
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	78 (98%)	2 (2%)	42	64
20	u	83/83 (100%)	82 (99%)	1 (1%)	63	75
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	w	57/57 (100%)	55 (96%)	2 (4%)	32	58
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	46 (98%)	1 (2%)	47	67
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	37 (97%)	1 (3%)	40	64
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%)	185 (100%)	1 (0%)	81	83
32	H	170/170 (100%)	168 (99%)	2 (1%)	63	75
33	I	172/172 (100%)	170 (99%)	2 (1%)	63	75
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	79
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	76
36	L	124/124 (100%)	123 (99%)	1 (1%)	73	79
37	M	104/104 (100%)	101 (97%)	3 (3%)	37	62
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%)	88 (99%)	1 (1%)	65	76
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	82 (99%)	1 (1%)	63	75
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	64 (98%)	1 (2%)	57	72
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	53 (96%)	2 (4%)	31	58
51	a	110/174 (63%)	109 (99%)	1 (1%)	70	78
All	All	4908/4972 (99%)	4862 (99%)	46 (1%)	68	78

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	D	1	MET
35	K	51	ILE
31	G	46	VAL
33	I	8	LEU
37	M	24	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
21	v	24	ASN
47	W	51	GLN
26	B	18	HIS
46	V	30	HIS
51	a	188	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	143 (9%)	3 (0%)
53	1	2902/2903 (99%)	330 (11%)	12 (0%)
54	2	119/120 (99%)	12 (10%)	1 (0%)
55	5	76/77 (98%)	24 (31%)	1 (1%)
56	4	17/18 (94%)	3 (17%)	0
57	7	75/76 (98%)	12 (16%)	1 (1%)
All	All	4727/4733 (99%)	524 (11%)	18 (0%)

5 of 524 RNA backbone outliers are listed below:

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

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	2756	U

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Mol	Chain	Res	Type
57	7	45	U
55	5	17(A)	U
53	1	1130	U
53	1	2391	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	PHE	7	101	59,57	10,11,12	0.73	0	8,13,15	0.36	0
59	FME	7	102	58	8,9,10	0.47	0	8,9,11	1.47	3 (37%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	PHE	7	101	59,57	-	1/5/6/8	0/1/1/1
59	FME	7	102	58	-	4/7/9/11	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	7	102	FME	CG-CB-CA	-2.37	105.62	112.87
59	7	102	FME	O-C-CA	-2.25	118.98	124.77
59	7	102	FME	C-CA-N	2.21	113.77	109.50

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	7	102	FME	O1-CN-N-CA
59	7	102	FME	O-C-CA-CB
59	7	102	FME	N-CA-CB-CG
58	7	101	PHE	N-CA-CB-CG
59	7	102	FME	CB-CG-SD-CE

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

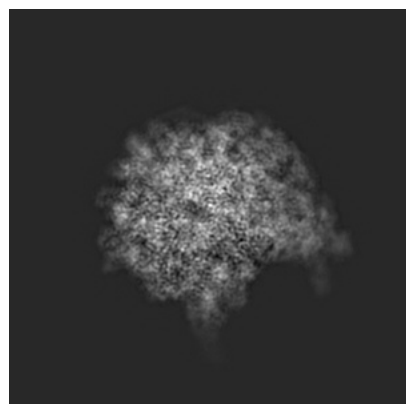
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21634. These allow visual inspection of the internal detail of the map and identification of artifacts.

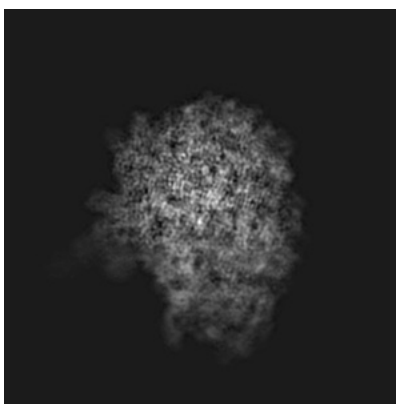
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

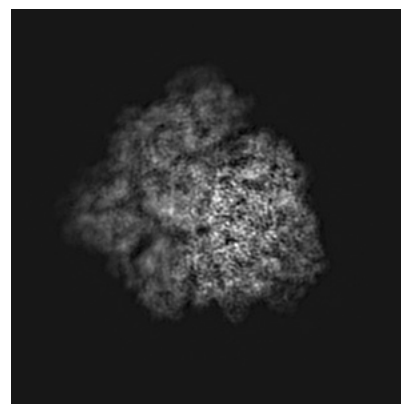
6.1.1 Primary map



X

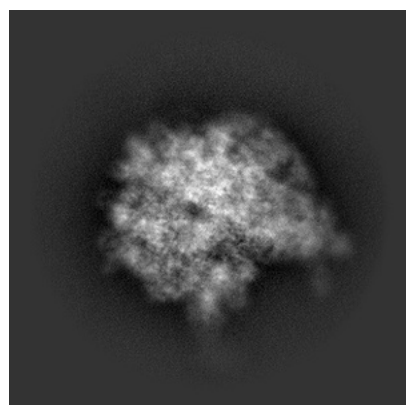


Y

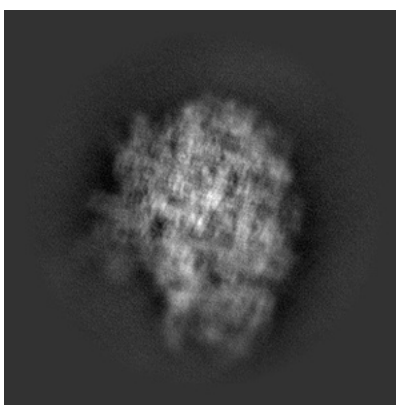


Z

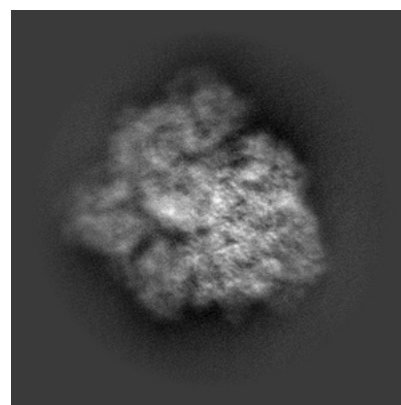
6.1.2 Raw map



X



Y

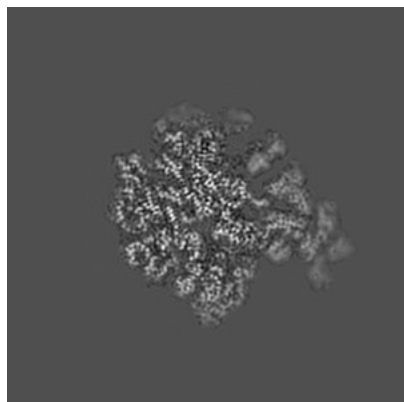


Z

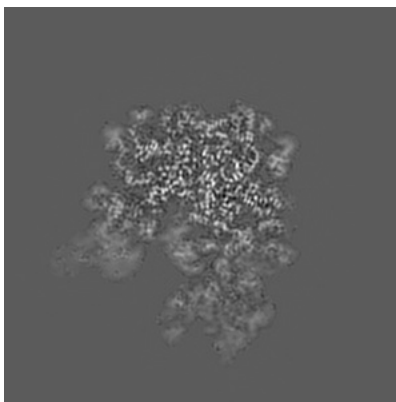
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

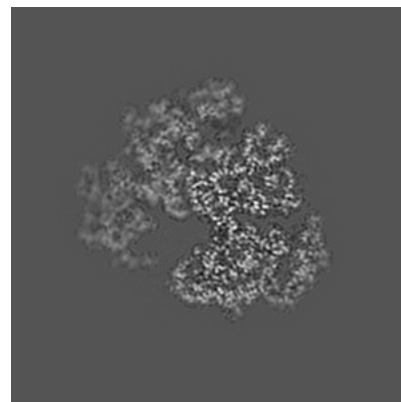
6.2.1 Primary map



X Index: 144

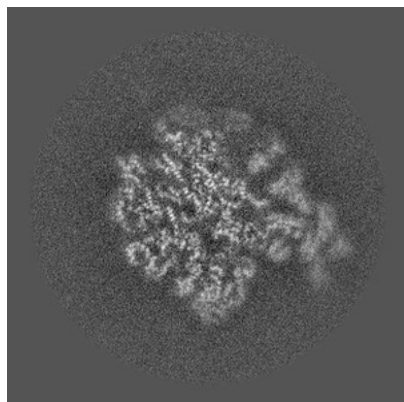


Y Index: 144

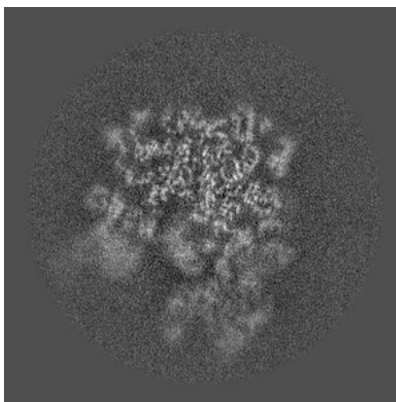


Z Index: 144

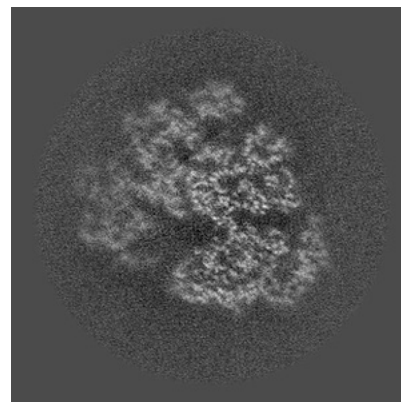
6.2.2 Raw map



X Index: 144



Y Index: 144

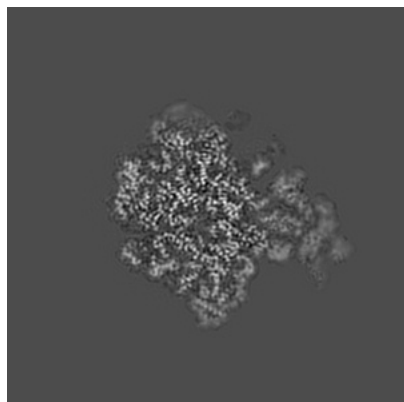


Z Index: 144

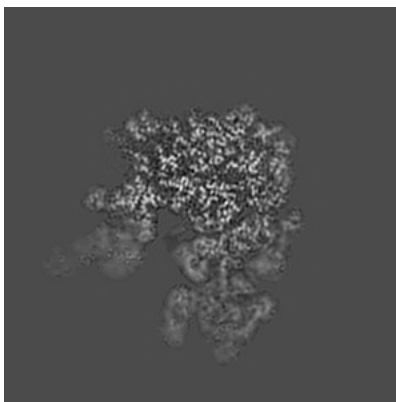
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

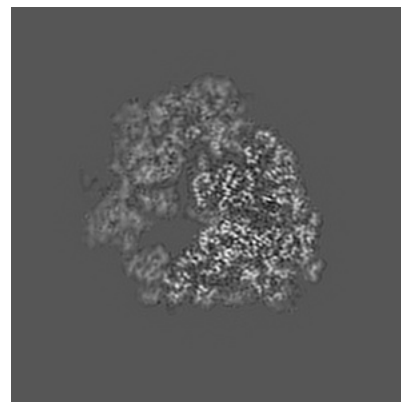
6.3.1 Primary map



X Index: 147

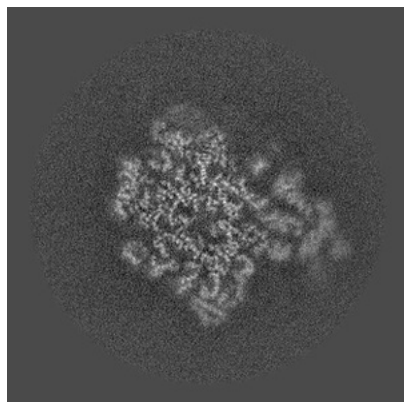


Y Index: 150

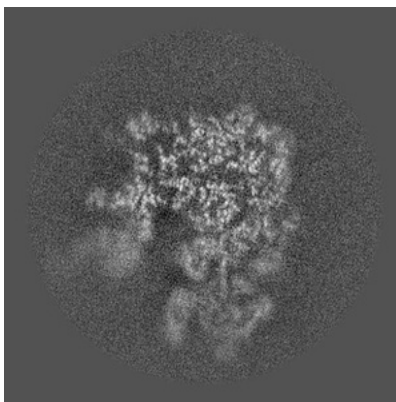


Z Index: 135

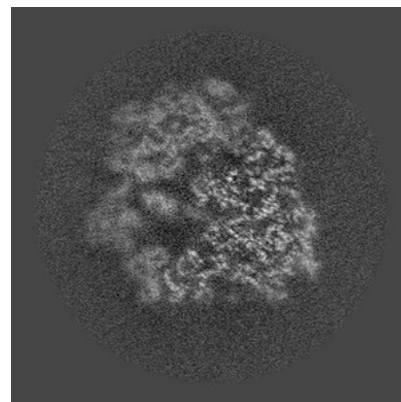
6.3.2 Raw map



X Index: 147



Y Index: 150

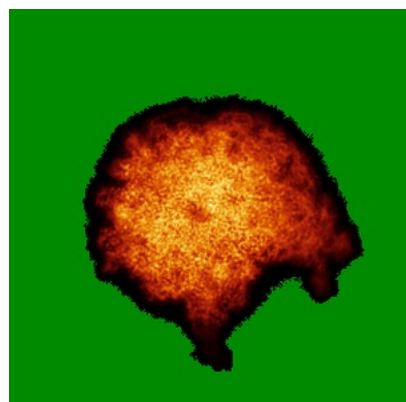


Z Index: 133

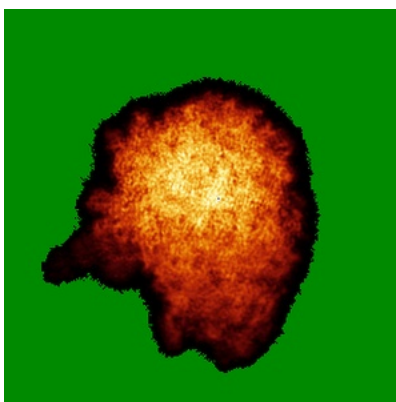
The images above show the largest variance slices of the map in three orthogonal directions.

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

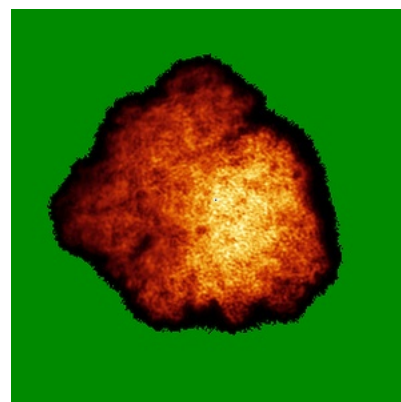
6.4.1 Primary map



X

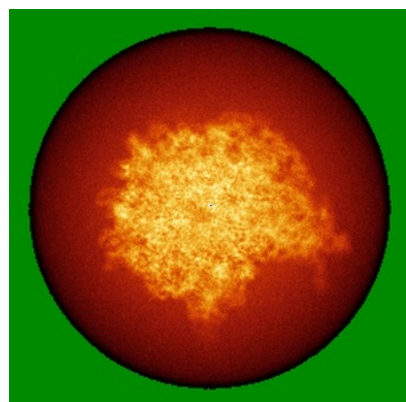


Y

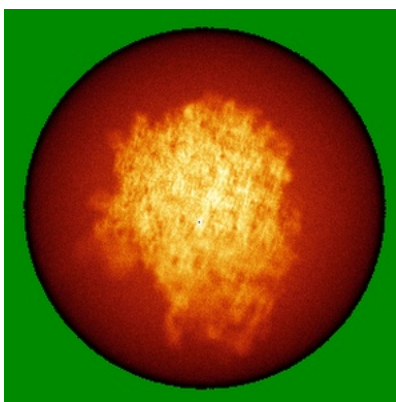


Z

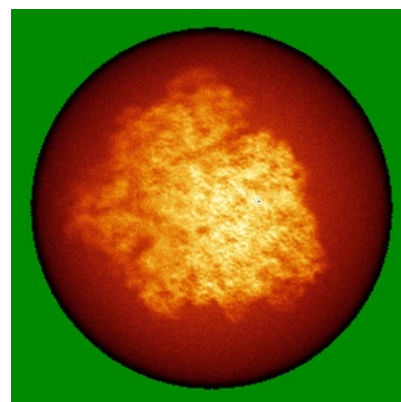
6.4.2 Raw map



X



Y



Z

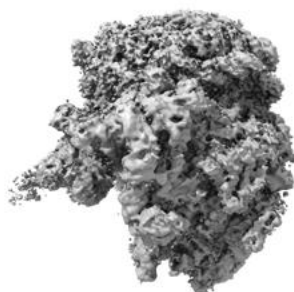
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



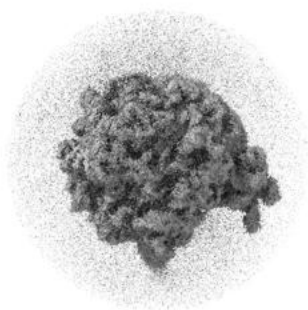
Y



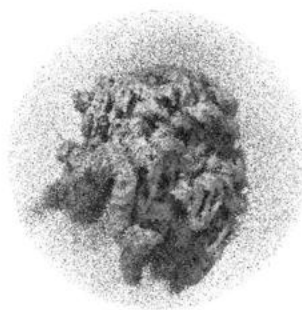
Z

The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

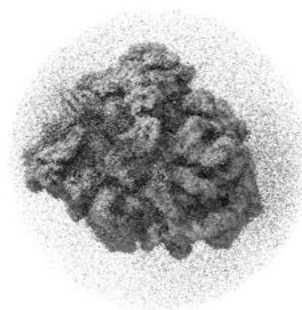
6.5.2 Raw map



X



Y



Z

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.

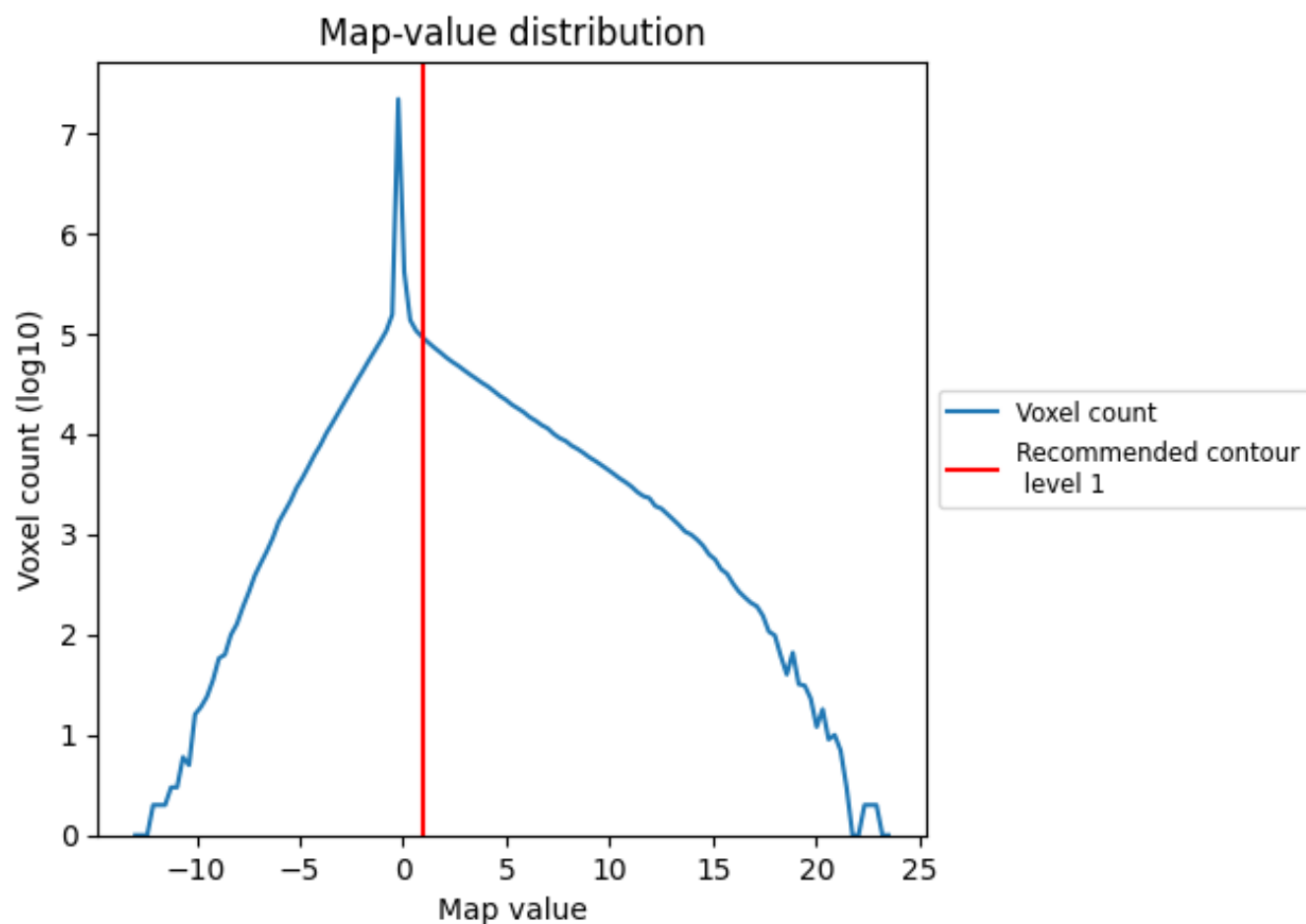
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

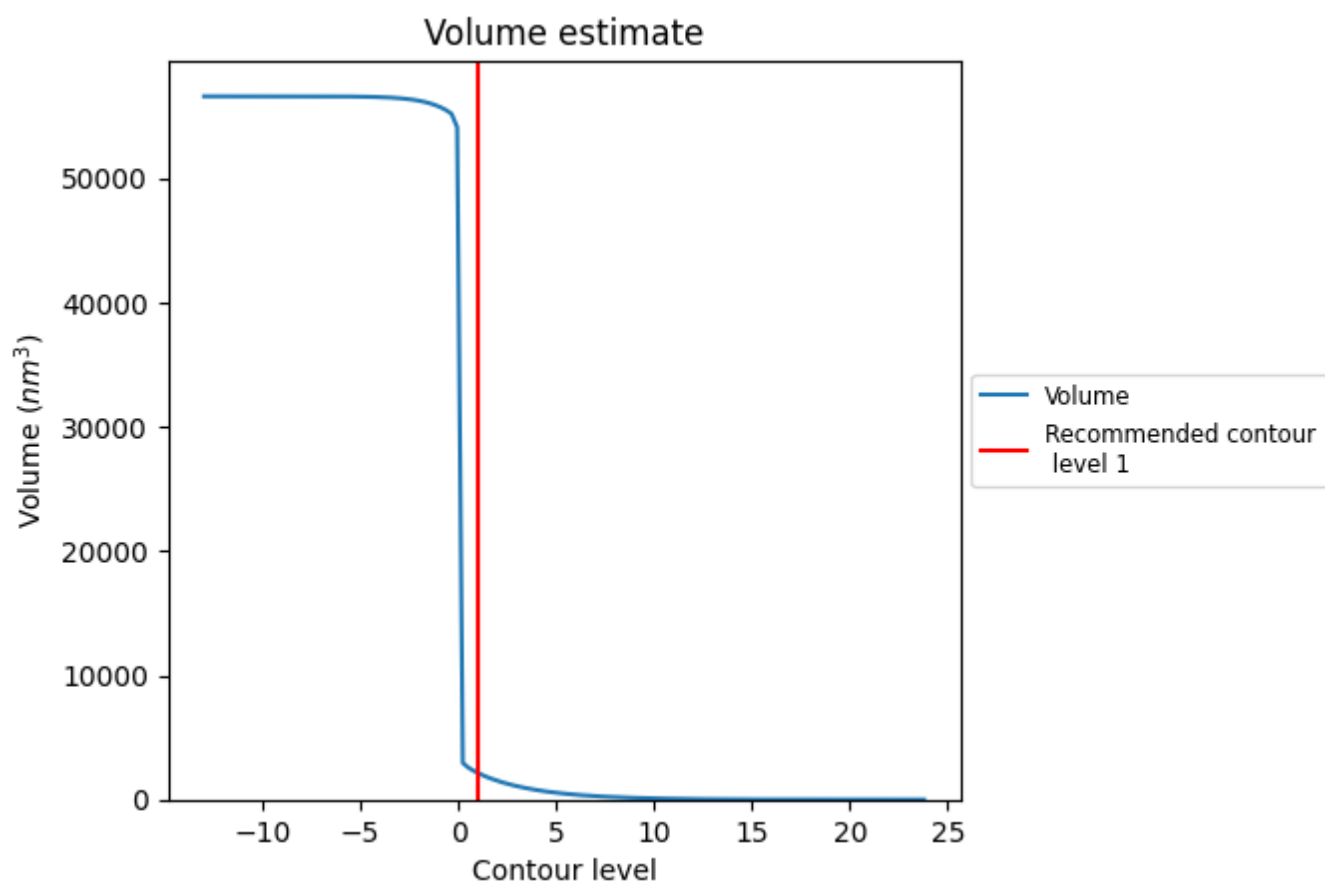
This section contains the results of statistical analysis of the map.

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.

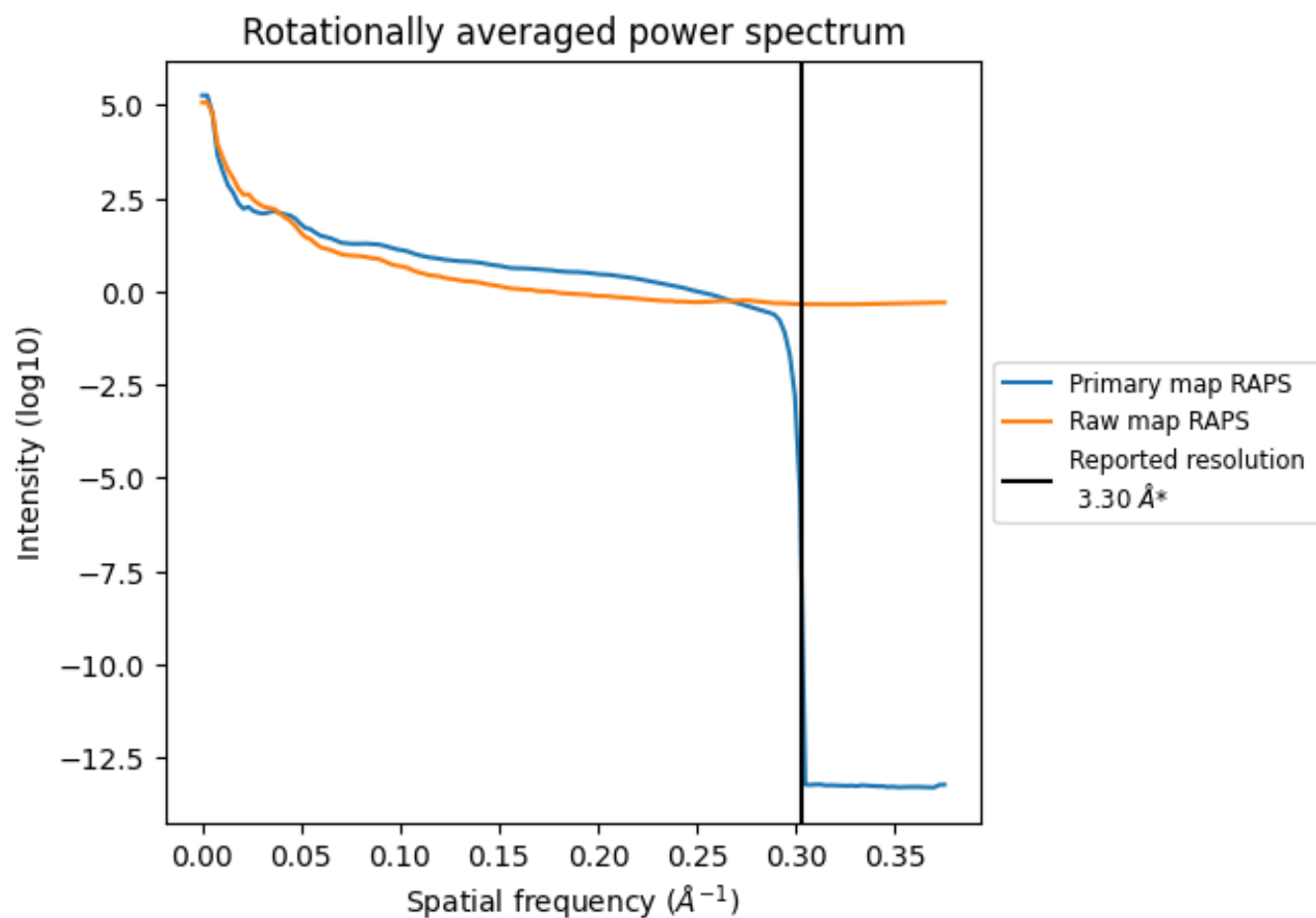
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2152 nm³; this corresponds to an approximate mass of 1944 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 ⓘ

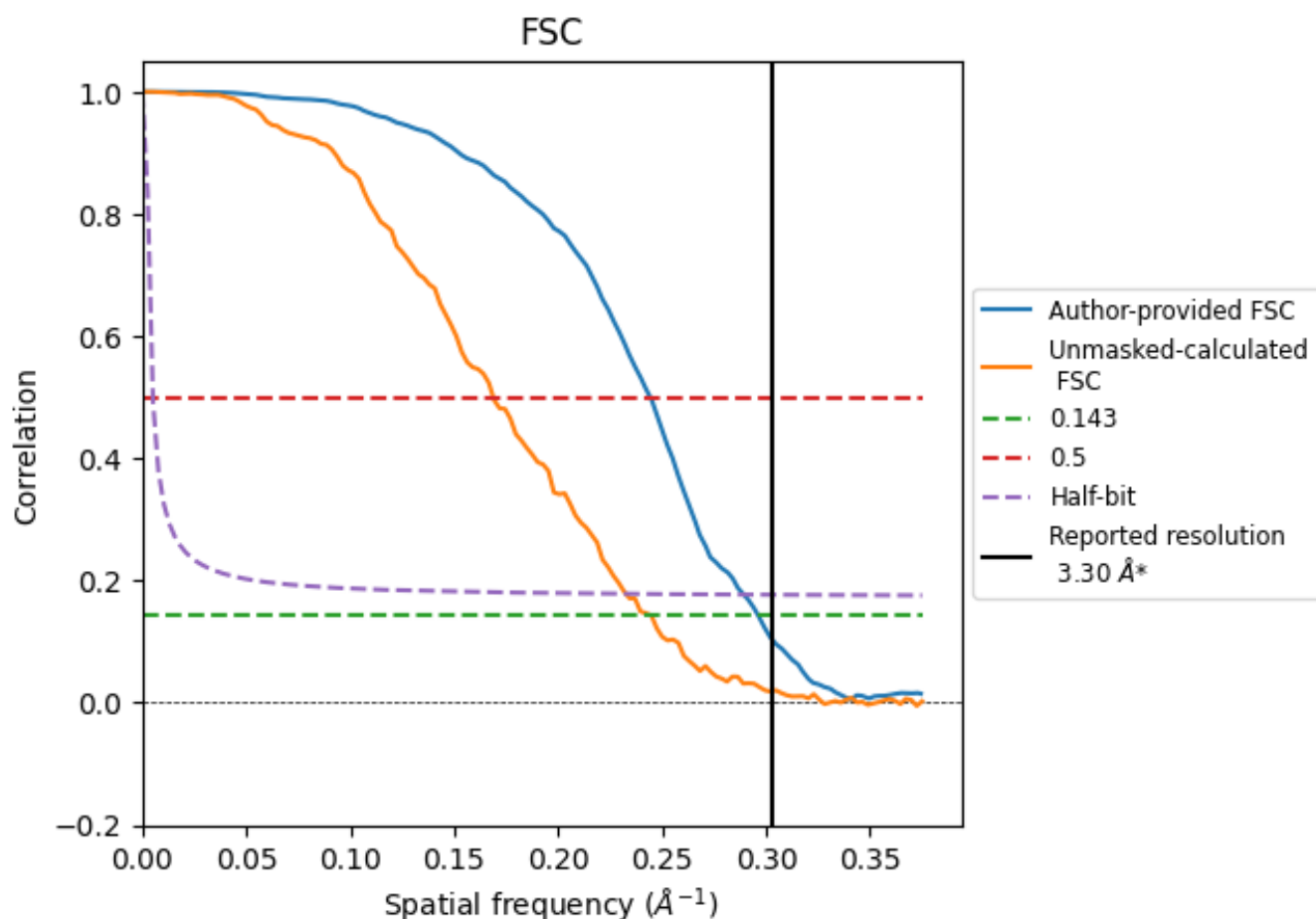


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

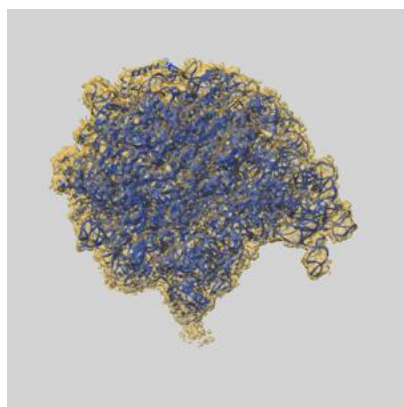
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.38	4.09	3.46
Unmasked-calculated*	4.09	5.92	4.30

*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 4.09 differs from the reported value 3.3 by more than 10 %

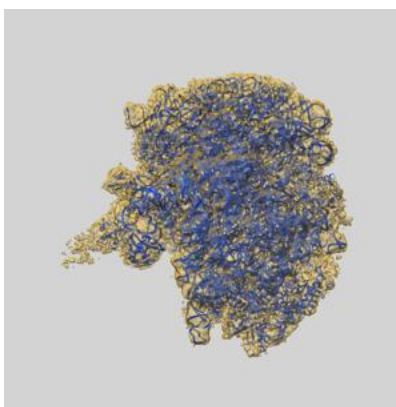
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21634 and PDB model 6WDF. Per-residue inclusion information can be found in section [3](#) on page [16](#).

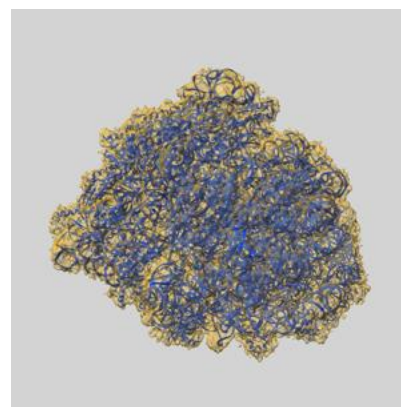
9.1 Map-model overlay [i](#)



X



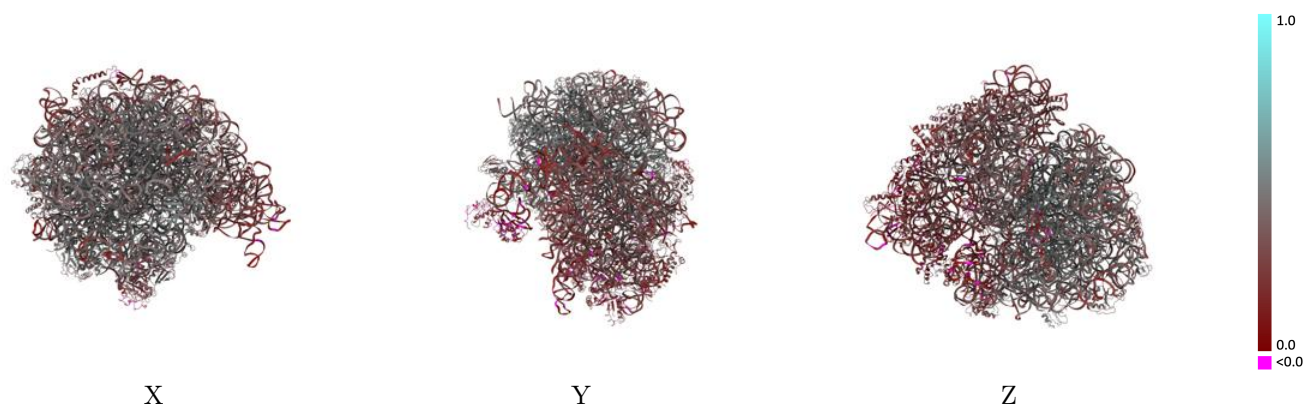
Y



Z

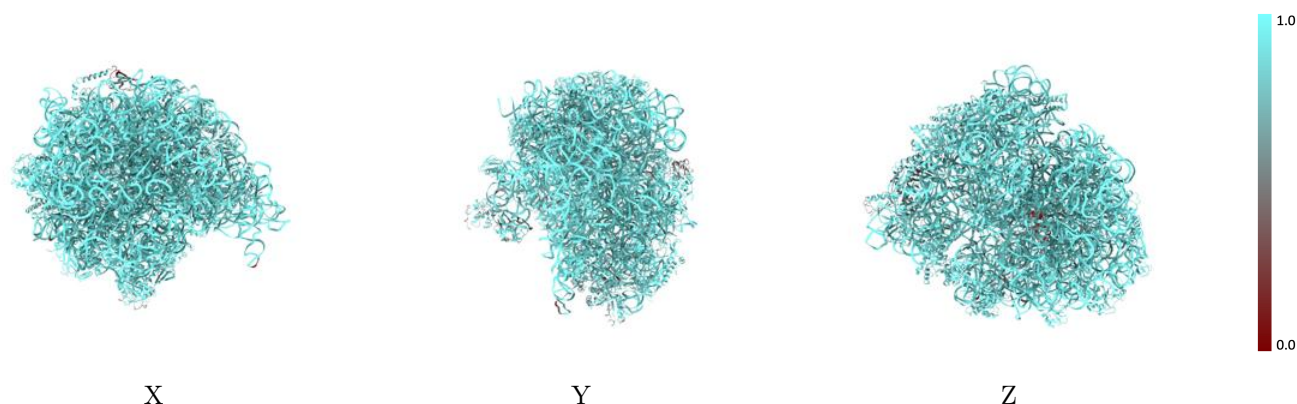
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



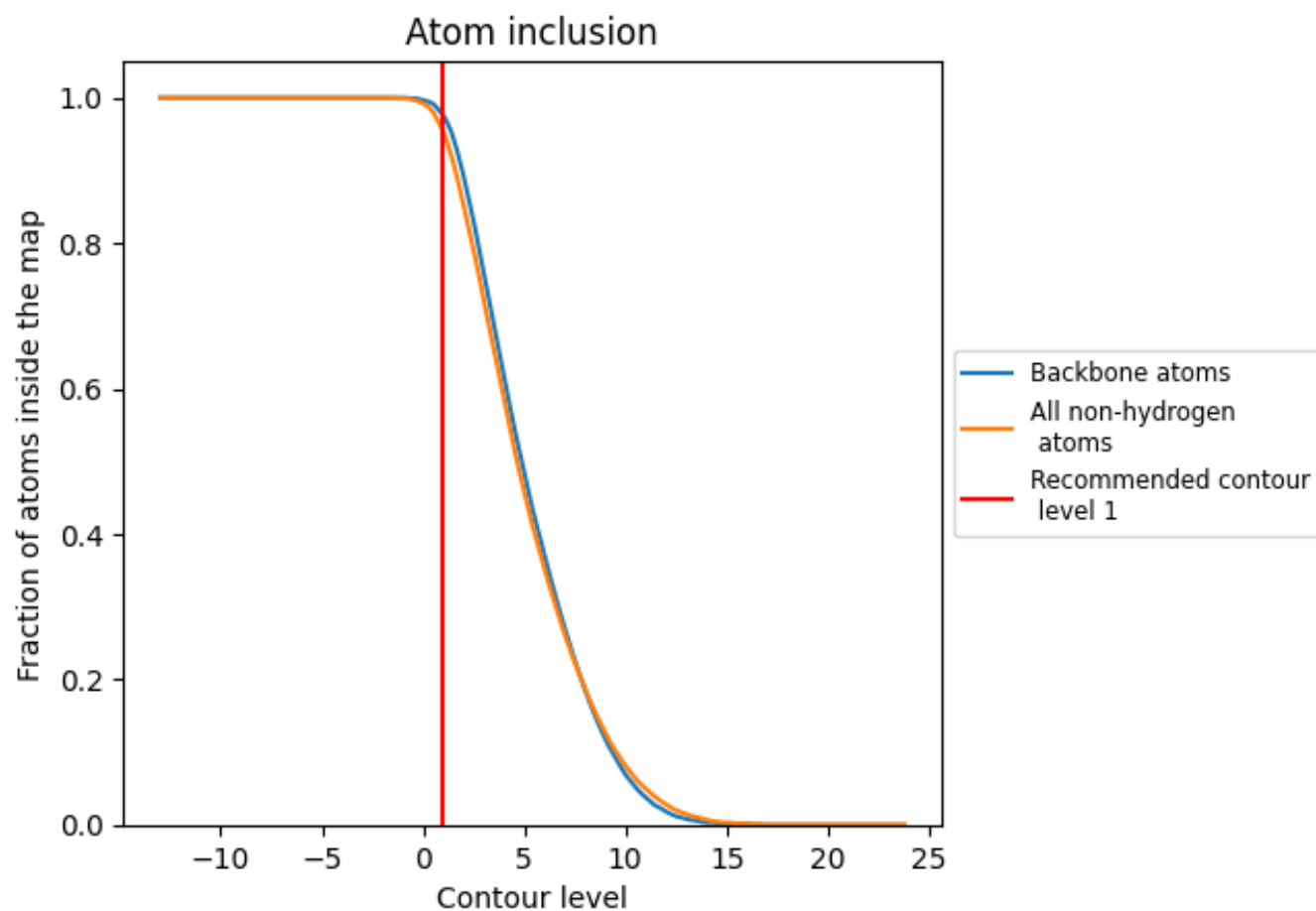
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9540	 0.3600
1	 0.9810	 0.4080
2	 0.9790	 0.3470
3	 0.9670	 0.2920
4	 0.8270	 0.1820
5	 0.9670	 0.2430
7	 0.9390	 0.2460
B	 0.9580	 0.4730
C	 0.8210	 0.4180
D	 0.9320	 0.4840
E	 0.9490	 0.5000
F	 0.8840	 0.4350
G	 0.8750	 0.2610
H	 0.8110	 0.2460
I	 0.8530	 0.2430
J	 0.9040	 0.3250
K	 0.9640	 0.3450
L	 0.8830	 0.2200
M	 0.9050	 0.3560
N	 0.8600	 0.2160
O	 0.7210	 0.2120
P	 0.9490	 0.3590
Q	 0.9330	 0.3770
R	 0.9010	 0.2200
S	 0.7800	 0.2150
T	 0.9360	 0.3700
U	 0.9010	 0.3160
V	 0.9340	 0.3480
W	 0.9260	 0.3430
X	 0.9390	 0.2330
Y	 0.8980	 0.2840
Z	 0.8690	 0.3090
a	 0.8770	 0.1790
b	 0.9650	 0.4860
c	 0.9480	 0.4780



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Chain	Atom inclusion	Q-score
d	 0.9460	 0.4330
e	 0.9370	 0.2620
f	 0.9700	 0.3940
g	 0.7090	 0.2330
h	 0.7330	 0.1710
i	 0.7610	 0.1180
j	 0.9660	 0.4770
k	 0.9440	 0.4670
l	 0.9460	 0.4580
m	 0.9430	 0.4600
n	 0.9640	 0.4720
o	 0.9410	 0.3880
p	 0.9600	 0.4550
q	 0.9470	 0.4670
r	 0.9620	 0.4560
s	 0.9380	 0.4660
t	 0.9500	 0.4400
u	 0.9520	 0.4060
v	 0.9570	 0.4430
w	 0.9500	 0.4740
x	 0.9650	 0.4740
y	 0.9620	 0.3730
z	 0.9520	 0.4510