



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:12 PM UTC

PDB ID : 6WD4 / pdb_00006wd4
EMDB ID : EMD-21623
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure II-B2)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

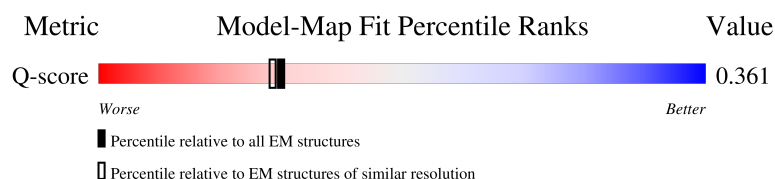
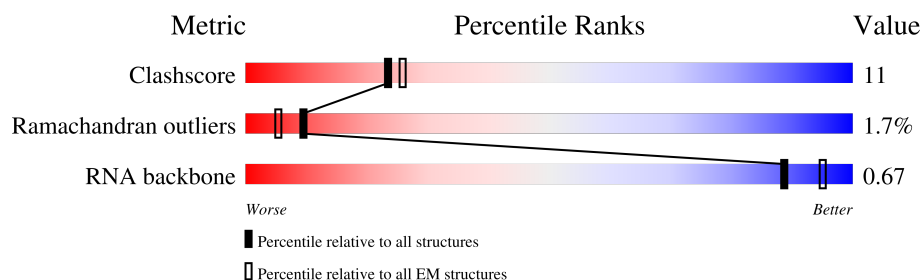
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

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



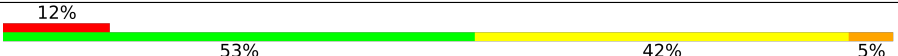
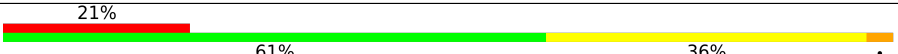
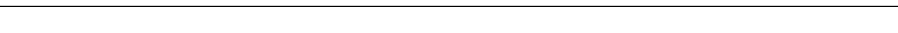
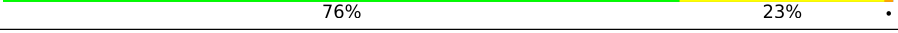
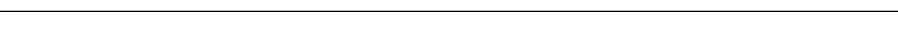
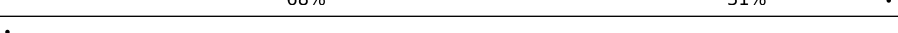
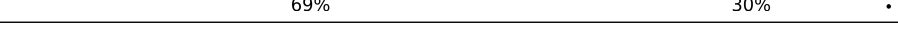
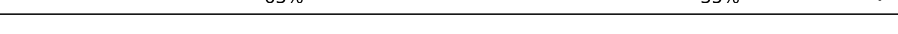
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	b	271	
2	c	209	
3	d	201	
4	e	177	

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Mol	Chain	Length	Quality of chain
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	
29	E	64	

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Mol	Chain	Length	Quality of chain
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	
54	2	120	

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Mol	Chain	Length	Quality of chain
55	5	77	73%21%6%
55	6	77	47%51%
56	4	18	50%44%6%
57	7	76	58%29%13%
58	8	400	9%62%28%8%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 153083 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	variant	GB 1036415628

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1370526515

- Molecule 55 is a RNA chain called tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
55	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 56 is a RNA chain called mRNA.

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

- Molecule 57 is a RNA chain called tRNA^{Phe}.

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

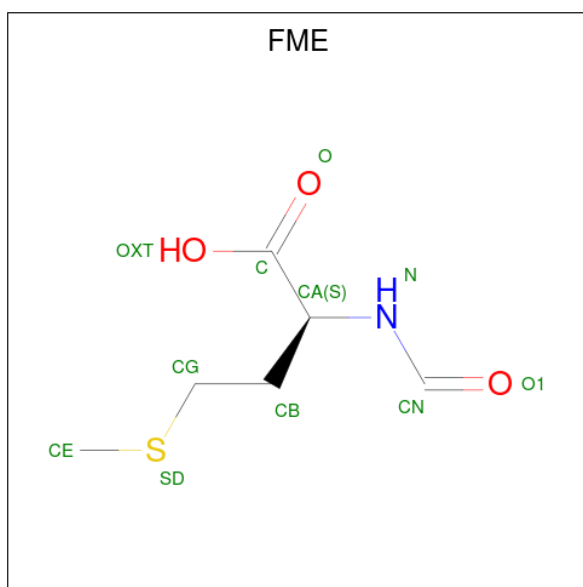
- Molecule 58 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	366	Total	C	N	O	S	0	0
			2833	1796	485	539	13		

There are 7 discrepancies between the modelled and reference sequences:

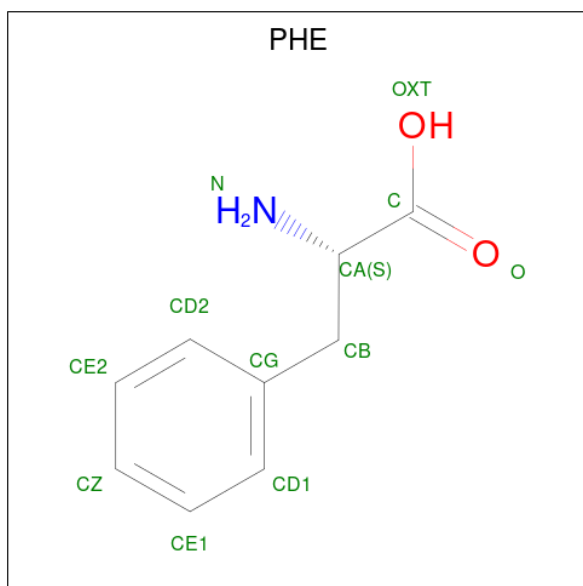
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag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

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



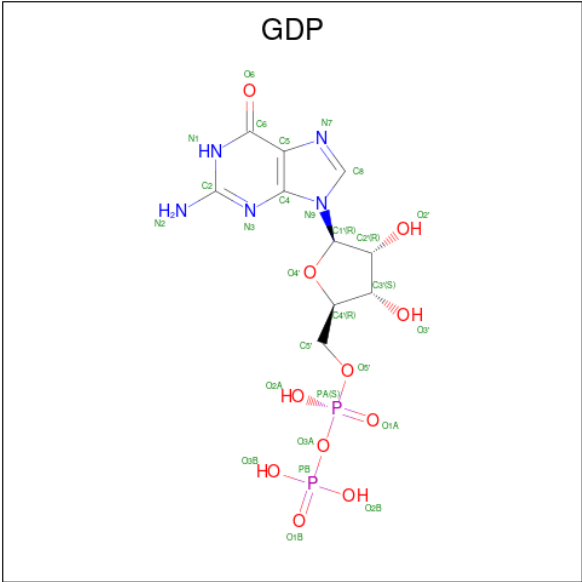
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

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



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

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

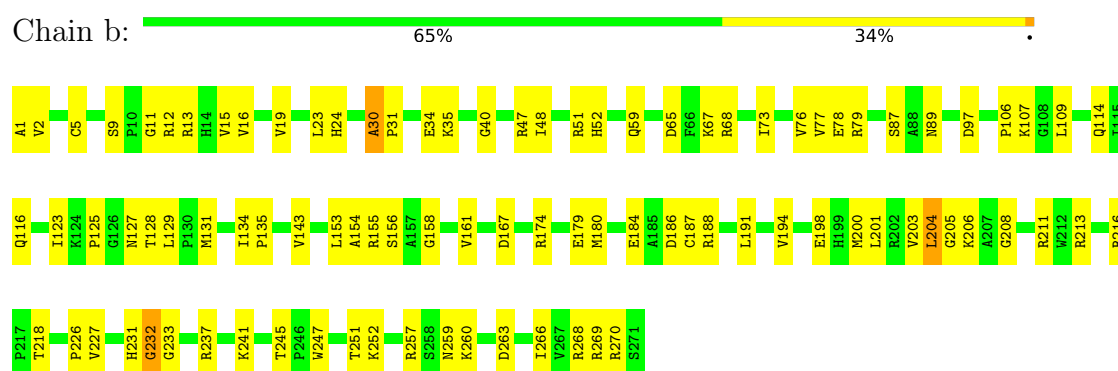


Mol	Chain	Residues	Atoms					AltConf
61	8	1	Total	C	N	O	P	0
			28	10	5	11	2	

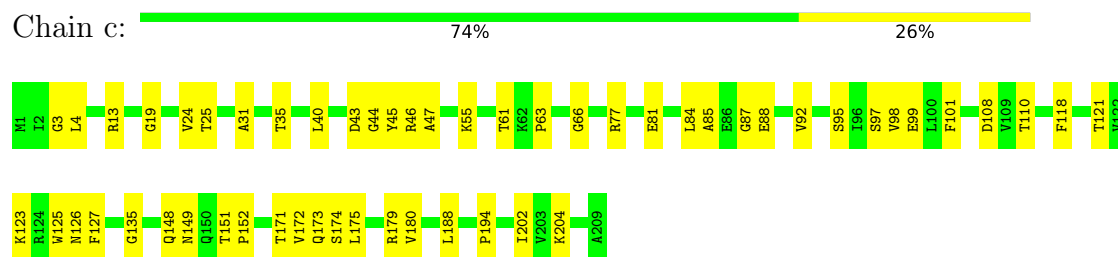
3 Residue-property plots

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.

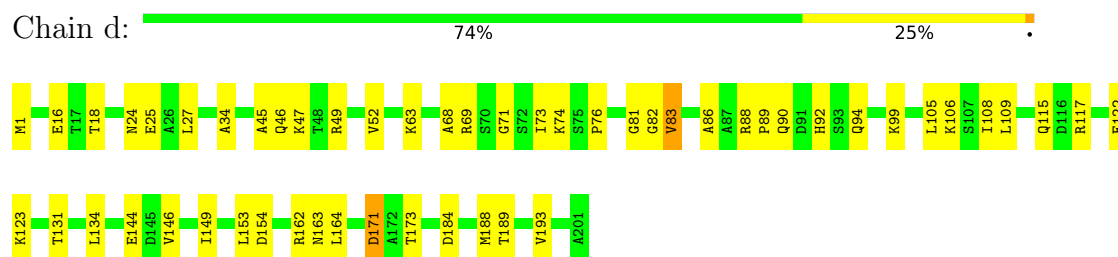
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

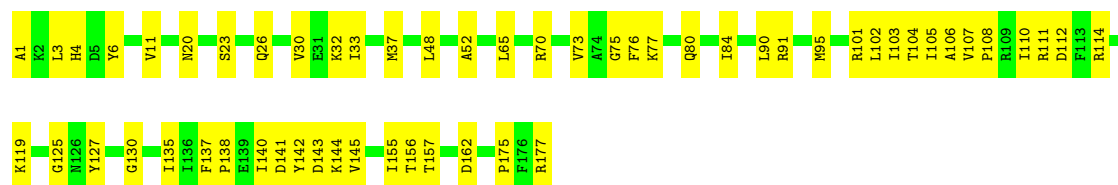


• Molecule 3: 50S ribosomal protein L4



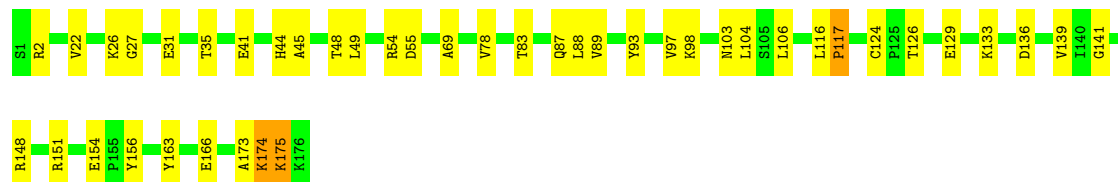
• Molecule 4: 50S ribosomal protein L5





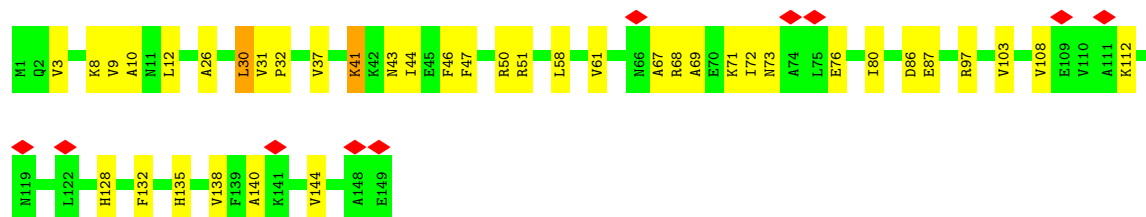
• Molecule 5: 50S ribosomal protein L6

Chain f: 76% 23% .



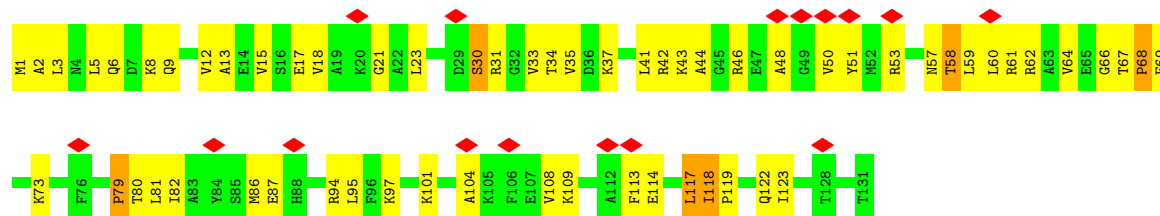
• Molecule 6: 50S ribosomal protein L9

Chain g: 7% 74% 25% .



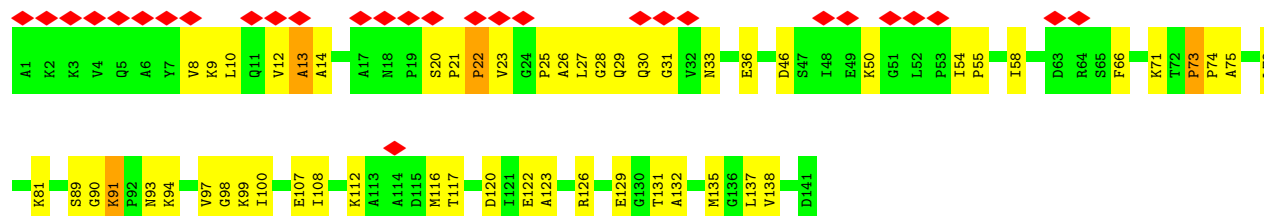
• Molecule 7: 50S ribosomal protein L10

Chain h: 12% 53% 42% 5% .

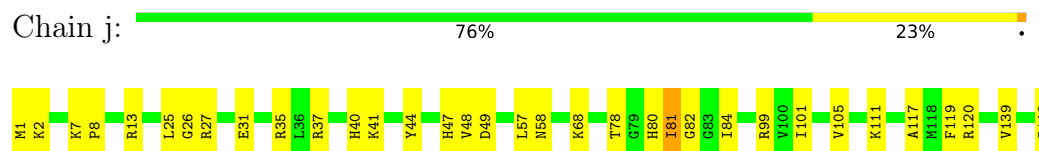


• Molecule 8: 50S ribosomal protein L11

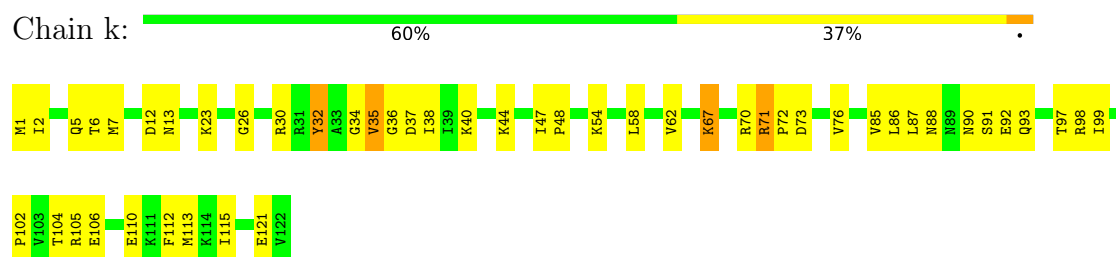
Chain i: 21% 61% 36% .



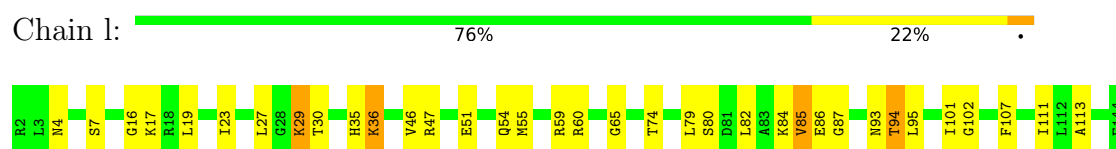
- Molecule 9: 50S ribosomal protein L13



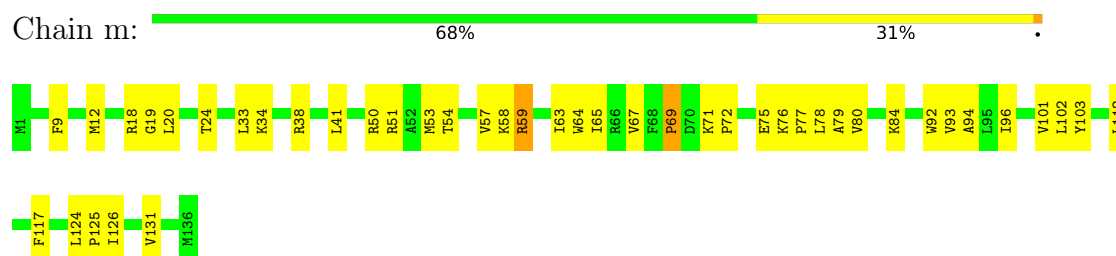
- Molecule 10: 50S ribosomal protein L14



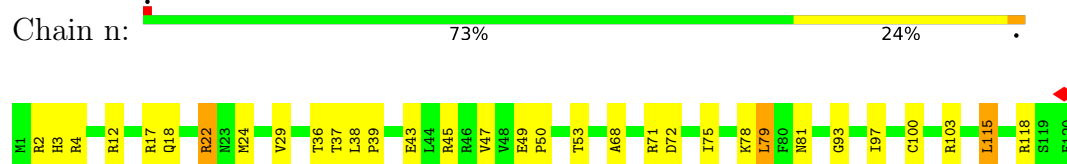
- Molecule 11: 50S ribosomal protein L15



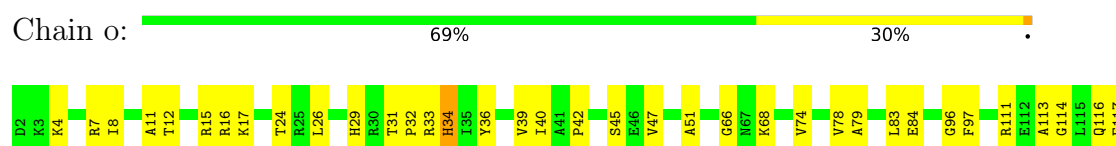
- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18



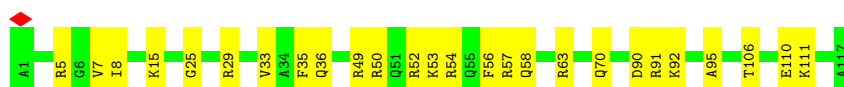
- Molecule 15: 50S ribosomal protein L19

Chain p:  60% 40%



- Molecule 16: 50S ribosomal protein L20

Chain q:  78% 22%



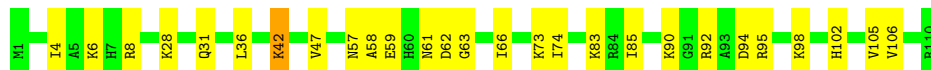
- Molecule 17: 50S ribosomal protein L21

Chain r:  79% 19% .



- Molecule 18: 50S ribosomal protein L22

Chain s:  75% 24% .



- Molecule 19: 50S ribosomal protein L23

Chain t:  63% 35% .



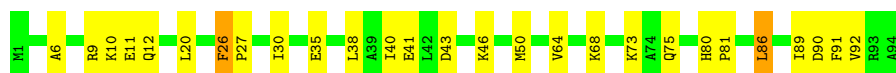
- Molecule 20: 50S ribosomal protein L24

Chain u:  76% 18% 6%



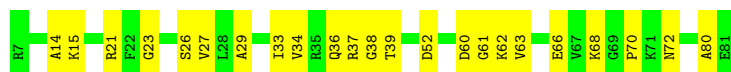
- Molecule 21: 50S ribosomal protein L25

Chain v:  71% 27% .



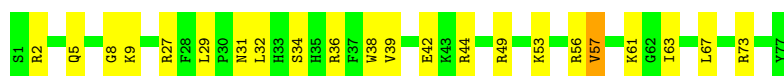
- Molecule 22: 50S ribosomal protein L27

Chain w: 69% 31%



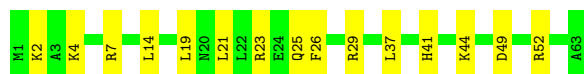
- Molecule 23: 50S ribosomal protein L28

Chain x: 71% 27%



- Molecule 24: 50S ribosomal protein L29

Chain y: 76% 24%



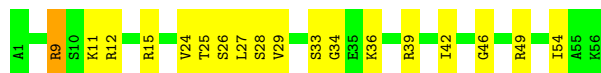
- Molecule 25: 50S ribosomal protein L30

Chain z: 76% 24%



- Molecule 26: 50S ribosomal protein L32

Chain B: 68% 30%



- Molecule 27: 50S ribosomal protein L33

Chain C: 64% 36%



- Molecule 28: 50S ribosomal protein L34

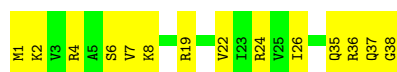
Chain D: 67% 33%



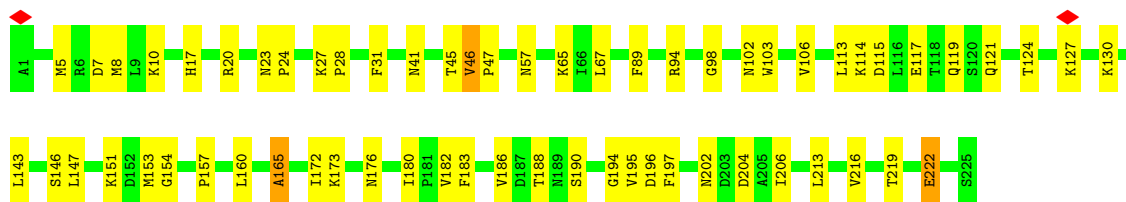
- Molecule 29: 50S ribosomal protein L35



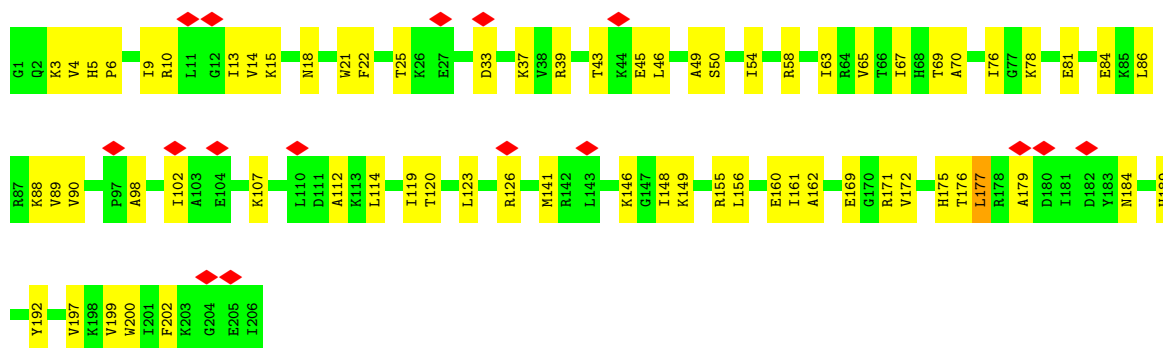
- Molecule 30: 50S ribosomal protein L36



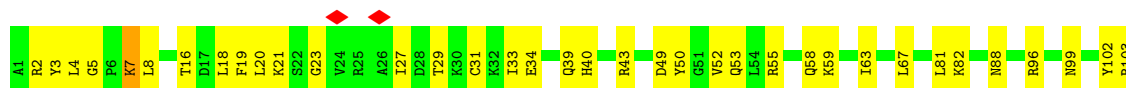
- Molecule 31: 30S ribosomal protein S2

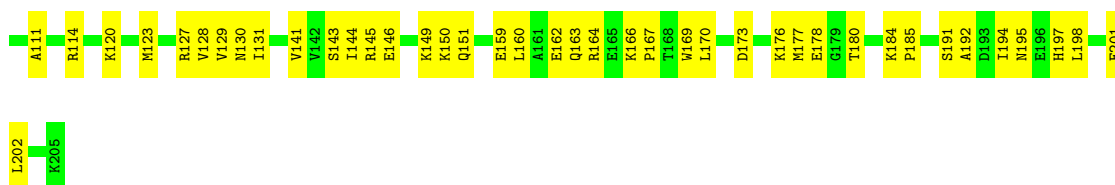


- Molecule 32: 30S ribosomal protein S3



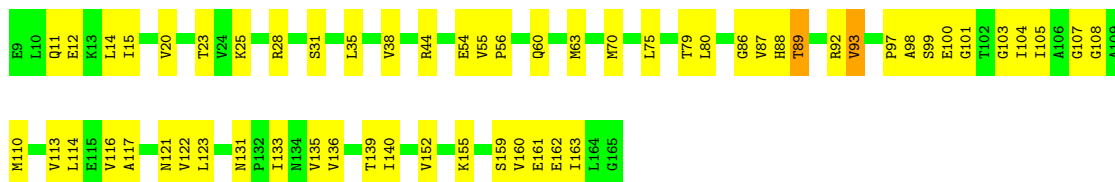
- Molecule 33: 30S ribosomal protein S4





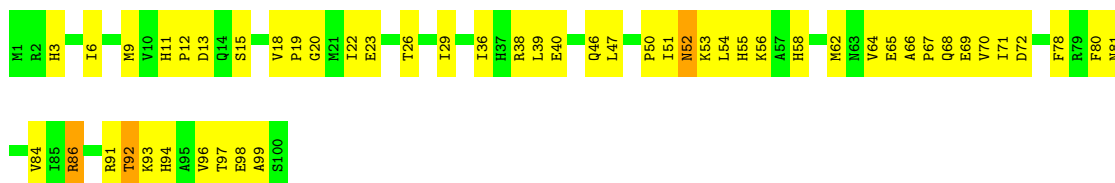
- Molecule 34: 30S ribosomal protein S5

Chain J: 63% 36%



- Molecule 35: 30S ribosomal protein S6

Chain K: 49% 48%



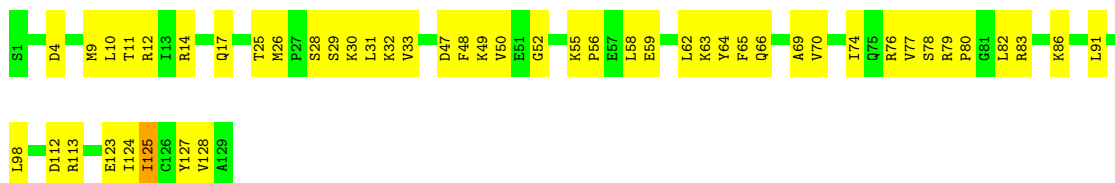
- Molecule 36: 30S ribosomal protein S7

Chain L: 70% 29%



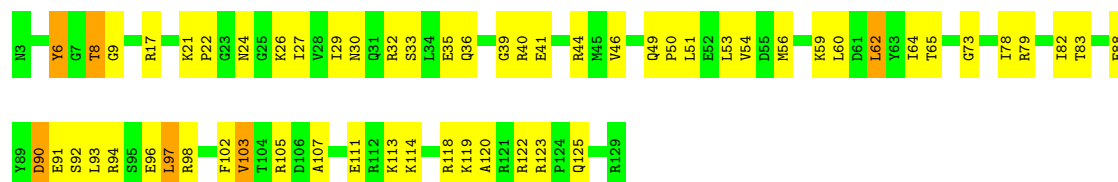
- Molecule 37: 30S ribosomal protein S8

Chain M: 62% 37%

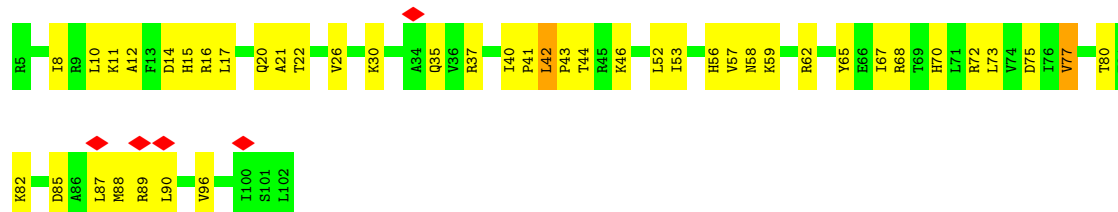


- Molecule 38: 30S ribosomal protein S9

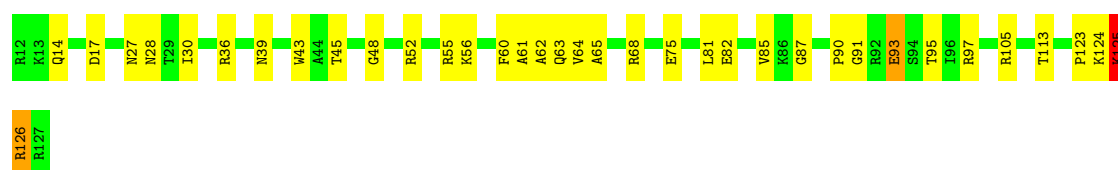
Chain N: 54% 41% 5%



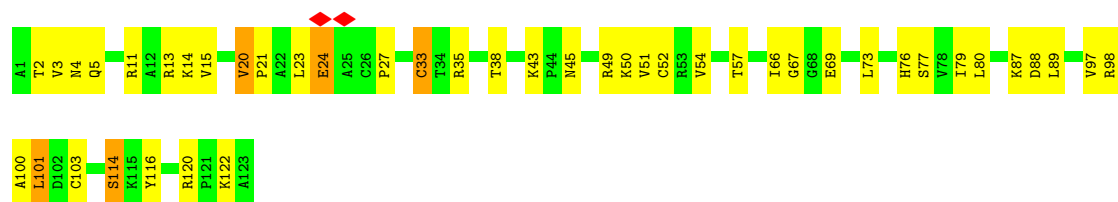
- Molecule 39: 30S ribosomal protein S10



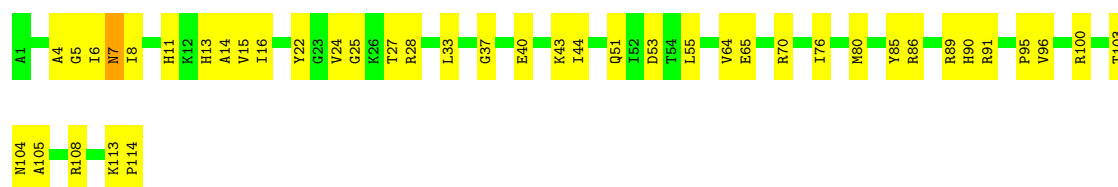
- Molecule 40: 30S ribosomal protein S11



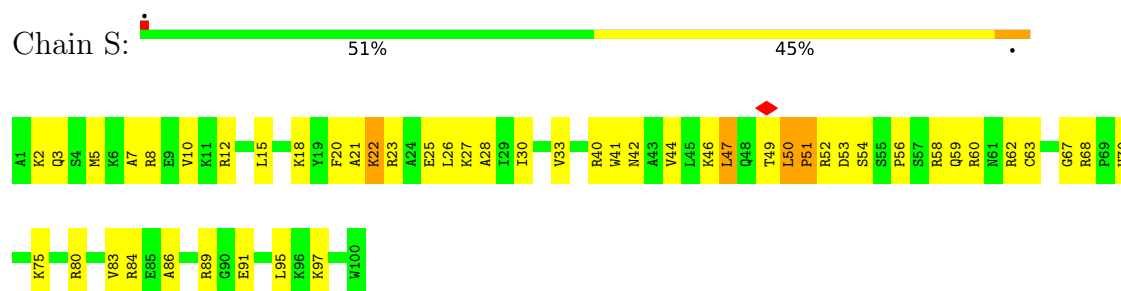
- Molecule 41: 30S ribosomal protein S12



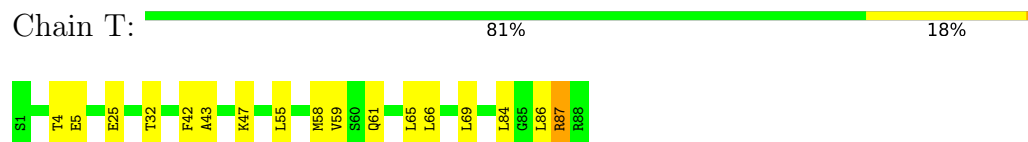
- Molecule 42: 30S ribosomal protein S13



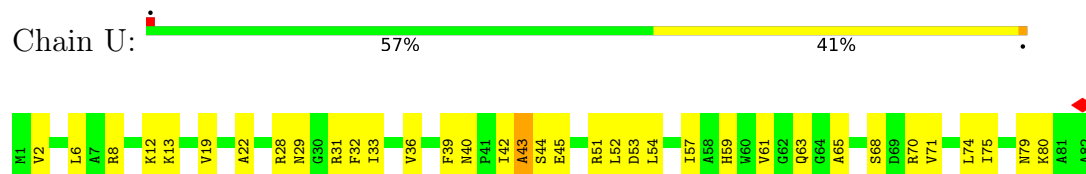
- Molecule 43: 30S ribosomal protein S14



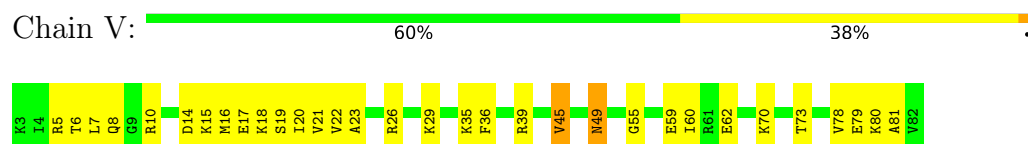
- Molecule 44: 30S ribosomal protein S15



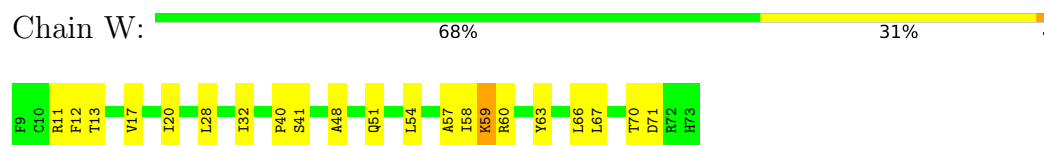
- Molecule 45: 30S ribosomal protein S16



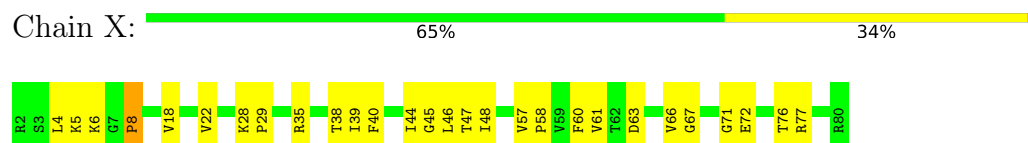
- Molecule 46: 30S ribosomal protein S17



- Molecule 47: 30S ribosomal protein S18

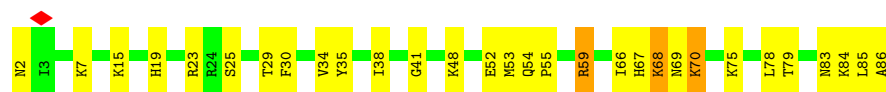


- Molecule 48: 30S ribosomal protein S19



- Molecule 49: 30S ribosomal protein S20

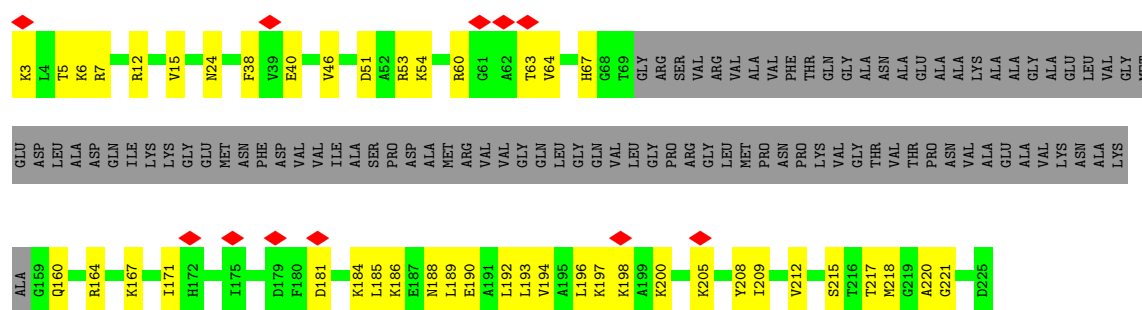




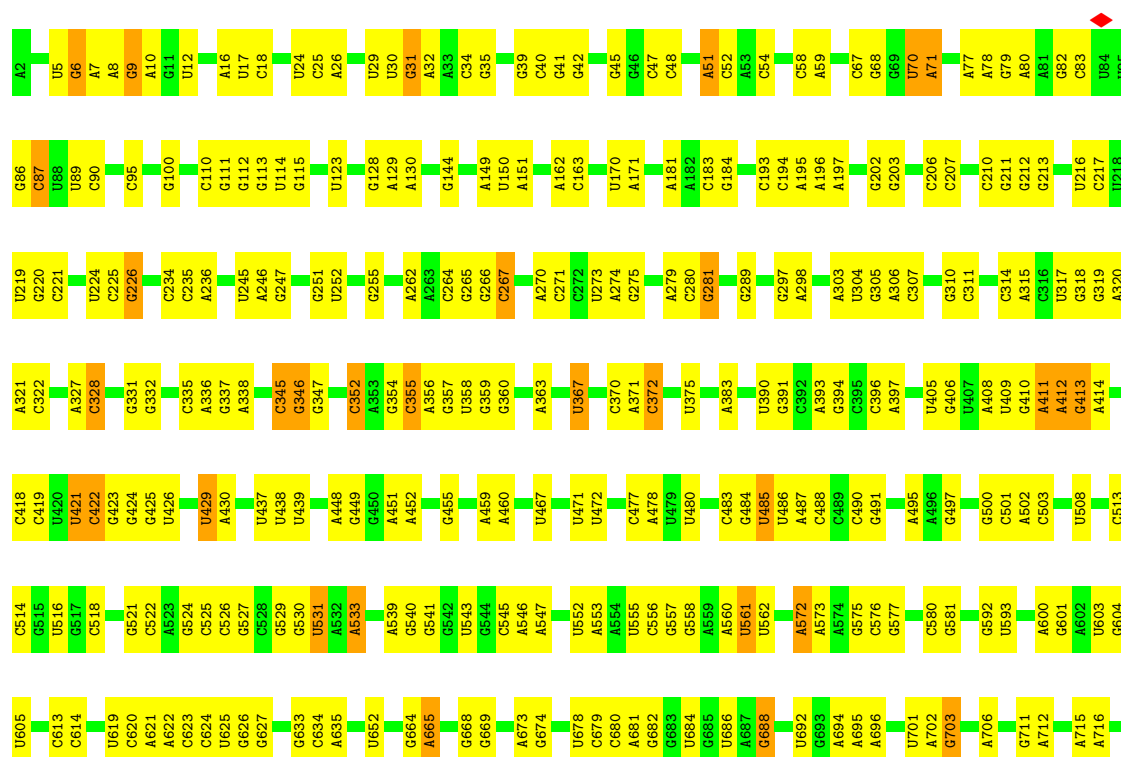
- Molecule 50: 30S ribosomal protein S21

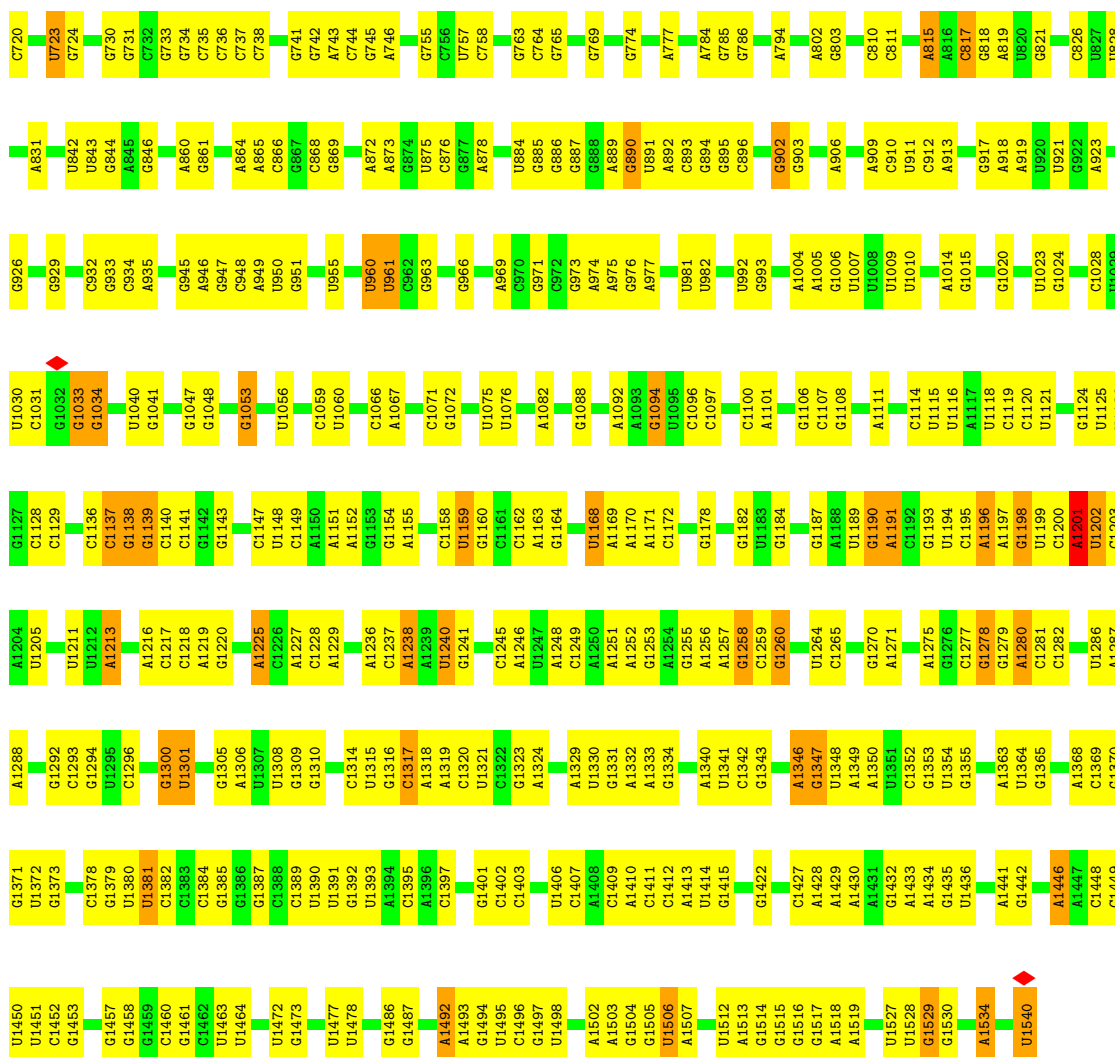


- Molecule 51: 50S ribosomal protein L1



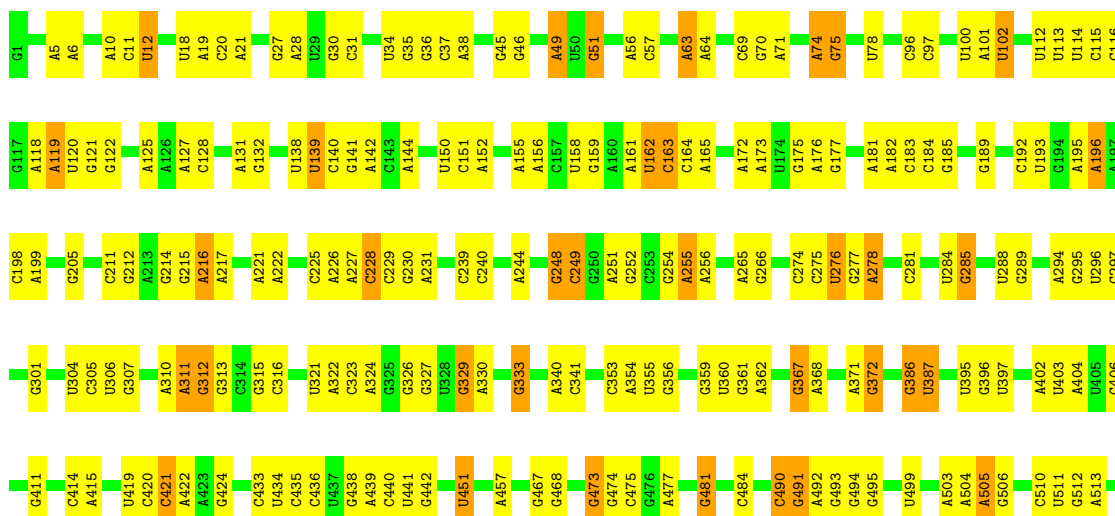
- Molecule 52: 16S ribosomal RNA



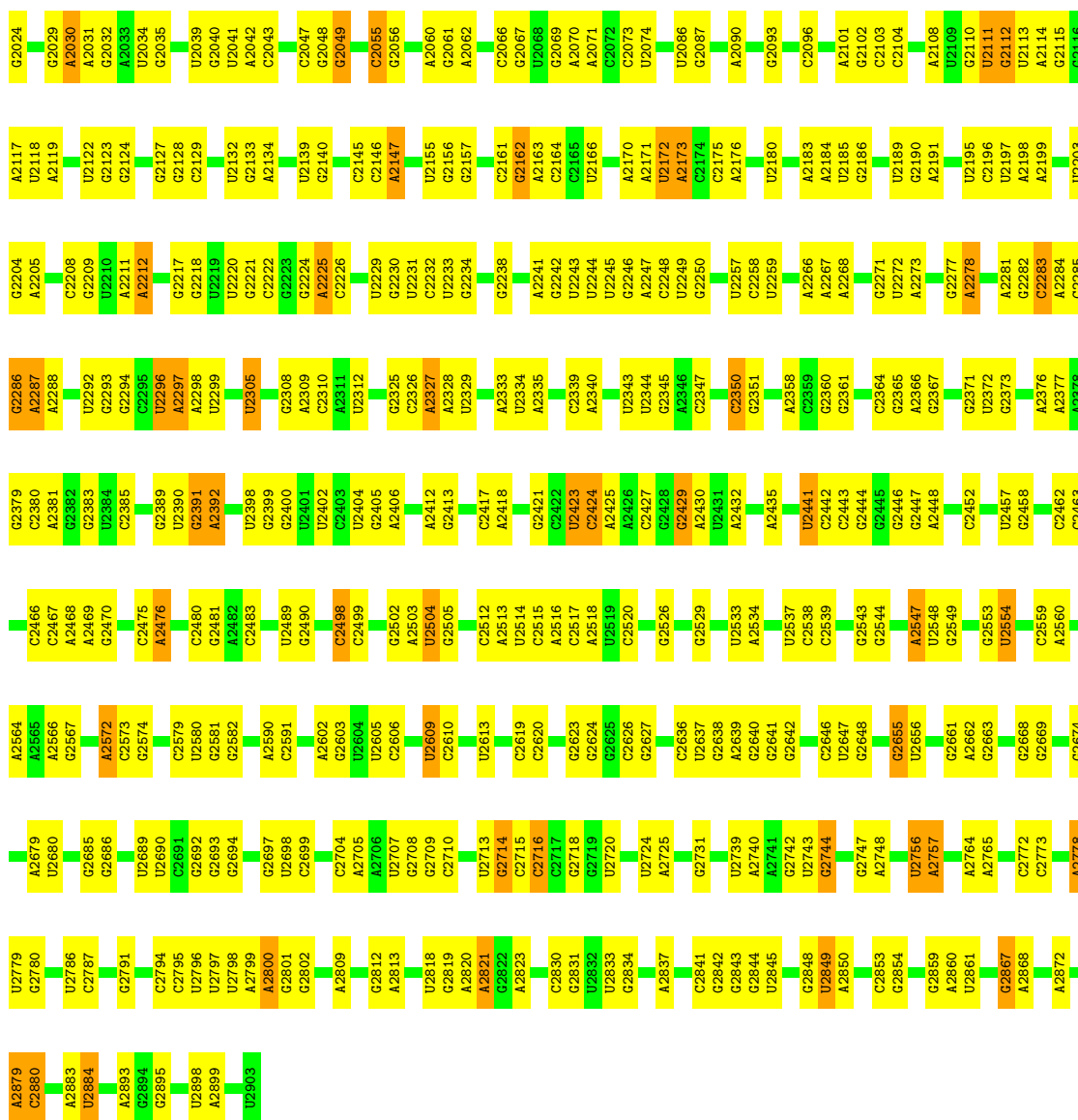


• Molecule 53: 23S ribosomal RNA

Chain 1: 57% 38% 5%

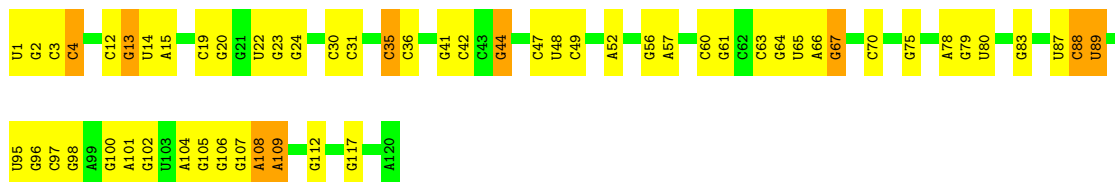


C1925	A1810	G1696	U1584	C1480	G1369	A1268	G1149	U1061	A975	U872	G785	G695	G597	C516
G1929	G1811	G1697	C1585	U1481	C1370	A1269	G1150	G1062	A983	C873	A792	G696	U598	C517
G1930	C1816	A1701	A1586	G1482	U1372	G1270	A1151	U1066	A984	C876	A793	G700	U599	G518
U1931	G1817	G1702	G1587	U1371	U1372	A1271	C1152	A1067	G989	A877	G796	U702	C601	G520
G1932	U1818	U1709	U1594	G1491	A1373	A1272	C1153	G1068	G990	A878	G797	U703	A602	C523
G1933	U1827	G1710	C1595	A1495	C1376	A1275	G1154	A1069	C992	C885	G805	U704	A603	G524
C1934	G1828	G1715	A1596	U1496	G1377	A1276	A1155	A1070	C993	A886	G806	A705	U607	
G1935	A1829	G1716	A1597	G1501	U1379	C1277	A1156	A1077	C994	A887	C807	A706		
A1936	C1830	G1717	G1598	U1502	A1383	C1278	G1170	U1078	C995	C890	U807	C717	C610	A528
A1937	G1831	U1720	U1602	A1503	A1384	G1280	G1171	A1079	A996	G891	G808	C718	C611	A529
A1938	C1832	G1721	A1603	U1506	C1386	A1285	A1176	C1079	G997		G809	C719	G612	G530
U1943	C1833			C1507	U1387	A1286	U1176	U1083	A1000	A896	U810	U720	A613	A531
U1944	U1834	C1726	A1608	A1508	A1387	A1287	G1177	U1084	A1001	C897	C812	A721	A614	A532
		C1727		A1509	G1388	G1288	G1178	A1085		C898	U813	A722	U534	G533
C1947	C1837	U1729	C1611	G1510	G1389		G1179	A1086	C1007	A899	C814	C723	A616	G535
G1948	U1851	C1730	G1612	U1515	U1394	C1297	U1180	G1087	A1008		C815	C724	G617	C542
		G1732	A1616	G1524	A1395	C1298	U1181	A1088	A1009	G907	C816	C725	G618	G543
U1955	U1856	C1733		C1525		C1299	U1182	A1089	U1012	A909	C817	C726	C619	G544
C1957	G1857	G1738	C1625	G1526	U1409	G1300	U1183	A1090	U1013	C908	C818	A727	G620	U545
C1958	A1858		A1626	G1527	G1410	A1301	U1184	G1091	A1014	A910	C819	C728	A627	
G1959	U1859	U1746	A1626	A1528	G1416	G1310	G1185	C1092	U1015	A911	C822	A730	G548	G549
	G1860	U1747		G1529	C1417	G1311	G1186	G1093	G1016	U913			G636	
U1963	G1861	U1747	A1637		G1418		G1187						A637	
G1964		A1754	G1642	A1535	A1419	U1316	U1198	A1103	U1019	U826	G738		G638	U554
C1965	G1866		G1643	C1536	G1317	U1317	U1199	C1104	A1020	U827	A739		U639	G555
A1966	G1867		C1644	G1537	A1420	U1318	G1206	U828	A1021	U829	A742		C640	
C1967	U1871	U1758	C1644	U1538	G1423	C1319	G1207	U830	G1022	A743	A744		U658	U558
	A1872	A1759	C1645	U1539	G1424	C1320	G1212	A933	G1023	A745	U746		C645	G559
A1970	A1873	C1764	C1646	U1540	G1427	U1329	U1219	U934		U934	U746		U646	
U1971	G1873	U1765	U1647	C1541	A1428	C1330	G1220	C935	G1026	A654	C747			A563
G1972	G1874	U1766	U1648	G1542	G1433	G1331	G1221	A833	A1028	U657	C748		U658	U567
	G1875		G1649	G1543	A1434	G1332	G1225	G834	A1029	U658	A749		U659	U568
A1978	A1876	A1773	G1663	G1543	A1435	G1333	A1226	U839	A1030	U659	A750		G659	U569
U1979	A1877	C1774	A1664	A1549	G1436	G1337	G1227	C840	A1033	U660	A751		C660	G570
G1980	G1878	U1775	A1665	C1560	U1437	G1338	G1227	A941	U1033	A661	A752		G661	U571
A1981	G1884	G1776	G1666	G1555	U1438	G1339	G1231	G942	A845	U662	U759		G662	A572
U1982	A1885		G1667	G1556	U1439	G1341	U1231	A943	U846		G760			U573
		U1779	A1668	G1560	A1439	G1342	G1232	U847	U847				G669	A574
U1991	C1893	A1780	A1669	C1561		G1343	G1238	C946	C851	A670	G763		A670	A575
G1992	C1894			U1562	C1447	U1344		A947	U852	C671	A764		C671	U576
U1993		A1784	A1672	C1563	G1448	G1123	G1238	C948	C853	C672	C765		C672	G577
C1996	A1900	U1785	G1673	C1564	U1449	G1124		G949	C854	C673	U766		C673	U580
G1997	A1901	A1786	G1674	C1565	C1345	G1125	C1243		C855	G674	U767		G674	C581
	C1902			C1566	U1352		U1250	G856	G856					A592
C2008	G1903	C1795	A1677	G1567	C1454	U1130	C1251	C957	G857	A677	G771		A677	G583
A2009	G1904	U1796		U1568	G1455	G1131	A1251	C961	C858					C584
G2010	C1905	C1797		C1569	C1461	U1132	A1252		C859	G682	G776		G682	G585
G2011	U1906	U1798	G1681	A1569	C1462	A1133	A1253	U967	U860	U686	G777		A586	
U2012	G1907	C1799	G1682	A1570	C1463	A1134	U1254	C968	A861	C587	G778		C687	G586
A2013	C1908	C1800	U1683	G1571	G1464	G1361	U1256	G969	G862	U687	U779		U688	
A2014	A1913	A1801	G1684	A1572	U1475	C1362	C1257	U970	A863	U688	G780			
					G1476		U1258	G971	G864		A781			U593
A2019	U1917	C1806	A1690	U1578	U1476	A1365	G1259	G972	A1053	C691	A782		C691	U594
	A1918	G1807	C1691	G1581	A1477	A1366		U973	C1054		A783			C595
U2022		A1808	G1478	G1581	A1477	A1367		A972	G1055					U596
C2023	C1924	A1809	G1695		G1479	G1368	A1264	A1143	U1058	G974			U694	



• Molecule 54: 5S ribosomal RNA

Chain 2: 52% 40% 8%



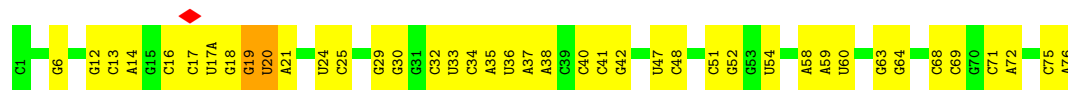
• Molecule 55: tRNA^{fMet}

Chain 5: 73% 21% 6%



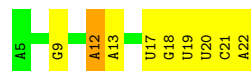
- Molecule 55: tRNA^{fMet}

Chain 6: 



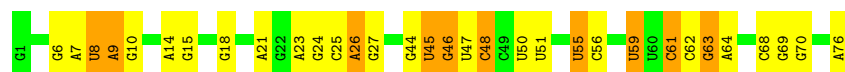
- Molecule 56: mRNA

Chain 4: 



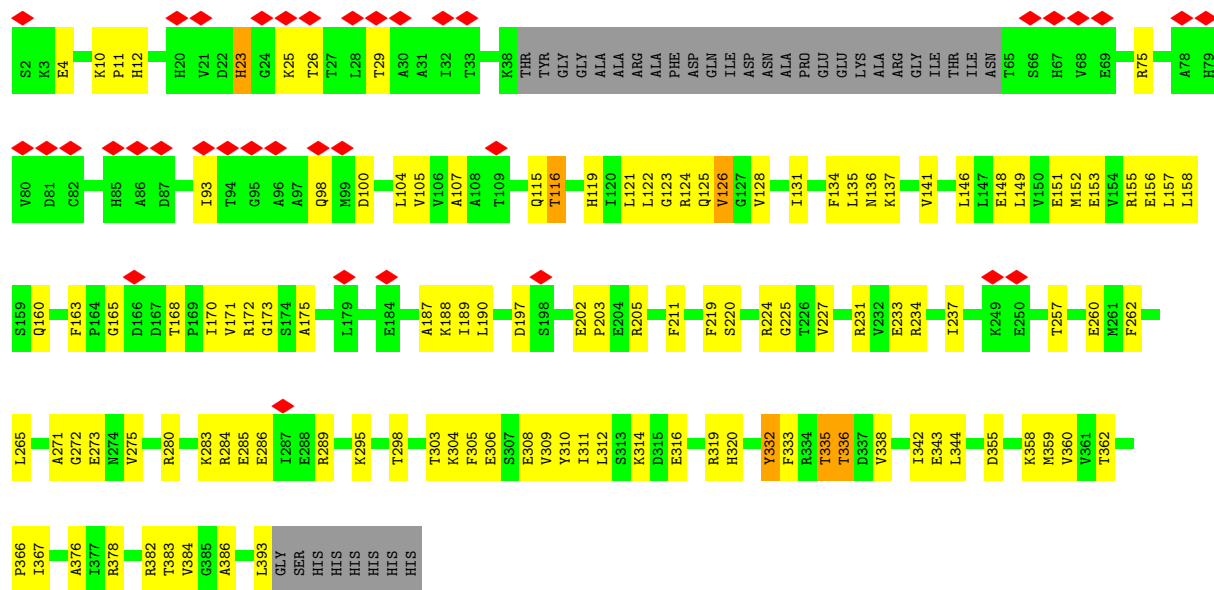
- Molecule 57: tRNA^{Phe}

Chain 7: 



- Molecule 58: Elongation factor Tu

Chain 8: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6805	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	18.305	Depositor
Minimum map value	-10.599	Depositor
Average map value	0.113	Depositor
Map value standard deviation	0.860	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: GDP, 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	0.30	0/2122	0.94	8/2852 (0.3%)
2	c	0.29	0/1586	0.84	1/2134 (0.0%)
3	d	0.28	0/1571	0.86	4/2113 (0.2%)
4	e	0.30	0/1435	0.90	4/1926 (0.2%)
5	f	0.30	0/1343	0.84	1/1816 (0.1%)
6	g	0.32	0/1122	0.93	4/1515 (0.3%)
7	h	0.33	0/1002	1.07	7/1350 (0.5%)
8	i	0.36	0/1046	0.98	7/1410 (0.5%)
9	j	0.29	0/1152	0.84	2/1551 (0.1%)
10	k	0.28	0/948	0.92	4/1268 (0.3%)
11	l	0.30	0/1054	0.96	2/1403 (0.1%)
12	m	0.29	0/1093	0.81	0/1460
13	n	0.30	0/974	0.93	6/1301 (0.5%)
14	o	0.30	0/902	0.87	2/1209 (0.2%)
15	p	0.28	0/929	0.83	1/1242 (0.1%)
16	q	0.28	0/960	0.89	3/1278 (0.2%)
17	r	0.29	0/829	0.88	2/1107 (0.2%)
18	s	0.27	0/864	0.89	1/1156 (0.1%)
19	t	0.27	0/745	0.86	1/994 (0.1%)
20	u	0.29	0/788	0.90	2/1051 (0.2%)
21	v	0.30	0/766	0.91	4/1025 (0.4%)
22	w	0.28	0/582	0.90	2/769 (0.3%)
23	x	0.28	0/635	0.82	2/848 (0.2%)
24	y	0.28	0/510	0.86	2/677 (0.3%)
25	z	0.30	0/453	0.77	1/605 (0.2%)
26	B	0.29	0/450	0.84	1/599 (0.2%)
27	C	0.31	0/417	0.82	1/554 (0.2%)
28	D	0.31	0/380	0.91	1/498 (0.2%)
29	E	0.29	0/513	0.89	3/676 (0.4%)
30	F	0.32	0/303	0.88	0/397
31	G	0.30	0/1788	0.91	6/2408 (0.2%)
32	H	0.32	0/1652	0.92	6/2225 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.29	0/1665	0.85	4/2227 (0.2%)
34	J	0.31	0/1170	1.00	8/1573 (0.5%)
35	K	0.32	0/836	0.97	1/1128 (0.1%)
36	L	0.30	0/1196	0.93	2/1602 (0.1%)
37	M	0.30	0/989	0.90	1/1326 (0.1%)
38	N	0.31	0/1034	0.94	6/1375 (0.4%)
39	O	0.33	0/797	0.93	4/1077 (0.4%)
40	P	0.33	0/886	0.97	3/1195 (0.3%)
41	Q	0.30	0/969	1.01	3/1300 (0.2%)
42	R	0.30	0/893	0.86	0/1193
43	S	0.29	0/817	0.89	4/1088 (0.4%)
44	T	0.28	0/722	0.89	1/964 (0.1%)
45	U	0.31	0/659	0.89	0/884
46	V	0.30	0/658	0.92	1/881 (0.1%)
47	W	0.33	0/545	0.97	3/731 (0.4%)
48	X	0.31	0/653	0.86	2/877 (0.2%)
49	Y	0.29	0/671	0.93	4/888 (0.5%)
50	Z	0.34	0/551	1.02	5/728 (0.7%)
51	a	0.31	0/1034	0.77	0/1387
52	3	0.41	0/36963	0.47	4/57662 (0.0%)
53	1	0.40	0/69796	0.48	2/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.40	0/1832	0.45	0/2855
55	6	0.41	0/1832	0.47	0/2855
56	4	0.41	0/436	0.47	0/679
57	7	0.40	0/1809	0.49	0/2819
58	8	0.32	0/2885	0.89	8/3902 (0.2%)
All	All	0.37	0/166084	0.62	157/247980 (0.1%)

There are no bond length outliers.

The worst 5 of 157 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	8	336	THR	N-CA-C	9.46	122.04	110.41
41	Q	20	VAL	N-CA-C	9.00	118.32	107.61
7	h	43	LYS	N-CA-C	-8.34	101.73	112.23
41	Q	114	SER	N-CA-C	-8.23	102.28	111.82
7	h	117	LEU	N-CA-C	8.21	122.96	109.24

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	76	0
2	c	1565	0	1616	39	0
3	d	1552	0	1619	43	0
4	e	1411	0	1447	42	0
5	f	1323	0	1374	30	0
6	g	1111	0	1148	25	0
7	h	989	0	1025	53	0
8	i	1032	0	1088	50	0
9	j	1129	0	1162	34	0
10	k	939	0	1012	42	0
11	l	1045	0	1117	25	0
12	m	1074	0	1157	38	0
13	n	961	0	1000	21	0
14	o	892	0	923	23	0
15	p	917	0	965	43	0
16	q	947	0	1022	21	0
17	r	816	0	839	14	0
18	s	857	0	922	20	0
19	t	739	0	807	31	0
20	u	780	0	834	16	0
21	v	753	0	780	18	0
22	w	575	0	592	13	0
23	x	625	0	655	17	0
24	y	509	0	543	16	0
25	z	449	0	491	9	0
26	B	444	0	461	15	0
27	C	410	0	440	13	0
28	D	377	0	418	15	0
29	E	504	0	574	14	0
30	F	302	0	343	16	0
31	G	1757	0	1787	38	0
32	H	1625	0	1699	51	0
33	I	1643	0	1710	63	0
34	J	1157	0	1199	42	0
35	K	818	0	808	42	0
36	L	1182	0	1240	35	0
37	M	979	0	1034	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	46	0
39	O	787	0	828	37	0
40	P	870	0	878	31	0
41	Q	955	0	1019	29	0
42	R	884	0	944	44	0
43	S	805	0	847	44	0
44	T	714	0	737	12	0
45	U	649	0	666	33	0
46	V	649	0	691	25	0
47	W	536	0	552	11	0
48	X	638	0	665	22	0
49	Y	665	0	714	22	0
50	Z	545	0	579	36	0
51	a	1027	0	1092	38	0
52	3	33012	0	16618	538	0
53	1	62317	0	31346	903	0
54	2	2568	0	1303	56	0
55	5	1640	0	836	17	0
55	6	1640	0	837	31	0
56	4	388	0	196	9	0
57	7	1619	0	821	38	0
58	8	2833	0	2857	79	0
59	5	10	0	10	0	0
60	7	11	0	8	2	0
61	8	28	0	12	0	0
All	All	153083	0	104134	2821	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 2821 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)
53:1:1906:G:H2'	53:1:1907:G:H5''	1.42	0.98
53:1:2277:G:H2'	53:1:2278:A:H5''	1.43	0.98
52:3:225:C:H2'	52:3:226:G:H5''	1.46	0.97
53:1:45:G:H5''	53:1:46:G:H5'	1.46	0.97
52:3:1259:C:H3'	52:3:1260:G:H5''	1.45	0.96

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	236/271 (87%)	208 (88%)	23 (10%)	5 (2%)	5	31
2	c	76/209 (36%)	66 (87%)	10 (13%)	0	100	100
3	d	183/201 (91%)	153 (84%)	28 (15%)	2 (1%)	11	42
4	e	175/177 (99%)	154 (88%)	19 (11%)	2 (1%)	11	42
5	f	116/176 (66%)	105 (90%)	8 (7%)	3 (3%)	4	28
6	g	101/149 (68%)	90 (89%)	10 (10%)	1 (1%)	12	43
7	h	129/131 (98%)	95 (74%)	28 (22%)	6 (5%)	2	18
8	i	139/141 (99%)	122 (88%)	15 (11%)	2 (1%)	9	37
9	j	140/142 (99%)	127 (91%)	12 (9%)	1 (1%)	18	50
10	k	120/122 (98%)	103 (86%)	14 (12%)	3 (2%)	4	29
11	l	141/143 (99%)	119 (84%)	16 (11%)	6 (4%)	2	19
12	m	134/136 (98%)	113 (84%)	19 (14%)	2 (2%)	8	36
13	n	118/120 (98%)	97 (82%)	19 (16%)	2 (2%)	7	34
14	o	114/116 (98%)	99 (87%)	13 (11%)	2 (2%)	6	34
15	p	112/114 (98%)	92 (82%)	20 (18%)	0	100	100
16	q	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
17	r	101/103 (98%)	85 (84%)	14 (14%)	2 (2%)	6	32
18	s	108/110 (98%)	92 (85%)	15 (14%)	1 (1%)	14	45
19	t	91/93 (98%)	83 (91%)	8 (9%)	0	100	100
20	u	100/102 (98%)	85 (85%)	10 (10%)	5 (5%)	1	17
21	v	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
22	w	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
23	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	y	61/63 (97%)	58 (95%)	3 (5%)	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%)	50 (93%)	4 (7%)	0	100	100
27	C	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
28	D	44/46 (96%)	36 (82%)	8 (18%)	0	100	100
29	E	62/64 (97%)	53 (86%)	7 (11%)	2 (3%)	3	25
30	F	36/38 (95%)	28 (78%)	8 (22%)	0	100	100
31	G	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
32	H	204/206 (99%)	187 (92%)	16 (8%)	1 (0%)	24	56
33	I	203/205 (99%)	172 (85%)	31 (15%)	0	100	100
34	J	155/157 (99%)	126 (81%)	25 (16%)	4 (3%)	4	28
35	K	98/100 (98%)	79 (81%)	12 (12%)	7 (7%)	1	12
36	L	149/151 (99%)	133 (89%)	16 (11%)	0	100	100
37	M	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	48
38	N	125/127 (98%)	101 (81%)	20 (16%)	4 (3%)	3	25
39	O	96/98 (98%)	82 (85%)	10 (10%)	4 (4%)	2	20
40	P	114/116 (98%)	89 (78%)	21 (18%)	4 (4%)	3	24
41	Q	121/123 (98%)	95 (78%)	18 (15%)	8 (7%)	1	13
42	R	112/114 (98%)	96 (86%)	13 (12%)	3 (3%)	4	27
43	S	98/100 (98%)	81 (83%)	15 (15%)	2 (2%)	6	32
44	T	86/88 (98%)	78 (91%)	7 (8%)	1 (1%)	10	40
45	U	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	4	29
46	V	78/80 (98%)	64 (82%)	12 (15%)	2 (3%)	4	28
47	W	63/65 (97%)	58 (92%)	2 (3%)	3 (5%)	2	17
48	X	77/79 (98%)	65 (84%)	10 (13%)	2 (3%)	4	28
49	Y	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	40
50	Z	63/65 (97%)	45 (71%)	12 (19%)	6 (10%)	0	7
51	a	130/223 (58%)	126 (97%)	4 (3%)	0	100	100
58	8	362/400 (90%)	329 (91%)	31 (9%)	2 (1%)	21	52
All	All	5997/6512 (92%)	5210 (87%)	683 (11%)	104 (2%)	9	34

5 of 104 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	204	LEU

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Mol	Chain	Res	Type
1	b	232	GLY
7	h	108	VAL
7	h	118	ILE
9	j	81	ILE

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	143 (9%)	5 (0%)
53	1	2902/2903 (99%)	330 (11%)	12 (0%)
54	2	119/120 (99%)	9 (7%)	1 (0%)
55	5	76/77 (98%)	6 (7%)	0
55	6	76/77 (98%)	6 (7%)	0
56	4	17/18 (94%)	3 (17%)	0
57	7	75/76 (98%)	14 (18%)	0
All	All	4803/4810 (99%)	511 (10%)	18 (0%)

5 of 511 RNA backbone outliers are listed below:

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

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	2326	C
54	2	88	C
53	1	2756	U
53	1	859	G
53	1	2296	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
61	GDP	8	501	-	29,30,30	1.44	4 (13%)	45,47,47	1.95	14 (31%)
60	PHE	7	101	57	10,11,12	0.73	0	8,13,15	0.25	0
59	FME	5	101	55	8,9,10	0.48	0	8,9,11	0.82	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
61	GDP	8	501	-	-	5/16/32/32	0/3/3/3
60	PHE	7	101	57	-	0/5/6/8	0/1/1/1
59	FME	5	101	55	-	1/7/9/11	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GDP	PB-O1B	3.97	1.62	1.50
61	8	501	GDP	O4'-C1'	2.31	1.47	1.42
61	8	501	GDP	PA-O3A	2.19	1.61	1.59
61	8	501	GDP	PB-O3B	2.01	1.62	1.54

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	C5-C4-N3	-5.65	119.39	128.39
61	8	501	GDP	C2-N3-C4	5.51	121.78	112.30
61	8	501	GDP	N9-C4-N3	4.04	134.03	125.95
61	8	501	GDP	C8-N7-C5	3.01	109.63	104.26
61	8	501	GDP	C2-N1-C6	-2.69	120.23	125.11

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

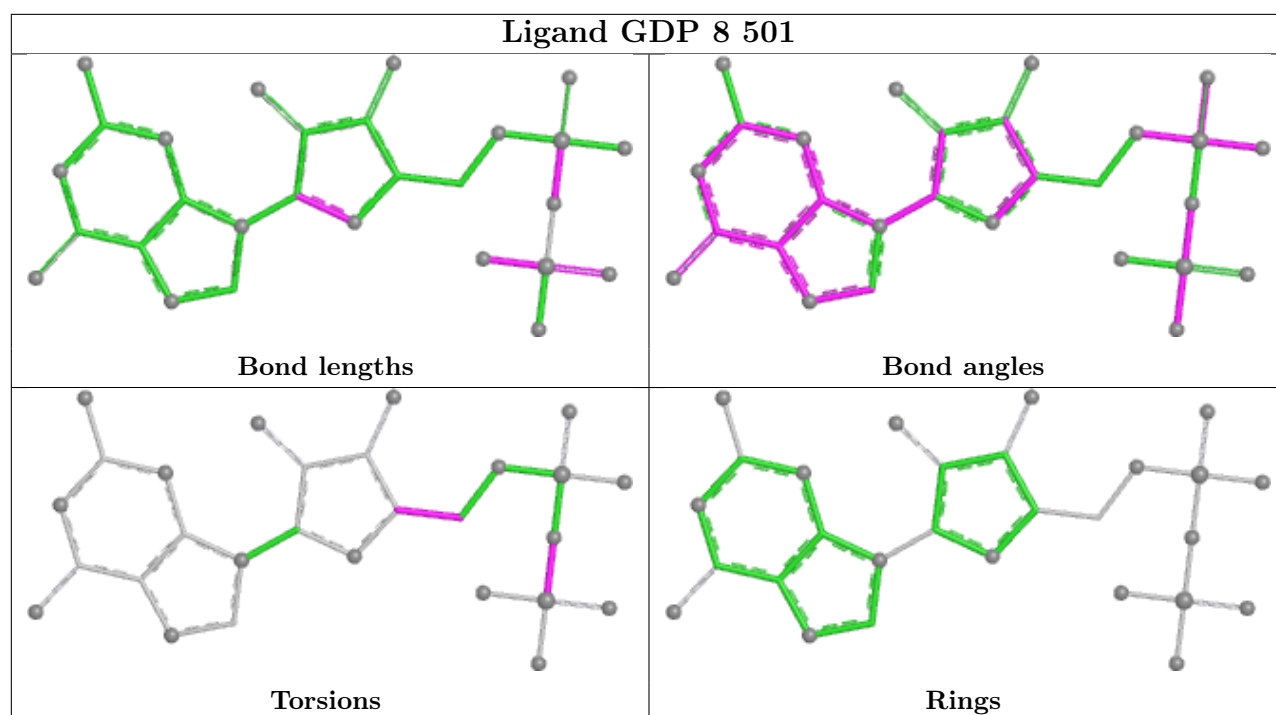
Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA
61	8	501	GDP	PA-O3A-PB-O2B
61	8	501	GDP	PA-O3A-PB-O3B
61	8	501	GDP	O4'-C4'-C5'-O5'
61	8	501	GDP	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

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

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

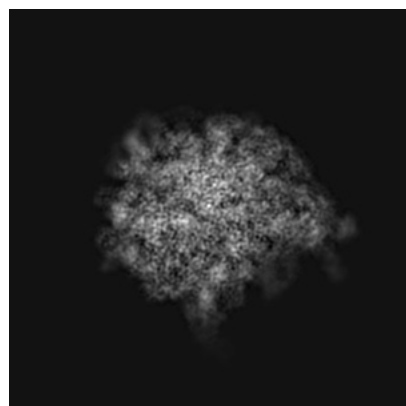
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21623. These allow visual inspection of the internal detail of the map and identification of artifacts.

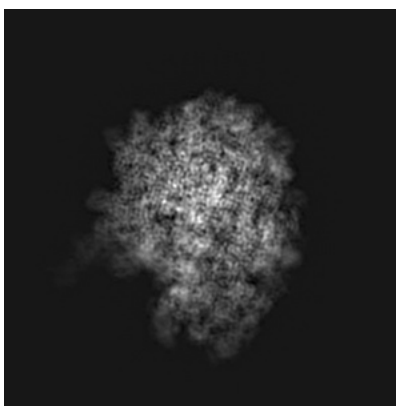
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

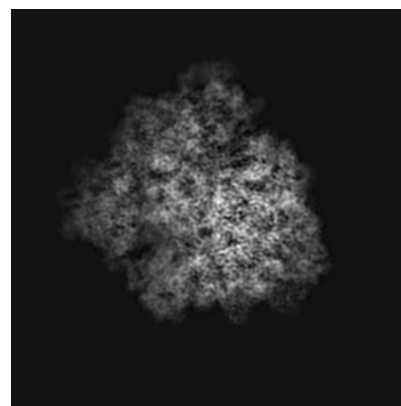
6.1.1 Primary map



X

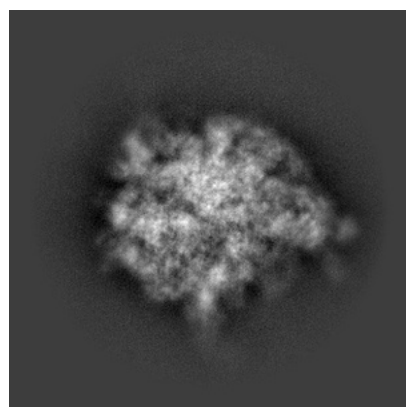


Y

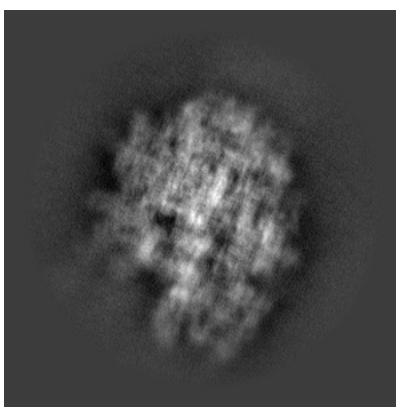


Z

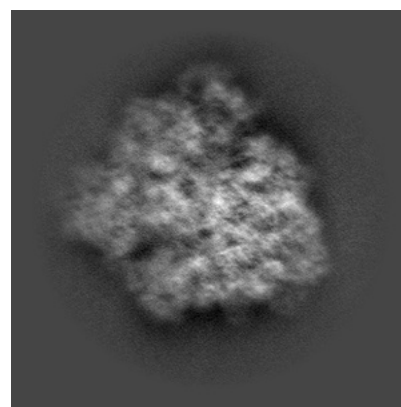
6.1.2 Raw map



X



Y

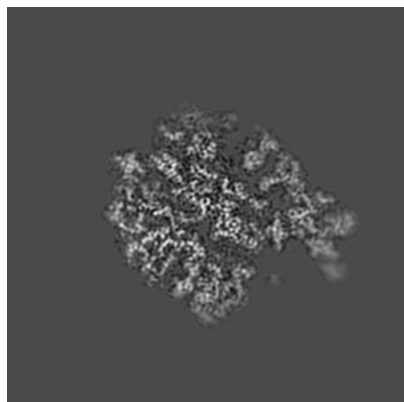


Z

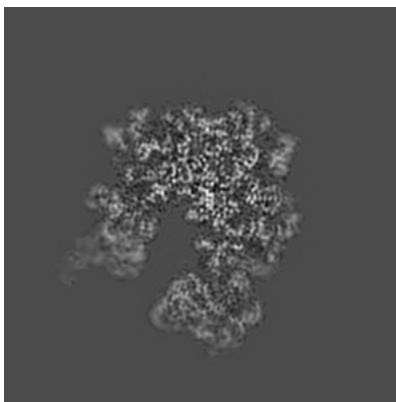
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

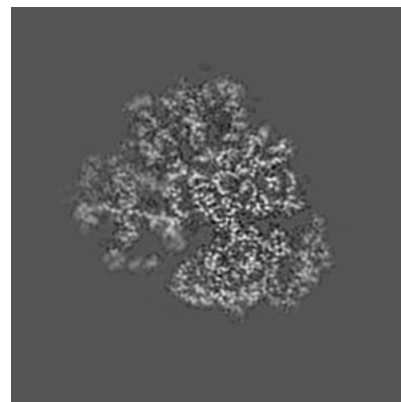
6.2.1 Primary map



X Index: 144

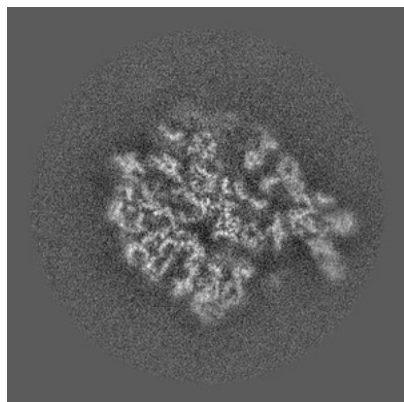


Y Index: 144

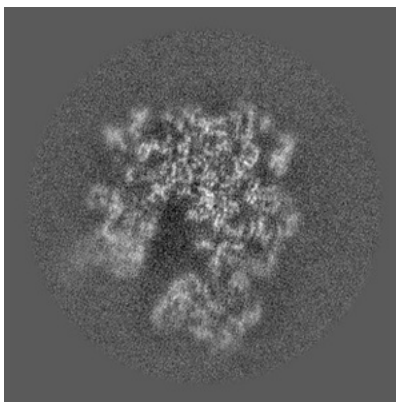


Z Index: 144

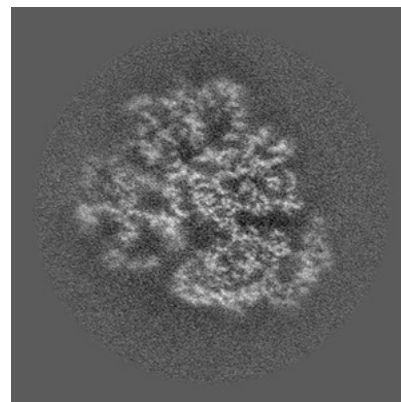
6.2.2 Raw map



X Index: 144



Y Index: 144

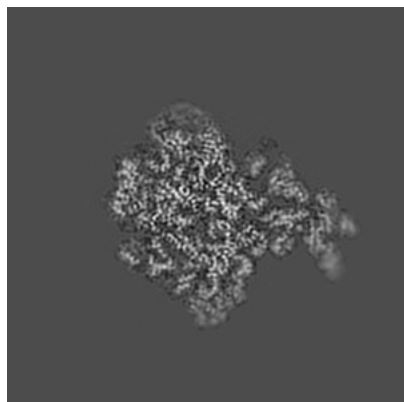


Z Index: 144

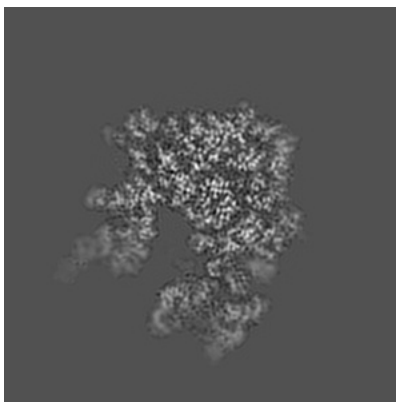
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

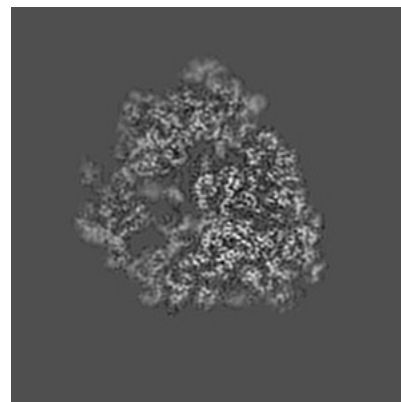
6.3.1 Primary map



X Index: 149

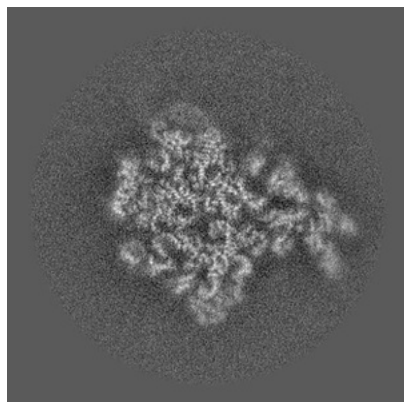


Y Index: 148

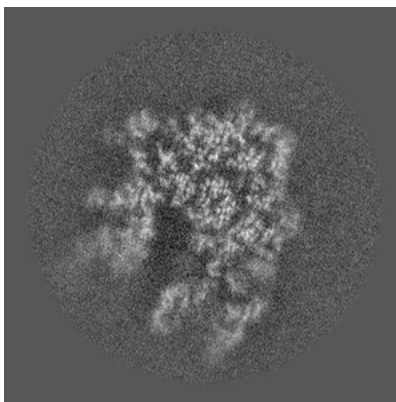


Z Index: 135

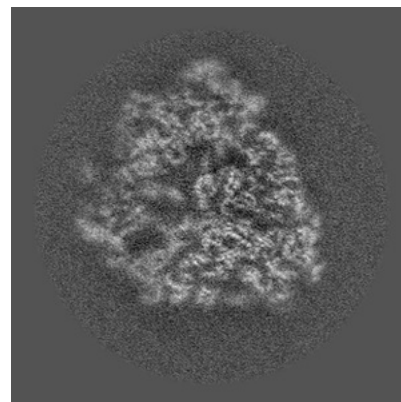
6.3.2 Raw map



X Index: 149



Y Index: 148

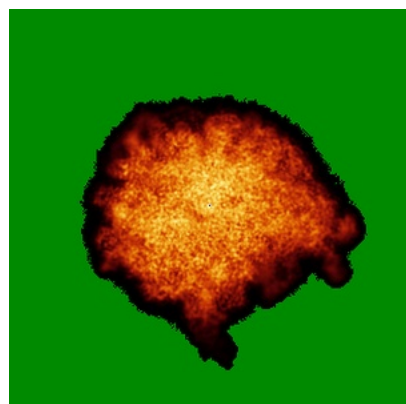


Z Index: 135

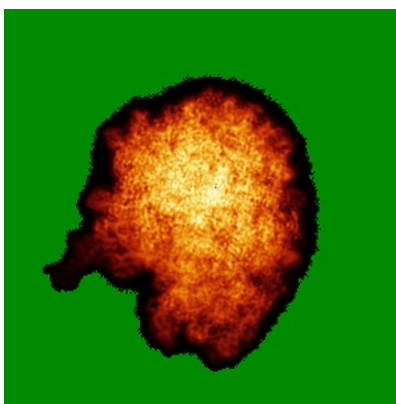
The images above show the largest variance slices of the map in three orthogonal directions.

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

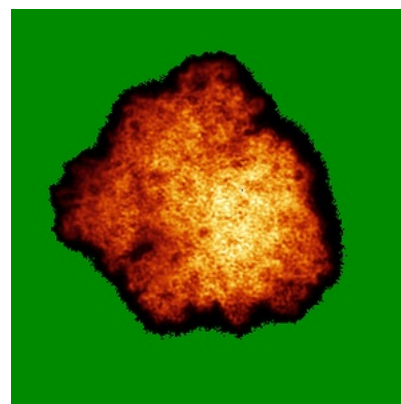
6.4.1 Primary map



X

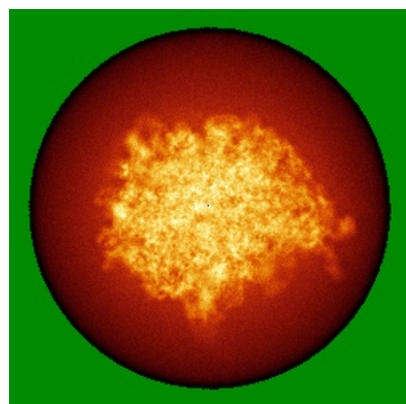


Y

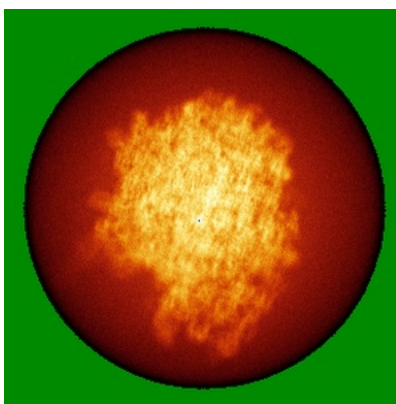


Z

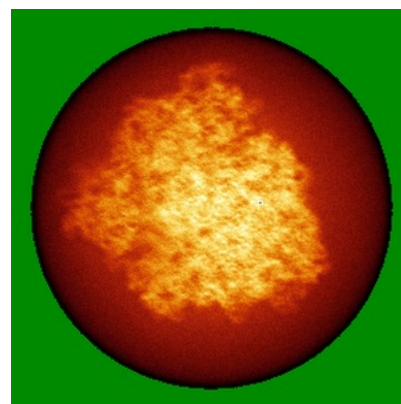
6.4.2 Raw map



X



Y

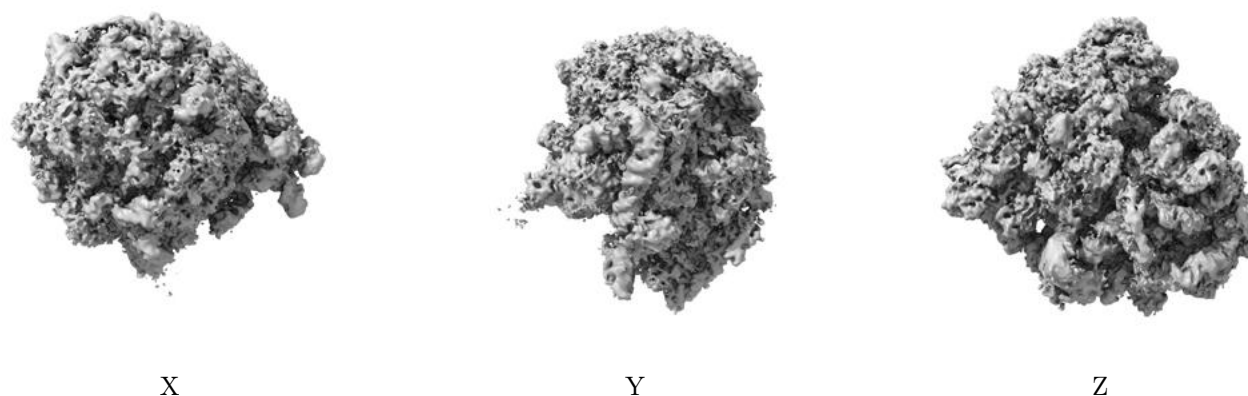


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

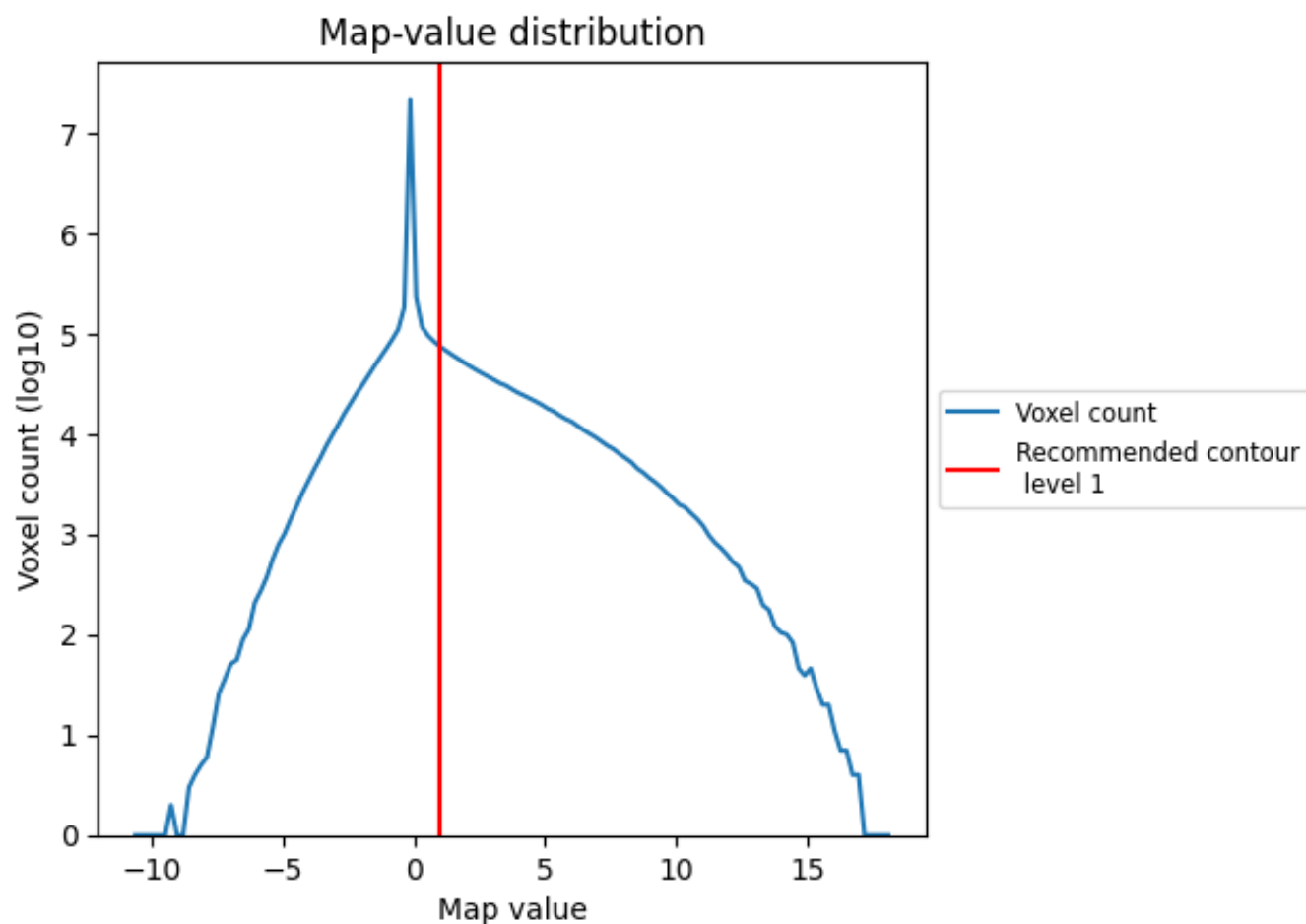
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

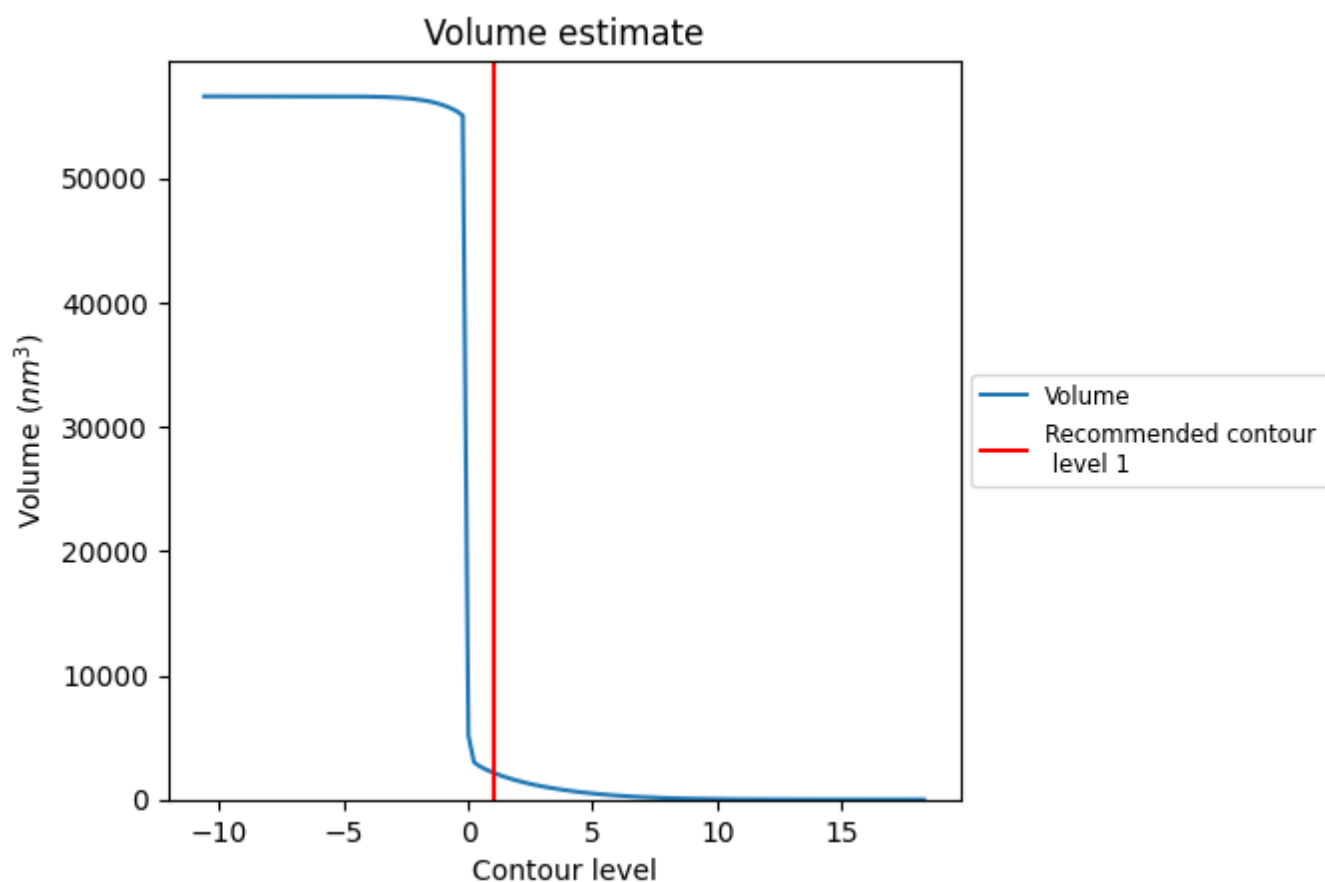
This section contains the results of statistical analysis of the map.

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.

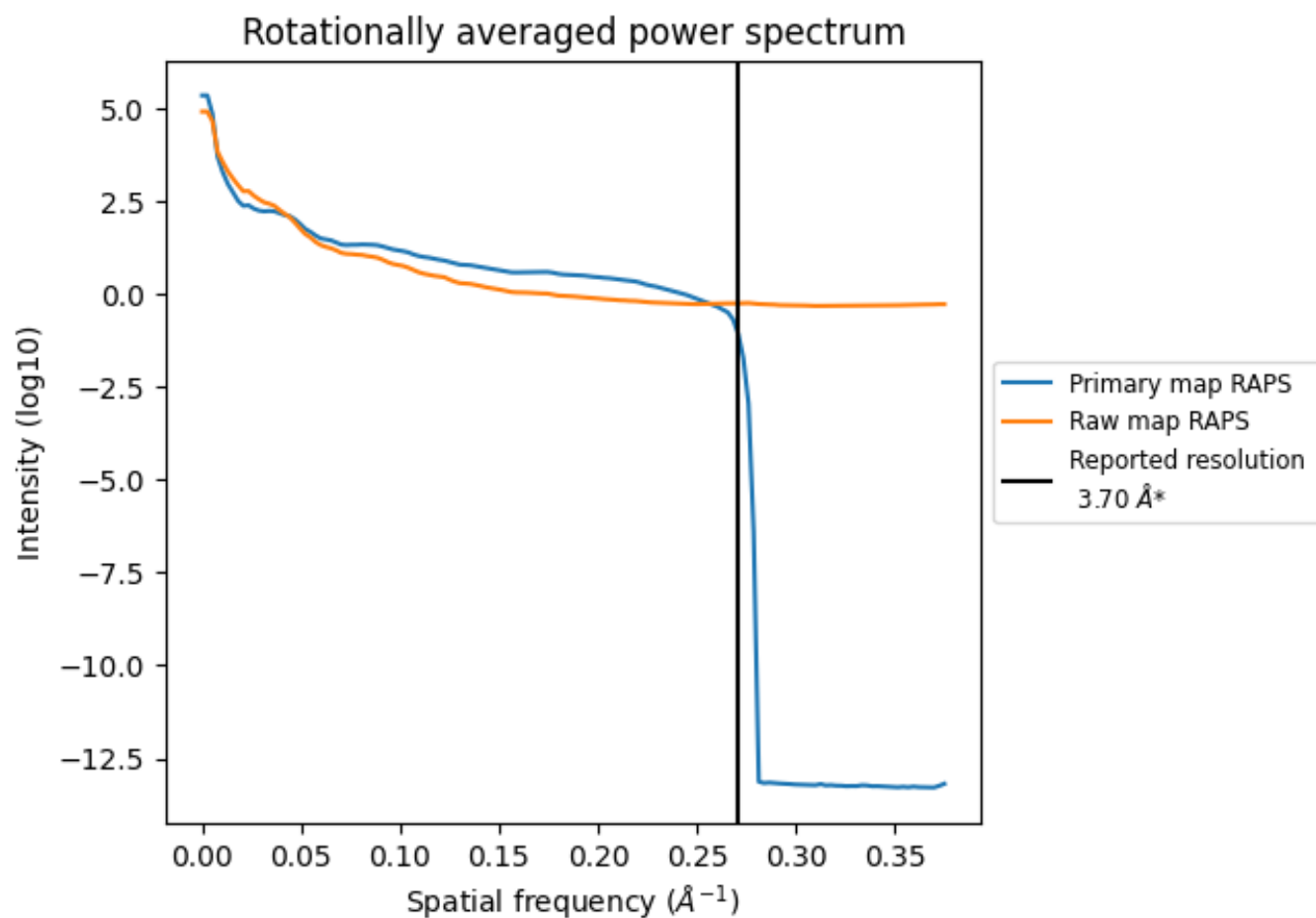
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2174 nm³; this corresponds to an approximate mass of 1964 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

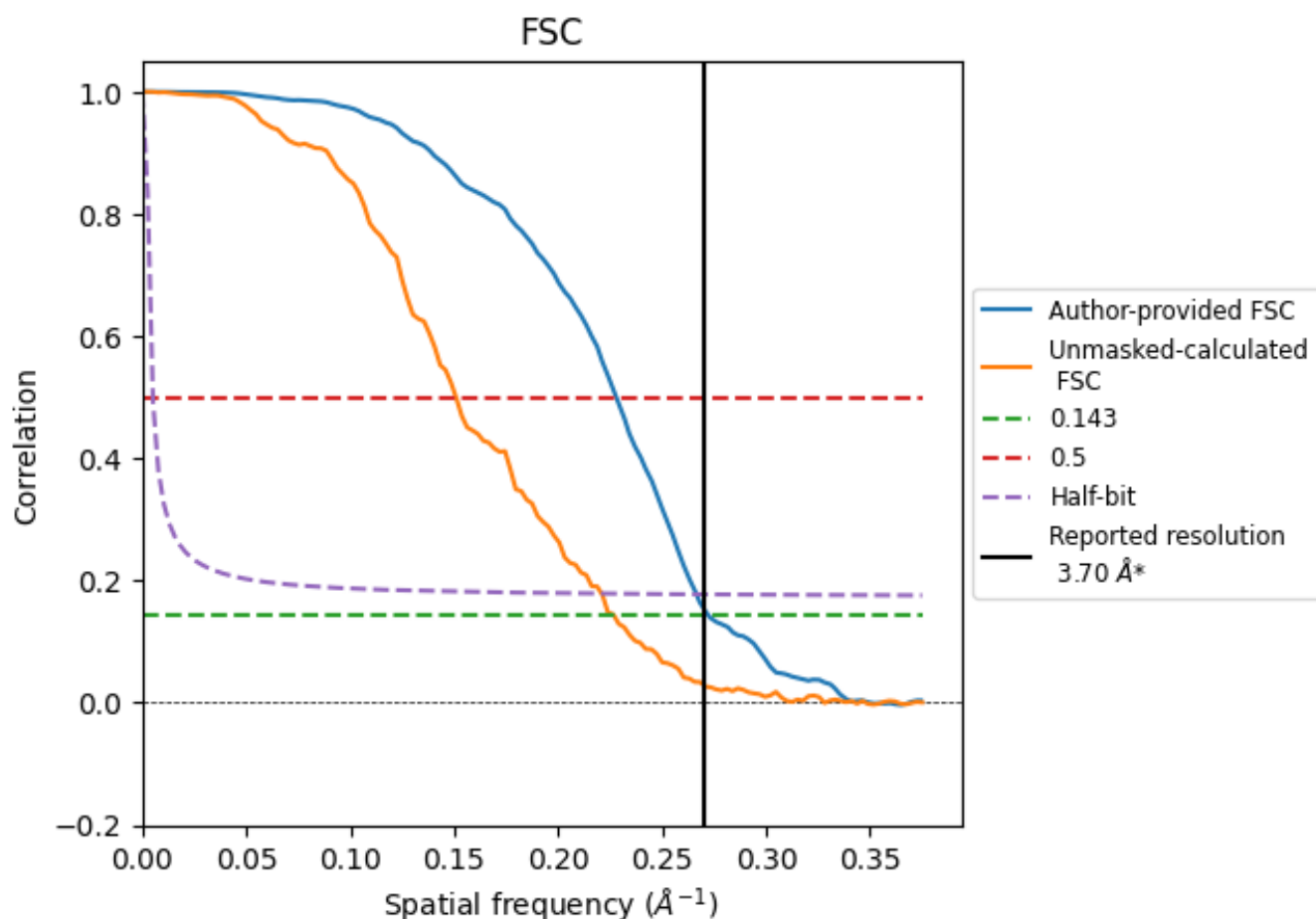


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.67	4.39	3.75
Unmasked-calculated*	4.41	6.63	4.53

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21623 and PDB model 6WD4. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)

This section was not generated.

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

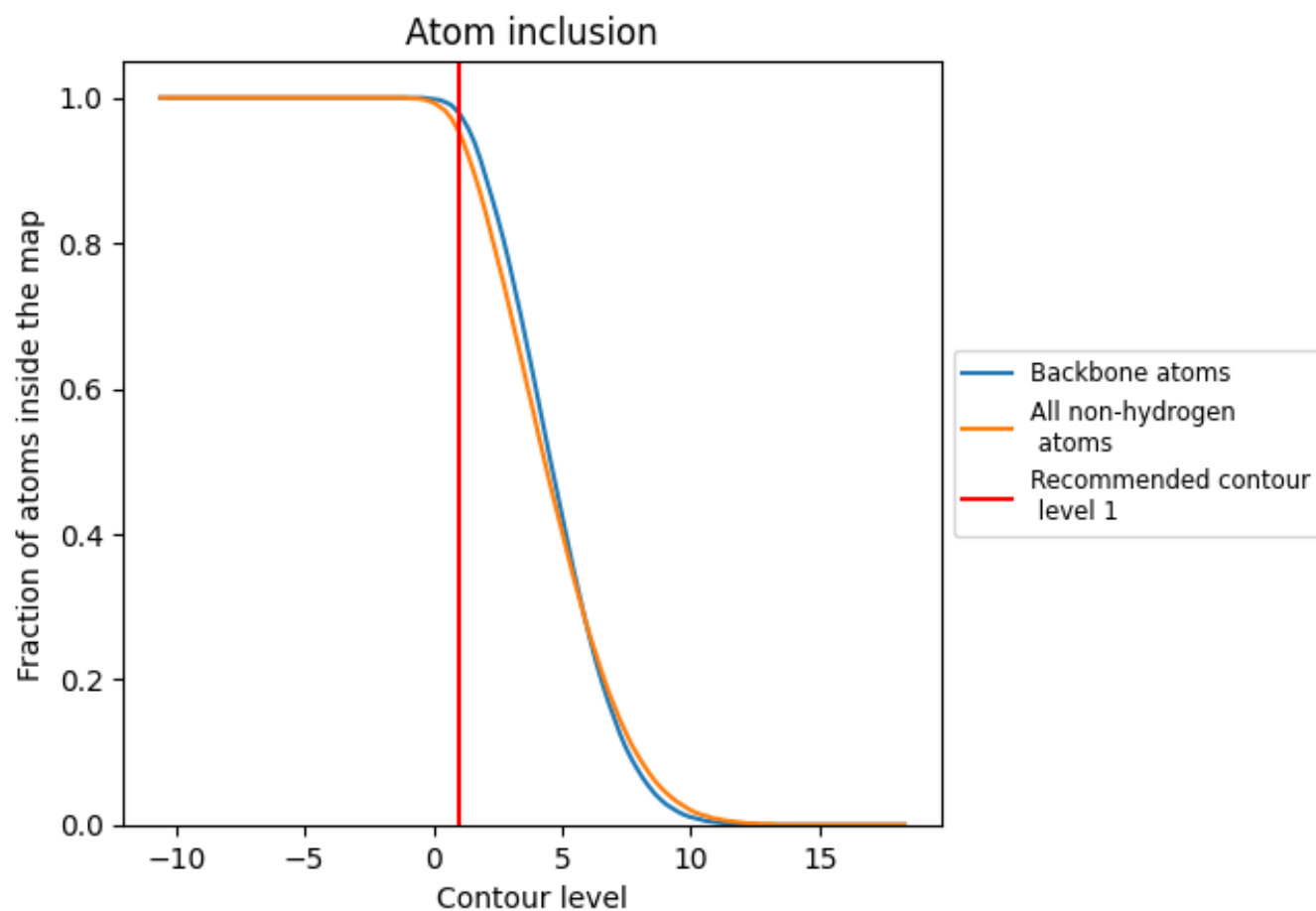


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

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	 0.9530	 0.3610
1	 0.9830	 0.3810
2	 0.9860	 0.3380
3	 0.9770	 0.3510
4	 0.8840	 0.2510
5	 0.9580	 0.3000
6	 0.8320	 0.1500
7	 0.9140	 0.1910
8	 0.8080	 0.1840
B	 0.9530	 0.4320
C	 0.8430	 0.3760
D	 0.9210	 0.4480
E	 0.9510	 0.4640
F	 0.8660	 0.4320
G	 0.8920	 0.3130
H	 0.7620	 0.3170
I	 0.8830	 0.3220
J	 0.9180	 0.3810
K	 0.9540	 0.3680
L	 0.9320	 0.3500
M	 0.9080	 0.3810
N	 0.9100	 0.3220
O	 0.7350	 0.2790
P	 0.9500	 0.3820
Q	 0.9050	 0.4120
R	 0.9350	 0.3450
S	 0.8220	 0.3330
T	 0.9510	 0.3770
U	 0.9120	 0.3880
V	 0.9160	 0.3960
W	 0.9400	 0.3680
X	 0.9570	 0.3300
Y	 0.9000	 0.3500
Z	 0.8650	 0.3070
a	 0.8340	 0.1500



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Chain	Atom inclusion	Q-score
b	 0.9540	 0.4520
c	 0.9450	 0.4470
d	 0.9420	 0.4060
e	 0.9260	 0.3360
f	 0.9660	 0.3690
g	 0.7930	 0.2920
h	 0.7840	 0.1630
i	 0.7250	 0.1970
j	 0.9510	 0.4400
k	 0.9310	 0.4460
l	 0.9600	 0.4240
m	 0.9250	 0.4470
n	 0.9500	 0.4360
o	 0.9460	 0.3720
p	 0.9360	 0.4320
q	 0.9280	 0.4250
r	 0.9510	 0.4130
s	 0.9210	 0.4300
t	 0.9270	 0.4040
u	 0.9300	 0.3860
v	 0.9470	 0.3920
w	 0.9450	 0.4570
x	 0.9600	 0.4310
y	 0.9300	 0.3350
z	 0.9340	 0.4310