



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:18 PM UTC

PDB ID : 7JSW / pdb_00007jsw
EMDB ID : EMD-22461
Title : ArfB Rescue of a 70S Ribosome stalled on truncated mRNA with a partial A-site codon (+2-III)
Authors : Carbone, C.E.; Korostelev, A.A.
Deposited on : 2020-08-16
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
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

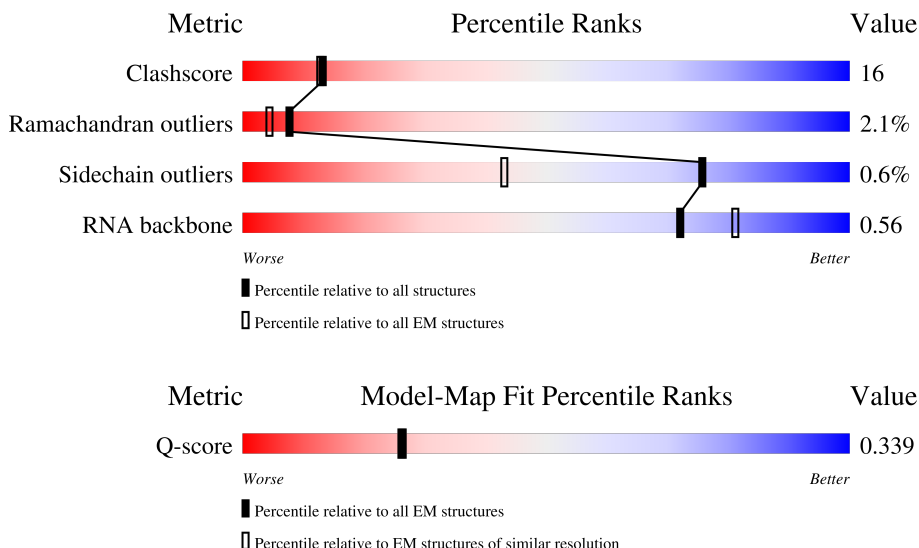
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

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



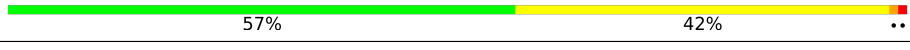
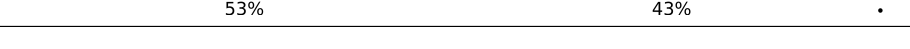
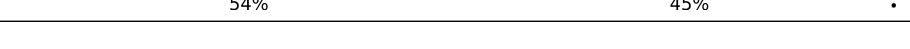
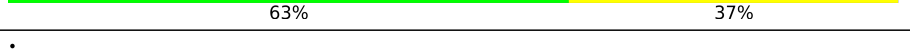
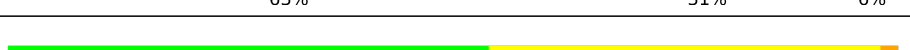
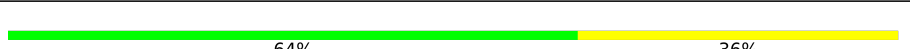
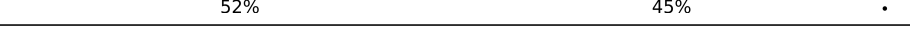
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	b	271	55% 44% .
2	c	209	56% 44%
3	d	201	64% 35% .

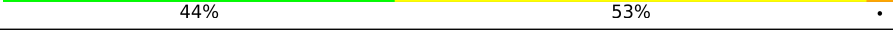
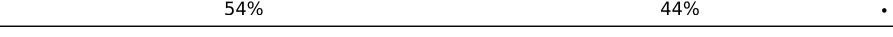
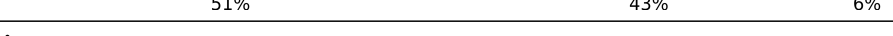
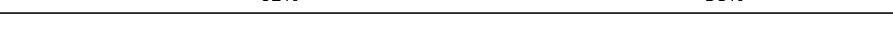
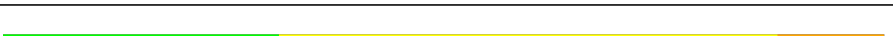
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	j	142	
8	k	122	
9	l	143	
10	m	136	
11	n	120	
12	o	116	
13	p	114	
14	q	117	
15	r	103	
16	s	110	
17	t	93	
18	u	102	
19	v	94	
20	w	75	
21	x	77	
22	y	63	
23	z	58	
24	B	56	
25	C	50	
26	D	46	
27	E	64	
28	F	38	

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Mol	Chain	Length	Quality of chain
29	G	225	
30	H	206	
31	I	205	
32	J	157	
33	K	100	
34	L	151	
35	M	129	
36	N	127	
37	O	98	
38	P	116	
39	Q	123	
40	R	114	
41	S	100	
42	T	88	
43	U	82	
44	V	80	
45	W	65	
46	X	79	
47	Y	85	
48	Z	65	
49	3	1539	
50	1	2903	
51	2	120	
52	5	77	
53	4	16	

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Mol	Chain	Length	Quality of chain
54	8	132	 13% 32% 47% 11% 9%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 144808 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 L13.

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

- Molecule 8 is a protein called 50S ribosomal protein L14.

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

- Molecule 9 is a protein called 50S ribosomal protein L15.

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

- Molecule 10 is a protein called 50S ribosomal protein L16.

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

- Molecule 11 is a protein called 50S ribosomal protein L17.

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

- Molecule 12 is a protein called 50S ribosomal protein L18.

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

- Molecule 13 is a protein called 50S ribosomal protein L19.

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

- Molecule 14 is a protein called 50S ribosomal protein L20.

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

- Molecule 15 is a protein called 50S ribosomal protein L21.

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

- Molecule 16 is a protein called 50S ribosomal protein L22.

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

- Molecule 17 is a protein called 50S ribosomal protein L23.

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

- Molecule 18 is a protein called 50S ribosomal protein L24.

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

- Molecule 19 is a protein called 50S ribosomal protein L25.

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

- Molecule 20 is a protein called 50S ribosomal protein L27.

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

- Molecule 21 is a protein called 50S ribosomal protein L28.

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

- Molecule 22 is a protein called 50S ribosomal protein L29.

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

- Molecule 23 is a protein called 50S ribosomal protein L30.

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

- Molecule 24 is a protein called 50S ribosomal protein L32.

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

- Molecule 25 is a protein called 50S ribosomal protein L33.

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

- Molecule 26 is a protein called 50S ribosomal protein L34.

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

- Molecule 27 is a protein called 50S ribosomal protein L35.

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

- Molecule 28 is a protein called 50S ribosomal protein L36.

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

- Molecule 29 is a protein called 30S ribosomal protein S2.

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S4.

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

- Molecule 32 is a protein called 30S ribosomal protein S5.

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

- Molecule 33 is a protein called 30S ribosomal protein S6.

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

- Molecule 34 is a protein called 30S ribosomal protein S7.

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

- Molecule 35 is a protein called 30S ribosomal protein S8.

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

- Molecule 36 is a protein called 30S ribosomal protein S9.

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

- Molecule 37 is a protein called 30S ribosomal protein S10.

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

- Molecule 38 is a protein called 30S ribosomal protein S11.

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

- Molecule 39 is a protein called 30S ribosomal protein S12.

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

- Molecule 40 is a protein called 30S ribosomal protein S13.

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

- Molecule 41 is a protein called 30S ribosomal protein S14.

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

- Molecule 42 is a protein called 30S ribosomal protein S15.

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

- Molecule 43 is a protein called 30S ribosomal protein S16.

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

- Molecule 44 is a protein called 30S ribosomal protein S17.

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

- Molecule 45 is a protein called 30S ribosomal protein S18.

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

- Molecule 46 is a protein called 30S ribosomal protein S19.

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

- Molecule 47 is a protein called 30S ribosomal protein S20.

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

- Molecule 48 is a protein called 30S ribosomal protein S21.

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

- Molecule 49 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	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 50 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	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 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	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 52 is a RNA chain called tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	4	16	Total	C	N	O	P	0	0
			353	158	74	105	16		

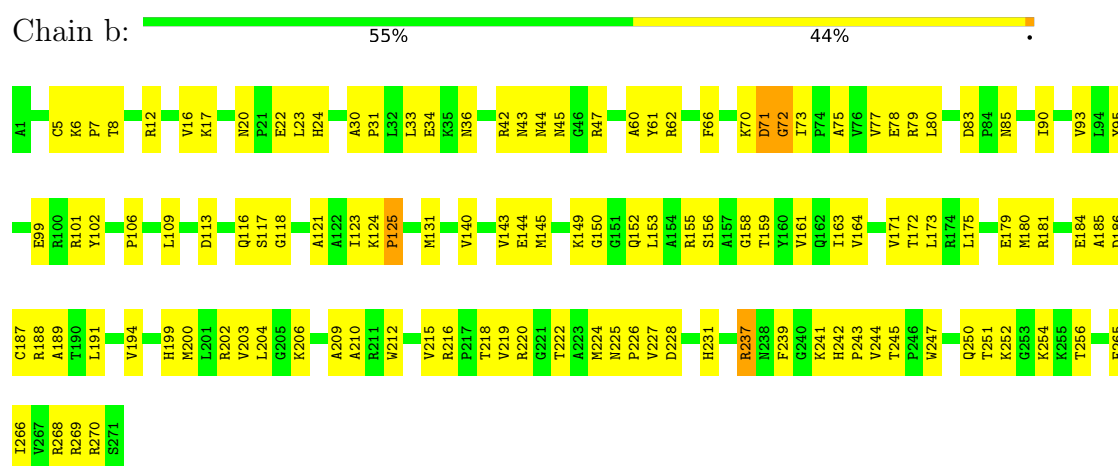
- Molecule 54 is a protein called Peptidyl-tRNA hydrolase ArfB.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	8	120	Total	C	N	O	S	0	0
			949	591	186	170	2		

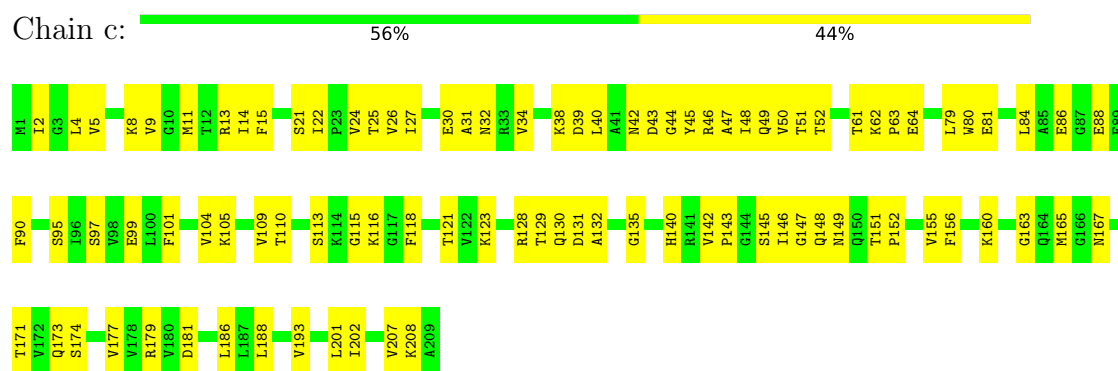
3 Residue-property plots

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

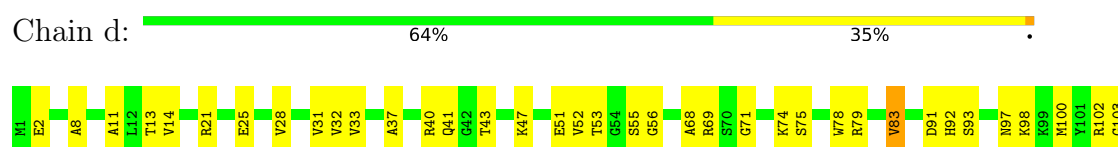
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3



• Molecule 3: 50S ribosomal protein L4

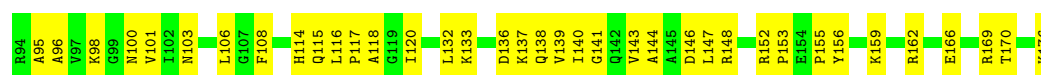
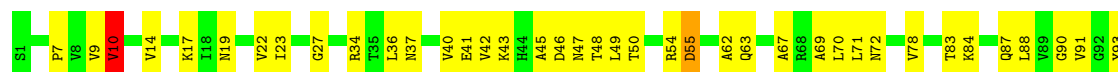




• Molecule 4: 50S ribosomal protein L5



• Molecule 5: 50S ribosomal protein L6



• Molecule 6: 50S ribosomal protein L9

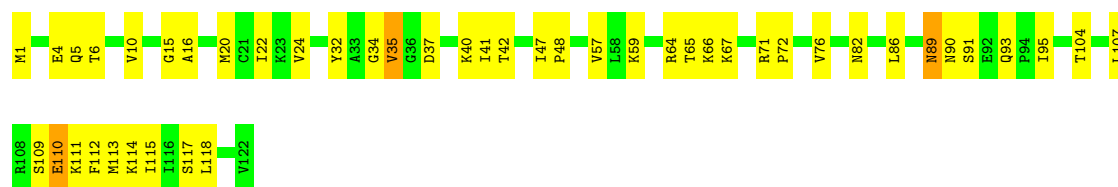


• Molecule 7: 50S ribosomal protein L13



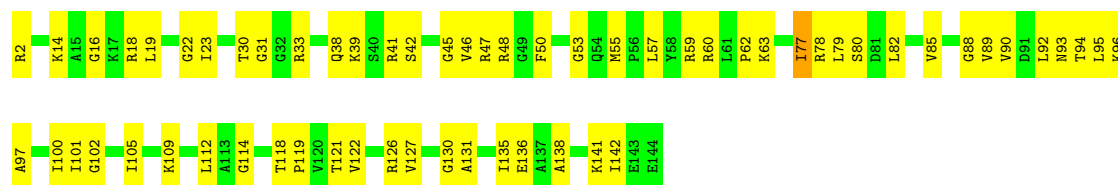
• Molecule 8: 50S ribosomal protein L14

Chain k:  62% 35%



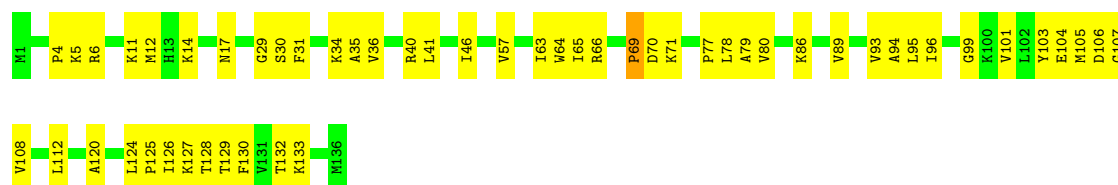
• Molecule 9: 50S ribosomal protein L15

Chain l:  57% 42%



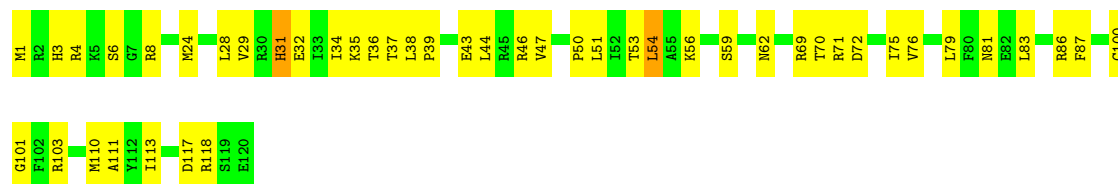
• Molecule 10: 50S ribosomal protein L16

Chain m:  61% 38%



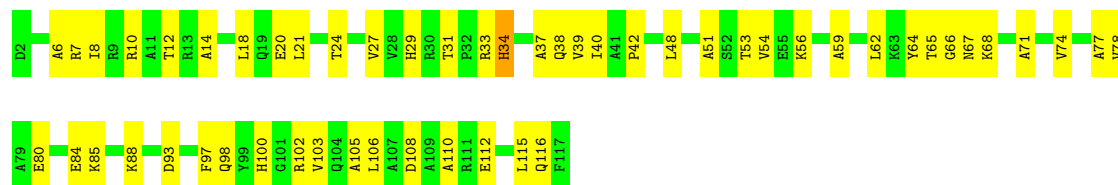
• Molecule 11: 50S ribosomal protein L17

Chain n:  62% 37%



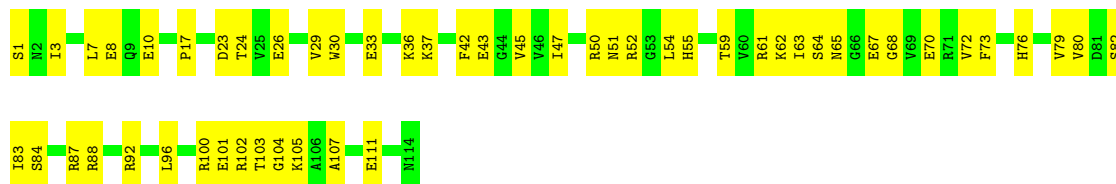
• Molecule 12: 50S ribosomal protein L18

Chain o:  54% 45%



• Molecule 13: 50S ribosomal protein L19

Chain p:  54% 46%



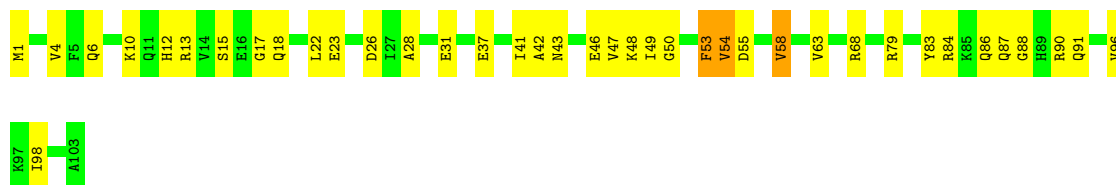
- Molecule 14: 50S ribosomal protein L20

Chain q:  71% 29%



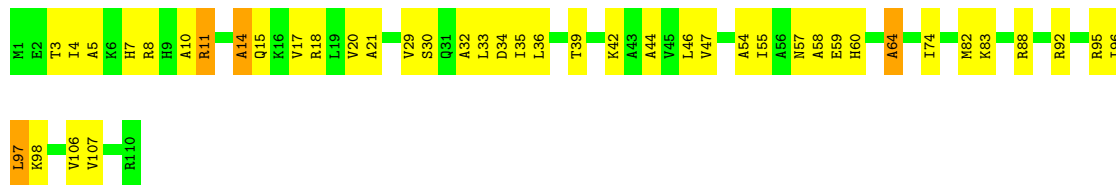
- Molecule 15: 50S ribosomal protein L21

Chain r:  62% 35% .



- Molecule 16: 50S ribosomal protein L22

Chain s:  61% 35% .



- Molecule 17: 50S ribosomal protein L23

Chain t:  63% 37%



- Molecule 18: 50S ribosomal protein L24

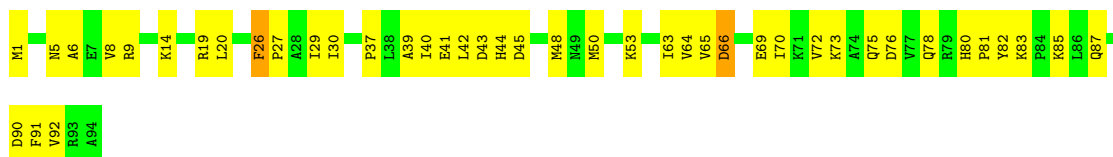
Chain u:  63% 31% 6%





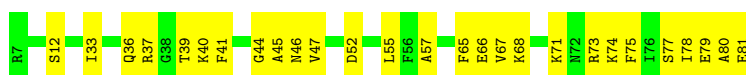
- Molecule 19: 50S ribosomal protein L25

Chain v: 54% 44% .



- Molecule 20: 50S ribosomal protein L27

Chain w: 64% 36% .



- Molecule 21: 50S ribosomal protein L28

Chain x: 58% 39% .



- Molecule 22: 50S ribosomal protein L29

Chain y: 65% 33% .



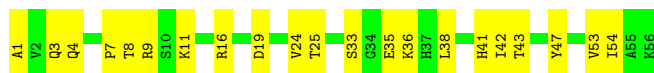
- Molecule 23: 50S ribosomal protein L30

Chain z: 52% 45% .



- Molecule 24: 50S ribosomal protein L32

Chain B: 62% 38% .



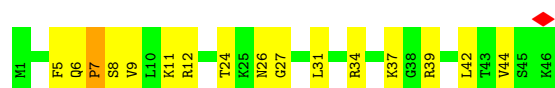
- Molecule 25: 50S ribosomal protein L33

Chain C:  60% 38% .



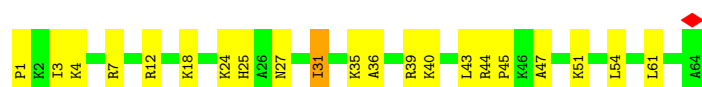
• Molecule 26: 50S ribosomal protein L34

Chain D:  65% 33% .



• Molecule 27: 50S ribosomal protein L35

Chain E:  67% 31% .



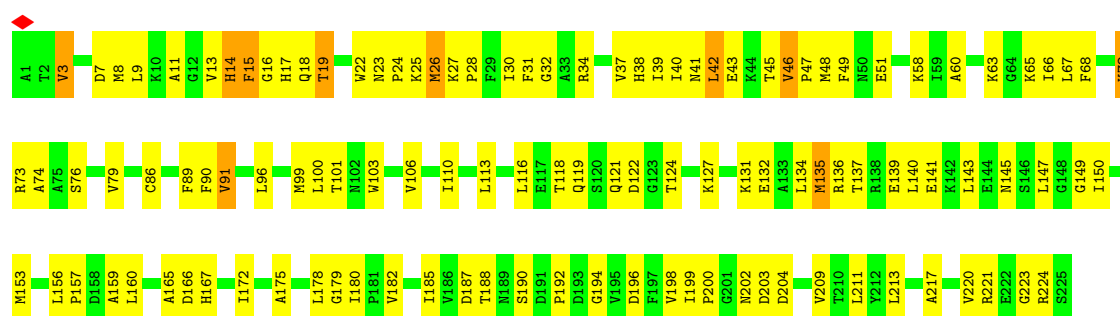
• Molecule 28: 50S ribosomal protein L36

Chain F:  55% 42% .



• Molecule 29: 30S ribosomal protein S2

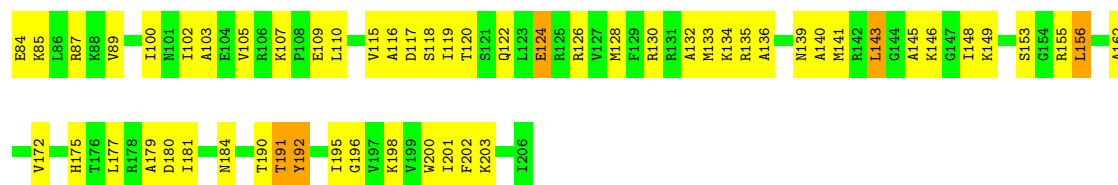
Chain G:  48% 47% .



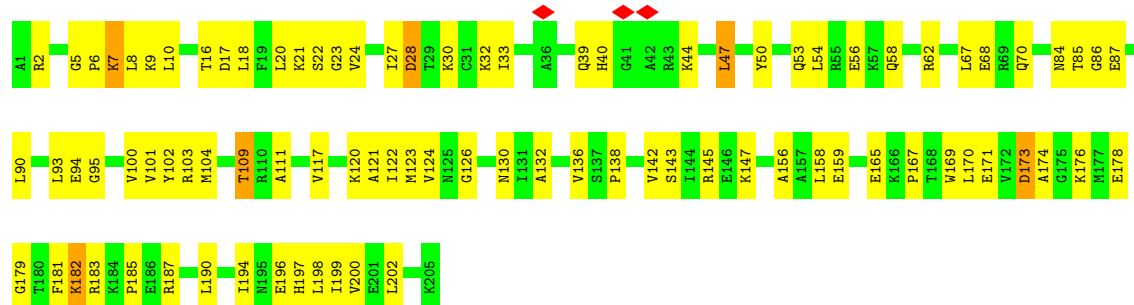
• Molecule 30: 30S ribosomal protein S3

Chain H:  54% 43% .

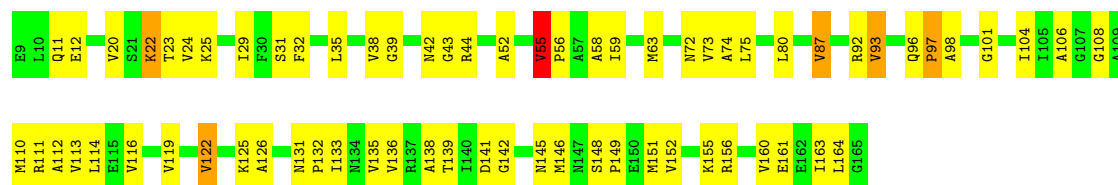




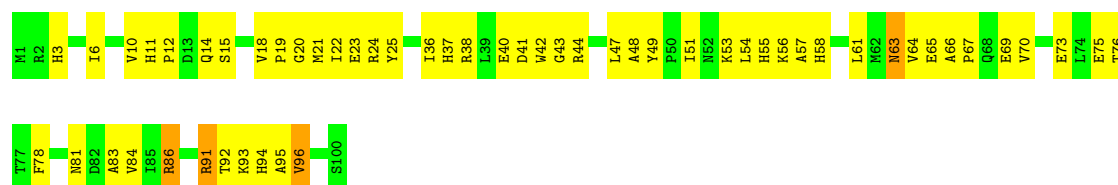
• Molecule 31: 30S ribosomal protein S4



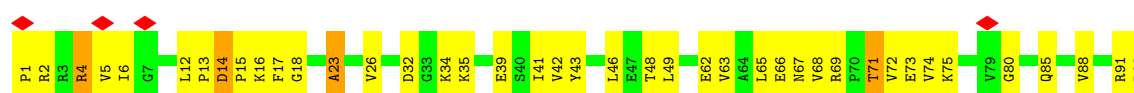
• Molecule 32: 30S ribosomal protein S5



• Molecule 33: 30S ribosomal protein S6



• Molecule 34: 30S ribosomal protein S7





- Molecule 35: 30S ribosomal protein S8

Chain M: 53% 47%



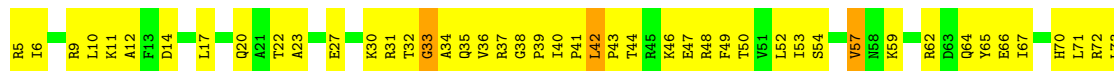
- Molecule 36: 30S ribosomal protein S9

Chain N: 54% 42% 5%



- Molecule 37: 30S ribosomal protein S10

Chain O: 44% 53%



- Molecule 38: 30S ribosomal protein S11

Chain P: 57% 41%

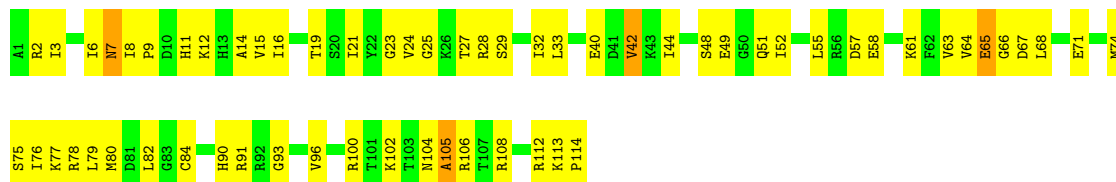


- Molecule 39: 30S ribosomal protein S12

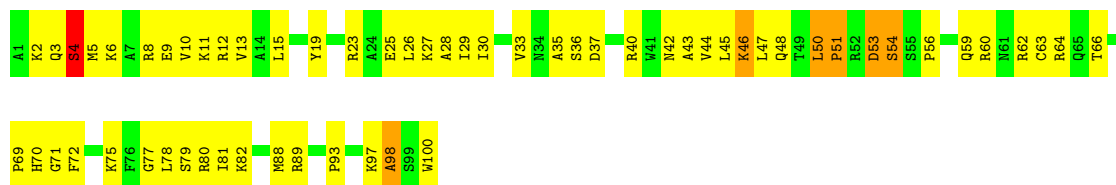
Chain Q: 54% 44%



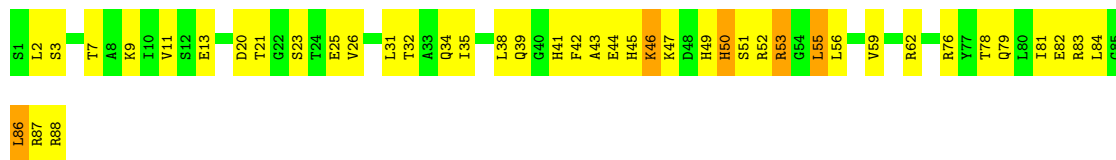
• Molecule 40: 30S ribosomal protein S13



• Molecule 41: 30S ribosomal protein S14



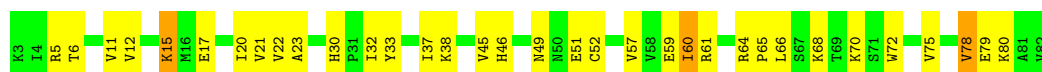
• Molecule 42: 30S ribosomal protein S15



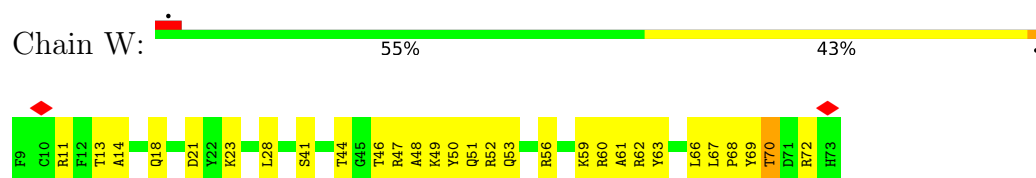
• Molecule 43: 30S ribosomal protein S16



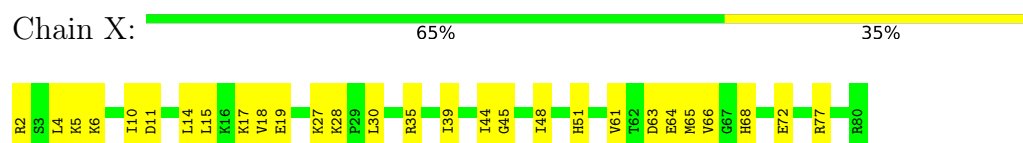
• Molecule 44: 30S ribosomal protein S17



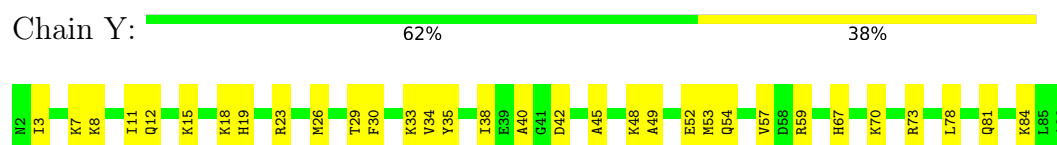
- Molecule 45: 30S ribosomal protein S18



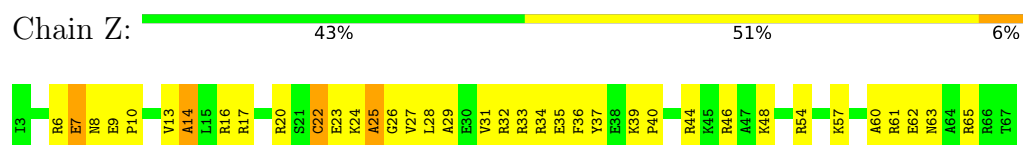
- Molecule 46: 30S ribosomal protein S19



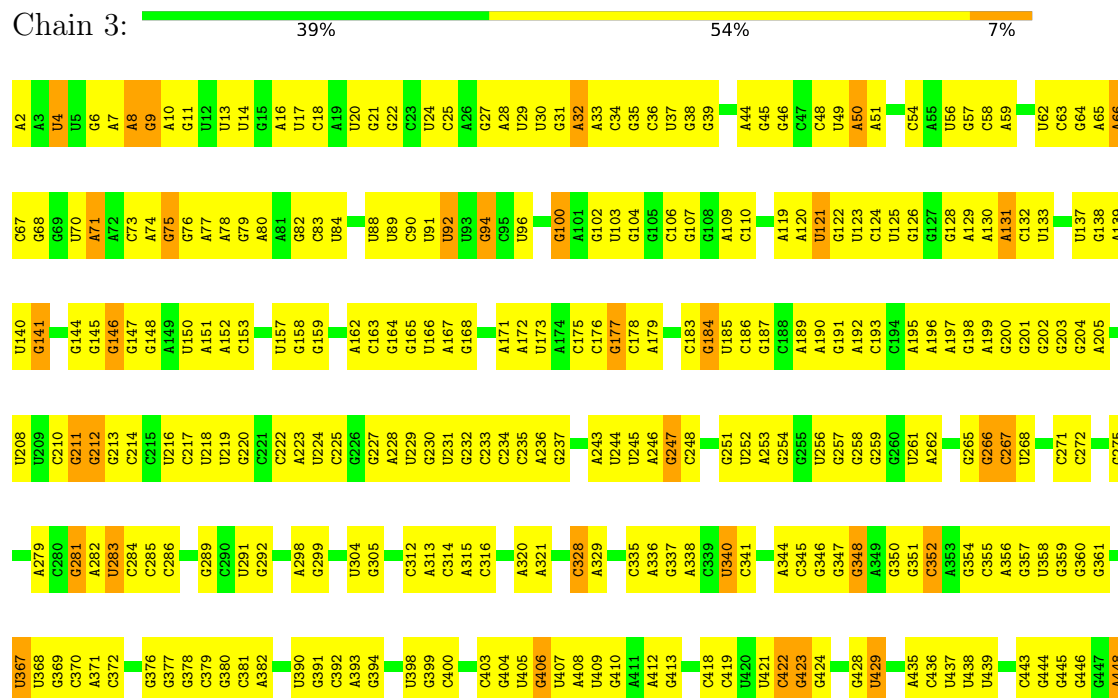
- Molecule 47: 30S ribosomal protein S20



- Molecule 48: 30S ribosomal protein S21



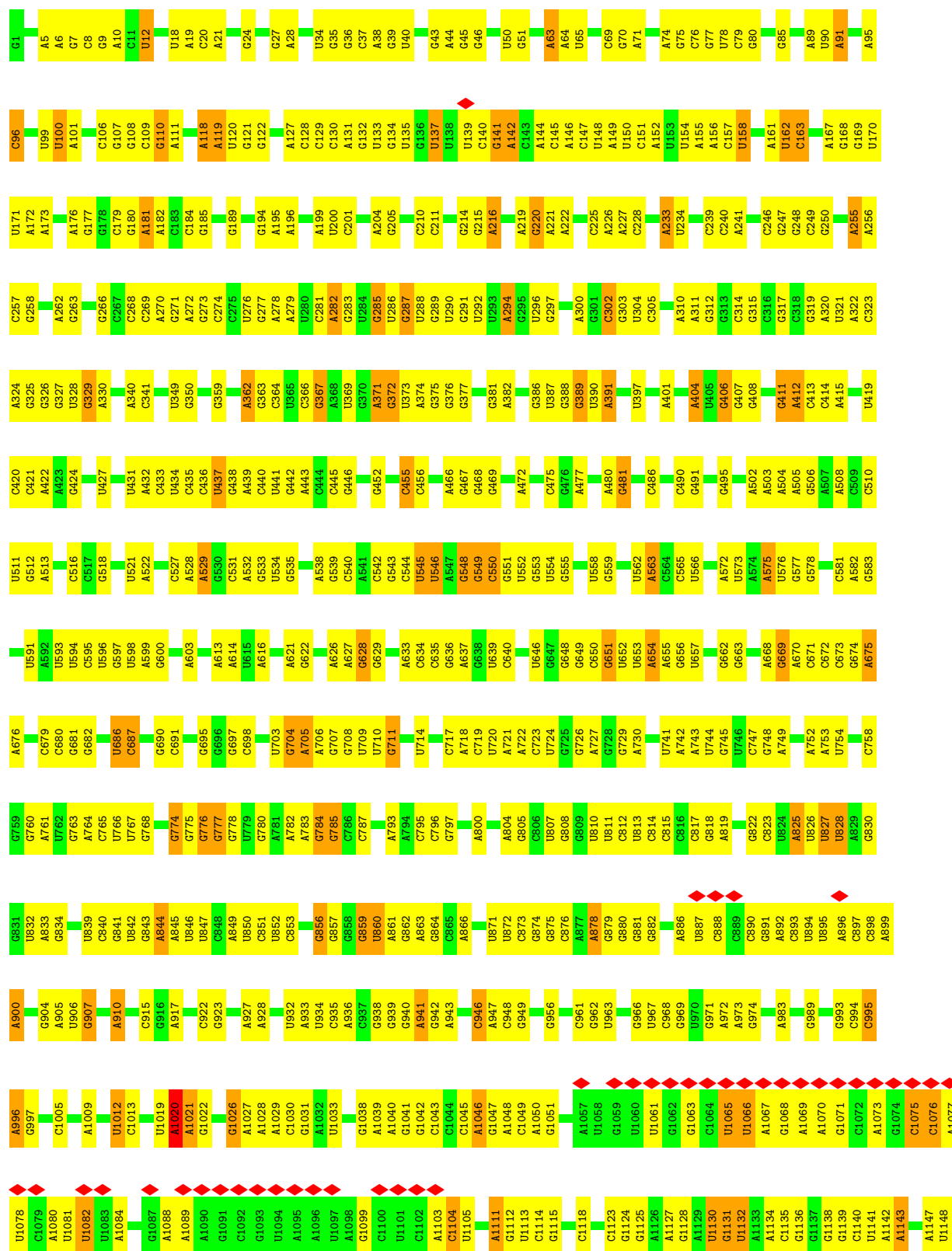
- Molecule 49: 16S ribosomal RNA



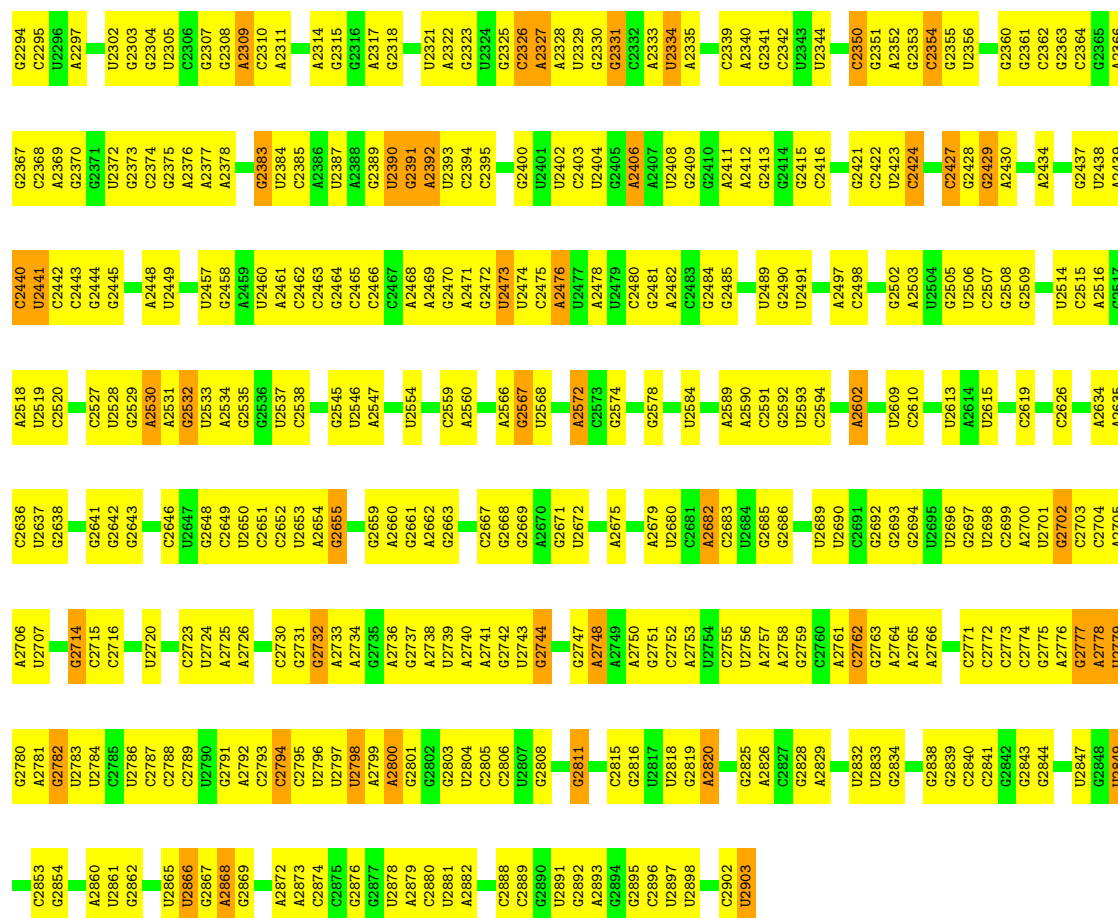
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A1507	U1440	A1360	C1282	C1214	G1142	A1067	U982	A914	G832	G745	U673	A597	U512	G450
U1512	A1441	G1361	U1286	G1215	G1143	A1067	U992	A914	G833	A746	A673	G597	C513	A451
A1513	G1442	A1362	U1287	C1216	A1144	C1071	A994	A914	G834	A747	G674	U598	C514	A452
G1514	C1443	A1363	C1218	A1217	A1145	G1072	G993	G917	U835	C750	A675	C599	G515	G453
G1515	U1444	A1363	C1218	A1219	A1146	U1073	C995	A918	G836	C750	A676	A600	G515	G454
G1516	U1445	U1372	A1289	G1220	C1147	U1074	A996	A919	C840	C754	U677	A601	C518	G455
A1517	U1446	G1373	G1290	G1220	U1148	U1075	U997	U920	C841	G754	U678	A602	G521	A459
G1518	A1447	A1374	G1221	G1221	C1149	U1075	C998	U921	U842	G755	C679	G603	C522	A460
A1519	C1448	A1375	C1296	G1222	A1150	U1078	C999	U921	U843	C758	C680	U605	A523	A461
G1520	C1449	U1376	U1297	C1223	U1159	A1081	C1001	C932	U844	A759	G682	G606	G524	G462
C1521	U1450	U1377	U1298	U1224	U1159	A1081	C1001	C933	G844	C759	G683	A607	C525	G462
U1522	U1451	A1378	U1299	A1225	C1162	G1084	G1002	C934	A845	C760	U686	A608	C526	U463
G1523	C1452	C1378	G1300	C1226	A1163	U1085	G1003	A936	G846	G761	U686	C613	C527	U464
C1524	G1453	U1380	C1302	A1227	A1163	U1085	A1004	C936	G847	U762	G687	C614	C528	U465
G1525	G1454	C1303	C1302	C1228	U1165	G1087	A1005	A937	U854	C764	G688	C615	G529	A466
C1526	G1455	C1382	G1304	A1229	U1165	G1087	G1006	A938	U855	G765	U689	G615	G530	U467
G1527	G1456	G1382	G1304	G1230	A1166	G1088	U1007	C940	C856	A766	U692	G616	U631	A468
U1528	A1457	C1383	G1305	G1231	A1167	G1089	U1008	G940	C857	A767	G693	G617	A532	C469
G1529	C1457	C1384	A1306	U1232	U1168	G1089	U1009	U943	U768	A768	A694	C621	A535	C470
U1530	G1458	G1385	U1307	C1233	A1169	G1094	U1010	U944	A860	C769	A695	A621	A535	U471
A1531	G1459	G1386	U1307	G1234	A1170	U1095	C1011	G944	G861	G769	A696	A622	C536	U472
C1532	C1460	C1387	U1309	U1235	A1171	C1096	A1012	G945	U861	G775	G700	C623	U539	U473
G1533	G1461	G1310	G1310	A1236	C1172	C1097	G1013	A946	U862	C776	U701	C624	A539	G474
A1534	G1461	C1311	C1237	U1311	U1173	C1098	G1014	C948	A864	A777	G702	C625	G540	C475
C1535	C1462	G1312	A1238	U1312	G1174	C1099	A1015	A949	A865	G778	A703	G626	G540	U476
U1540	C1467	U1313	U1318	G1241	A1175	C1100	A1016	U950	C868	C779	G704	G627	U543	C477
U1471	U1471	C1395	U1315	G1242	A1176	A1101	U1017	G951	U868	A780	A704	G628	G544	A478
U1472	U1472	A1396	U1315	C1245	G1181	A1105	A1019	U952	C869	C779	A704	G628	G544	A478
U1473	U1473	C1397	G1317	U1246	G1182	G1106	A1019	U952	U870	A777	A704	G628	G544	A478
U1474	U1474	A1398	A1318	U1247	U1183	G1107	G1033	G963	U871	G785	C708	A630	A546	U480
U1475	U1475	A1398	A1318	U1247	U1183	G1107	G1033	G963	U872	G786	C708	C631	A547	G481
U1476	U1476	G1401	G1323	U1248	G1184	C1109	G1034	G963	U873	C786	C708	C632	G548	A482
U1477	U1477	C1404	A1324	C1249	G1187	A1110	U1029	U957	U874	A794	G711	C633	C549	C483
U1478	U1478	A1405	A1250	C1250	G1187	A1111	U1029	U957	U875	C795	A712	C634	C549	G484
C1479	C1479	G1405	A1251	A1251	G1188	C1112	C1031	U960	A878	C795	G713	C635	U555	U485
A1480	A1480	U1330	U1330	A1252	U1189	C1113	U961	U960	C879	C796	G714	U636	C556	U486
U1481	U1481	G1331	G1253	A1252	U1189	C1113	U961	U960	C879	C796	G714	U636	C556	U486
G1482	G1482	A1408	G1331	G1253	G1190	C1114	C1033	C962	C880	C797	A715	C637	A560	A487
U1483	U1483	C1409	A1254	A1254	A1191	U1115	G1034	C962	C881	U801	A716	U638	U561	C488
U1484	U1484	A1332	G1255	G1255	C1192	U1115	G1034	C963	C882	A802	U717	U638	U561	C489
U1485	U1485	A1333	G1255	G1255	C1192	U1115	G1034	C963	C882	A802	U717	U638	U561	C489
G1486	G1486	C1411	G1334	A1256	G1193	A1036	U1036	G966	C883	C805	A718	C643	U562	C490
G1487	G1487	C1412	U1335	A1257	U1194	A1036	U1036	G966	C883	C805	A718	C643	U562	C490
U1488	U1488	C1413	C1336	G1258	C1195	U1121	C1037	U966	U884	C806	G722	U644	A563	G491
U1489	U1489	G1259	G1259	G1259	A1196	U1121	C1037	U966	U884	C806	G722	U644	A563	G491
C1490	C1490	U1414	A1340	G1260	A1197	U1122	G1047	A969	G837	C806	G723	C647	G566	C493
G1491	G1491	G1415	U1341	G1260	G1198	U1123	U1049	A969	G837	C806	G723	C647	G566	C493
A1492	A1492	U1341	U1341	G1260	G1198	U1123	U1049	A969	G837	C806	G723	C647	G566	C493
A1493	A1493	C1263	C1263	C1263	U1201	G1124	G1049	G971	A899	A815	A729	C651	A572	A495
G1494	G1494	U1284	U1284	U1284	A1201	G1124	G1049	G971	A899	A815	A729	C651	A572	A495
U1495	U1495	C1265	C1265	C1265	A1202	U1126	C1053	A974	C890	C817	G730	U652	A573	A496
C1496	C1496	A1346	G1266	G1266	U1202	U1126	C1053	A974	C890	C817	G730	U652	A573	A496
G1497	G1497	G1347	G1266	G1266	C1203	U1126	C1053	A974	C890	C817	G730	U652	A573	A496
U1498	U1498	U1348	G1266	G1266	A1204	A1130	A1056	G977	C894	G821	G733	G654	C576	A498
A1499	A1499	U1348	G1266	G1266	U1205	A1130	A1056	G977	C894	G821	G733	G654	C576	A498
U1499	U1499	U1348	G1266	G1266	U1205	A1130	A1056	G977	C894	G821	G733	G654	C576	A498
A1500	A1500	A1349	U1274	U1274	G1206	G1133	G1057	A978	G902	G824	C735	C658	C501	G500
C1501	C1501	A1350	A1275	A1275	G1206	G1133	G1057	A978	G902	G824	C735	C658	C501	G500
A1502	A1502	U1351	U1276	U1276	G1207	G1133	G1057	A978	G902	G824	C735	C658	C501	G500
G1503	G1503	A1351	G1276	G1276	G1207	G1133	G1057	A978	G902	G824	C735	C658	C501	G500
A1504	A1504	C1352	C1277	C1277	C1209	C1336	G1061	U981	A906	A825	C736	U661	C502	A502
G1504	G1504	G1353	G1278	G1278	C1209	C1336	G1061	U981	A906	A825	C736	U661	C502	A502
U1505	U1505	G1353	G1278	G1278	C1209	C1336	G1061	U981	A906	A825	C736	U661	C502	A502
U1505	U1505	U1354	G1279	G1279	C1210	G1139	U1062	C984	A909	U828	G741	A665	G592	A509
U1505	U1505	G1355	G1355	A1280	U1212	C1140	G1064	C985	U911	G830	A743	G667	U593	A510

• Molecule 50: 23S ribosomal RNA

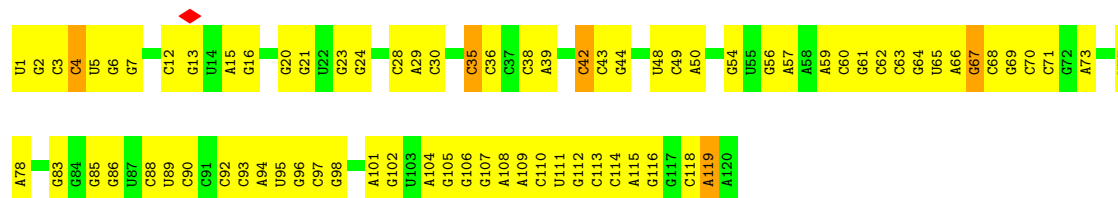
Chain 1:  45% 48% 8%



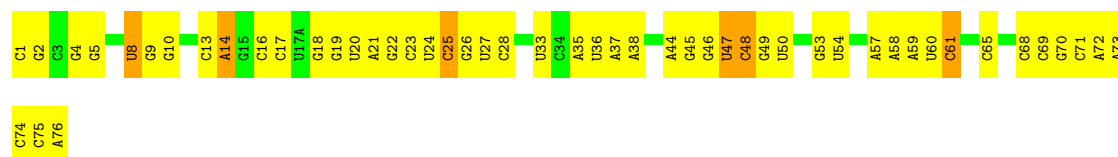
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C2214	A2147	C2078	U1991	C1908	C1830	U1758	C1685	U1584	G1511	U1440	G1356	U1258	C1150
C2215	G2216	U2079	G1992	C1909	G1831	A1759	C1686	A1586	C1512	U1442	C1357	G1259	A1151
G2217	U2149	U2080	U1993	G1910	C1832	G1760	G1687		C1513	U1443	G1358		C1152
	U2151	U2081	C1950		U1833				G1514	G1444		G1265	G1154
G2221	G2152	C2083	U1995	A1913	U1834	G1764	U1692	A1591	A1515	U1445	C1363	G1266	A1155
C2222	C2153	C2084	C1996	C1914	U1835	U1765	U1693	C1592	G1516	G1446	G1364	U1267	
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A2225	G2155	G2086	A1998		G1838		G1695	U1594	A1522	U1448	A1366	G1270	G1160
	G2156	U2087	C1999	C1920	G1839	U1769		A1596	U1523	G1449	G1367	A1272	C1161
G2228	G2157	A2088	C2001	U1923	G1842	C1771	A1700	A1597	G1524		G1368	U1273	G1162
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U2231	G2162	A2094	A2006		G1845	A1774	C1704	A1603	G1455		C1376	G1278	A1165
C2232	A2163	C2096	G2010	A1928	G1846	U1775	A1705	C1604	G1456		G1377	G1279	G1166
U2233	C2164	A2097	G2011	G1929	A1847	G1776	C1706	C1605	U1457		U1378	G1280	C1167
G2234	G2165		G2012	G1930	A1848		G1707	C1606	U1458		U1379	G1281	G1168
	U2166	A2101	A2013	U1931	C1849	A1780	G1708	C1607	G1459		A1383	G1282	A1169
G2238	U2167	G2102	A2017	C1934	G1850	U1781	U1709	C1608	U1460		A1384	G1283	C1170
G2239	G2168	C2103	U2017	G1935		U1782	G1710	C1609	C1536		A1385	A1284	G1171
U2240	A2169	C2104	G2018	A1936	G1856	A1783	A1711	A1609	G1537		C1386	A1285	C1172
A2241	A2170	U2105	A2019	A1937	G1857	A1784	U1712	G1611	G1538		A1387	A1286	U1173
G2242	A2171	U2106		A1938	A1858	A1785	U1713	G1611	U1539			A1287	U1174
U2243	U2172	G2107				A1786	U1714	A1616	G1540			G1288	A1175
U2244	A2173		U2022		G1862		G1715		C1541		U1391	C1289	U1176
G2248	C2174	A2109	C2023	C1942		A1791	U1716	G1627	U1542			G1290	G1177
U2249	G2175	G2110	G2024	U1943	A1866	G1792	A1545	G1628	A1474		U1394	G1291	C1178
U2249	A2176	U2111	C2025	U1944	G1867	C1793	G1646	G1629	G1475		A1395	G1292	U1179
G2249	C2177	U2112	A2030	G1947	G1868	A1795	A1547				U1396	G1293	U1180
U2257	G2178	U2113	A2031	G1948	C1870	U1796	A1548		G1478		U1397	U1294	U1181
C2258	G2179	A2114	G2034	G1949	A1871	G1797	G1724		G1479				G1182
	U2180		U2035	U1955	G1872	G1798	U1725	G1645	U1481		U1405	G1300	U1183
U2262	U2181	U2118	G2036		A1873	G1799	A1551	G1646	G1482		U1406	A1301	U1184
A2266	U2182	A2119	U2039	G1958	C1874	A1801	U1554	U1648	G1483		U1409	G1302	G1185
A2267	A2183	G2120	G2040	G1959	G1875	A1802			G1484		U1410	G1303	G1186
A2268	U2184	U2121	U2041	G1960	A1876	A1803			G1485		U1411	A1304	G1187
G2269	U2185	G2122	A2042	U1961	A1877	A1804			U1486		U1412	C1305	
A2270	G2186	G2123	C2043	U1962		U1812			U1487		A1413	C1306	
G2271	G2190	G2124	G2044	G1963	U1880	A1815	G1730	A1654			G1416	G1309	G1193
U2272	A2191	A2126	C2047	G1964	G1881	A1816	U1732	G1658	A1490		G1417	G1310	U1199
G2273	C2193	G2127	G2048	C1965	U1882	G1817	G1733	G1659	G1491		G1418	G1311	
	U2194	G2128		C1967	U1883	U1818	U1735	A1664	G1492		A1419	C1314	G1212
G2276	U2195		C2055	G1968	G1884		G1737	G1665	C1493		A1420	G1315	U1224
G2277	C2196	U2131	G2056	A1969	A1885	U1812	G1738	G1666	A1494		G1421	U1316	G1225
A2281	U2197	U2132	A2060	U1970	A1889	A1815	A1739	U1671	A1495		G1422	G1317	C1229
C2282	A2198	G2133	G2061	G1972	A1890	G1816	G1740	A1672	A1496		G1423	U1326	A1230
C2283	A2199		A2062	G1973	G1891	U1817	C1741	G1673	U1497		G1424	A1327	
G2284	C2200	G2136		G1979	C1894	U1818	A1745	G1674	G1500			G1429	G1248
G2285	G2204	U2137	C2066	U1979	C1895	A1819	A1746	A1675	G1501		G1430	A1328	U1249
G2286	C2205	U2139	G2069	G1980	G1896	U1820	U1747	A1676	A1502		A1433	U1329	G1250
A2287	G2206	G2140	A2070	U1981	C1822	A1821	C1748	A1677	A1503		A1434	U1344	G1251
A2288	C2207	U2141	A2071	U1982	A1899	G1823		A1678	A1504		A1435	U1345	G1252
C2208	C2208	A2142	A2072	U1987	A1900	G1826	G1752	A1679	A1505		G1436	U1346	A1253
U2291	U2292	C2143	C2072	G1988	A1901	U1827	G1753	U1680	U1506		G1437	C1348	U1254
G2293	U2210	C2144	U2076	G1989	G1906	A1828	A1755	G1681	C1507		U1438	G1349	G1256



• Molecule 51: 5S ribosomal RNA

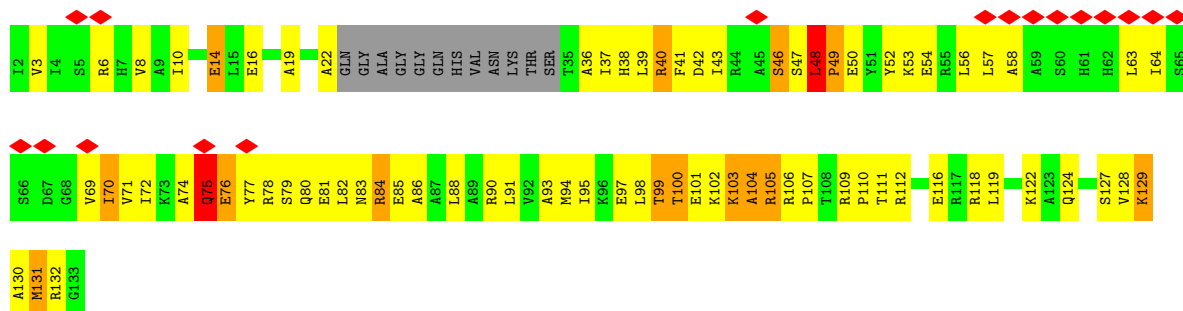


• Molecule 52: tRNAfMet



• Molecule 53: mRNA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7464	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	12.365	Depositor
Minimum map value	-5.856	Depositor
Average map value	0.096	Depositor
Map value standard deviation	0.614	Depositor
Recommended contour level	0.592	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 ⓘ

5.1 Standard geometry ⓘ

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	0.85	2/2852 (0.1%)
2	c	0.30	0/1586	0.80	0/2134
3	d	0.30	0/1571	0.81	5/2113 (0.2%)
4	e	0.33	0/1435	0.91	4/1926 (0.2%)
5	f	0.33	0/1343	0.85	3/1816 (0.2%)
6	g	0.32	0/1122	0.92	3/1515 (0.2%)
7	j	0.29	0/1152	0.83	3/1551 (0.2%)
8	k	0.30	0/948	0.95	3/1268 (0.2%)
9	l	0.30	0/1054	0.94	4/1403 (0.3%)
10	m	0.30	0/1093	0.83	1/1460 (0.1%)
11	n	0.29	0/974	0.82	1/1301 (0.1%)
12	o	0.29	0/902	0.89	3/1209 (0.2%)
13	p	0.30	0/929	0.82	0/1242
14	q	0.29	0/960	0.88	3/1278 (0.2%)
15	r	0.30	0/829	0.84	1/1107 (0.1%)
16	s	0.28	0/864	0.90	1/1156 (0.1%)
17	t	0.28	0/745	0.80	1/994 (0.1%)
18	u	0.29	0/788	0.87	4/1051 (0.4%)
19	v	0.32	0/766	0.85	2/1025 (0.2%)
20	w	0.27	0/582	0.86	1/769 (0.1%)
21	x	0.28	0/635	0.89	2/848 (0.2%)
22	y	0.28	0/510	0.90	0/677
23	z	0.29	0/453	0.88	3/605 (0.5%)
24	B	0.29	0/450	0.84	1/599 (0.2%)
25	C	0.30	0/417	0.81	1/554 (0.2%)
26	D	0.31	0/380	0.97	3/498 (0.6%)
27	E	0.33	0/513	0.80	0/676
28	F	0.31	0/303	0.81	0/397
29	G	0.33	0/1788	0.94	10/2408 (0.4%)
30	H	0.31	0/1652	0.88	4/2225 (0.2%)
31	I	0.31	0/1665	0.91	4/2227 (0.2%)
32	J	0.34	0/1170	0.95	5/1573 (0.3%)
33	K	0.35	0/836	0.93	1/1128 (0.1%)
34	L	0.31	0/1196	0.93	6/1602 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	M	0.30	0/989	0.84	0/1326
36	N	0.32	0/1034	0.94	5/1375 (0.4%)
37	O	0.33	0/797	0.87	0/1077
38	P	0.34	0/886	0.95	4/1195 (0.3%)
39	Q	0.31	0/969	0.92	3/1300 (0.2%)
40	R	0.34	0/893	1.01	3/1193 (0.3%)
41	S	0.31	0/817	1.06	5/1088 (0.5%)
42	T	0.29	0/722	0.99	4/964 (0.4%)
43	U	0.33	0/659	0.88	1/884 (0.1%)
44	V	0.30	0/658	0.89	1/881 (0.1%)
45	W	0.35	0/545	0.92	1/731 (0.1%)
46	X	0.37	0/653	0.84	0/877
47	Y	0.29	0/671	0.98	3/888 (0.3%)
48	Z	0.36	0/551	1.03	4/728 (0.5%)
49	3	0.39	0/36963	0.48	1/57662 (0.0%)
50	1	0.38	0/69796	0.49	1/108888 (0.0%)
51	2	0.40	0/2872	0.48	0/4479
52	5	0.41	0/1832	0.48	0/2855
53	4	0.44	0/398	0.51	0/620
54	8	0.37	0/959	1.11	12/1285 (0.9%)
All	All	0.37	0/157397	0.62	133/235483 (0.1%)

There are no bond length outliers.

The worst 5 of 133 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	8	129	LYS	N-CA-C	-10.14	100.86	113.02
54	8	99	THR	N-CA-C	-8.15	102.34	111.14
24	B	53	VAL	N-CA-C	7.75	118.55	110.72
32	J	22	LYS	N-CA-C	-7.67	105.88	114.62
42	T	43	ALA	N-CA-C	-7.59	103.28	112.54

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	104	0
2	c	1565	0	1616	74	0
3	d	1552	0	1619	55	0
4	e	1411	0	1447	63	0
5	f	1323	0	1374	59	0
6	g	1111	0	1148	53	0
7	j	1129	0	1162	49	0
8	k	939	0	1012	34	0
9	l	1045	0	1117	62	0
10	m	1074	0	1157	43	0
11	n	961	0	1000	47	0
12	o	892	0	923	36	0
13	p	917	0	965	48	0
14	q	947	0	1022	28	0
15	r	816	0	839	37	0
16	s	857	0	922	37	0
17	t	739	0	807	27	0
18	u	780	0	834	27	0
19	v	753	0	780	37	0
20	w	575	0	592	18	0
21	x	625	0	655	29	0
22	y	509	0	543	16	0
23	z	449	0	491	28	0
24	B	444	0	461	20	0
25	C	410	0	440	17	0
26	D	377	0	418	17	0
27	E	504	0	574	19	0
28	F	302	0	343	15	0
29	G	1757	0	1787	93	0
30	H	1625	0	1699	74	0
31	I	1643	0	1710	82	0
32	J	1157	0	1199	54	0
33	K	818	0	808	60	0
34	L	1182	0	1240	58	0
35	M	979	0	1034	52	0
36	N	1022	0	1070	62	0
37	O	787	0	828	48	0
38	P	870	0	878	48	0
39	Q	955	0	1019	58	0
40	R	884	0	944	57	0
41	S	805	0	847	58	0
42	T	714	0	737	35	0
43	U	649	0	666	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	V	649	0	691	32	0
45	W	536	0	552	19	0
46	X	638	0	665	31	0
47	Y	665	0	714	25	0
48	Z	545	0	579	39	0
49	3	33012	0	16619	771	0
50	1	62317	0	31346	1228	0
51	2	2568	0	1303	75	0
52	5	1640	0	837	38	0
53	4	353	0	175	8	0
54	8	949	0	1009	83	0
All	All	144808	0	97374	3906	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 16.

The worst 5 of 3906 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)
54:8:106:ARG:H	54:8:107:PRO:HA	1.07	1.18
50:1:2170:A:H2'	50:1:2171:A:H4'	1.40	1.00
38:P:28:ASN:HD21	38:P:56:LYS:HE2	1.26	1.00
5:f:96:ALA:HB3	5:f:103:ASN:HD21	1.27	0.99
39:Q:113:ARG:HB2	39:Q:118:VAL:HB	1.43	0.99

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%)	227 (84%)	38 (14%)	4 (2%)	8 36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	c	207/209 (99%)	183 (88%)	22 (11%)	2 (1%)	12	43
3	d	199/201 (99%)	166 (83%)	30 (15%)	3 (2%)	8	36
4	e	175/177 (99%)	139 (79%)	31 (18%)	5 (3%)	3	25
5	f	174/176 (99%)	151 (87%)	21 (12%)	2 (1%)	11	41
6	g	147/149 (99%)	118 (80%)	21 (14%)	8 (5%)	1	16
7	j	140/142 (99%)	130 (93%)	9 (6%)	1 (1%)	18	51
8	k	120/122 (98%)	102 (85%)	15 (12%)	3 (2%)	4	28
9	l	141/143 (99%)	114 (81%)	26 (18%)	1 (1%)	18	51
10	m	134/136 (98%)	117 (87%)	16 (12%)	1 (1%)	18	51
11	n	118/120 (98%)	103 (87%)	15 (13%)	0	100	100
12	o	114/116 (98%)	105 (92%)	8 (7%)	1 (1%)	14	45
13	p	112/114 (98%)	91 (81%)	21 (19%)	0	100	100
14	q	115/117 (98%)	106 (92%)	8 (7%)	1 (1%)	14	45
15	r	101/103 (98%)	72 (71%)	26 (26%)	3 (3%)	3	25
16	s	108/110 (98%)	97 (90%)	9 (8%)	2 (2%)	6	32
17	t	91/93 (98%)	75 (82%)	15 (16%)	1 (1%)	11	41
18	u	100/102 (98%)	78 (78%)	19 (19%)	3 (3%)	3	25
19	v	92/94 (98%)	80 (87%)	10 (11%)	2 (2%)	5	30
20	w	73/75 (97%)	63 (86%)	9 (12%)	1 (1%)	9	37
21	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
22	y	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	7	35
23	z	56/58 (97%)	47 (84%)	9 (16%)	0	100	100
24	B	54/56 (96%)	46 (85%)	8 (15%)	0	100	100
25	C	48/50 (96%)	37 (77%)	11 (23%)	0	100	100
26	D	44/46 (96%)	37 (84%)	7 (16%)	0	100	100
27	E	62/64 (97%)	53 (86%)	8 (13%)	1 (2%)	7	35
28	F	36/38 (95%)	29 (81%)	6 (17%)	1 (3%)	4	26
29	G	223/225 (99%)	186 (83%)	30 (14%)	7 (3%)	3	25
30	H	204/206 (99%)	175 (86%)	25 (12%)	4 (2%)	6	32
31	I	203/205 (99%)	169 (83%)	29 (14%)	5 (2%)	4	28
32	J	155/157 (99%)	124 (80%)	27 (17%)	4 (3%)	4	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	K	98/100 (98%)	68 (69%)	26 (26%)	4 (4%)	2	20
34	L	149/151 (99%)	130 (87%)	17 (11%)	2 (1%)	9	38
35	M	127/129 (98%)	112 (88%)	14 (11%)	1 (1%)	16	48
36	N	125/127 (98%)	94 (75%)	25 (20%)	6 (5%)	2	17
37	O	96/98 (98%)	77 (80%)	13 (14%)	6 (6%)	1	14
38	P	114/116 (98%)	94 (82%)	18 (16%)	2 (2%)	6	33
39	Q	121/123 (98%)	90 (74%)	28 (23%)	3 (2%)	4	28
40	R	112/114 (98%)	97 (87%)	13 (12%)	2 (2%)	6	33
41	S	98/100 (98%)	77 (79%)	15 (15%)	6 (6%)	1	14
42	T	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	10	40
43	U	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	4	28
44	V	78/80 (98%)	68 (87%)	9 (12%)	1 (1%)	9	38
45	W	63/65 (97%)	56 (89%)	6 (10%)	1 (2%)	7	35
46	X	77/79 (98%)	66 (86%)	11 (14%)	0	100	100
47	Y	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
48	Z	63/65 (97%)	47 (75%)	12 (19%)	4 (6%)	1	14
54	8	116/132 (88%)	84 (72%)	23 (20%)	9 (8%)	1	11
All	All	5637/5749 (98%)	4732 (84%)	788 (14%)	117 (2%)	8	31

5 of 117 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
7	j	81	ILE
8	k	89	ASN
8	k	110	GLU
12	o	34	HIS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	215 (100%)	1 (0%)	81	81
2	c	164/164 (100%)	164 (100%)	0	100	100
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	77
6	g	114/114 (100%)	112 (98%)	2 (2%)	51	67
7	j	116/116 (100%)	116 (100%)	0	100	100
8	k	103/103 (100%)	101 (98%)	2 (2%)	50	66
9	l	102/102 (100%)	102 (100%)	0	100	100
10	m	109/109 (100%)	109 (100%)	0	100	100
11	n	100/100 (100%)	98 (98%)	2 (2%)	48	65
12	o	86/86 (100%)	86 (100%)	0	100	100
13	p	99/99 (100%)	99 (100%)	0	100	100
14	q	89/89 (100%)	89 (100%)	0	100	100
15	r	84/84 (100%)	82 (98%)	2 (2%)	43	62
16	s	93/93 (100%)	92 (99%)	1 (1%)	65	73
17	t	80/80 (100%)	80 (100%)	0	100	100
18	u	83/83 (100%)	83 (100%)	0	100	100
19	v	78/78 (100%)	78 (100%)	0	100	100
20	w	57/57 (100%)	57 (100%)	0	100	100
21	x	67/67 (100%)	67 (100%)	0	100	100
22	y	55/55 (100%)	55 (100%)	0	100	100
23	z	48/48 (100%)	48 (100%)	0	100	100
24	B	47/47 (100%)	47 (100%)	0	100	100
25	C	45/45 (100%)	45 (100%)	0	100	100
26	D	38/38 (100%)	38 (100%)	0	100	100
27	E	51/51 (100%)	51 (100%)	0	100	100
28	F	34/34 (100%)	34 (100%)	0	100	100
29	G	186/186 (100%)	186 (100%)	0	100	100
30	H	170/170 (100%)	167 (98%)	3 (2%)	51	67
31	I	172/172 (100%)	170 (99%)	2 (1%)	63	72
32	J	119/119 (100%)	117 (98%)	2 (2%)	53	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	K	87/87 (100%)	87 (100%)	0	100	100
34	L	124/124 (100%)	124 (100%)	0	100	100
35	M	104/104 (100%)	103 (99%)	1 (1%)	68	74
36	N	105/105 (100%)	105 (100%)	0	100	100
37	O	86/86 (100%)	86 (100%)	0	100	100
38	P	89/89 (100%)	89 (100%)	0	100	100
39	Q	103/103 (100%)	103 (100%)	0	100	100
40	R	92/92 (100%)	92 (100%)	0	100	100
41	S	83/83 (100%)	82 (99%)	1 (1%)	63	72
42	T	76/76 (100%)	74 (97%)	2 (3%)	40	60
43	U	65/65 (100%)	64 (98%)	1 (2%)	57	69
44	V	74/74 (100%)	73 (99%)	1 (1%)	59	70
45	W	56/56 (100%)	56 (100%)	0	100	100
46	X	70/70 (100%)	70 (100%)	0	100	100
47	Y	65/65 (100%)	65 (100%)	0	100	100
48	Z	55/55 (100%)	55 (100%)	0	100	100
54	8	100/108 (93%)	96 (96%)	4 (4%)	28	52
All	All	4689/4697 (100%)	4661 (99%)	28 (1%)	76	79

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	I	109	THR
54	8	119	LEU
32	J	97	PRO
54	8	16	GLU
32	J	55	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 135 such sidechains are listed below:

Mol	Chain	Res	Type
40	R	104	ASN
42	T	79	GLN
47	Y	51	ASN
13	p	11	GLN

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Mol	Chain	Res	Type
13	p	6	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
49	3	1538/1539 (99%)	222 (14%)	0
50	1	2902/2903 (99%)	454 (15%)	10 (0%)
51	2	119/120 (99%)	12 (10%)	0
52	5	76/77 (98%)	14 (18%)	0
53	4	15/16 (93%)	3 (20%)	0
All	All	4650/4655 (99%)	705 (15%)	10 (0%)

5 of 705 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
49	3	4	U
49	3	6	G
49	3	8	A
49	3	9	G
49	3	22	G

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	1	2326	C
50	1	2391	G
50	1	2756	U
50	1	1020	A
50	1	1130	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

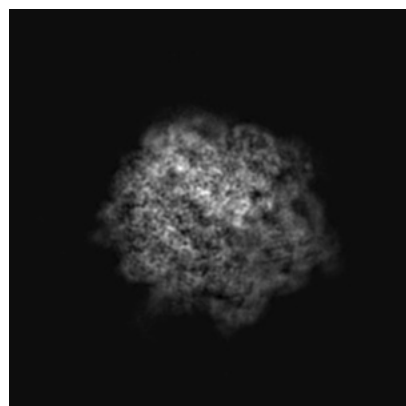
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22461. These allow visual inspection of the internal detail of the map and identification of artifacts.

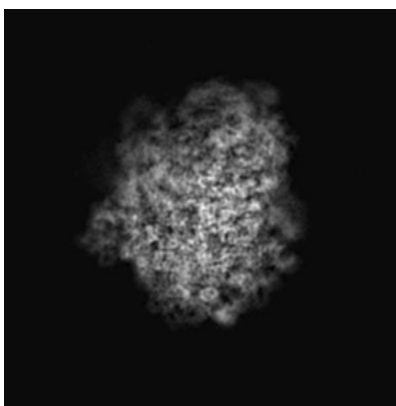
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

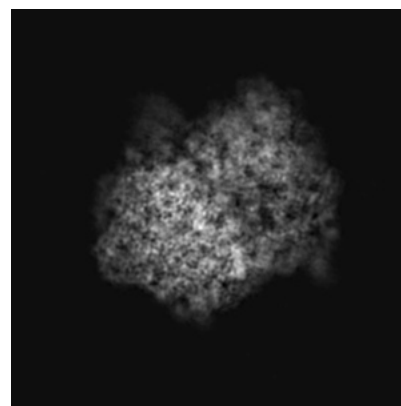
6.1.1 Primary map



X

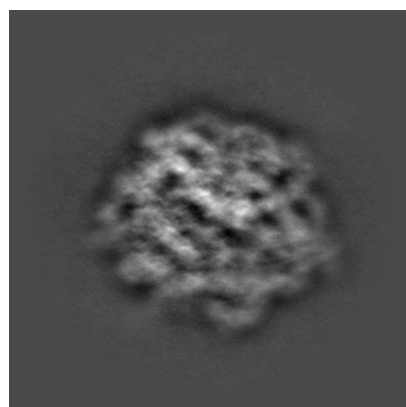


Y

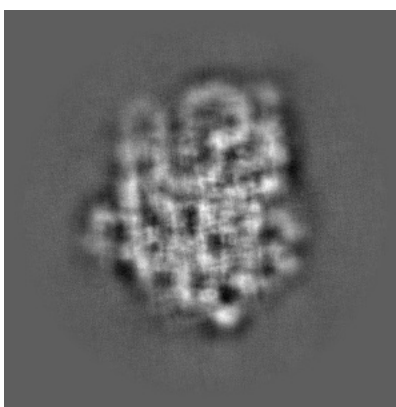


Z

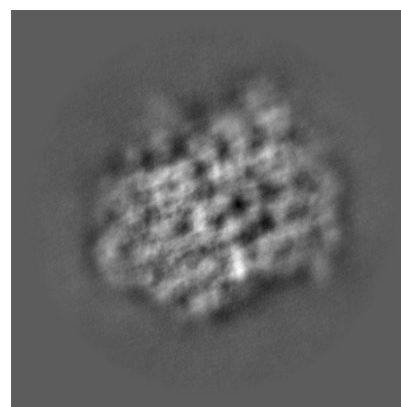
6.1.2 Raw map



X



Y

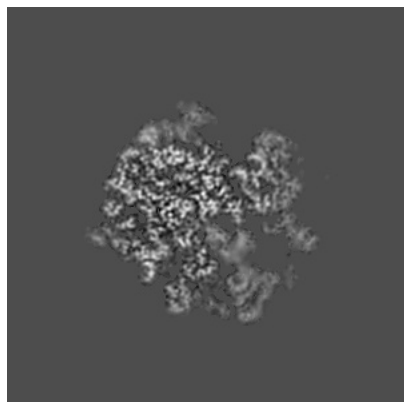


Z

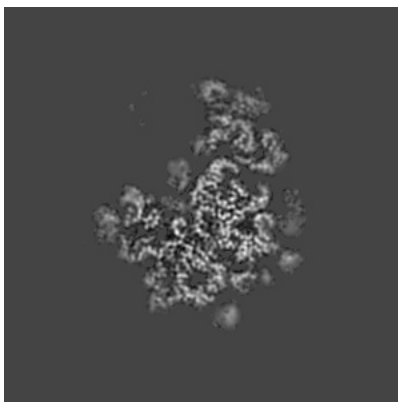
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

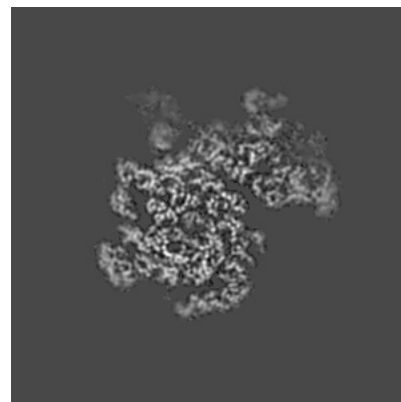
6.2.1 Primary map



X Index: 224

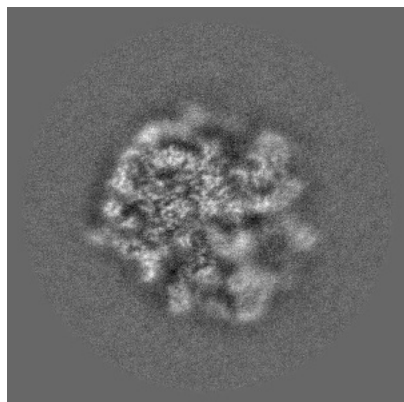


Y Index: 224

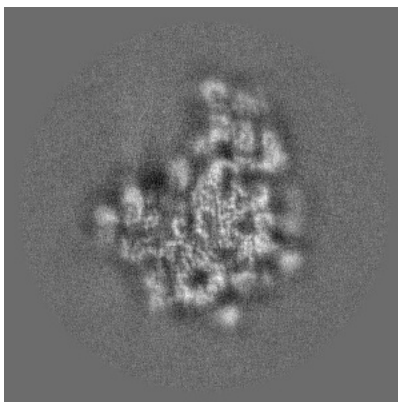


Z Index: 224

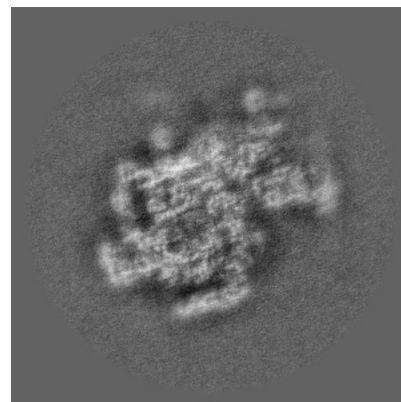
6.2.2 Raw map



X Index: 224



Y Index: 224

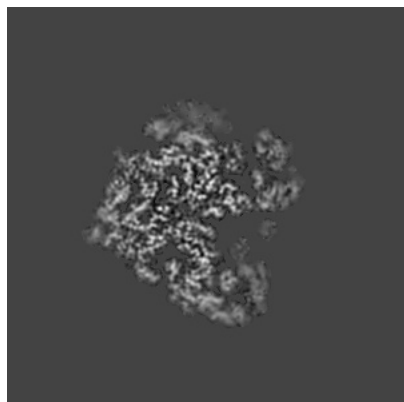


Z Index: 224

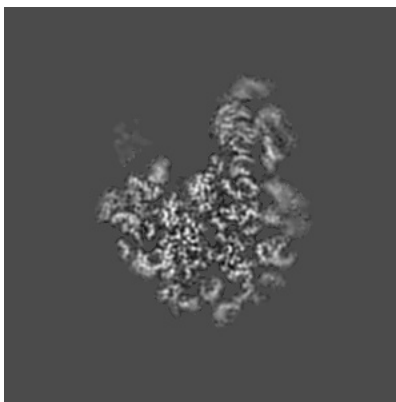
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

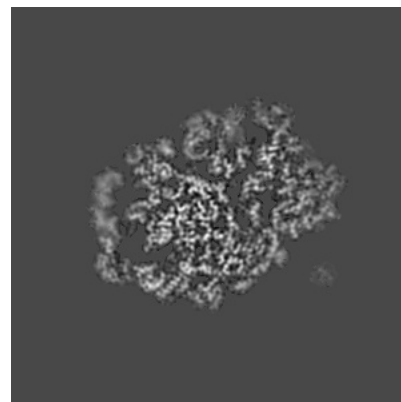
6.3.1 Primary map



X Index: 211

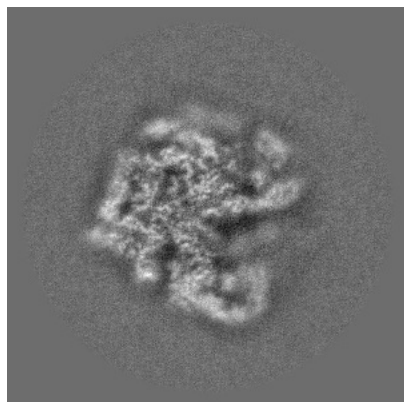


Y Index: 201

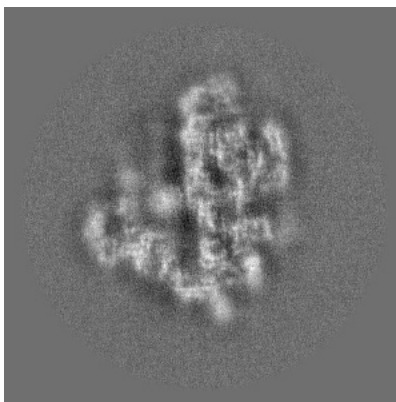


Z Index: 246

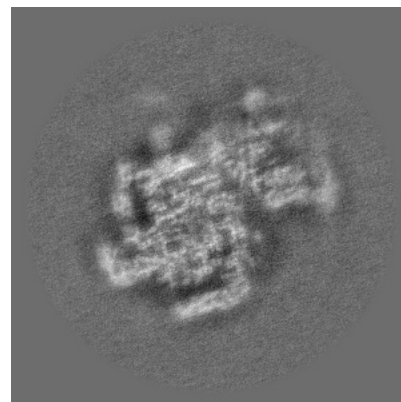
6.3.2 Raw map



X Index: 213



Y Index: 257

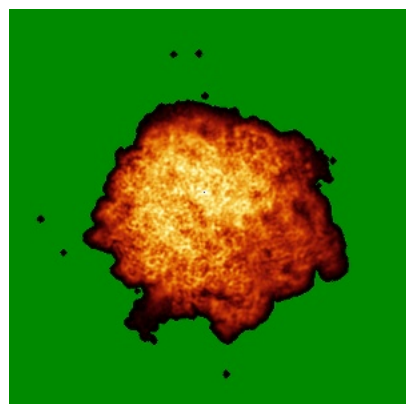


Z Index: 222

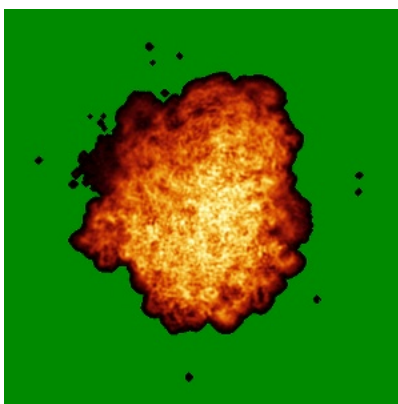
The images above show the largest variance slices of the map in three orthogonal directions.

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

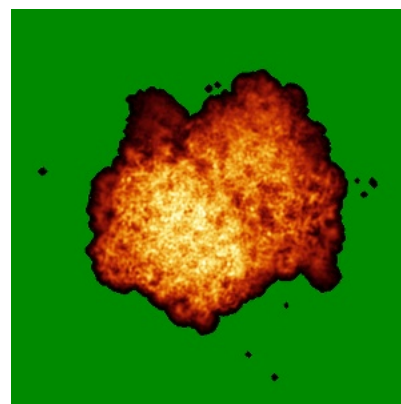
6.4.1 Primary map



X

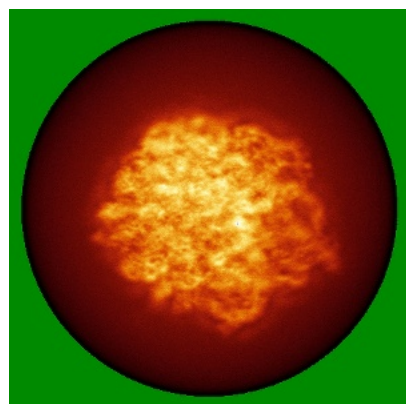


Y

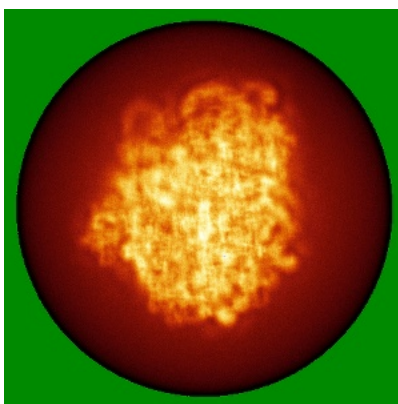


Z

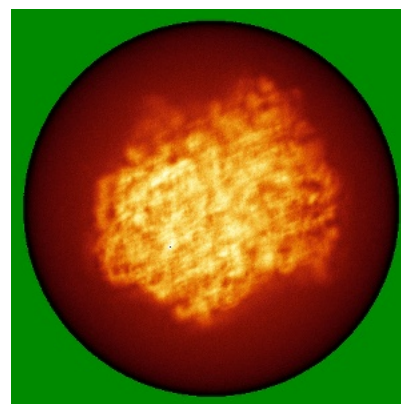
6.4.2 Raw map



X



Y

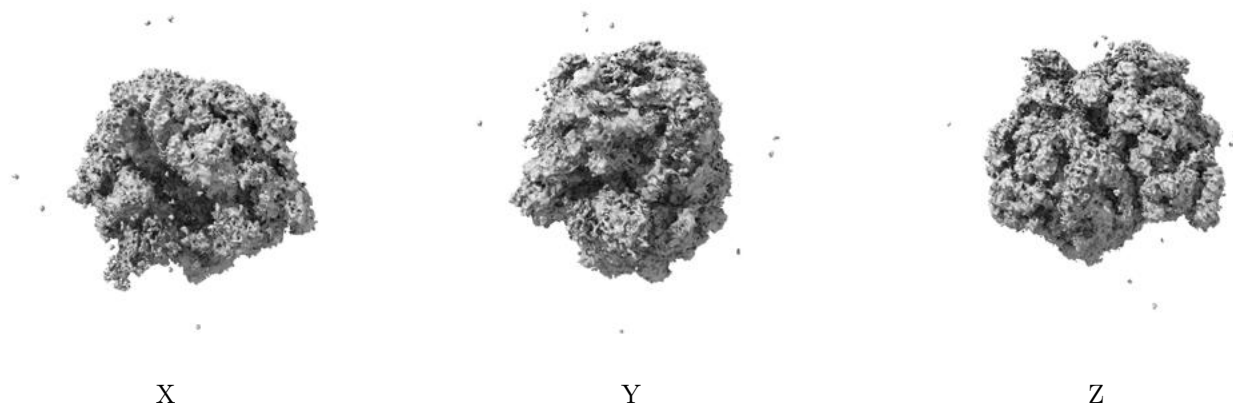


Z

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.

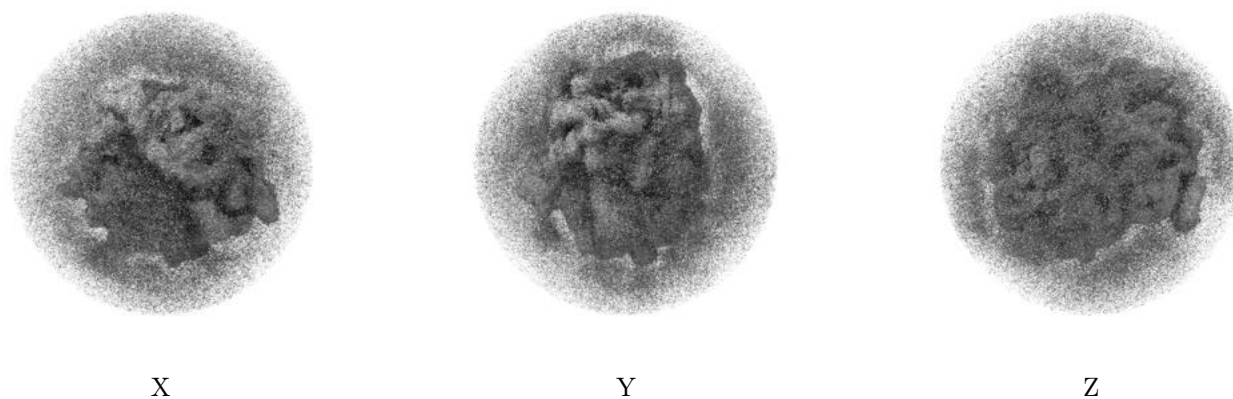
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.592. 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.

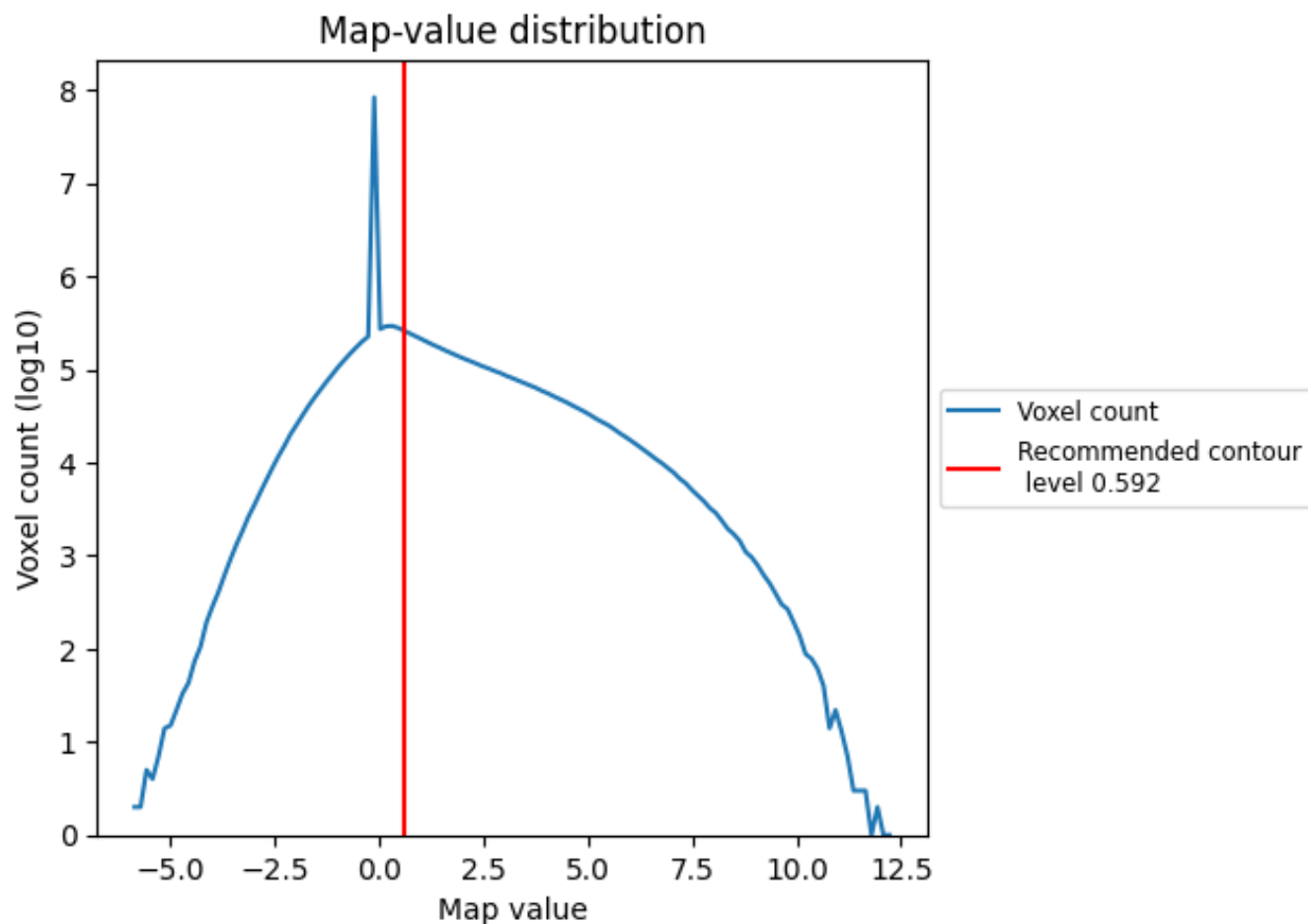
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

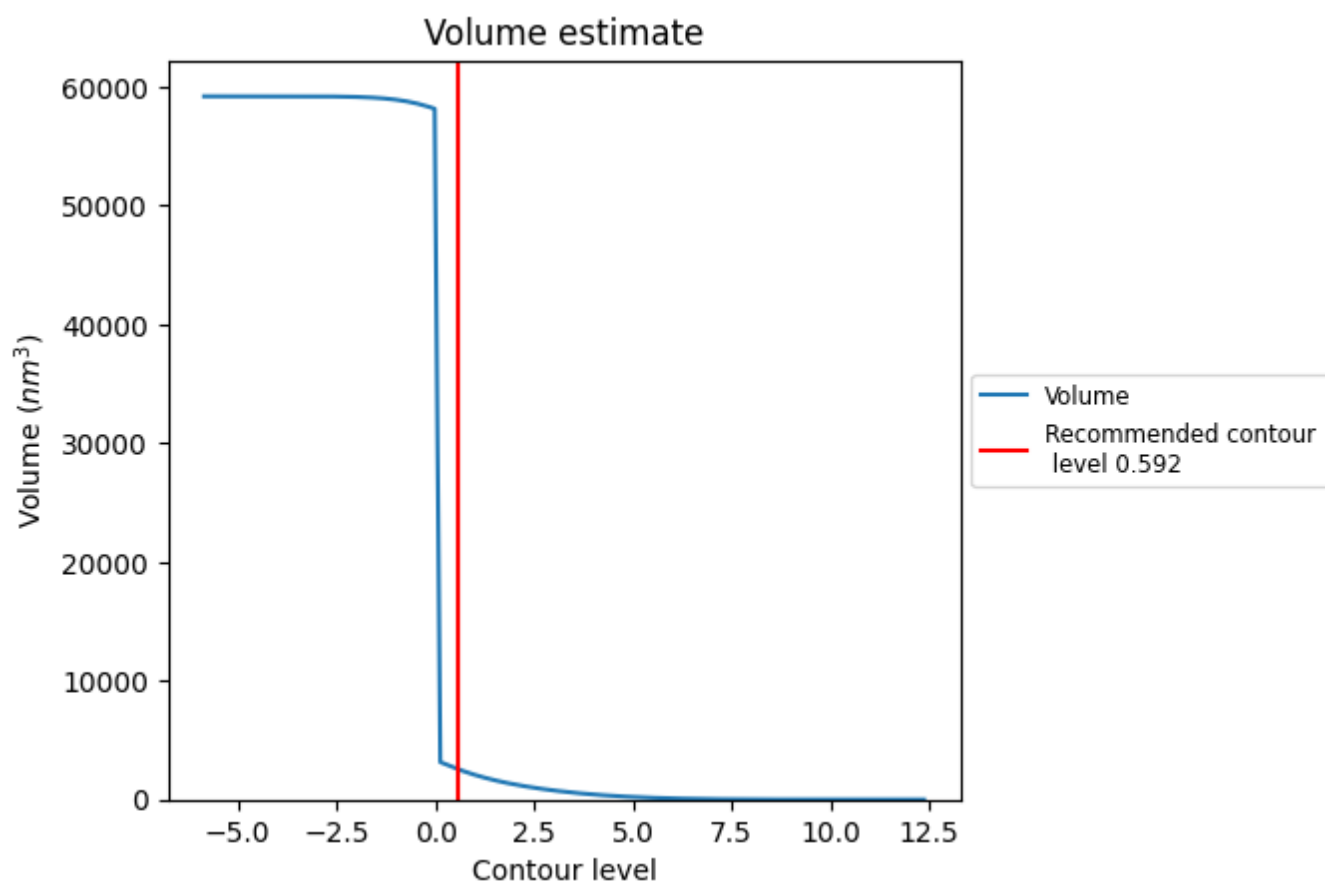
This section contains the results of statistical analysis of the map.

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.

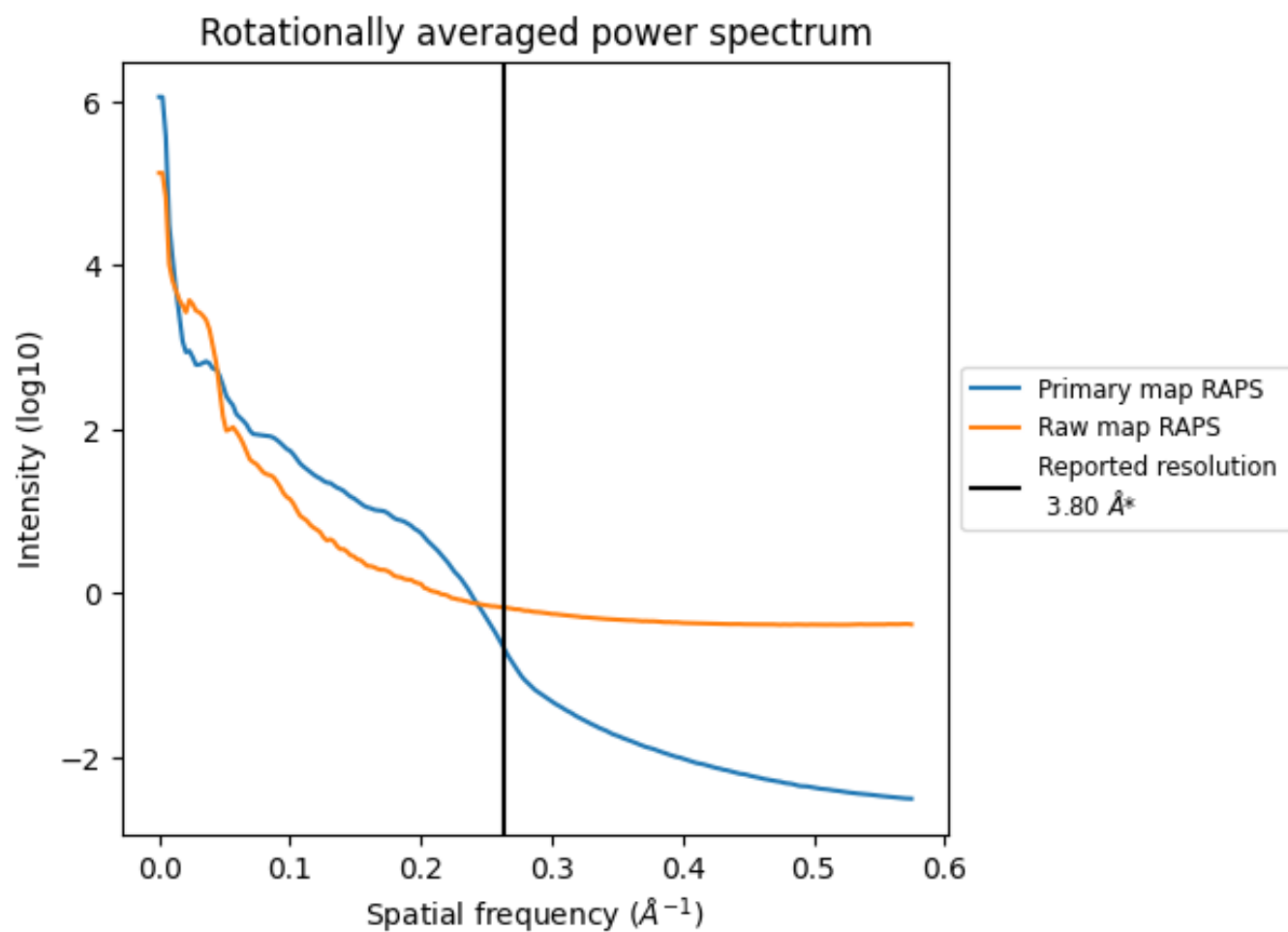
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2536 nm^3 ; this corresponds to an approximate mass of 2291 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

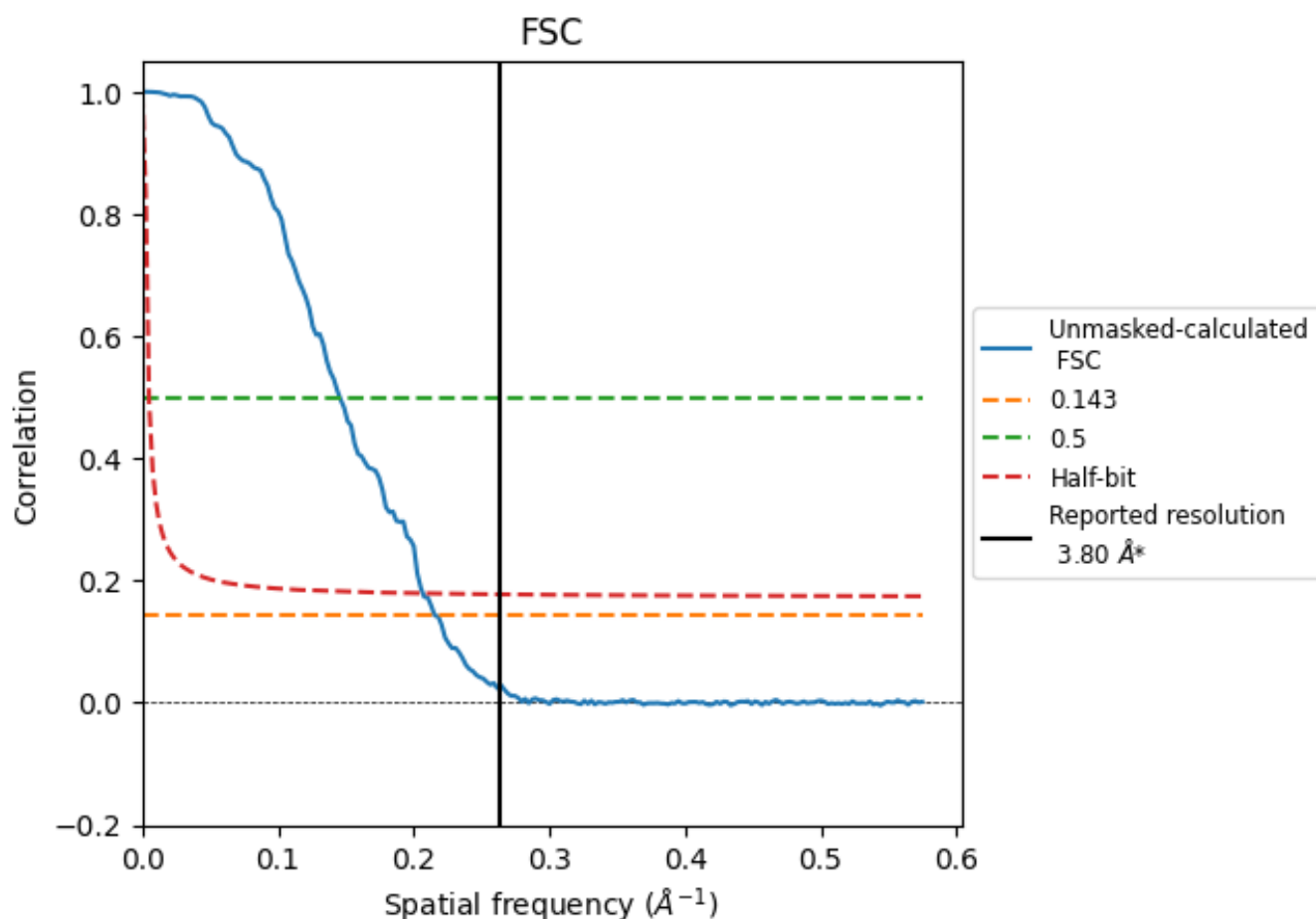


*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

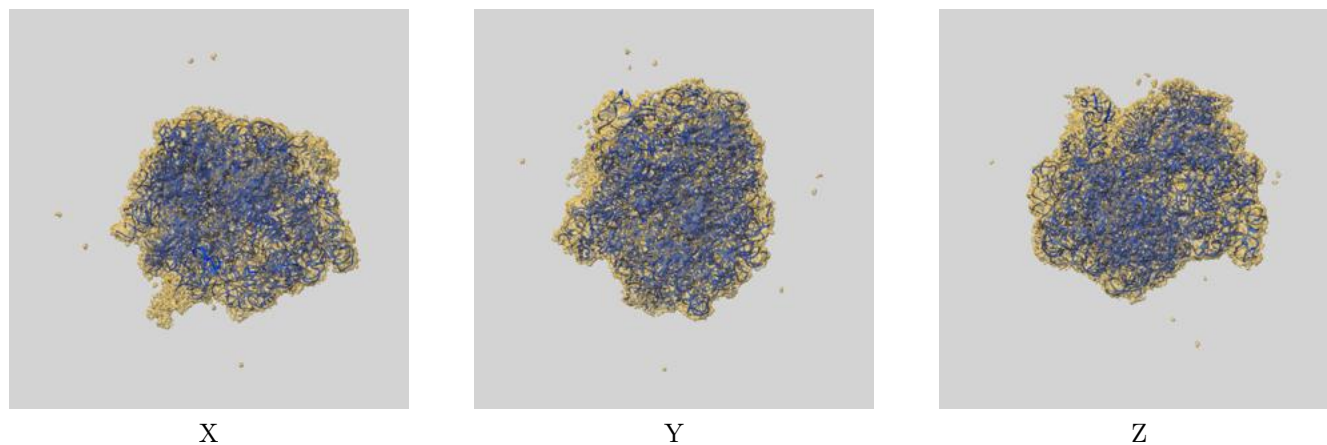
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.64	6.87	4.84

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

9 Map-model fit [i](#)

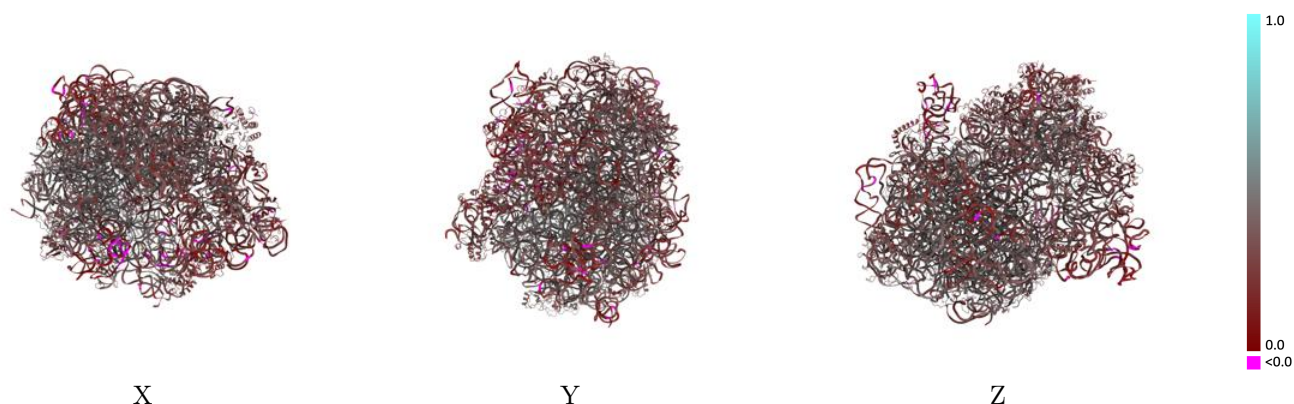
This section contains information regarding the fit between EMDB map EMD-22461 and PDB model 7JSW. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



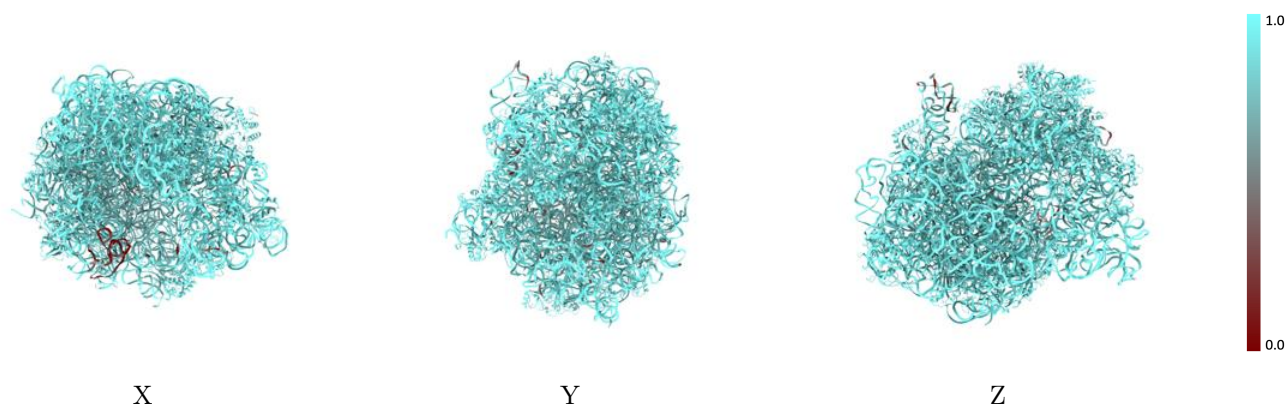
The images above show the 3D surface view of the map at the recommended contour level 0.592 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



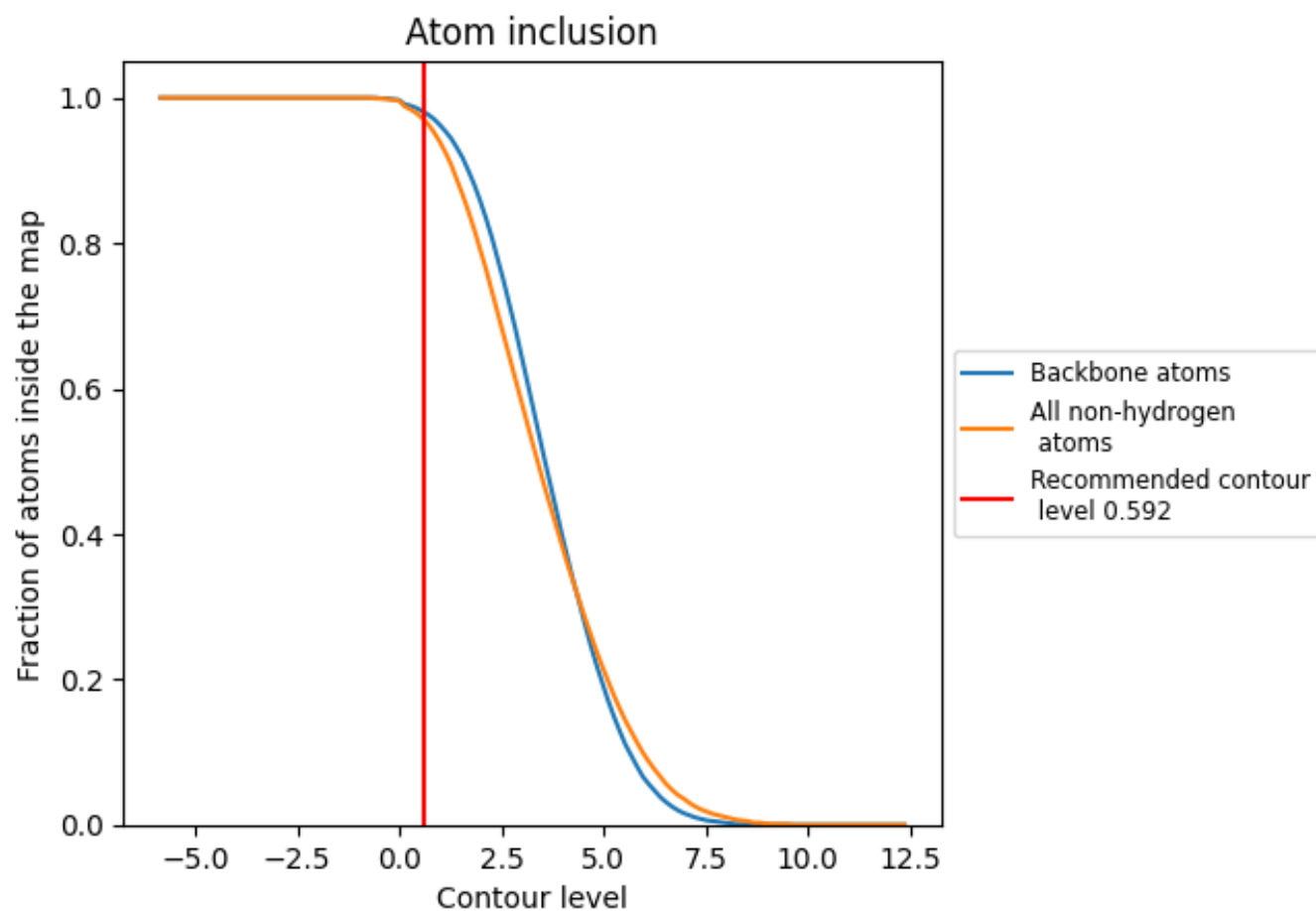
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.592).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (0.592) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.3390
1	 0.9710	 0.3530
2	 0.9900	 0.2920
3	 0.9860	 0.3110
4	 0.9800	 0.2840
5	 0.9400	 0.2280
8	 0.7990	 0.2150
B	 0.9600	 0.4140
C	 0.9750	 0.3980
D	 0.9520	 0.4270
E	 0.9250	 0.4070
F	 0.9620	 0.3810
G	 0.9650	 0.3040
H	 0.9510	 0.3320
I	 0.9450	 0.2990
J	 0.9710	 0.3650
K	 0.9760	 0.3140
L	 0.9430	 0.2640
M	 0.9650	 0.3440
N	 0.9440	 0.2610
O	 0.9230	 0.2810
P	 0.9680	 0.3250
Q	 0.9700	 0.3950
R	 0.9770	 0.2660
S	 0.9680	 0.2920
T	 0.9680	 0.3180
U	 0.9540	 0.3300
V	 0.9750	 0.3510
W	 0.9130	 0.3130
X	 0.9940	 0.2500
Y	 0.9710	 0.3090
Z	 0.9030	 0.2660
b	 0.9550	 0.4150
c	 0.9610	 0.4160
d	 0.9690	 0.3780



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Chain	Atom inclusion	Q-score
e	 0.9690	 0.2420
f	 0.9750	 0.3050
g	 0.9080	 0.2760
j	 0.9580	 0.3970
k	 0.9660	 0.4170
l	 0.9670	 0.4100
m	 0.9660	 0.4040
n	 0.9770	 0.4130
o	 0.9840	 0.3270
p	 0.9810	 0.3980
q	 0.9580	 0.4000
r	 0.9750	 0.4040
s	 0.9550	 0.4130
t	 0.9680	 0.3930
u	 0.9670	 0.3670
v	 0.9800	 0.3630
w	 0.9480	 0.4080
x	 0.9800	 0.3980
y	 0.9780	 0.3320
z	 0.9700	 0.4070