



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:10 PM UTC

PDB ID : 6WD6 / pdb_00006wd6
EMDB ID : EMD-21625
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure II-C2)
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

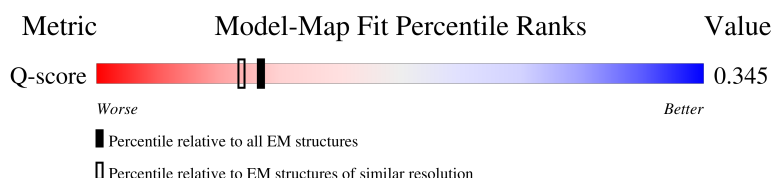
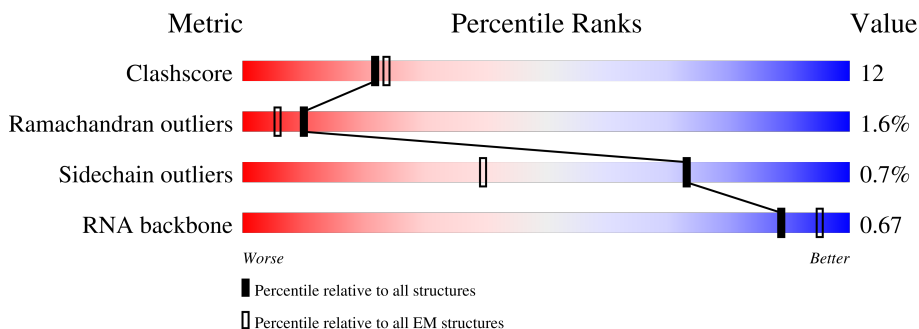
1 Overall quality at a glance

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.



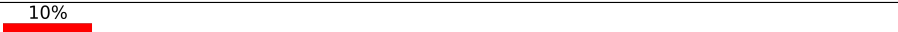
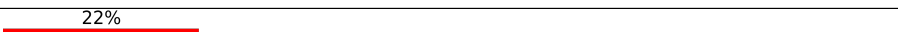
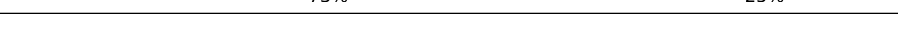
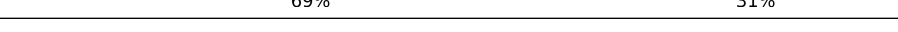
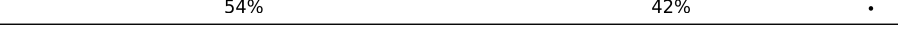
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

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

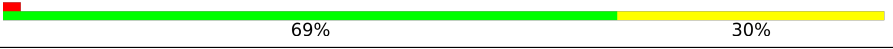
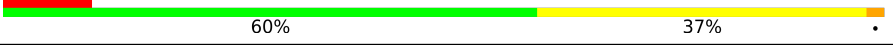
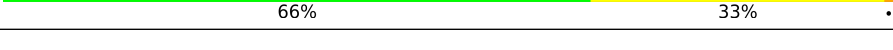
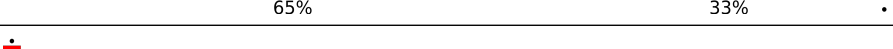
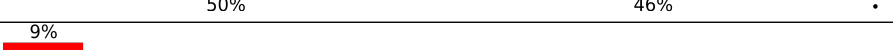
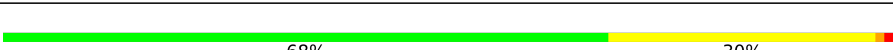
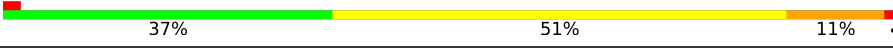
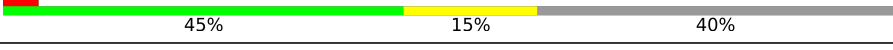
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	

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

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Mol	Chain	Length	Quality of chain
54	2	120	50% 42% 8%
55	5	77	68% 26% 6%
55	6	77	53% 44%
56	4	18	50% 50%
57	7	76	53% 37% 11%
58	8	400	28% 60% 32% 7%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 153103 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 802133627

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

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 55 is a RNA chain called 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		

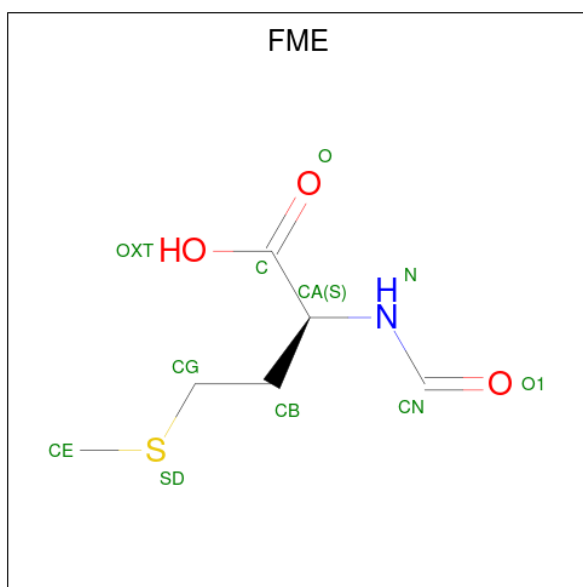
- Molecule 58 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	371	Total	C	N	O	S	0	0
			2853	1804	490	546	13		

There are 7 discrepancies between the modelled and reference sequences:

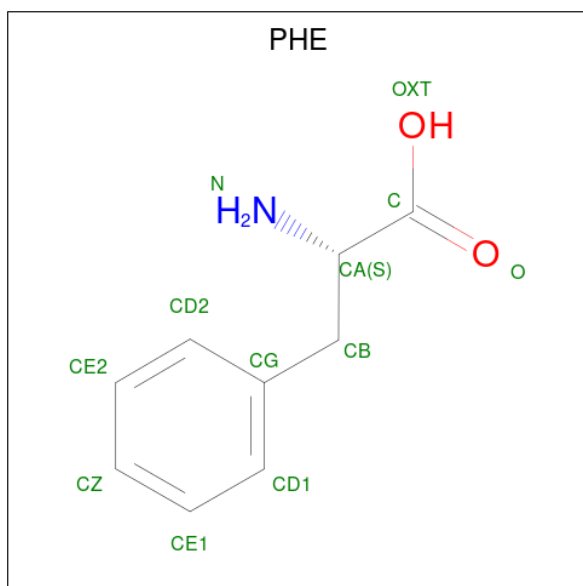
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag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

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



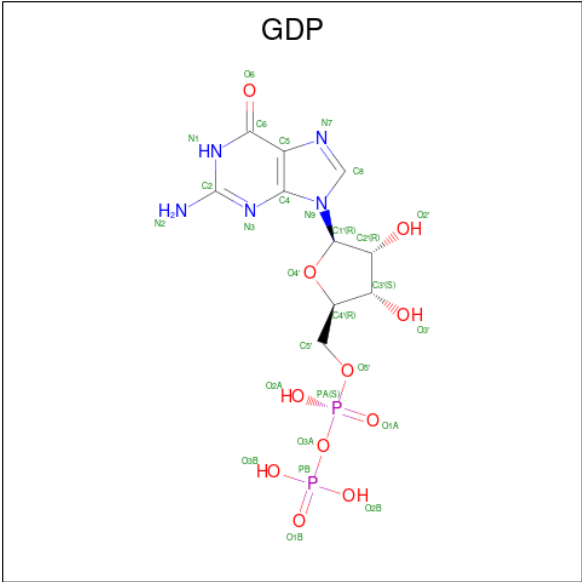
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

- 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		

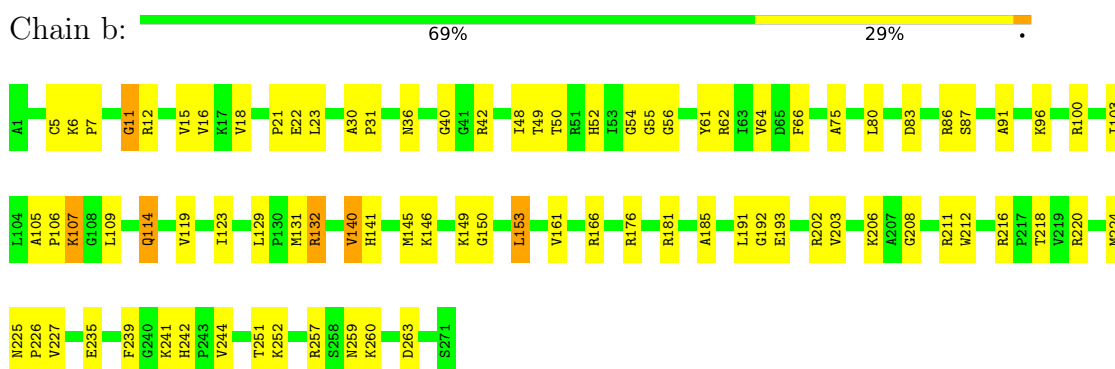
- Molecule 61 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



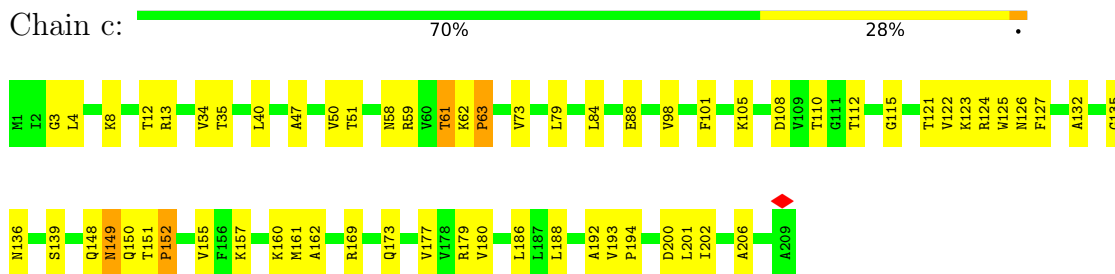
3 Residue-property plots

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.

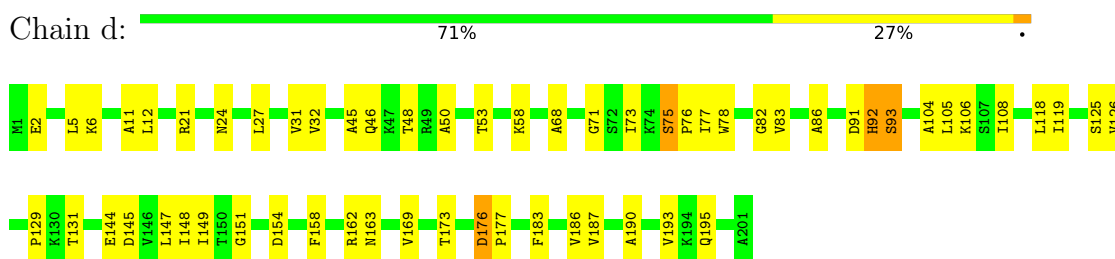
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

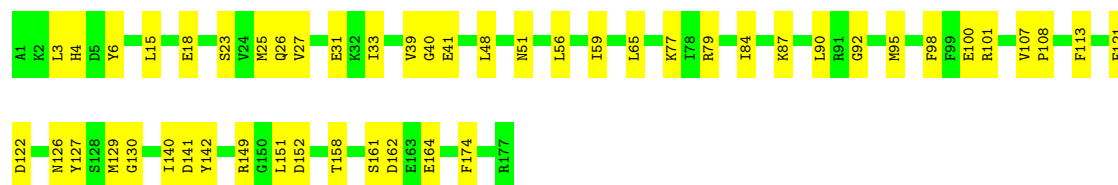


- Molecule 3: 50S ribosomal protein L4



- Molecule 4: 50S ribosomal protein L5





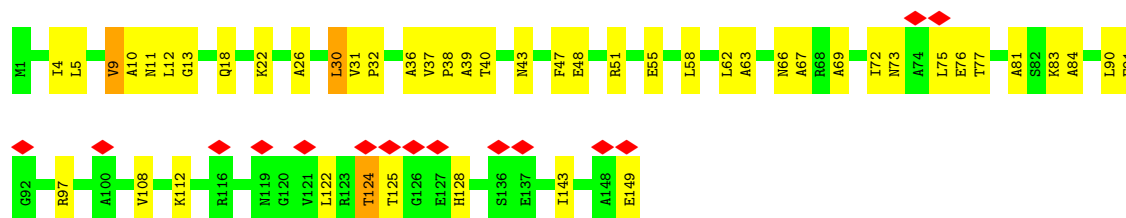
• Molecule 5: 50S ribosomal protein L6

Chain f: 79% 19% .



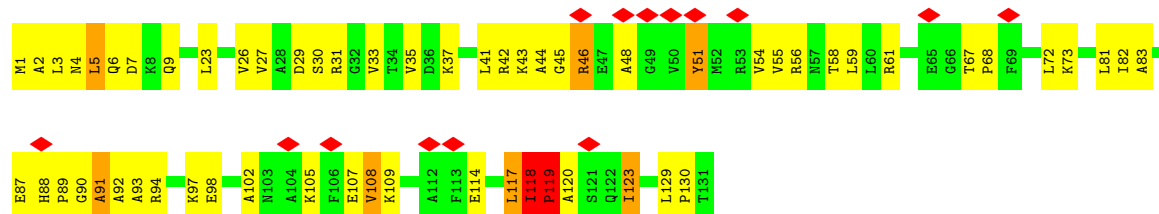
• Molecule 6: 50S ribosomal protein L9

Chain g: 10% 68% 30% .



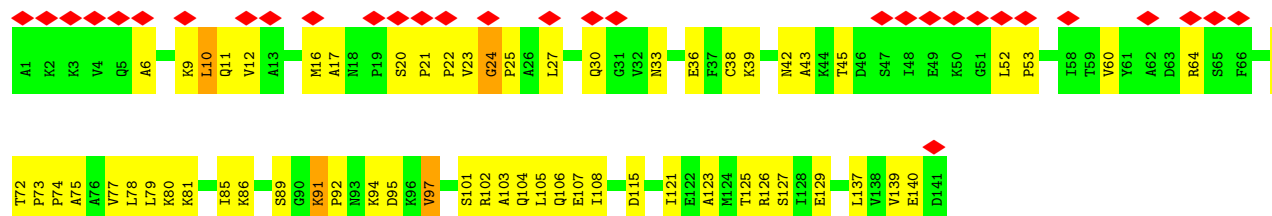
• Molecule 7: 50S ribosomal protein L10

Chain h: 11% 53% 40% 5% .



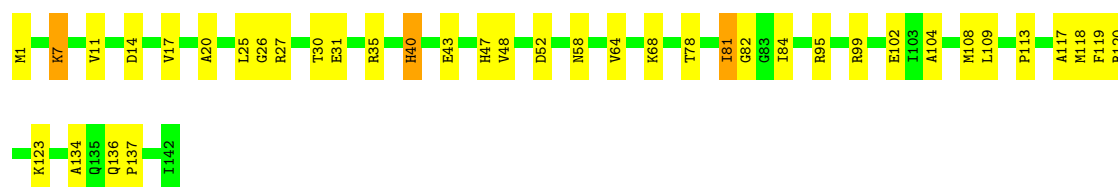
• Molecule 8: 50S ribosomal protein L11

Chain i: 22% 56% 41% .

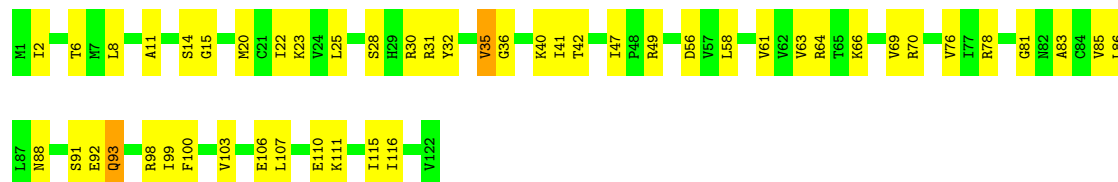


• Molecule 9: 50S ribosomal protein L13

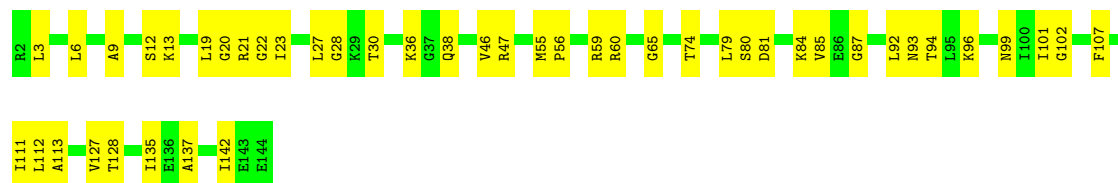
Chain j: 73% 25% .



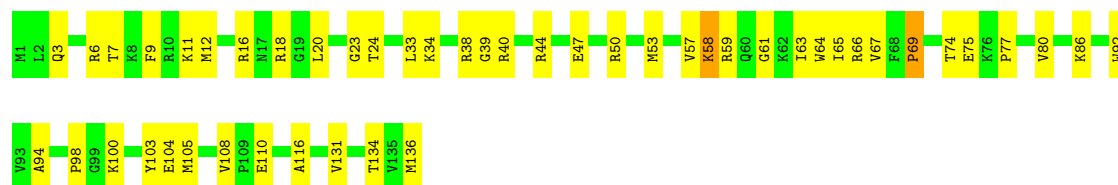
• Molecule 10: 50S ribosomal protein L14



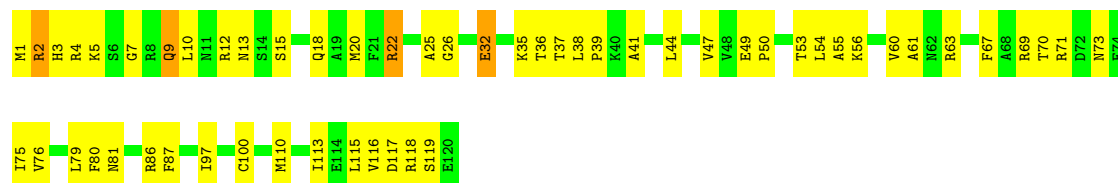
• Molecule 11: 50S ribosomal protein L15



• Molecule 12: 50S ribosomal protein L16

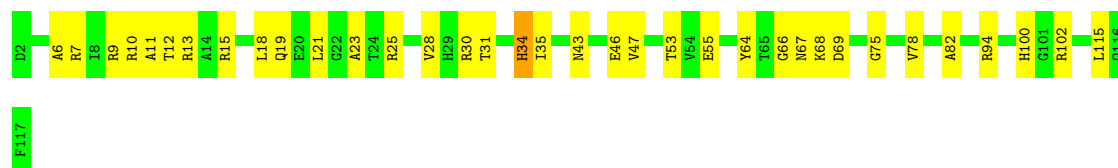


• Molecule 13: 50S ribosomal protein L17



• Molecule 14: 50S ribosomal protein L18





- Molecule 15: 50S ribosomal protein L19

Chain p: 67% 32%



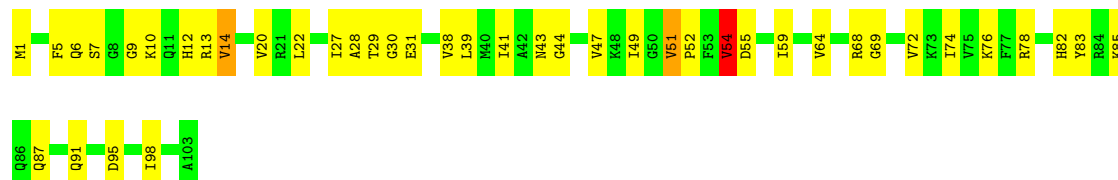
- Molecule 16: 50S ribosomal protein L20

Chain q: 81% 18%



- Molecule 17: 50S ribosomal protein L21

Chain r: 59% 38%



- Molecule 18: 50S ribosomal protein L22

Chain s: 66% 33%



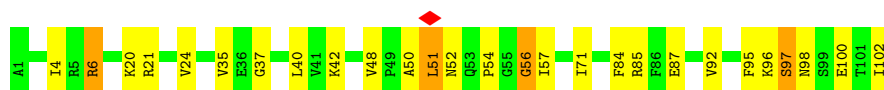
- Molecule 19: 50S ribosomal protein L23

Chain t: 73% 25%



- Molecule 20: 50S ribosomal protein L24

Chain u:  74% 23%



- Molecule 21: 50S ribosomal protein L25

Chain v:  76% 24%



- Molecule 22: 50S ribosomal protein L27

Chain w:  76% 24%



- Molecule 23: 50S ribosomal protein L28

Chain x:  71% 29%



- Molecule 24: 50S ribosomal protein L29

Chain y:  67% 33%



- Molecule 25: 50S ribosomal protein L30

Chain z:  74% 26%



- Molecule 26: 50S ribosomal protein L32

Chain B:  77% 23%



- Molecule 27: 50S ribosomal protein L33

Chain C:  68% 30%



- Molecule 28: 50S ribosomal protein L34

Chain D:  76% 22%



- Molecule 29: 50S ribosomal protein L35

Chain E:  75% 20% 5%



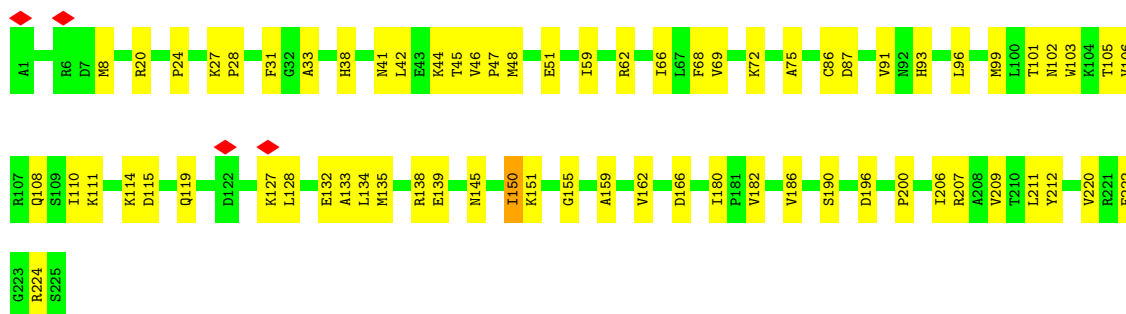
- Molecule 30: 50S ribosomal protein L36

Chain F:  74% 26%



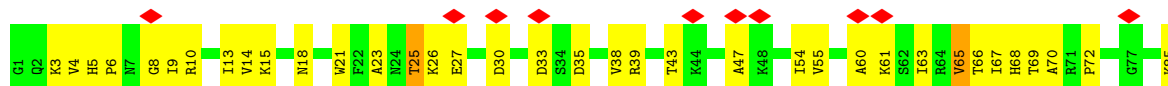
- Molecule 31: 30S ribosomal protein S2

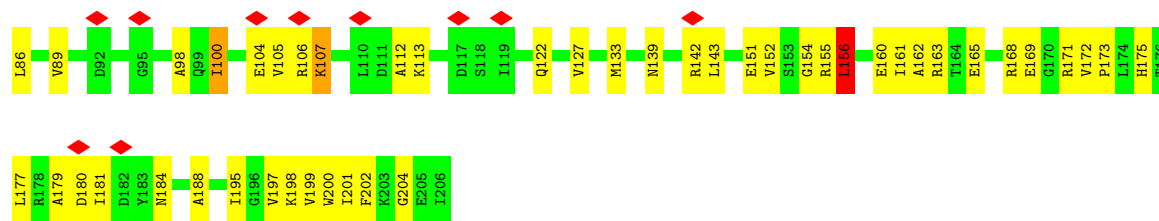
Chain G:  69% 30%



- Molecule 32: 30S ribosomal protein S3

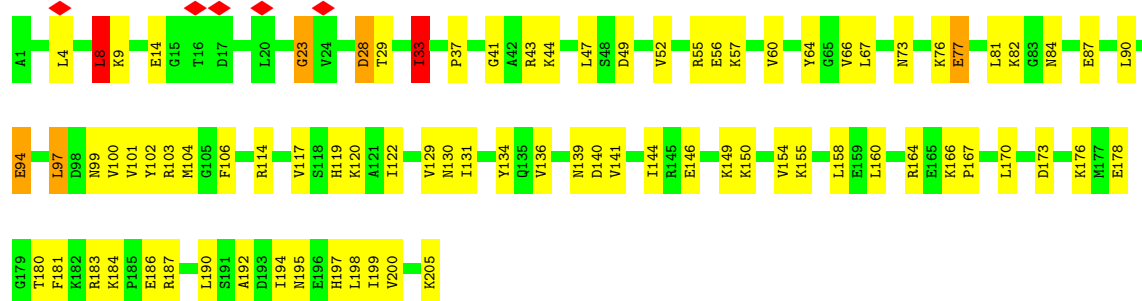
Chain H:  10% 60% 37%





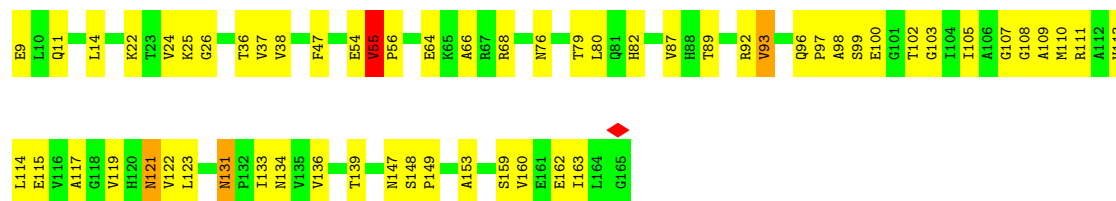
- Molecule 33: 30S ribosomal protein S4

Chain I: 60% 37% ..



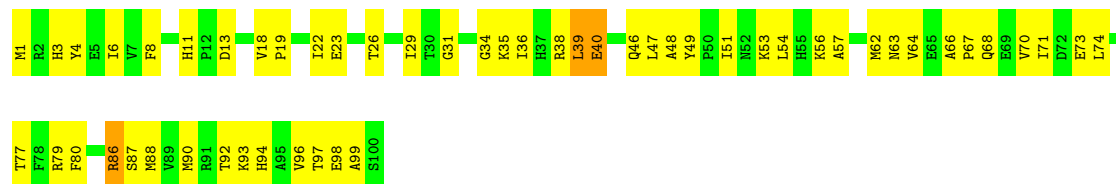
- Molecule 34: 30S ribosomal protein S5

Chain J: 62% 35% ..



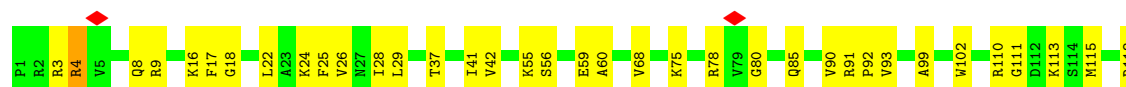
- Molecule 35: 30S ribosomal protein S6

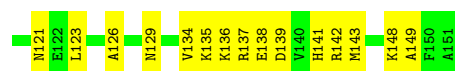
Chain K: 47% 50% .



- Molecule 36: 30S ribosomal protein S7

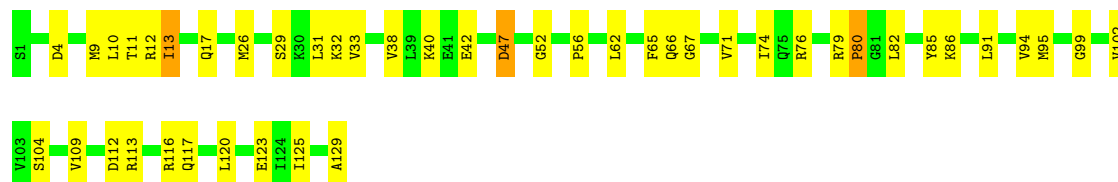
Chain L: 66% 33% .





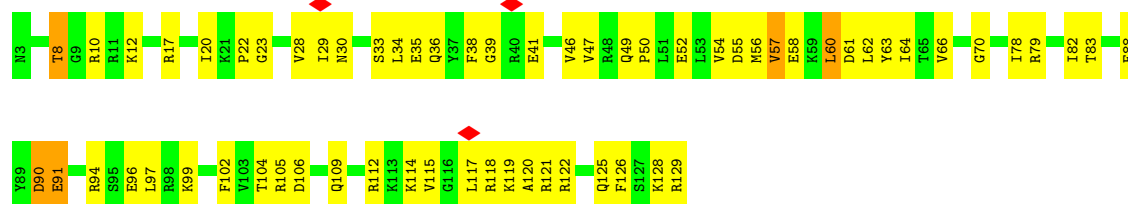
- Molecule 37: 30S ribosomal protein S8

Chain M: 65% 33%



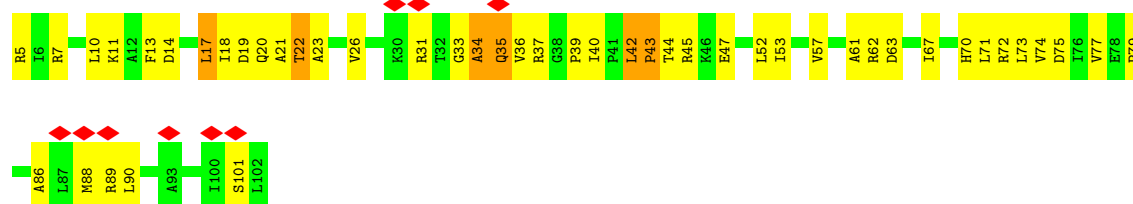
- Molecule 38: 30S ribosomal protein S9

Chain N: 50% 46%



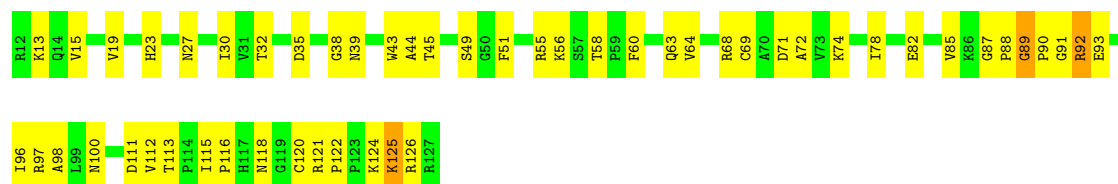
- Molecule 39: 30S ribosomal protein S10

Chain O: 9% 52% 42% 6%



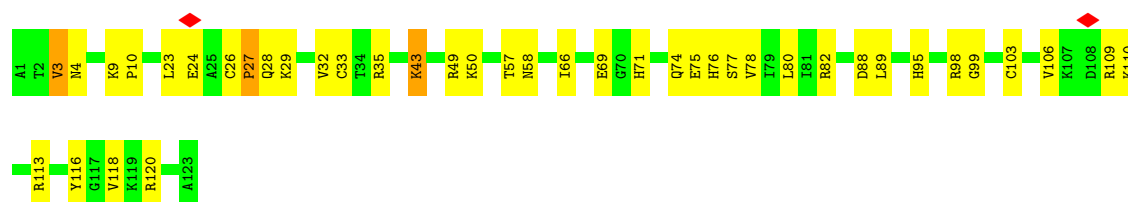
- Molecule 40: 30S ribosomal protein S11

Chain P: 55% 42%



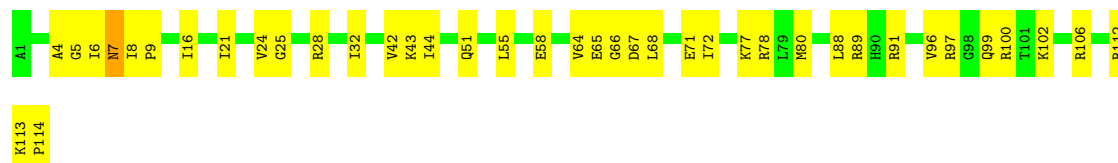
- Molecule 41: 30S ribosomal protein S12

Chain Q: 67% 31%



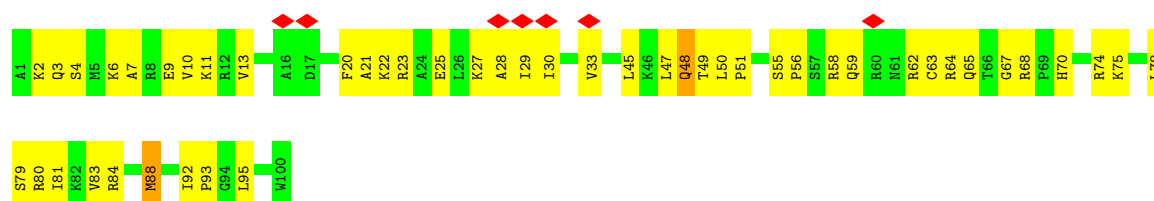
- Molecule 42: 30S ribosomal protein S13

Chain R: 65% 34% .



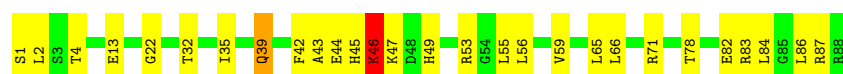
- Molecule 43: 30S ribosomal protein S14

Chain S: 7% 52% 46% .



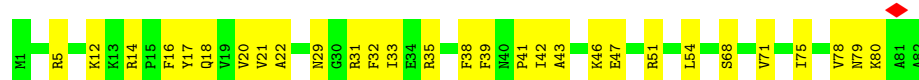
- Molecule 44: 30S ribosomal protein S15

Chain T: 68% 30% ..



- Molecule 45: 30S ribosomal protein S16

Chain U: 65% 35%

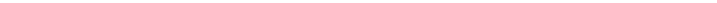


- Molecule 46: 30S ribosomal protein S17

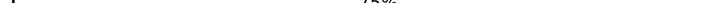
Chain V: 56% 41% .



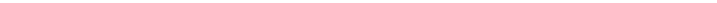
- Molecule 47: 30S ribosomal protein S18

- Chain X:  73% 27%

Category	Count
R2	10
S3	10
L4	10
K5	10
F9	10
L14	10
K17	10
V18	10
K28	10
P29	10
L30	10
R35	10
R36	10
I39	10
I48	10
V57	10
P58	10
T62	10
M65	10
H68	10
F73	10
A74	10
P75	10
R80	10

- Chain Y:  75% 25%

A horizontal bar chart showing the distribution of 1800 items across 20 categories. The categories are labeled R2, I3, K4, K7, A10, E14, N20, R23, R24, S25, M26, K27, R28, K32, A36, E39, Q54, P55, H67, K70, R73, N83, K84, L85, and A86. The bars are colored in a repeating pattern of green, yellow, and red. A red diamond icon is positioned above the R2 category.

- Chain Z:  37% 51% 11%

I3
V4
K5
R6
E7
N8
E9
P10
F11
D12
V13
A14
L15
R16
R17
F18
K19
R20
S21
C22
E23
K24
A25
L28
V31
R34
E35
F36
Y37
F38
K39
P40
T41
T42
F43
E44
K45
R46
A47
K48
A49
K53
A56
K57
K58
L59
A60
R61
A64
R65
R66
R67

- Chain a:

ALA	ASP	GLN	ILE	LYS	LYS	GLY	GLU	MET	PHE	ASP	VAL	VAL	ILE	ALA	ARG	VAL	VAL	GLY	GLN	LEU	GLY	GLN	VAL	LEU	GLY	PRO	PRO	ASN	PRO	PRO	LYS	VAL	THR	THR	PRO	ASN	VAL	ALA	GLU	ALA	VAL	LYS	ASN	ALA	LYS	ALA	ALA	Cys9
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------

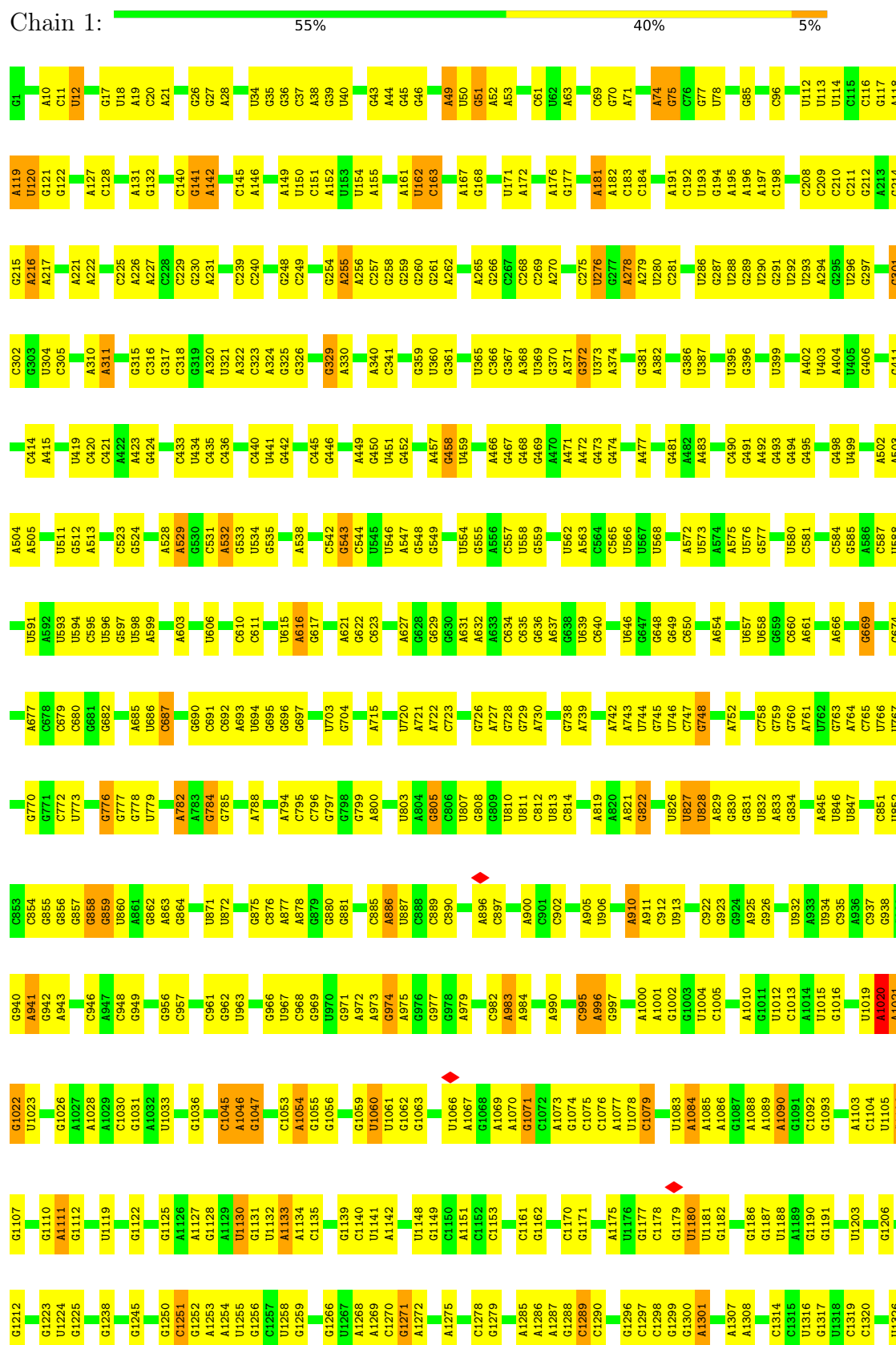
Keyword	Number of Publications
V161	10
N165	9
D166	8
K167	7
N168	6
G169	5
I170	4
T174	3
K177	2
D181	1
K184	1
L185	1
N188	1
L189	1
L192	1
L193	1
L196	1
K205	10
G206	9
K210	10
I214	8
G219	7
V222	6
D225	5

- Chain 3: 56% 40% .

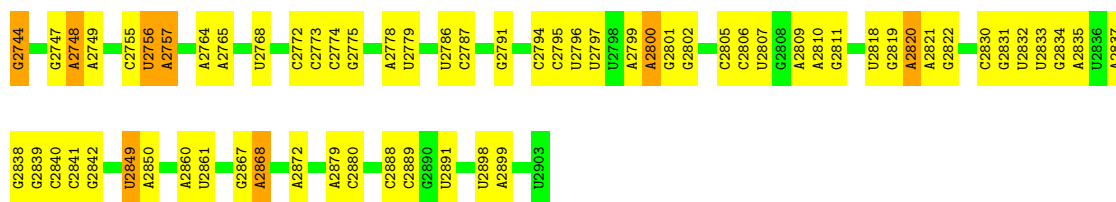
A2
A3
U4
U5
G6
A7
A8
G9
A10
G11
U12
A16
U17
C18
A19
G22
C23
U24
C25
A26
U29
U30
G31
A32
A33
C34
G35
G39
C40
G41
G42
C43
A44
G45
C48
U49
A50
A51
U56
G57
C58
A59
G67
G68
G69
U70
A71
A77
A78
G79
A80

G1459	G1369	U1298	C1203	G1107	A1004	C910	A814	A712	C618	G651	A408	A315	C210	G82
G1460	G1370	A1299	A1204	G1108	A1005	U911	A815	A715	U619	C522	U409	U323	G211	C83
G1461	G1371	G1300	U1205	U1008	G1006	A912	A816	A716	A621	A523	G410	U323	G212	U84
U1464	A1374	A1301	A1213	U1118	U1008	A918	A818	A717	C624	C525	G412	A327	G213	U85
A1465	A1375	G1304	A1216	U1119	C1011	A919	U820	A718	U625	C526	G413	A328	U216	G86
A1468	C1378	G1305	G1217	U1120	A1012	U920	U821	C719	U628	G530	C418	A329	U217	C87
G1475	G1379	G1306	C1218	U1122	A1013	A921	A825	G720	A629	U531	C419	G332	U218	C90
A1476	G1380	G1309	G1219	U1123	A1014	G922	A826	G722	G628	U532	U420	C335	U219	U91
U1477	U1381	G1310	G1220	G1124	G1015	A923	U827	U723	A629	A533	U421	A336	U220	U92
U1478	C1382	A1311	G1221	U1125	C924	G925	U828	G724	G633	A534	G422	A337	G221	U93
U1391	U1391	U1312	G1222	U1126	A1019	G926	U829	A728	U636	G537	G424	A338	U224	G94
G1392	G1392	C1314	A1225	G1127	G1020	G926	U830	A729	U637	G538	G425	A339	C225	C95
U1485	U1393	G1315	C1226	C1128	U1023	G933	U831	G730	U638	G539	C426	C340	G226	G100
G1486	G1394	G1316	A1227	U1129	G1024	C934	U834	G731	A640	A539	G428	C345	U229	A101
G1487	C1395	G1317	C1228	G1137	U1030	A935	U835	G732	U641	G540	U429	G346	G230	G112
A1482	A1398	A1318	A1229	G1138	C1028	C936	U836	G733	A642	G541	U430	G347	U231	G113
A1493	C1400	A1319	C1230	G1139	U1029	A937	U843	G734	G645	U543	U437	G348	G232	U114
G1494	G1401	G1320	G1231	U1148	U1030	A938	G844	C735	G646	U544	U438	G349	C235	G123
U1495	C1402	G1323	A1236	C1149	G1031	G939	A845	C736	U653	A547	U439	G350	A236	U123
G1496	G1403	A1324	C1237	A1150	C1032	G945	G846	C737	U654	A547	A448	G351	A237	C132
U1497	G1409	G1328	A1238	U1158	G1034	A946	C857	G741	U659	U552	G449	C352	G237	G132
U1498	A1410	C1329	A1239	C1159	U1038	G947	G858	G742	U662	A553	G450	C354	A243	G144
A1502	C1412	U1330	G1240	U1169	C1039	U950	U865	A743	U663	U554	A451	C355	U244	G145
A1503	A1413	G1331	G1241	C1162	U1049	G951	A866	G744	A663	U555	U452	C356	U245	G146
G1504	U1414	A1332	C1243	U1163	U1052	U952	G867	G745	G664	C556	U458	G360	A246	G147
G1505	G1415	A1333	G1244	G1164	U1053	G954	G868	G748	A665	C557	U459	G361	G247	G148
U1506	G1422	G1334	A1251	U1168	C1054	G955	G869	A749	U671	U559	A460	G362	G251	A149
U1507	A1429	A1339	A1252	A1169	U1060	U956	A872	C750	U672	U561	A461	A363	U252	U150
U1512	A1430	U1341	G1253	A1170	C1055	U960	C876	C754	U673	U562	U464	U367	G255	A152
G1514	A1431	G1342	A1254	A1171	U1061	U961	G877	C755	G674	A563	A465	U368	U261	A161
G1515	G1432	G1343	G1255	G1174	U1062	G966	A878	C756	A676	U564	A466	G369	A262	A162
G1516	A1433	A1344	A1256	G1175	C1071	A969	C879	U757	U677	U571	U467	C370	G266	C163
U1517	A1434	C1345	C1259	U1182	G1072	G970	A880	C764	U678	A572	C477	C372	C267	U166
A1518	U1436	U1346	G1260	U1183	U1073	G971	U884	C765	C680	A574	A478	G376	G267	A167
G1524	A1437	U1347	A1261	G1184	G1074	A974	G885	G769	U684	C576	C483	G376	A279	U166
G1525	G1438	A1348	A1273	G1187	U1078	A975	G886	G769	G688	C577	G484	A381	C279	A167
G1526	U1440	C1350	A1274	U1188	U1078	G976	G887	A777	U688	C578	U485	A382	G281	A171
U1527	C1351	U1352	A1275	U1189	A1081	A977	G888	A777	G691	A579	U486	C387	C285	C183
G1529	G1442	G1353	G1278	G1190	A1082	A982	A889	G784	G691	C580	G497	G388	C286	G184
G1530	C1443	U1354	G1279	A1191	A1082	U982	G890	A784	U701	G581	C501	A389	G289	C193
U1533	U1444	G1355	A1280	C1192	A1092	A983	U891	G785	A702	U584	A502	U390	G289	C194
A1534	U1445	G1356	C1281	G1193	A1093	C984	A900	A794	G703	A600	C503	C396	U304	A195
U1537	A1446	U1357	U1286	U1194	G1094	U986	A901	C795	A704	G601	A503	A397	U304	A196
U1537	C1448	C1359	A1287	C1195	U1095	U986	G902	C796	G705	A602	U512	U398	G305	A197
C1449	C1449	A1288	A1288	G1198	C1096	U992	G903	C797	A706	U603	U512	U398	A306	G202
U1540	C1452	A1363	C1293	U1199	C1097	G993	U904	C797	U707	G604	C514	C400	C307	G203
U1540	G1453	U1364	G1294	U1199	C1098	G993	U905	A802	C708	U605	G515	U405	G310	G204
U1540	U1458	G1365	G1294	C1200	C1100	C1001	A906	G803	U709	G606	U516	G406	C311	A205
U1540	U1458	A1368	G1297	A1201	A1101	G1002	A909	U813	G711	C613	C518	U407	C314	C206
U1540	U1458	A1368	G1297	A1202	A1102	G1003	A909	U813	G711	C613	C518	U407	C314	C207

● Molecule 53: 23S ribosomal RNA

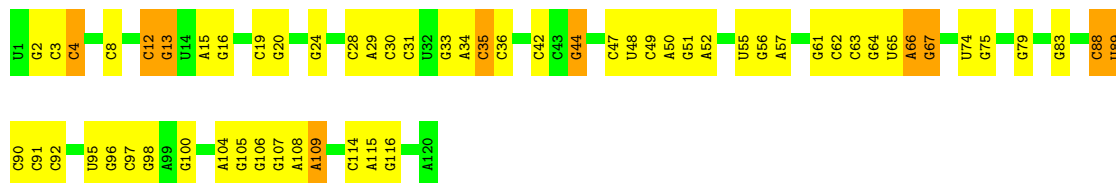


G2641	G2646	G2647	G2648	G2655	G2671	G2672	G2673	G2674	G2675	G2676	G2677	G2678	G2679	G2680	G2681	G2682	G2686	G2687	G2688	G2689	G2690	G2696	G2697	G2698	G2699	G2704	G2705	G2706	G2710	G2714	G2715	G2716	G2717	G2718	G2719	G2720	G2728	G2730	G2731	G2732	G2733	G2737	G2738	G2739	G2740	G2741	G2742	G2743																																																																																																																																																																							
G2350	G2351	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2376	G2377	G2378	G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2391	G2392	G2393	G2402	G2403	G2404	G2405	G2406	G2407	G2415	G2416	G2421	G2422	G2423	G2424	G2425	G2429	G2430	G2431	G2432	G2435	G2441	G2442	G2443	G2444	G2448	G2457	G2458	G2459																																																																																																																																																																								
G2462	G2463	G2469	G2470	G2475	G2476	G2477	G2478	G2479	G2480	G2481	G2484	G2489	G2490	G2499	G2491	G2498	G2499	G2502	G2503	G2504	G2505	G2508	G2509	G2510	G2511	G2512	G2513	G2514	G2515	G2516	G2517	G2518	G2527	G2528	G2529	G2530	G2531	G2532	G2533	G2534	G2537	G2538	G2543	G2544	G2545	G2546	G2547	G2548	G2549																																																																																																																																																																						
G2553	G2554	G2555	G2556	G2557	G2561	G2562	G2563	G2564	G2565	G2566	G2567	G2572	G2573	G2574	G2579	G2580	G2581	G2582	G2583	G2584	G2585	G2589	G2590	G2591	G2592	G2599	G2602	G2605	G2606	G2609	G2610	G2613	G2614	G2615	G2616	G2617	G2618	G2619	G2623	G2624	G2628	G2629	G2636	G2637	G2638	G2639	G2640																																																																																																																																																																								
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A2101	G2102	G2106	G2107	G2108	G2109	G2110	G2111	G2112	G2113	G2114	G2117	G2118	G2119	G2120	G2121	G2122	G2123	G2124	G2125	G2126	G2127	G2128	G2129	G2130	G2131	G2132	G2133	G2134	G2139	G2140	G2146	G2147	G2148	G2149	G2153	G2154	G2155	G2156	G2157	G2162	G2163	G2164	G2170	G2171	G2172	G2173	G2176	G2177	G2178	G2179	G2183																																																																																																																																																																				
G1828	A1829	C1833	C1837	U1841	G1842	A1848	G1849	A1853	A1854	U1855	C1856	G1857	A1858	U1859	G1860	G1861	A1871	A1872	G1873	C1874	G1875	C1881	U1882	U1883	G1884	A1885	G1888	A1889	A1890	C1893	C1894	A1900	A1901	G1902	G1903	G1904	C1905	G1906	G1907	C1908	G1909	G1910	A1913	U1917	A1918	U1919	C1920																																																																																																																																																																								
U1923	C1924	C1925	G1929	G1930	U1931	G1933	A1936	A1937	A1938	U1943	U1946	C1947	U1955	G1956	C1957	U1963	G1964	C1965	A1966	C1967	A1970	U1971	G1972	U1979	G1980	G1989	C1990	U1991	G1992	C1993	C1996	C1997	A1998	C1999	G2000	C2008	A2009	G2010	G2011	G2012	A2013	U2017	U2022	C2023																																																																																																																																																																											
G2024	G2025	U2026	G2027	U2028	G2029	A2030	A2031	G2032	U2033	A2034	G2035	C2036	G2039	G2040	U2041	A2042	C2043	C2047	G2048	G2049	A2052	C2055	G2056	A2060	G2061	A2062	C2066	G2067	U2068	G2069	A2070	A2071	C2072	G2073	U2074	U2075	C2078	U2079	A2080	G2086	G2087	A2088	C2089	G2093	C2096	A2097	U2098	U2099	G2100																																																																																																																																																																						
G1327	A1328	U1329	A1330	G1331	G1332	A1336	G1341	G1342	G1343	A1344	C1345	G1346	C1351	U1352	A1353	A1354	C1357	G1358	C1363	G1364	A1365	A1366	G1367	G1368	G1369	C1370	G1371	A1372	A1373	C1376	G1377	A1378	U1379	A1383	C1386	A1387	U1394	A1395	C1398	C1404	U1405	G1409	U1410	U1411	U1412	A1413																																																																																																																																																																									
G1416	C1417	G1418	A1419	A1420	G1421	G1424	G1425	G1429	G1430	A1431	G1435	G1436	G1441	U1442	U1443	G1444	G1445	C1446	G1447	G1448	C1454	U1458	G1459	U1460	C1461	U1463	G1464	C1465	G1466	G1467	G1468	G1469	G1470	G1475	U1476	G1482	U1486	U1487	A1490	G1491	A1494	A1495	C1498	G1499	G1500	G1501	U1506	C1507	A1508	A1509	A1510	U1512	G1513																																																																																																																																																																		
A1515	G1516	G1517	A1518	G1519	C1520	C1521	C1522	C1523	C1524	C1525	C1526	C1527	C1528	C1529	C1530	C1531	C1532	C1533	C1534	C1535	C1536	C1537	C1538	C1539	C1540	C1541	C1542	C1543	C1544	C1545	C1546	C1547	C1548	C1549	C1550	C1551	C1552	C1553	C1554	C1555	C1556	C1557	C1558	C1559	C1560	C1561	C1562	C1563	C1564	C1565	C1566	C1567	C1568	C1569	C1570	C1571	C1572	C1573	C1574	C1575	C1576	C1577	C1578	C1579	C1580	C1581	C1582	C1583	C1584	C1585	C1586	C1587	C1588	C1589	C1590	C1591	C1592	C1593	C1594	C1595	C1596	C1597	C1598	C1599	C1600	C1601	C1602	C1603	C1604	C1605	C1606	C1607	C1608	C1609	C1610	C1611	C1612	C1613	C1614	C1615	C1616	C1617	C1618	C1619	C1620	C1621	C1622	C1623	C1624	C1625	C1626	C1627	C1628	C1629	C1630	C1631	C1632	C1633	C1634	C1635	C1636	C1637	C1638	C1639	C1640	C1641	C1642	C1643	C1644	C1645	C1646	C1647	C1648	C1649	C1650	C1651	C1652	C1653	C1654	C1655	C1656	C1657	C1658	C1659	C1660	C1661	C1662	C1663	C1664	C1665	C1666	C1667	C1668	C1669	C1670	C1671	C1672	C1673	C1674	C1675	C1676	C1677	C1678	C1679	C1680	C1681	C1682	C1683	C1684	C1685	C1686	C1687	C1688	C1689	C1690	C1691	C1692	C1693	C1694	C1695	C1696	C1697	C1698	C1699	C1700	C1701	C1702	C1703	C1704	C1705	C1706	C1707	C1708	C1709	C1710	C1711	C1712	C1713	C1714	C1715	C1716	C1717	C1718	C1719	C1720	C1721	C1722	C1723	C1724	C1725	C1726	C1727	C1728	C1729	C1730
G1738	A1739	G1740	U1741	G1742	U1743	U1744	U1745	U1746	U1747	U1748	U1749	U1750	U1751	U1752	U1753	U1754	U1755	U1756	U1757	U1758	U1759	U1760	U1761	U1762	U1763	U1764	U1765	U1766	U1767	U1768	U1769	U1770	U1771	U1772	U1773	U1774	U1775	U1776	U1777	U1778	U1779	U1780	U1781	U1782	U1783	U1784	U1785	U1786	U1787	U1788	U1789	U1790	U1791	U1792	U1793	U1794	U1795	U1796	U1797	U1798	U1799	U1800	U1801	U1802	U1803	U1804	U1805	U1806	U1807	U1808	U1809	U1810	U1811	U1812	U1813	U1814	U1815	U1816	U1817	U1818	U1819	U1820	U1821	U1822	U1823	U1824	U1825	U1826	U1827																																																																																																																														
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U1923	C1924	C1925	G1929	G1930	U1931	G1933	A1936	A1937	A1938	U1943	U1946	C1947	U1955	G1956	C1957	U1963	G1964	C1965	A1966	C1967	A1970	U1971	G1972	U1979	G1980	G1989	C1990	U1991	G1992	C1993	C1996	C1997	A1998	C1999	G2000	C2008	A2009	G2010	G2011	G2012	A2013	U2017	U2022	C2023																																																																																																																																																																											
G2024	G2025	U2026	G2027	U2028	G2029	A2030	A2031	G2032	U2033	A2034	G2035	C2036	G2039	G2040	U2041	A2042	C2043	C2047	G2048	G2049	A2052	C2055	G2056	A2060	G2061	A2062	C2066	G2067	U2068	G2069	A2070	A2071	C2072	G2073	U2074	U2075	C2078	U2079	A2080	G2086	G2087	A2088	C2089	G2093	C2096	A2097	U2098	U2099	G2100																																																																																																																																																																						
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G2350	G2351	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2376	G2377	G2378	G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2391	G2392	G2393	G2402	G2403	G2404	G2405	G2406	G2407	G2415	G2416	G2421	G2422	G2423	G2424	G2425	G2429	G2430	G2431	G2432	G2435	G2441	G2442	G2443	G2444	G2448	G2457	G2458	G2459																																																																																																																																																																								
C2462	C2463	A24																																																																																																																																																																																																																					



- Molecule 54: 5S ribosomal RNA

Chain 2: 50% 42% 8%



- Molecule 55: tRNAfMet

Chain 5: 68% 26% 6%



- Molecule 55: tRNAfMet

Chain 6: 53% 44% 3%



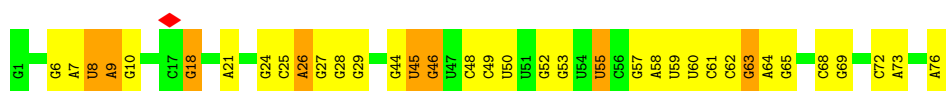
- Molecule 56: mRNA

Chain 4: 50% 50%



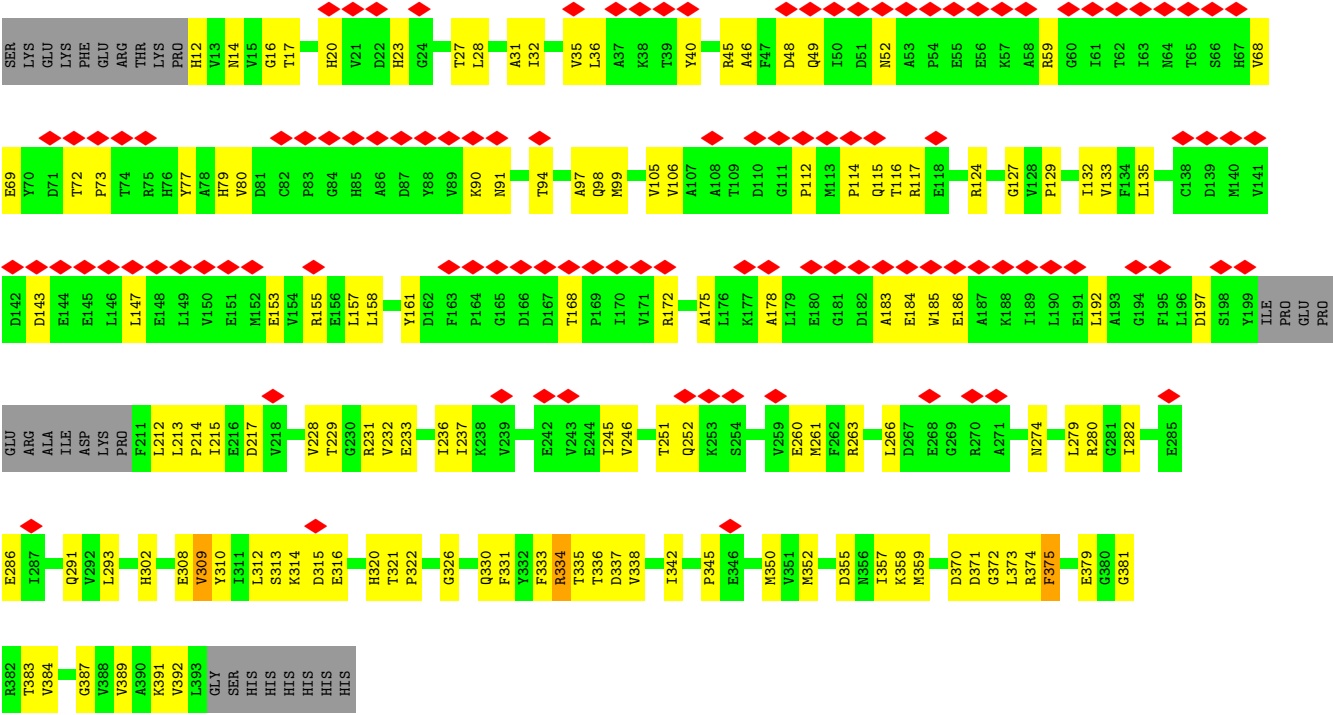
- Molecule 57: tRNAPhe

Chain 7: 53% 37% 11%



- Molecule 58: Elongation factor Tu

Chain 8: 28% 60% 32% 7%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6311	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	16.931	Depositor
Minimum map value	-9.315	Depositor
Average map value	0.111	Depositor
Map value standard deviation	0.831	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	0.93	4/2852 (0.1%)
2	c	0.29	0/1586	0.85	4/2134 (0.2%)
3	d	0.29	0/1571	0.92	6/2113 (0.3%)
4	e	0.30	0/1435	0.83	1/1926 (0.1%)
5	f	0.31	0/1343	0.89	2/1816 (0.1%)
6	g	0.32	0/1122	1.02	7/1515 (0.5%)
7	h	0.34	0/1002	1.05	9/1350 (0.7%)
8	i	0.37	0/1046	1.05	7/1410 (0.5%)
9	j	0.29	0/1152	0.87	4/1551 (0.3%)
10	k	0.29	0/948	0.95	2/1268 (0.2%)
11	l	0.29	0/1054	0.94	3/1403 (0.2%)
12	m	0.29	0/1093	0.87	2/1460 (0.1%)
13	n	0.29	0/974	0.98	8/1301 (0.6%)
14	o	0.28	0/902	0.86	2/1209 (0.2%)
15	p	0.28	0/929	0.81	1/1242 (0.1%)
16	q	0.29	0/960	0.92	6/1278 (0.5%)
17	r	0.30	0/829	0.87	3/1107 (0.3%)
18	s	0.28	0/864	0.83	1/1156 (0.1%)
19	t	0.28	0/745	0.86	3/994 (0.3%)
20	u	0.28	0/788	0.86	0/1051
21	v	0.28	0/766	0.90	1/1025 (0.1%)
22	w	0.29	0/582	0.88	1/769 (0.1%)
23	x	0.28	0/635	0.88	2/848 (0.2%)
24	y	0.27	0/510	0.90	3/677 (0.4%)
25	z	0.30	0/453	0.76	0/605
26	B	0.28	0/450	0.84	1/599 (0.2%)
27	C	0.34	0/417	0.90	0/554
28	D	0.31	0/380	0.95	0/498
29	E	0.30	0/513	0.85	1/676 (0.1%)
30	F	0.32	0/303	0.87	1/397 (0.3%)
31	G	0.30	0/1788	0.87	5/2408 (0.2%)
32	H	0.32	0/1652	0.90	5/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	0.93	10/2227 (0.4%)
34	J	0.31	0/1170	0.92	5/1573 (0.3%)
35	K	0.32	0/836	0.96	4/1128 (0.4%)
36	L	0.29	0/1196	0.90	1/1602 (0.1%)
37	M	0.29	0/989	0.93	2/1326 (0.2%)
38	N	0.31	0/1034	0.89	1/1375 (0.1%)
39	O	0.33	0/797	0.91	3/1077 (0.3%)
40	P	0.32	0/886	0.98	5/1195 (0.4%)
41	Q	0.32	0/969	0.96	2/1300 (0.2%)
42	R	0.31	0/893	0.92	4/1193 (0.3%)
43	S	0.31	0/817	0.90	2/1088 (0.2%)
44	T	0.28	0/722	0.93	4/964 (0.4%)
45	U	0.30	0/659	0.89	2/884 (0.2%)
46	V	0.30	0/658	0.93	2/881 (0.2%)
47	W	0.31	0/545	0.90	3/731 (0.4%)
48	X	0.31	0/653	0.84	0/877
49	Y	0.29	0/671	0.92	2/888 (0.2%)
50	Z	0.34	0/551	1.03	4/728 (0.5%)
51	a	0.30	0/1034	0.77	0/1387
52	3	0.41	0/36963	0.47	3/57662 (0.0%)
53	1	0.40	0/69796	0.48	1/108888 (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	0.46	0/2855
56	4	0.40	0/436	0.46	0/679
57	7	0.40	0/1809	0.48	0/2819
58	8	0.32	0/2903	0.91	7/3928 (0.2%)
All	All	0.37	0/166102	0.62	162/248006 (0.1%)

There are no bond length outliers.

The worst 5 of 162 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	S	49	THR	N-CA-C	-8.94	101.63	112.54
7	h	43	LYS	N-CA-C	-8.56	101.44	112.23
3	d	73	ILE	N-CA-C	-8.28	104.96	112.90
6	g	11	ASN	N-CA-C	7.97	120.67	111.11
33	I	176	LYS	N-CA-C	-7.73	102.94	113.30

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	75	0
2	c	1565	0	1616	46	0
3	d	1552	0	1619	39	0
4	e	1411	0	1447	38	0
5	f	1323	0	1374	24	0
6	g	1111	0	1148	31	0
7	h	989	0	1025	63	0
8	i	1032	0	1088	46	0
9	j	1129	0	1162	41	0
10	k	939	0	1012	43	0
11	l	1045	0	1117	36	0
12	m	1074	0	1157	33	0
13	n	961	0	1000	41	0
14	o	892	0	923	31	0
15	p	917	0	965	34	0
16	q	947	0	1022	15	0
17	r	816	0	839	34	0
18	s	857	0	922	25	0
19	t	739	0	807	21	0
20	u	780	0	834	20	0
21	v	753	0	780	18	0
22	w	575	0	592	14	0
23	x	625	0	655	17	0
24	y	509	0	543	18	0
25	z	449	0	491	10	0
26	B	444	0	461	10	0
27	C	410	0	440	18	0
28	D	377	0	418	10	0
29	E	504	0	574	16	0
30	F	302	0	343	8	0
31	G	1757	0	1787	47	0
32	H	1625	0	1699	76	0
33	I	1643	0	1710	63	0
34	J	1157	0	1199	44	0
35	K	818	0	808	37	0
36	L	1182	0	1240	54	0
37	M	979	0	1034	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	57	0
39	O	787	0	828	41	0
40	P	870	0	878	43	0
41	Q	955	0	1019	32	0
42	R	884	0	944	31	0
43	S	805	0	847	48	0
44	T	714	0	737	18	0
45	U	649	0	666	25	0
46	V	649	0	691	31	0
47	W	536	0	552	23	0
48	X	638	0	665	19	0
49	Y	665	0	714	19	0
50	Z	545	0	579	46	0
51	a	1027	0	1092	27	0
52	3	33012	0	16618	576	0
53	1	62317	0	31346	968	0
54	2	2568	0	1303	63	0
55	5	1640	0	836	20	0
55	6	1640	0	837	29	0
56	4	388	0	196	7	0
57	7	1619	0	821	35	0
58	8	2853	0	2860	92	0
59	5	10	0	10	0	0
60	7	11	0	8	3	0
61	8	28	0	12	0	0
All	All	153103	0	104137	2978	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 2978 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)
31:G:186:VAL:HG13	31:G:190:SER:HB2	1.44	0.97
53:1:45:G:H5''	53:1:46:G:H5'	1.46	0.97
58:8:98:GLN:HG2	58:8:387:GLY:O	1.65	0.96
24:y:43:LEU:HD23	53:1:61:C:H5''	1.49	0.94
33:I:190:LEU:HD12	33:I:192:ALA:H	1.30	0.94

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%)	236 (88%)	32 (12%)	1 (0%)	30	60
2	c	207/209 (99%)	180 (87%)	24 (12%)	3 (1%)	9	37
3	d	199/201 (99%)	174 (87%)	21 (11%)	4 (2%)	6	32
4	e	175/177 (99%)	158 (90%)	17 (10%)	0	100	100
5	f	174/176 (99%)	159 (91%)	12 (7%)	3 (2%)	7	34
6	g	147/149 (99%)	130 (88%)	16 (11%)	1 (1%)	18	50
7	h	129/131 (98%)	94 (73%)	28 (22%)	7 (5%)	1	16
8	i	139/141 (99%)	120 (86%)	17 (12%)	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%)	116 (82%)	23 (16%)	2 (1%)	9	37
12	m	134/136 (98%)	122 (91%)	9 (7%)	3 (2%)	5	31
13	n	118/120 (98%)	99 (84%)	18 (15%)	1 (1%)	16	48
14	o	114/116 (98%)	103 (90%)	10 (9%)	1 (1%)	14	45
15	p	112/114 (98%)	96 (86%)	16 (14%)	0	100	100
16	q	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
17	r	101/103 (98%)	84 (83%)	15 (15%)	2 (2%)	6	32
18	s	108/110 (98%)	94 (87%)	13 (12%)	1 (1%)	14	45
19	t	91/93 (98%)	81 (89%)	10 (11%)	0	100	100
20	u	100/102 (98%)	84 (84%)	12 (12%)	4 (4%)	2	21
21	v	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	w	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
23	x	75/77 (97%)	68 (91%)	6 (8%)	1 (1%)	9	38
24	y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	7	35
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%)	49 (91%)	5 (9%)	0	100	100
27	C	48/50 (96%)	41 (85%)	6 (12%)	1 (2%)	5	31
28	D	44/46 (96%)	36 (82%)	7 (16%)	1 (2%)	5	30
29	E	62/64 (97%)	53 (86%)	7 (11%)	2 (3%)	3	25
30	F	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
31	G	223/225 (99%)	205 (92%)	18 (8%)	0	100	100
32	H	204/206 (99%)	189 (93%)	14 (7%)	1 (0%)	24	56
33	I	203/205 (99%)	173 (85%)	28 (14%)	2 (1%)	12	43
34	J	155/157 (99%)	129 (83%)	22 (14%)	4 (3%)	4	28
35	K	98/100 (98%)	77 (79%)	19 (19%)	2 (2%)	6	32
36	L	149/151 (99%)	135 (91%)	13 (9%)	1 (1%)	18	50
37	M	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	7	35
38	N	125/127 (98%)	99 (79%)	21 (17%)	5 (4%)	2	21
39	O	96/98 (98%)	74 (77%)	16 (17%)	6 (6%)	1	14
40	P	114/116 (98%)	93 (82%)	16 (14%)	5 (4%)	2	19
41	Q	121/123 (98%)	99 (82%)	15 (12%)	7 (6%)	1	15
42	R	112/114 (98%)	95 (85%)	14 (12%)	3 (3%)	4	27
43	S	98/100 (98%)	83 (85%)	14 (14%)	1 (1%)	12	43
44	T	86/88 (98%)	76 (88%)	9 (10%)	1 (1%)	10	40
45	U	80/82 (98%)	72 (90%)	6 (8%)	2 (2%)	4	29
46	V	78/80 (98%)	64 (82%)	12 (15%)	2 (3%)	4	28
47	W	63/65 (97%)	57 (90%)	6 (10%)	0	100	100
48	X	77/79 (98%)	60 (78%)	16 (21%)	1 (1%)	9	38
49	Y	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
50	Z	63/65 (97%)	41 (65%)	15 (24%)	7 (11%)	0	5
51	a	130/223 (58%)	130 (100%)	0	0	100	100
58	8	367/400 (92%)	344 (94%)	20 (5%)	3 (1%)	16	48
All	All	6286/6512 (96%)	5490 (87%)	696 (11%)	100 (2%)	10	35

5 of 100 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL

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Mol	Chain	Res	Type
5	f	45	ALA
5	f	174	LYS
6	g	9	VAL
7	h	108	VAL

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%)	214 (99%)	2 (1%)	70	75
2	c	164/164 (100%)	162 (99%)	2 (1%)	63	72
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	79
4	e	148/148 (100%)	147 (99%)	1 (1%)	76	77
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	77
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	75
7	h	100/100 (100%)	98 (98%)	2 (2%)	48	64
8	i	109/109 (100%)	108 (99%)	1 (1%)	70	75
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	74
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	72
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	74
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	72
18	s	93/93 (100%)	91 (98%)	2 (2%)	45	63
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	v	78/78 (100%)	78 (100%)	0	100	100
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	185 (100%)	1 (0%)	81	80
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	79
33	I	172/172 (100%)	169 (98%)	3 (2%)	53	67
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	76
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	73
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	74
38	N	105/105 (100%)	103 (98%)	2 (2%)	50	65
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	62
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	82 (99%)	1 (1%)	63	72
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	65 (100%)	0	100	100
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	64 (98%)	1 (2%)	57	68
50	Z	55/55 (100%)	51 (93%)	4 (7%)	13	40
51	a	110/174 (63%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	8	304/332 (92%)	302 (99%)	2 (1%)	76	77
All	All	5212/5304 (98%)	5175 (99%)	37 (1%)	73	77

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	O	42	LEU
58	8	23	HIS
43	S	88	MET
50	Z	37	TYR
14	o	28	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 118 such sidechains are listed below:

Mol	Chain	Res	Type
19	t	70	HIS
58	8	52	ASN
32	H	122	GLN
58	8	14	ASN
46	V	30	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	133 (8%)	4 (0%)
53	1	2902/2903 (99%)	324 (11%)	9 (0%)
54	2	119/120 (99%)	10 (8%)	2 (1%)
55	5	76/77 (98%)	7 (9%)	0
55	6	76/77 (98%)	7 (9%)	0
56	4	17/18 (94%)	2 (11%)	0
57	7	75/76 (98%)	14 (18%)	0
All	All	4803/4810 (99%)	497 (10%)	15 (0%)

5 of 497 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G

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Mol	Chain	Res	Type
52	3	31	G
52	3	32	A

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	1475	G
54	2	66	A
53	1	2286	G
54	2	88	C
53	1	2391	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
59	FME	5	101	55	8,9,10	0.49	0	8,9,11	1.11	1 (12%)
60	PHE	7	101	57	10,11,12	0.71	0	8,13,15	0.23	0
61	GDP	8	501	-	29,30,30	1.43	3 (10%)	45,47,47	2.15	15 (33%)

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
59	FME	5	101	55	-	1/7/9/11	-
60	PHE	7	101	57	-	1/5/6/8	0/1/1/1
61	GDP	8	501	-	-	4/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GDP	PA-O3A	3.70	1.63	1.59
61	8	501	GDP	PA-O1A	3.23	1.62	1.50
61	8	501	GDP	PB-O2B	2.28	1.63	1.54

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	C2-N3-C4	5.59	121.92	112.30
61	8	501	GDP	C5-C4-N3	-5.53	119.58	128.39
61	8	501	GDP	O3B-PB-O1B	4.34	127.73	110.83
61	8	501	GDP	N9-C4-N3	4.03	134.02	125.95
61	8	501	GDP	O3B-PB-O2B	-3.92	93.09	107.80

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
60	7	101	PHE	O-C-CA-CB
61	8	501	GDP	PA-O3A-PB-O2B
61	8	501	GDP	O4'-C4'-C5'-O5'
61	8	501	GDP	C3'-C4'-C5'-O5'

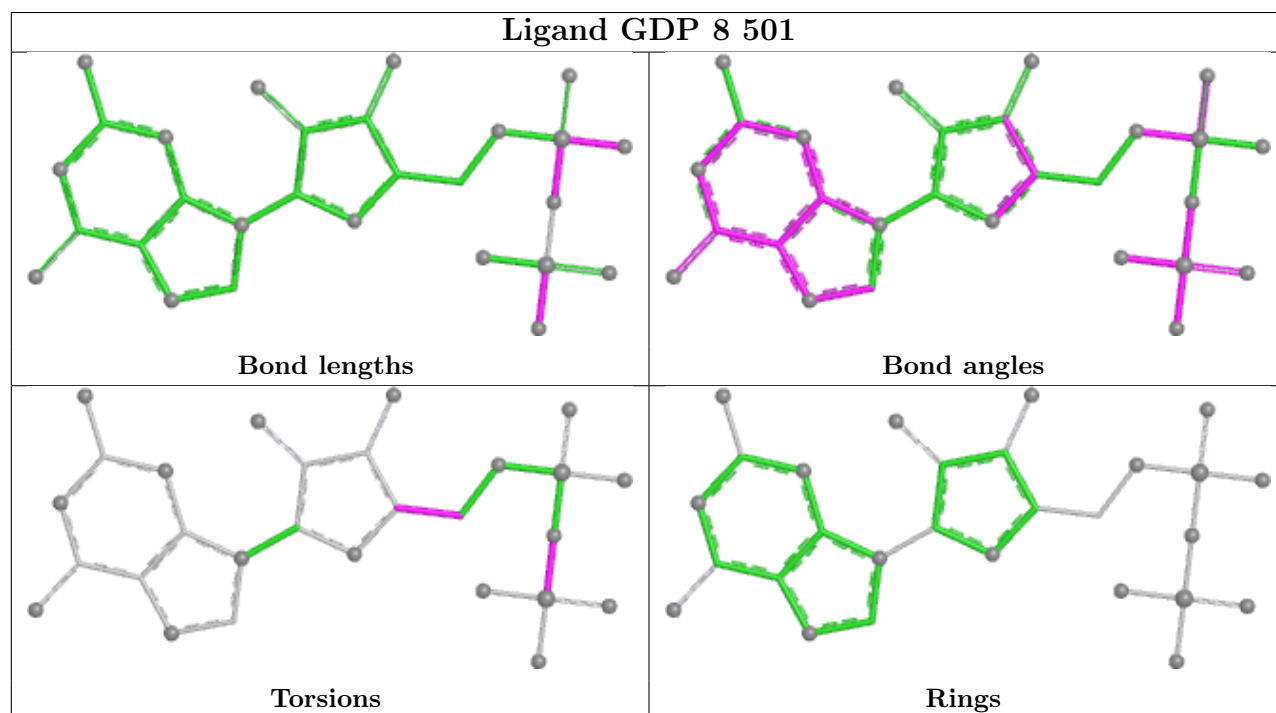
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	7	101	PHE	3	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.

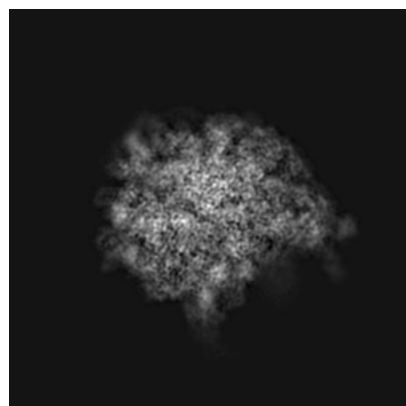
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21625. These allow visual inspection of the internal detail of the map and identification of artifacts.

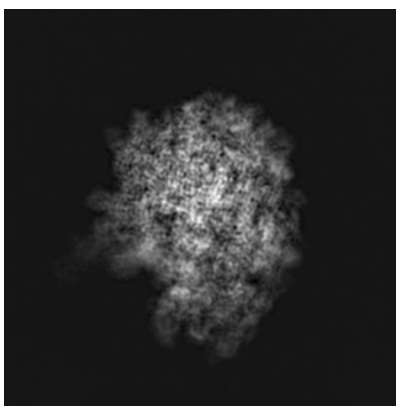
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

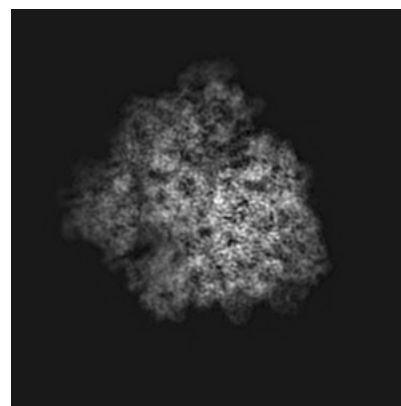
6.1.1 Primary map



X

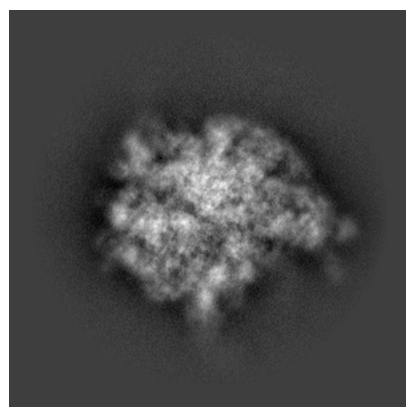


Y

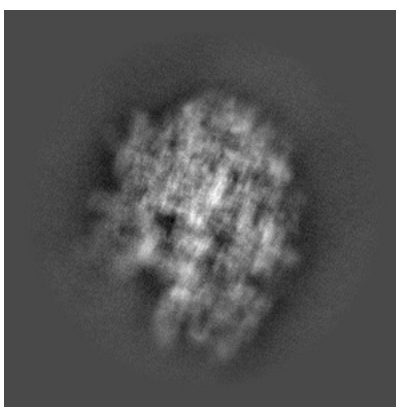


Z

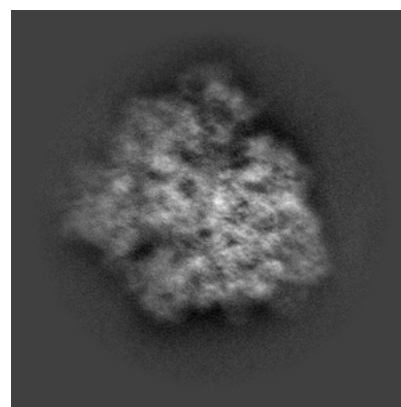
6.1.2 Raw map



X



Y

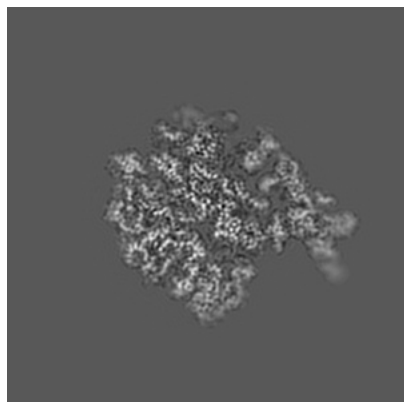


Z

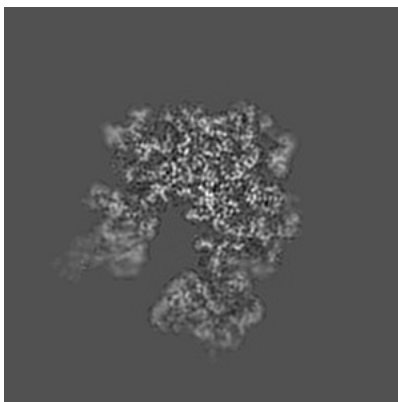
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

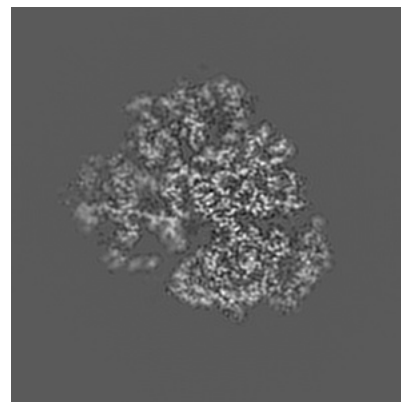
6.2.1 Primary map



X Index: 144

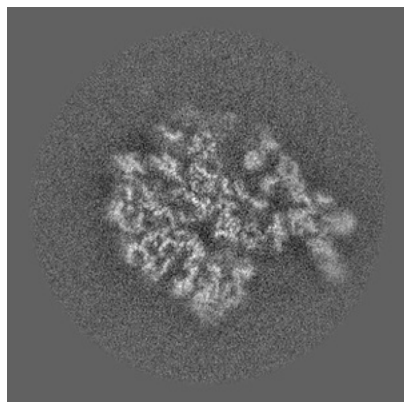


Y Index: 144

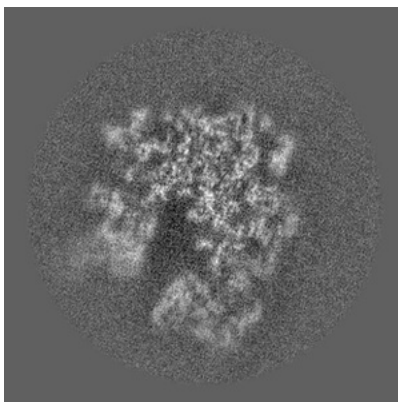


Z Index: 144

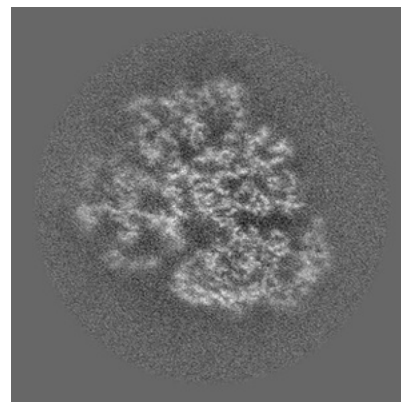
6.2.2 Raw map



X Index: 144



Y Index: 144

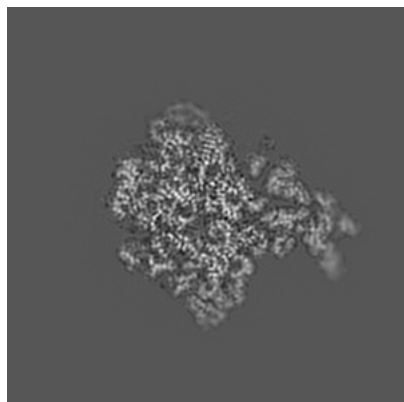


Z Index: 144

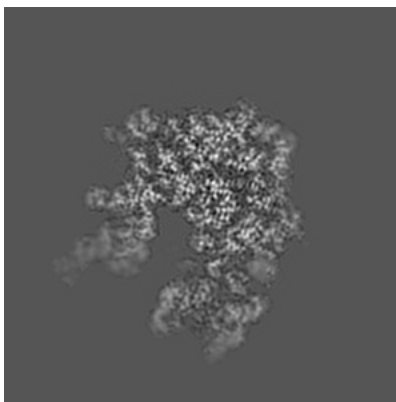
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

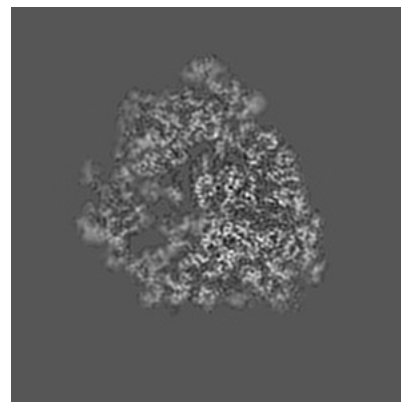
6.3.1 Primary map



X Index: 149

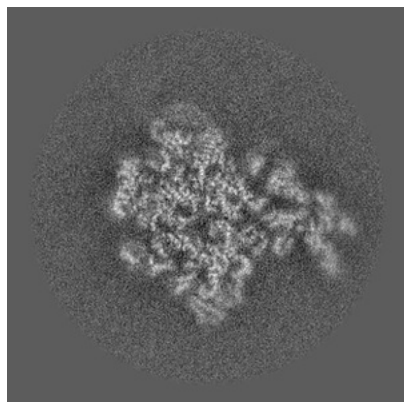


Y Index: 148

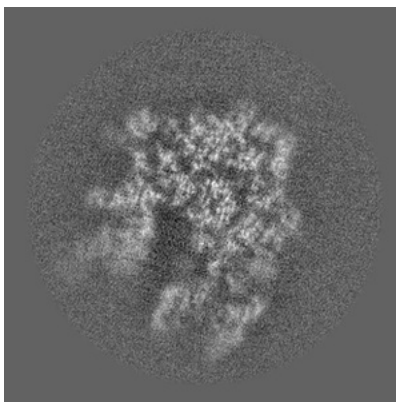


Z Index: 135

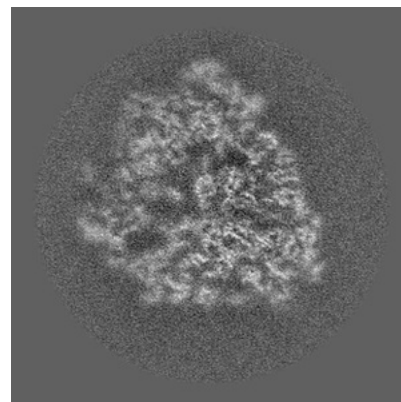
6.3.2 Raw map



X Index: 149



Y Index: 148

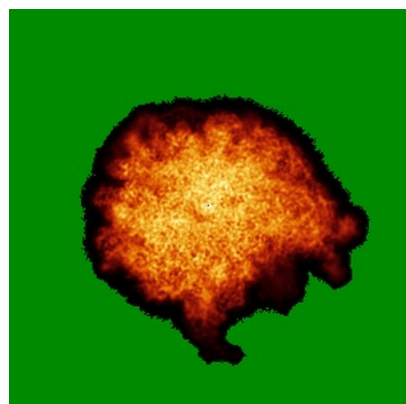


Z Index: 135

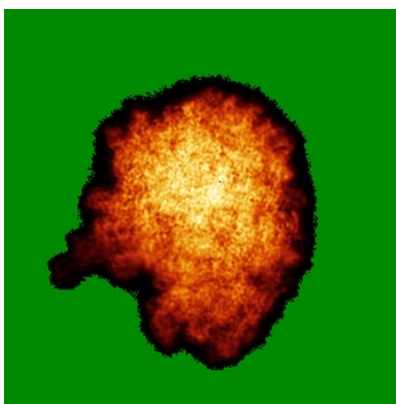
The images above show the largest variance slices of the map in three orthogonal directions.

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

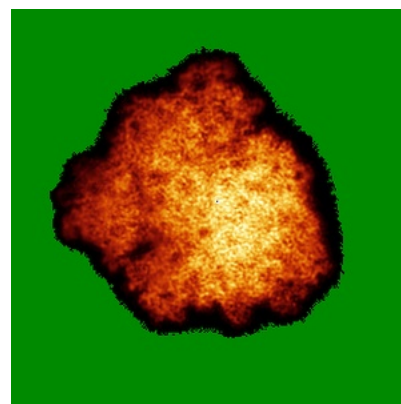
6.4.1 Primary map



X

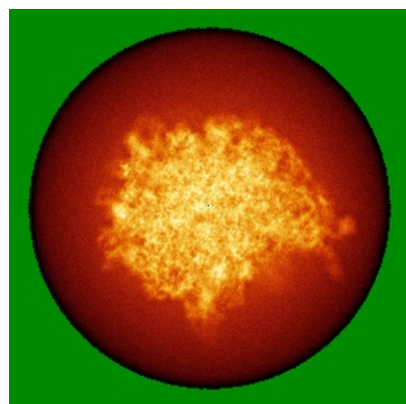


Y

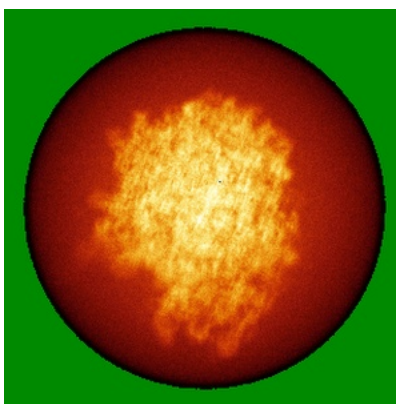


Z

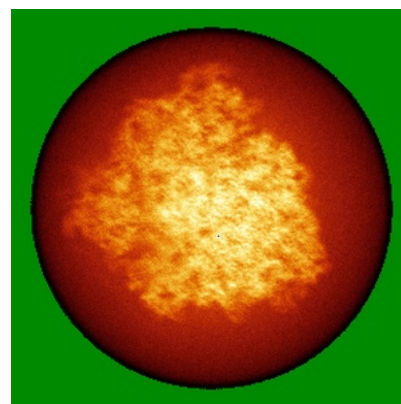
6.4.2 Raw map



X



Y

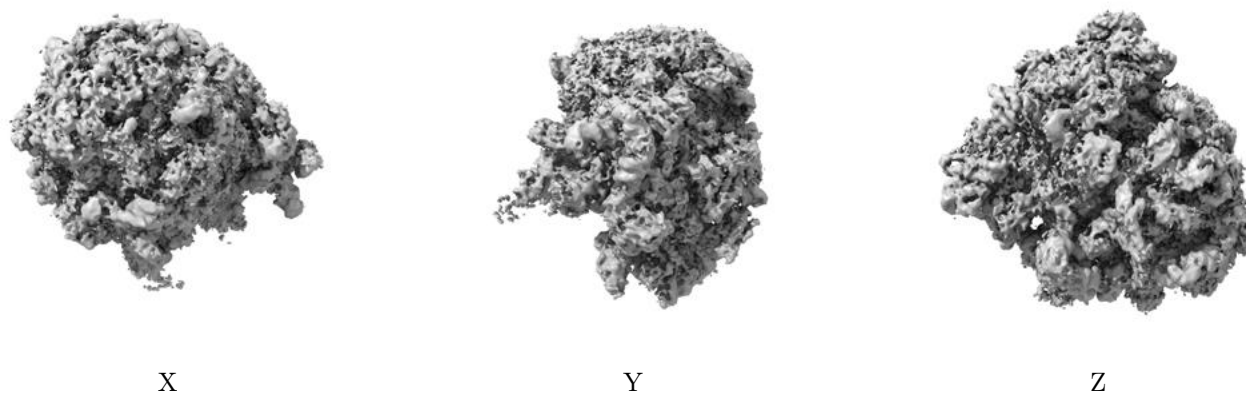


Z

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.

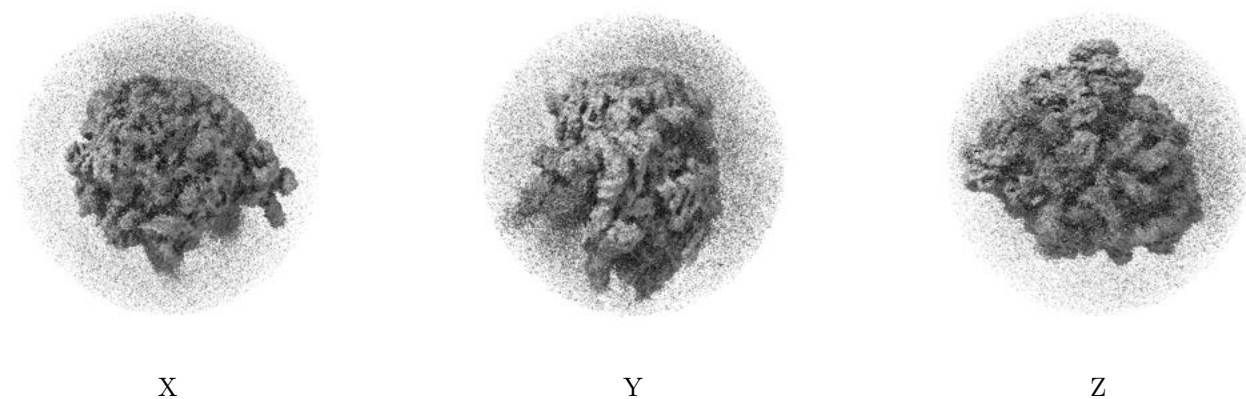
6.5 Orthogonal surface views [i](#)

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.

6.5.2 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.

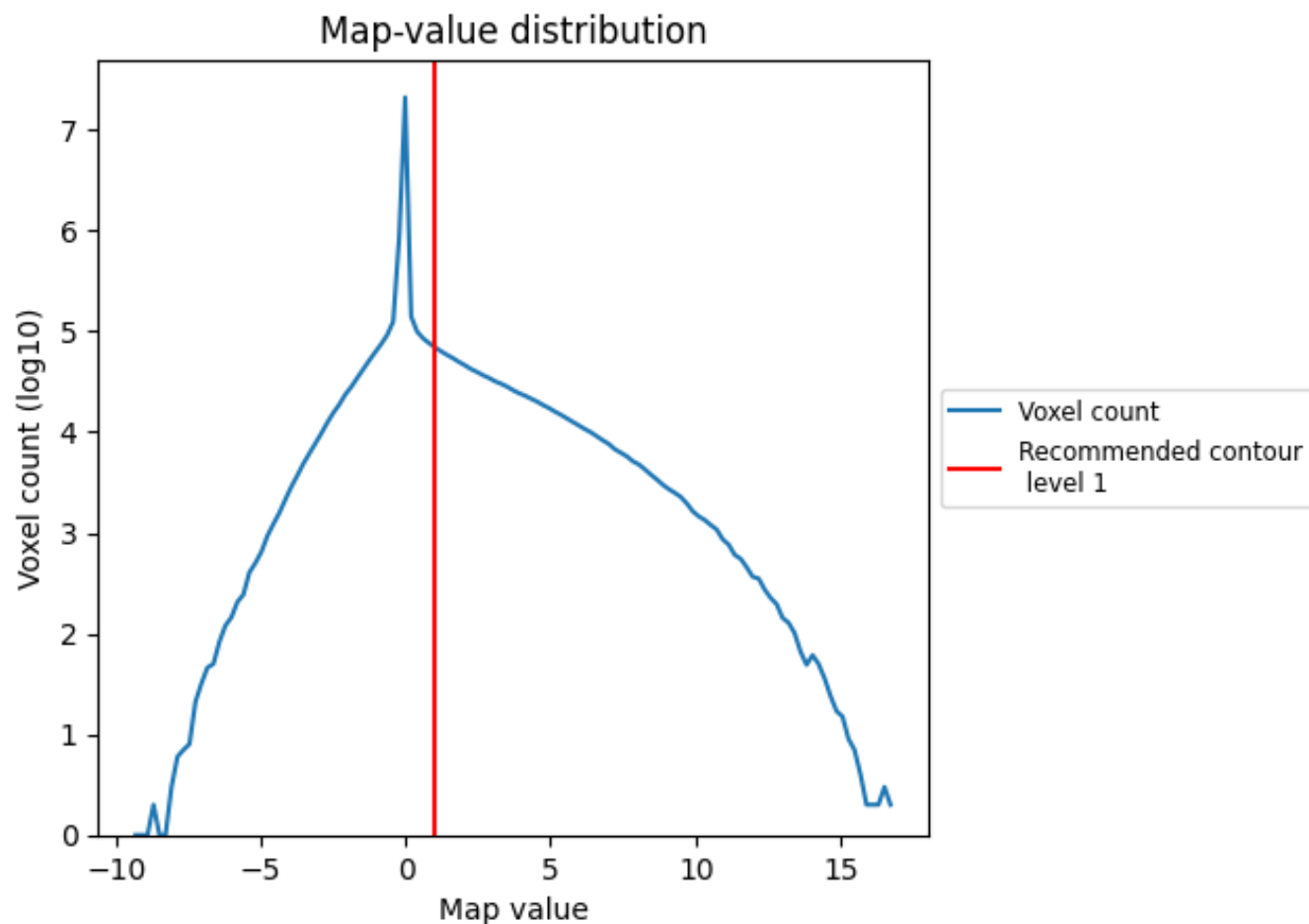
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

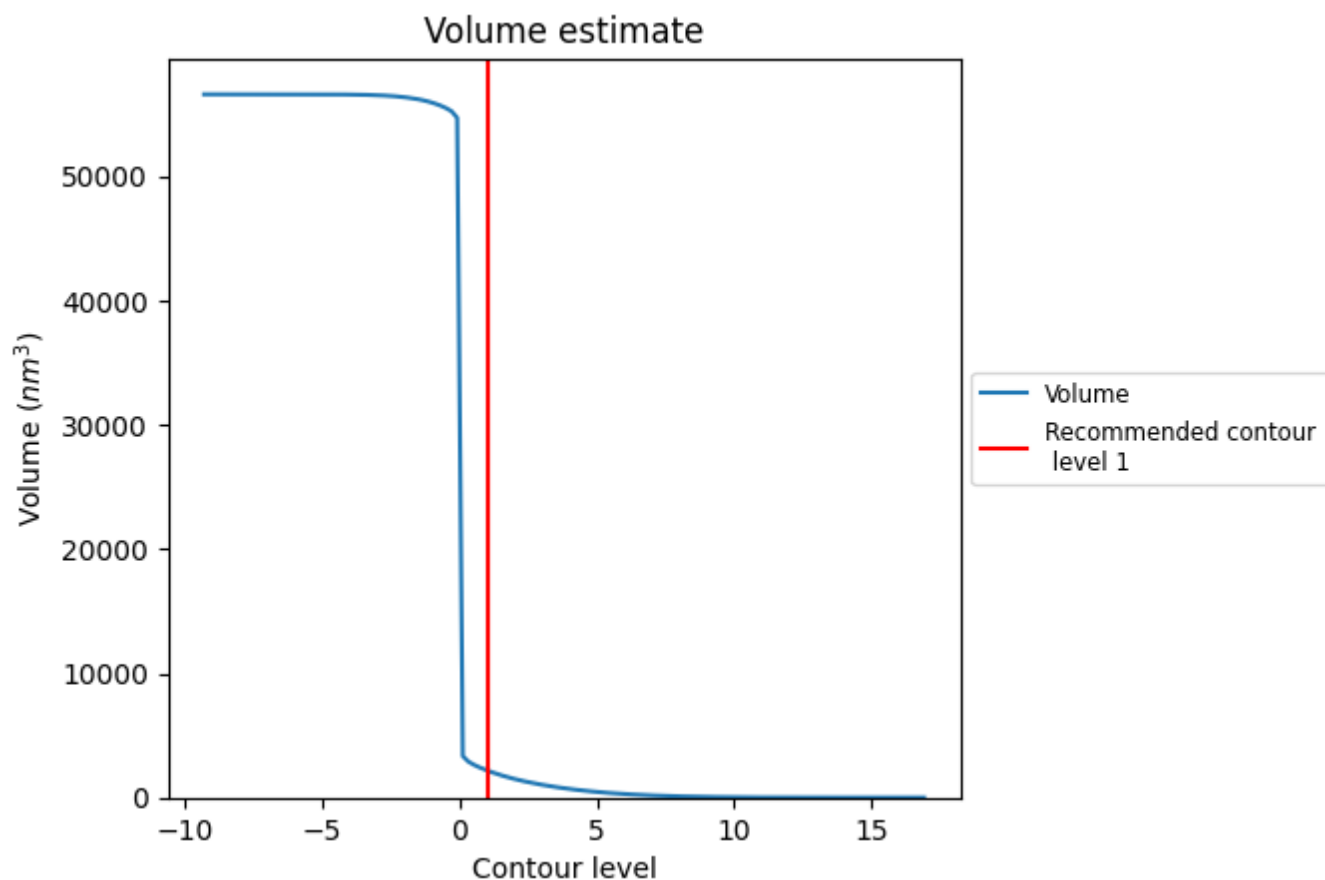
This section contains the results of statistical analysis of the map.

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.

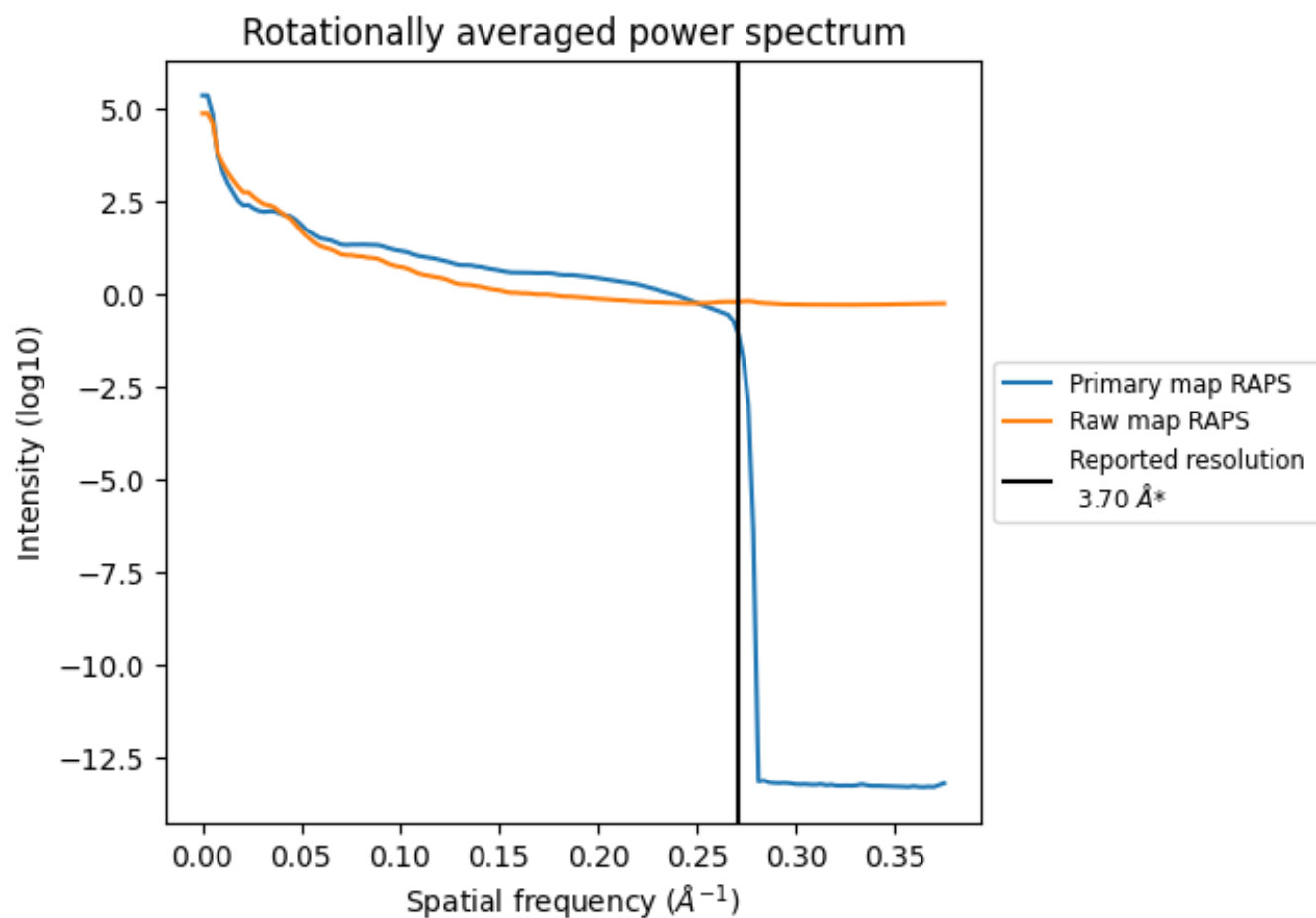
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2183 nm³; this corresponds to an approximate mass of 1972 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 ⓘ

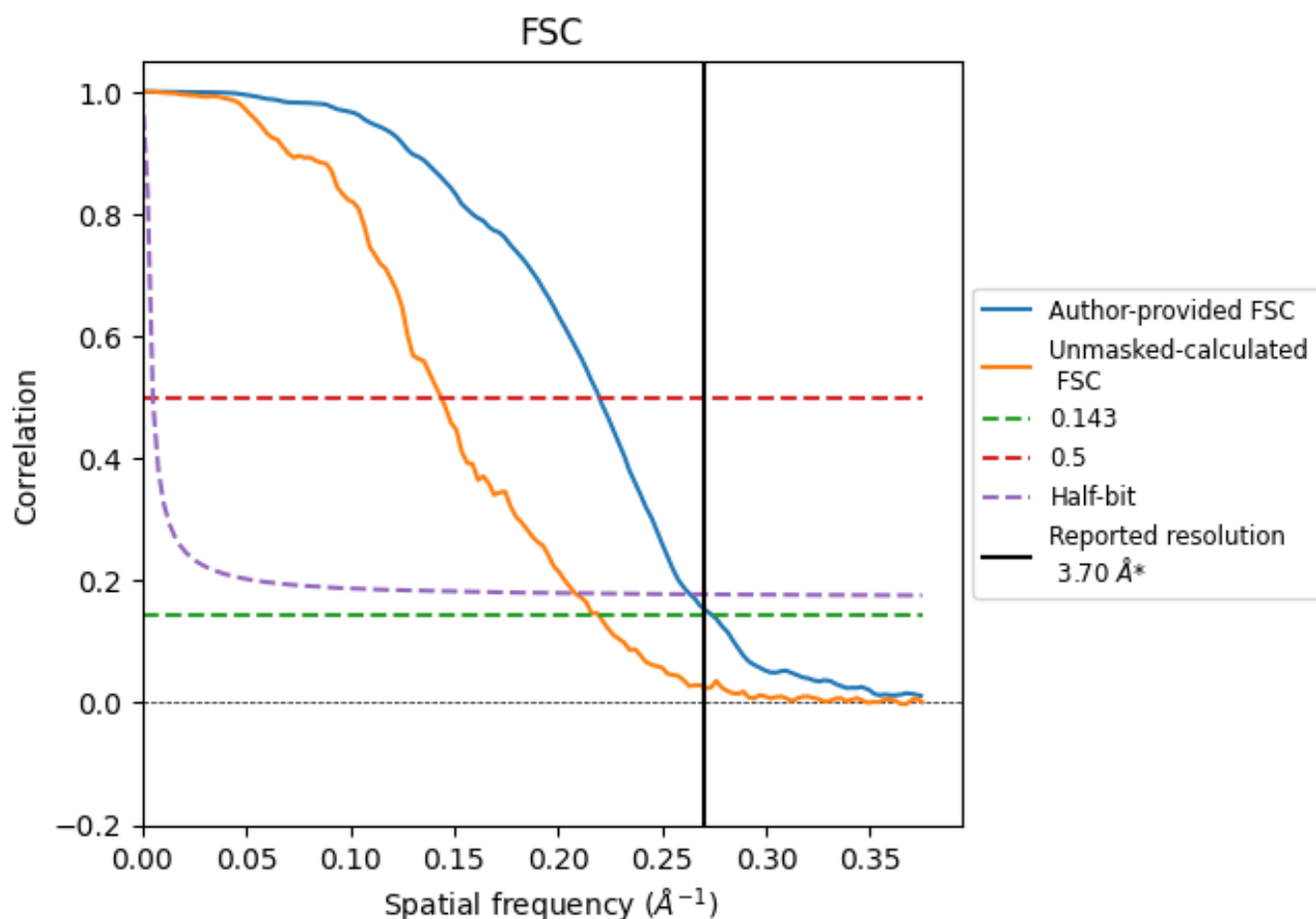


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates

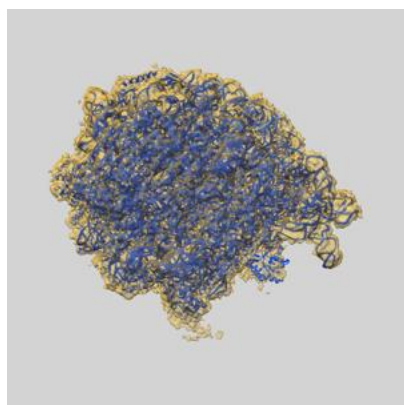
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.65	4.55	3.80
Unmasked-calculated*	4.56	6.96	4.80

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

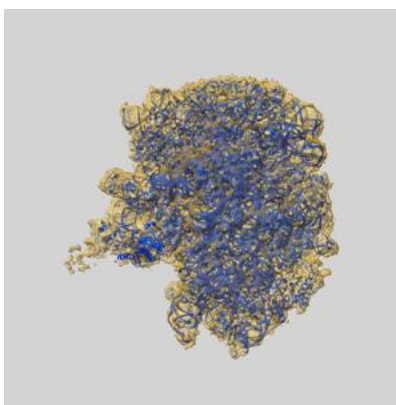
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21625 and PDB model 6WD6. Per-residue inclusion information can be found in section [3](#) on page [17](#).

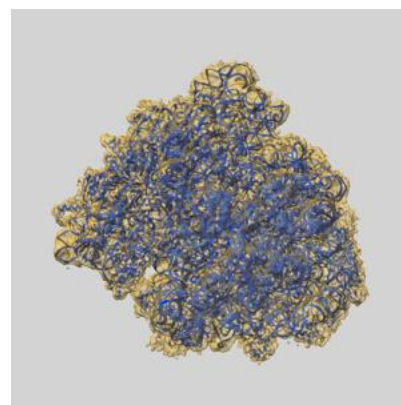
9.1 Map-model overlay [i](#)



X



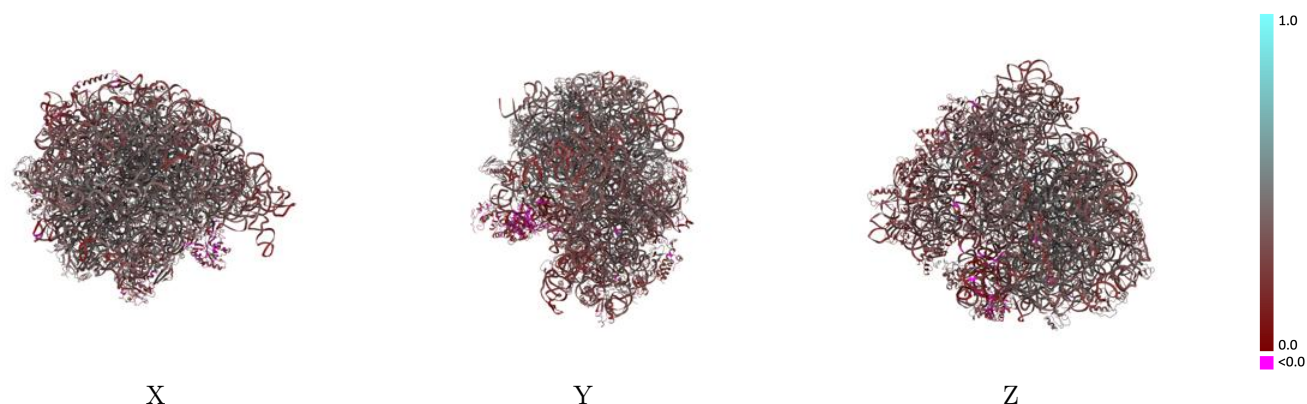
Y



Z

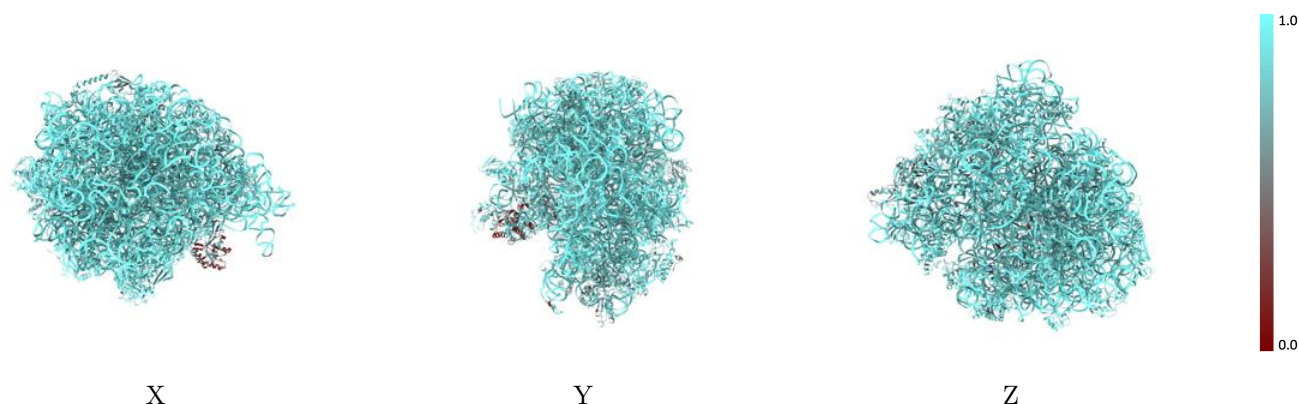
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



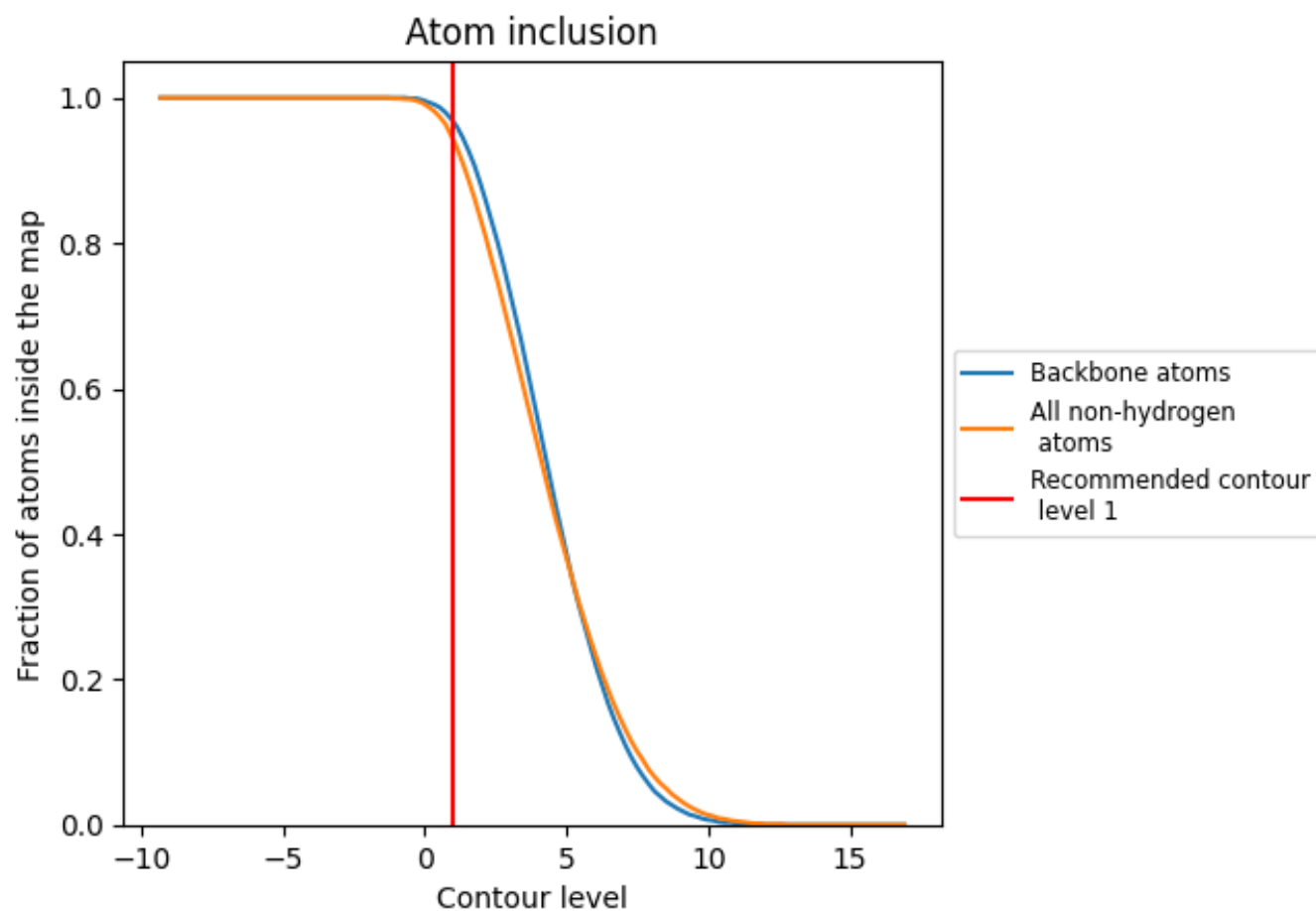
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	 0.9430	 0.3450
1	 0.9820	 0.3710
2	 0.9830	 0.3330
3	 0.9740	 0.3330
4	 0.8840	 0.2180
5	 0.9640	 0.2920
6	 0.8310	 0.1480
7	 0.9040	 0.1590
8	 0.6280	 0.1350
B	 0.9350	 0.4230
C	 0.8480	 0.3640
D	 0.9070	 0.4310
E	 0.9250	 0.4420
F	 0.8360	 0.3810
G	 0.8570	 0.3060
H	 0.7050	 0.2990
I	 0.8580	 0.2940
J	 0.9120	 0.3690
K	 0.9450	 0.3380
L	 0.9070	 0.2980
M	 0.9160	 0.3650
N	 0.8650	 0.2790
O	 0.6800	 0.2750
P	 0.9470	 0.3800
Q	 0.9090	 0.3920
R	 0.9060	 0.2870
S	 0.7380	 0.2750
T	 0.9350	 0.3690
U	 0.8840	 0.3670
V	 0.9130	 0.3710
W	 0.9150	 0.3430
X	 0.9530	 0.2710
Y	 0.8690	 0.3290
Z	 0.8360	 0.2720
a	 0.8090	 0.1420



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Chain	Atom inclusion	Q-score
b	 0.9480	 0.4470
c	 0.9430	 0.4320
d	 0.9330	 0.3870
e	 0.9290	 0.3030
f	 0.9540	 0.3330
g	 0.7820	 0.2630
h	 0.7710	 0.1500
i	 0.7100	 0.1490
j	 0.9390	 0.4230
k	 0.9120	 0.4410
l	 0.9470	 0.4190
m	 0.9250	 0.4190
n	 0.9310	 0.4220
o	 0.9260	 0.3360
p	 0.9360	 0.4190
q	 0.9380	 0.4210
r	 0.9570	 0.4110
s	 0.9070	 0.4250
t	 0.9460	 0.4130
u	 0.9280	 0.3580
v	 0.9570	 0.3880
w	 0.9280	 0.4320
x	 0.9380	 0.4250
y	 0.9150	 0.3060
z	 0.9290	 0.4060