



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 05:38 AM UTC

PDB ID : 6WD5 / pdb_00006wd5
EMDB ID : EMD-21624
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure II-C1)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.60 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

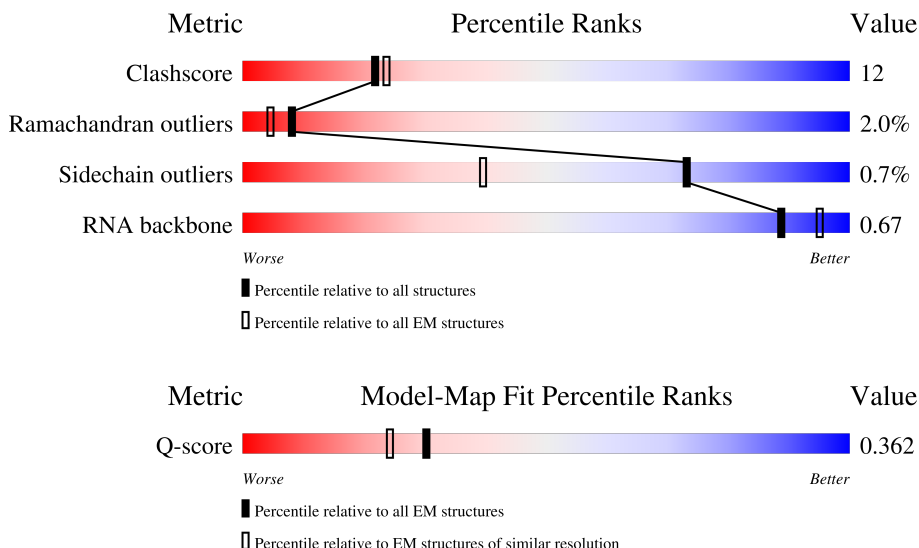
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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.



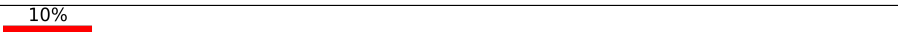
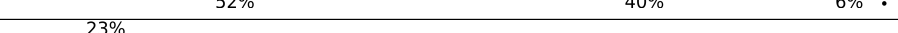
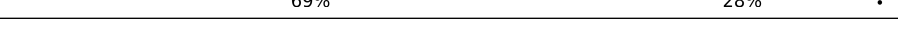
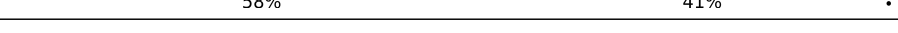
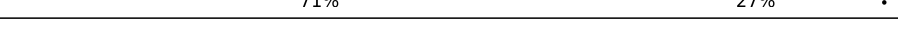
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	

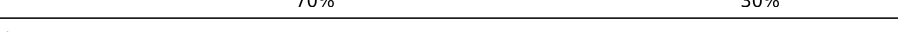
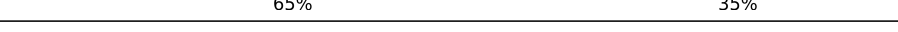
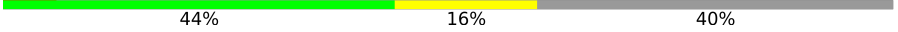
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Mol	Chain	Length	Quality of chain
4	e	177	 66% 33% .
5	f	176	 69% 30% .
6	g	149	 7% 62% 36% .
7	h	131	 10% 52% 40% 6% .
8	i	141	 23% 58% 38% . .
9	j	142	 77% 20% .
10	k	122	 60% 39% .
11	l	143	 69% 28% .
12	m	136	 66% 30% . .
13	n	120	 60% 38% . .
14	o	116	 67% 29% .
15	p	114	 58% 41% .
16	q	117	 74% 25% .
17	r	103	 71% 27% . .
18	s	110	 75% 25%
19	t	93	 . 71% 27% .
20	u	102	 66% 32% .
21	v	94	 68% 30% . .
22	w	75	 73% 27%
23	x	77	 68% 31% .
24	y	63	 67% 30% .
25	z	58	 78% 22%
26	B	56	 57% 41% .
27	C	50	 . 74% 24% .
28	D	46	 . 65% 30% . .

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Mol	Chain	Length	Quality of chain
29	E	64	 66% 33% .
30	F	38	 66% 32% .
31	G	225	 69% 29% .
32	H	206	 12% 67% 31% .
33	I	205	 64% 35% .
34	J	157	 59% 39% ..
35	K	100	 45% 51% .
36	L	151	 66% 32% .
37	M	129	 59% 40% .
38	N	127	 52% 45% .
39	O	98	 15% 62% 33% . .
40	P	116	 60% 34% . .
41	Q	123	 61% 33% 6% .
42	R	114	 62% 34% .
43	S	100	 9% 56% 42% .
44	T	88	 70% 30%
45	U	82	 65% 35%
46	V	80	 61% 35% .
47	W	65	 57% 43%
48	X	79	 63% 34% .
49	Y	85	 72% 27% .
50	Z	65	 43% 45% 9% .
51	a	223	 6% 44% 16% 40%
52	3	1539	 55% 41% .
53	1	2903	 56% 38% 5%

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Mol	Chain	Length	Quality of chain
54	2	120	56% 38% 7%
55	5	77	70% 29%
55	6	77	61% 38%
56	4	18	6% 56% 44%
57	7	76	58% 33% 9%
58	8	400	22% 58% 35% 6%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 153135 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	375	Total	C	N	O	S	0	0
			2885	1826	496	550	13		

There are 7 discrepancies between the modelled and reference sequences:

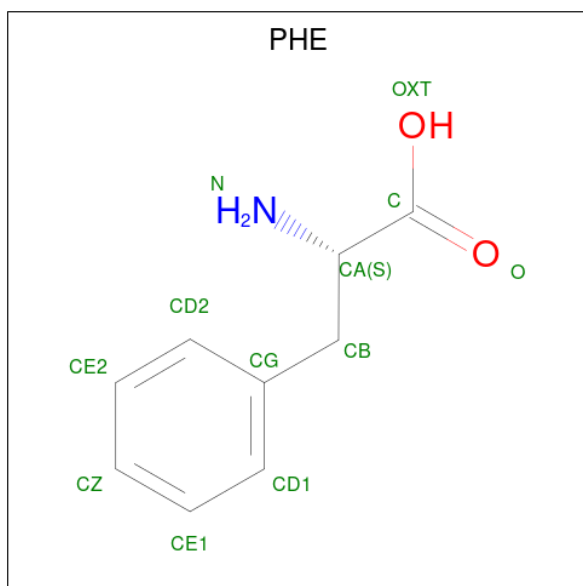
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag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

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



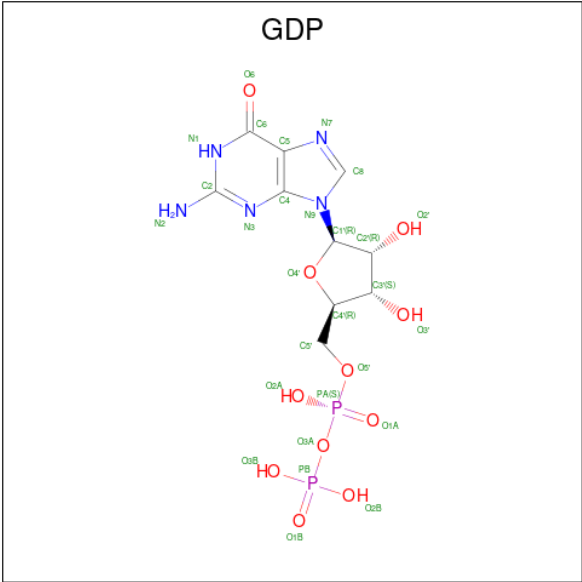
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

- 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		

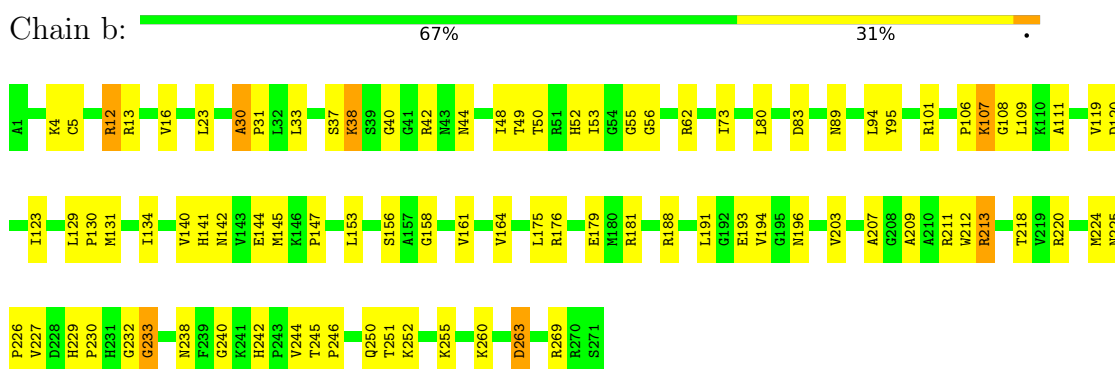
- Molecule 61 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



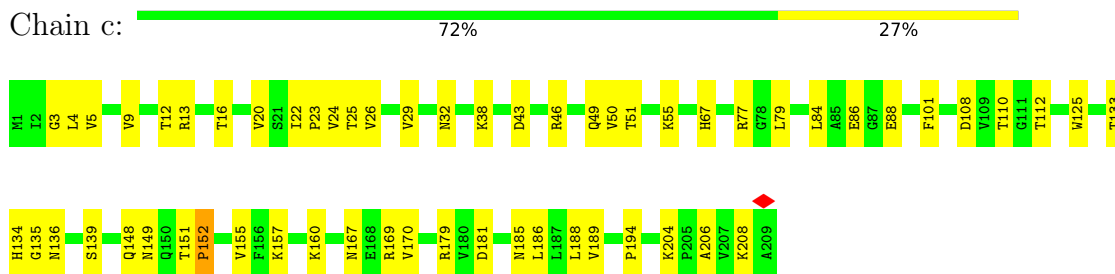
3 Residue-property plots

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.

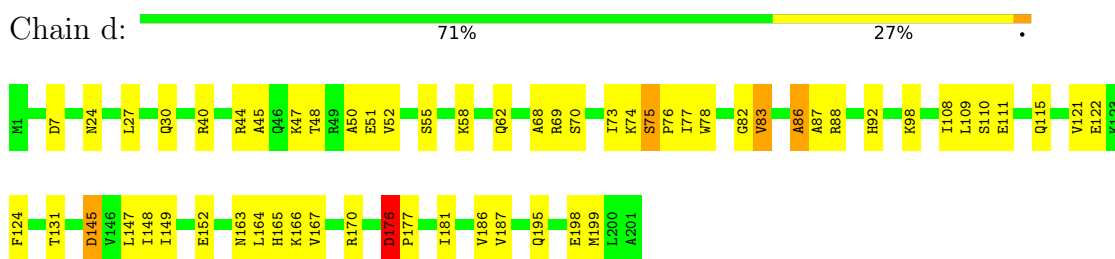
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

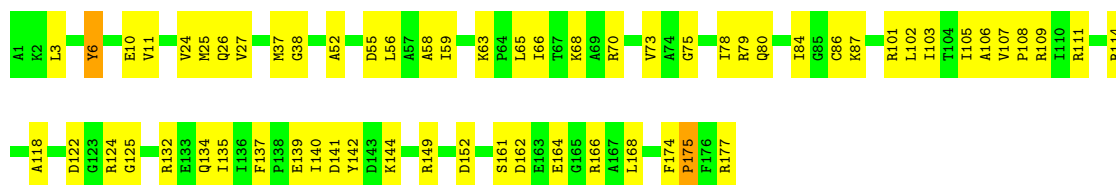


- Molecule 3: 50S ribosomal protein L4



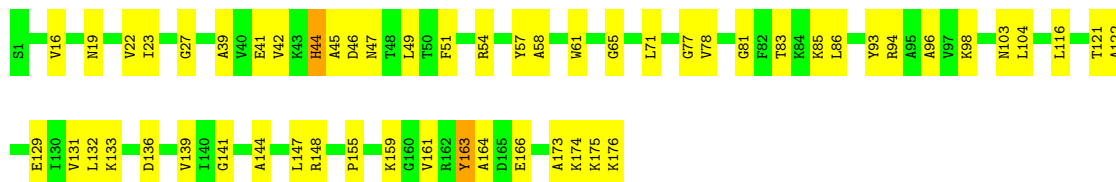
- Molecule 4: 50S ribosomal protein L5





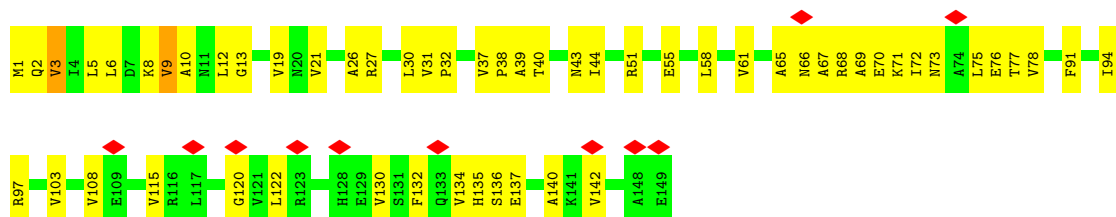
• Molecule 5: 50S ribosomal protein L6

Chain f: 69% 30% .



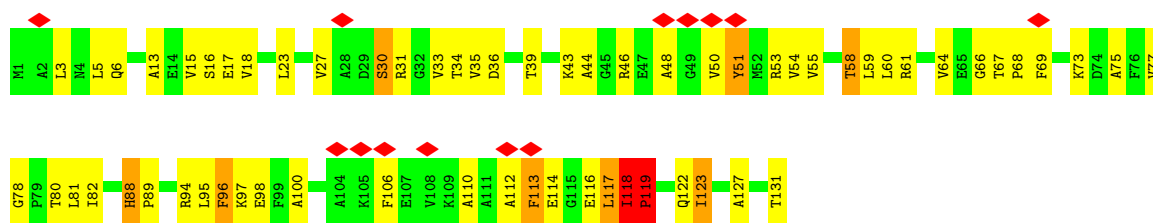
• Molecule 6: 50S ribosomal protein L9

Chain g: 7% 62% 36% .



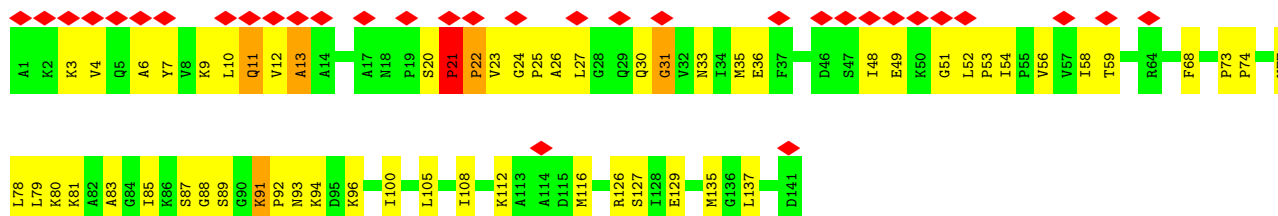
• Molecule 7: 50S ribosomal protein L10

Chain h: 10% 52% 40% 6% .



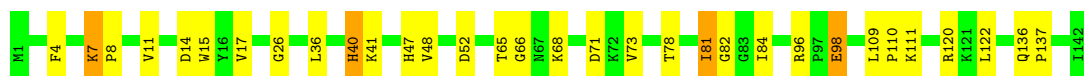
• Molecule 8: 50S ribosomal protein L11

Chain i: 23% 58% 38% . .



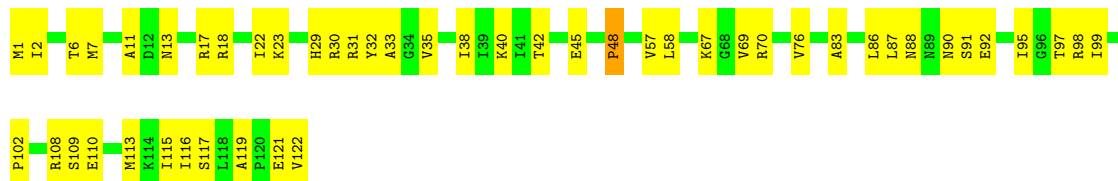
- Molecule 9: 50S ribosomal protein L13

Chain j:  77% 20% .



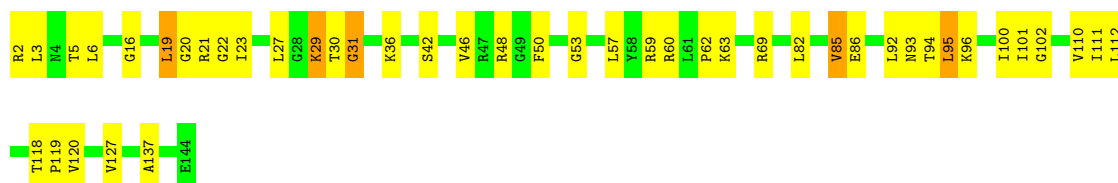
- Molecule 10: 50S ribosomal protein L14

Chain k:  60% 39% .



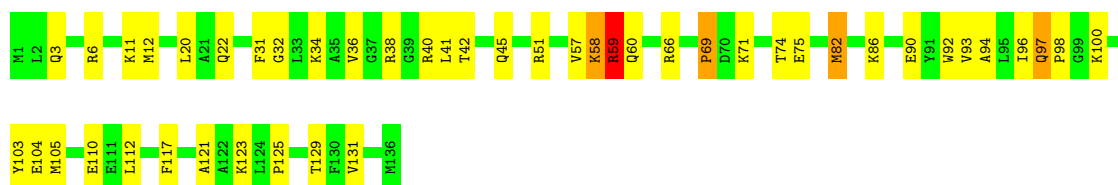
- Molecule 11: 50S ribosomal protein L15

Chain l:  69% 28% .



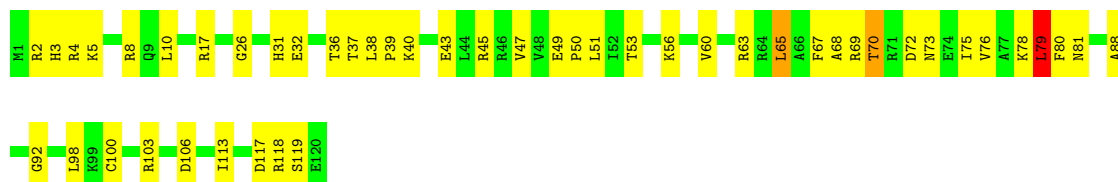
- Molecule 12: 50S ribosomal protein L16

Chain m:  66% 30% . .



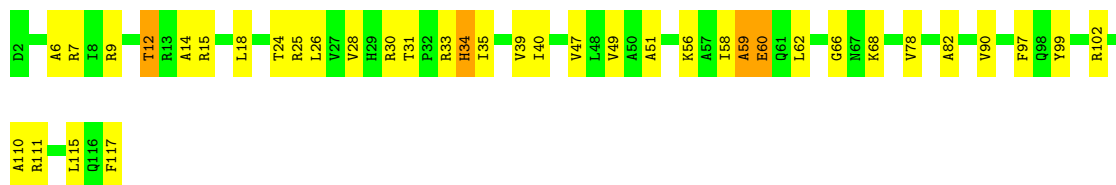
- Molecule 13: 50S ribosomal protein L17

Chain n:  60% 38% . .



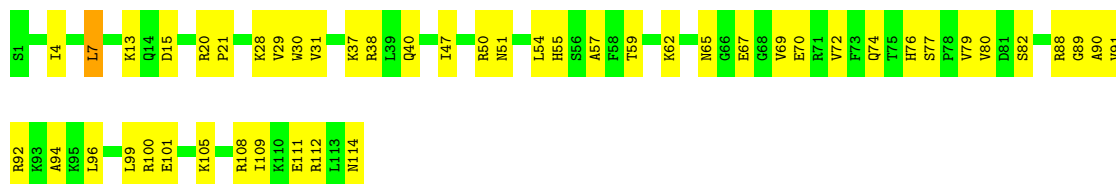
- Molecule 14: 50S ribosomal protein L18

Chain o:  67% 29% .



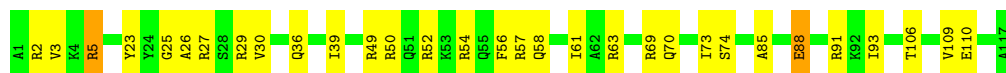
- Molecule 15: 50S ribosomal protein L19

Chain p:  58% 41% .



- Molecule 16: 50S ribosomal protein L20

Chain q:  74% 25% .



- Molecule 17: 50S ribosomal protein L21

Chain r:  71% 27% ..



- Molecule 18: 50S ribosomal protein L22

Chain s:  75% 25%



- Molecule 19: 50S ribosomal protein L23

Chain t:  71% 27% .



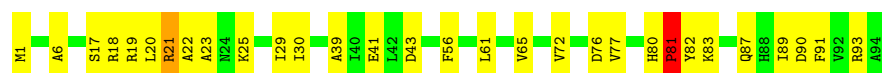
- Molecule 20: 50S ribosomal protein L24

Chain u:  66% 32% .



- Molecule 21: 50S ribosomal protein L25

Chain v:  68% 30% ..



- Molecule 22: 50S ribosomal protein L27

Chain w:  73% 27%



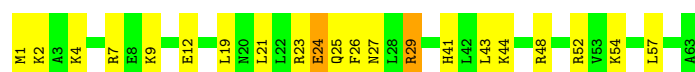
- Molecule 23: 50S ribosomal protein L28

Chain x:  68% 31% .



- Molecule 24: 50S ribosomal protein L29

Chain y:  67% 30% .



- Molecule 25: 50S ribosomal protein L30

Chain z:  78% 22%

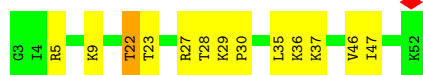
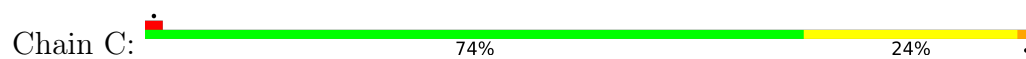


- Molecule 26: 50S ribosomal protein L32

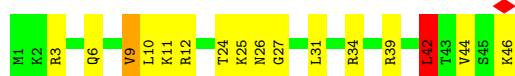
Chain B:  57% 41% .



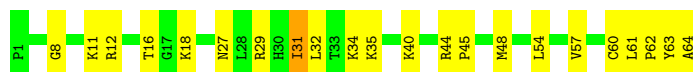
- Molecule 27: 50S ribosomal protein L33



- Molecule 28: 50S ribosomal protein L34



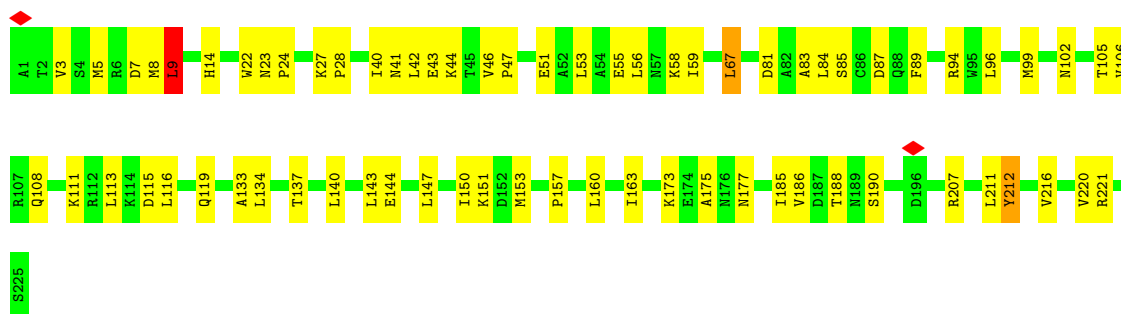
- Molecule 29: 50S ribosomal protein L35



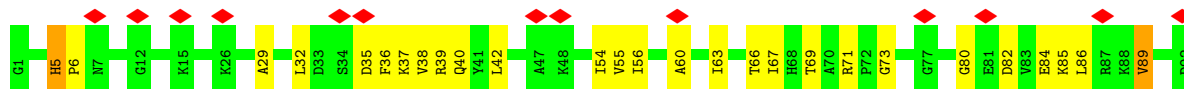
- Molecule 30: 50S ribosomal protein L36



- Molecule 31: 30S ribosomal protein S2

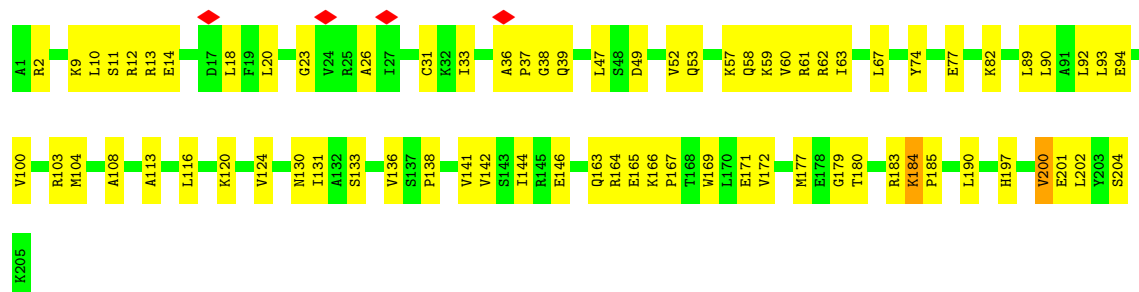


- Molecule 32: 30S ribosomal protein S3

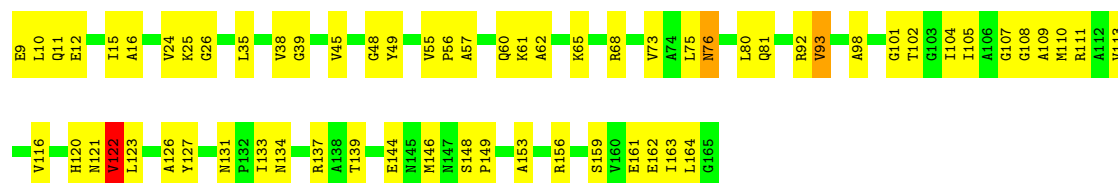




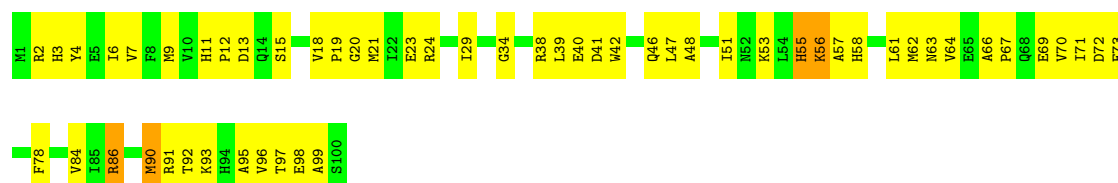
• Molecule 33: 30S ribosomal protein S4



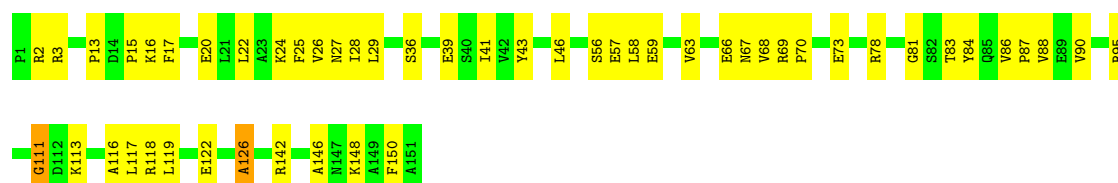
• Molecule 34: 30S ribosomal protein S5



• Molecule 35: 30S ribosomal protein S6



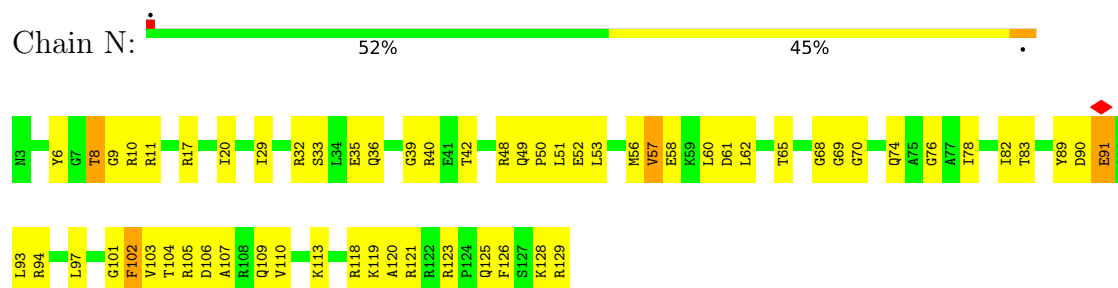
• Molecule 36: 30S ribosomal protein S7



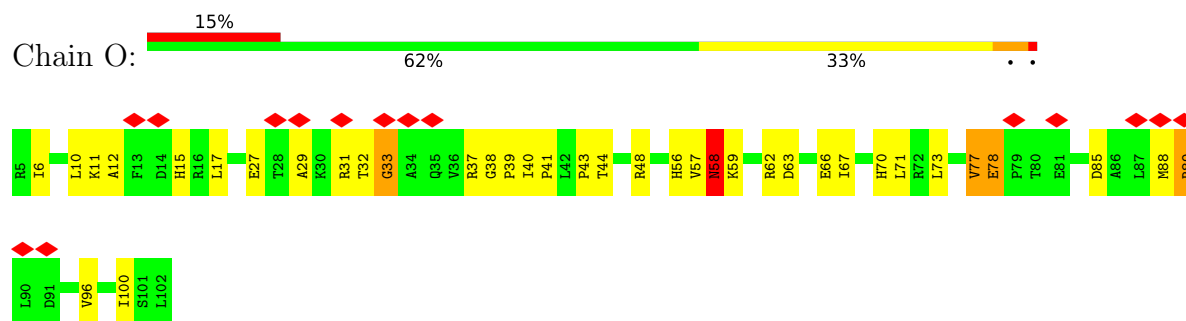
- Molecule 37: 30S ribosomal protein S8



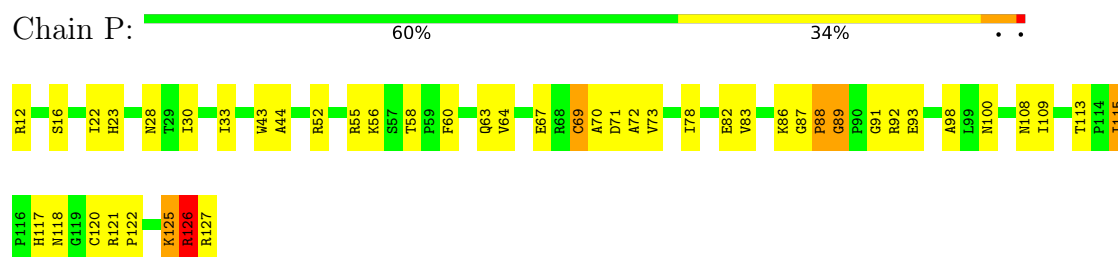
- Molecule 38: 30S ribosomal protein S9



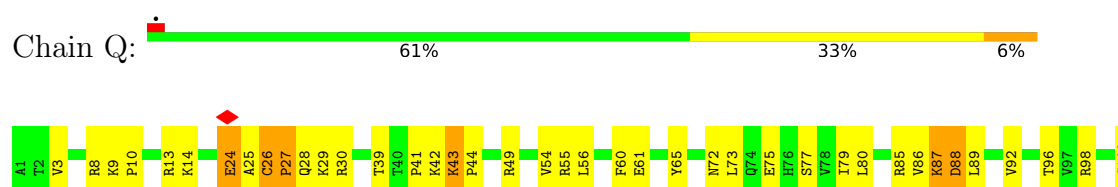
- Molecule 39: 30S ribosomal protein S10



- Molecule 40: 30S ribosomal protein S11



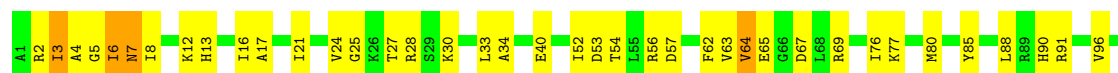
- Molecule 41: 30S ribosomal protein S12





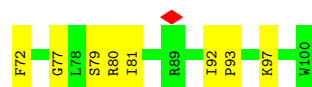
- Molecule 42: 30S ribosomal protein S13

Chain R: 62% 34%



- Molecule 43: 30S ribosomal protein S14

Chain S: 9% 56% 42%



- Molecule 44: 30S ribosomal protein S15

Chain T: 70% 30%



- Molecule 45: 30S ribosomal protein S16

Chain U: 65% 35%



- Molecule 46: 30S ribosomal protein S17

Chain V: 61% 35%



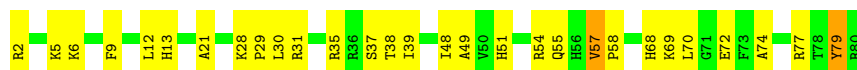
- Molecule 47: 30S ribosomal protein S18

Chain W: 57% 43%



- Molecule 48: 30S ribosomal protein S19

Chain X: 63% 34%



- Molecule 49: 30S ribosomal protein S20

Chain Y: 72% 27%



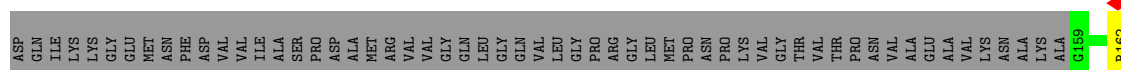
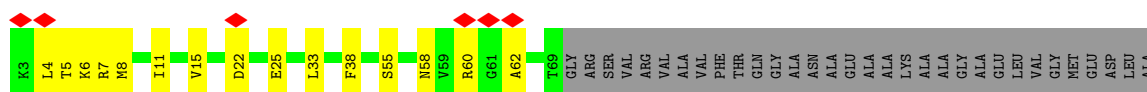
- Molecule 50: 30S ribosomal protein S21

Chain Z: 43% 45% 9%



- Molecule 51: 50S ribosomal protein L1

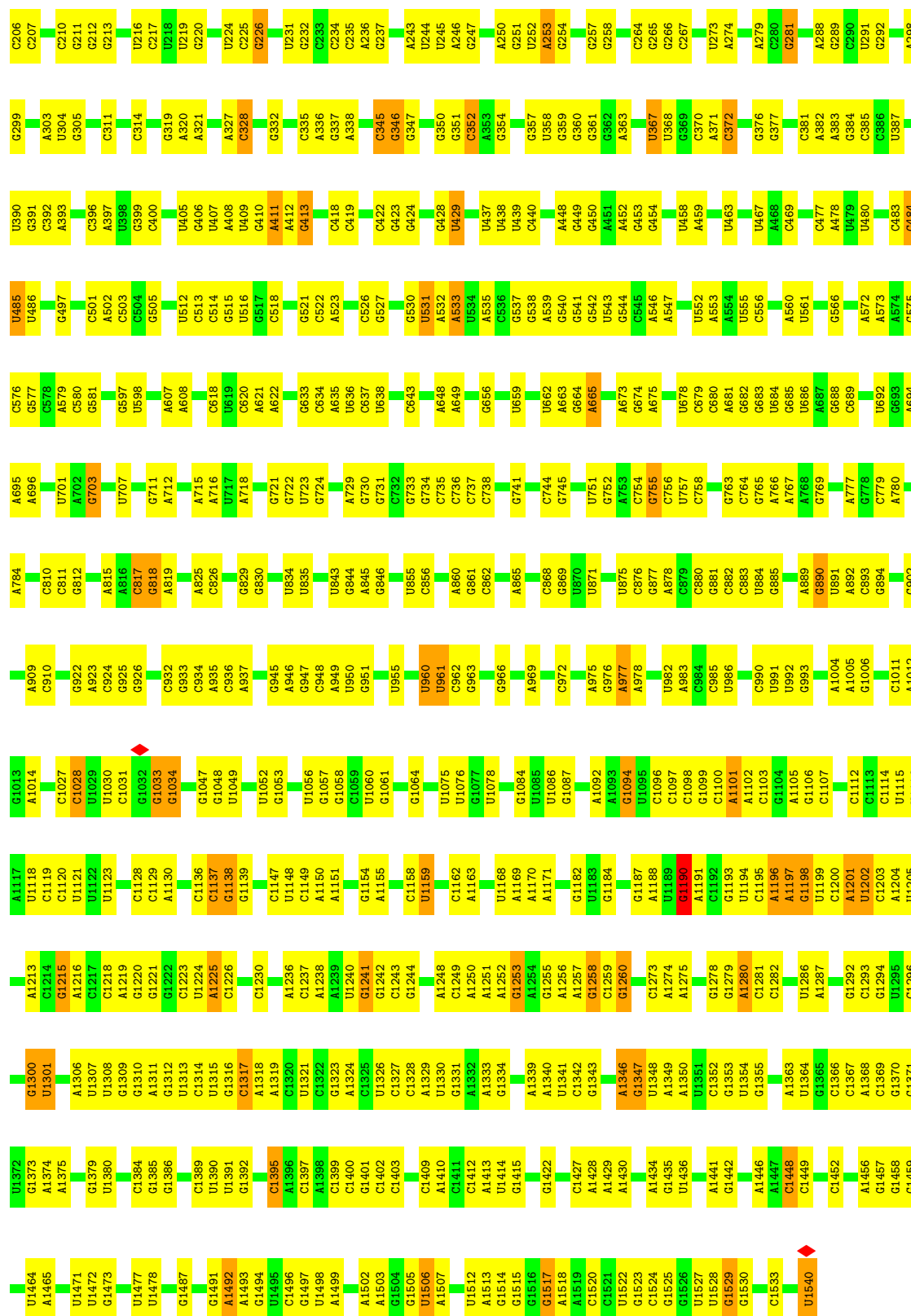
Chain a: 6% 44% 16% 40%



- Molecule 52: 16S ribosomal RNA

Chain 3: 55% 41%





● Molecule 53: 23S ribosomal RNA

Chain 1: 56% 38% 5%

C1357	G1250	G1138	G1059	U970	C885	A782	G697	A616	G533	U441	A310	C210	U112	G1
A1358	C1251	G1139	U1060	G971	U871	A783	U703	G617	U534	G442	A311	C211	U113	A10
G1359	A1252	C1140	U1061	A972	U872	G784	U704	A621	G535	A443	A312	G214	A118	C11
G1360	U1253	U1141	U1062	A973	C873	G785	A705	G622	G536	C444	G319	G215	A119	U12
G1361	U1254	A1142	U1063	A974	G874	A786	G708	A627	G537	G445	A320	A216	U120	U18
A1365	G1255	G1143	U1064	G975	G875	C786	U709	G628	C542	U451	U321	A221	G121	A19
A1366	G1256	G1144	U1065	G976	C876	G787	U710	G629	G543	A452	A322	A222	U139	C20
G1367	G1257	C1145	U1066	A977	A877	G788	U711	A633	C544	G453	C323	G225	C140	A21
G1368	G1258	U1146	U1067	A978	A878	G789	U712	G634	U545	A454	A324	G226	G141	C22
A1373	C1259	C1147	U1068	A979	G879	G790	U713	C635	U546	G455	A325	G227	G142	G23
A1378	A1268	G1153	G1071	C982	A886	A800	A715	G636	A547	A466	G329	G228	C143	G24
U1379	G1269	U1154	G1072	A983	U887	G801	A716	G637	A548	G467	A330	G229	A144	U25
A1383	G1270	A1155	U1073	G989	U888	A802	C717	A638	G549	G468	A340	G230	C145	G26
A1378	A1271	G1156	U1074	G990	C889	G803	A718	G639	U554	U473	C341	A231	C146	G27
U1387	A1272	U1157	G1075	G991	A890	G804	C719	G640	G555	G474	C353	G239	U148	U34
A1388	A1273	C1158	U1076	G992	A891	G805	U720	C645	U558	G475	A354	C240	A149	G35
G1401	U1274	G1161	U1077	G993	A892	G806	A721	U646	G559	G476	G359	G249	U150	G36
U1402	A1275	G1162	U1078	G994	C897	U807	U722	C650	C560	A477	U360	G248	C151	C37
C1386	C1278	A1175	U1083	G995	A898	G808	C723	G651	G561	A478	G361	C249	U153	A38
A1387	G1279	U1176	U1084	G996	A899	G809	U724	A654	U562	A479	G362	G250	U154	G43
U1394	A1285	G1177	A1085	G997	A900	U810	G725	A655	C564	A480	U365	G251	A155	G44
C1398	A1286	C1178	U1086	G998	A901	U811	G726	A656	U565	A481	G366	G252	G45	G45
G1401	U1287	U1179	U1087	G999	A902	U812	A727	G657	G566	A482	U367	G253	G46	G46
U1402	G1288	U1180	U1088	G1002	A903	U813	G728	A658	U567	A483	U368	G254	U158	A49
U1412	C1295	U1181	U1089	G1003	A904	U814	G729	A659	A574	A484	U369	G255	A160	U50
A1413	G1296	U1182	U1090	G1004	A905	U815	A730	A660	A575	A485	U370	G256	U162	G51
G1416	C1297	U1183	U1091	G1005	A906	U816	G731	A661	U576	A486	G371	G257	C163	C61
C1417	G1298	U1184	U1092	G1006	A907	U817	G732	A662	G577	A487	U387	G260	A167	U62
U1419	U1299	U1185	U1093	G1007	A908	U818	G733	A663	U580	A488	U395	G261	G168	A63
A1420	G1300	U1186	U1094	G1008	A909	U819	A734	A664	C581	A489	U396	G262	U174	A64
A1434	A1301	G1191	U1095	G1009	A910	U820	U744	A665	U581	U499	G396	G263	G175	U65
G1435	C1306	U1192	U1096	G1010	A911	U821	G745	A666	A582	A502	A404	G264	G178	C89
G1436	U1309	U1193	U1097	G1011	A912	U822	G746	A667	A583	A503	U405	G265	C179	G70
C1437	C1319	U1203	U1098	G1012	A913	U823	G747	A668	C584	A504	G406	G266	G180	A71
U1438	G1320	A1204	U1099	G1013	A914	U824	A752	A669	C585	A505	U419	G267	A181	A74
A1439	U1326	U1205	U1100	G1014	A915	U825	C758	A670	C586	G512	G411	G268	G188	G75
U1440	A1327	G1206	U1101	U1015	A916	U826	G759	A671	U588	A513	C414	G269	U191	U78
G1441	U1328	U1207	U1102	U1016	A917	U827	A761	A672	U589	A514	C415	G270	A192	A83
U1442	A1329	G1212	U1103	A1020	A918	U828	U762	A673	U593	C517	U416	G271	C193	A84
C1443	C1330	A1213	U1104	A1021	A919	U829	G763	A674	C594	G518	U417	G272	U194	C86
C1447	G1331	U1224	U1105	G1022	A920	U830	A764	A675	C595	U519	U418	G273	G195	C87
G1448	C1332	G1225	U1106	G1023	A921	U831	C765	A676	C596	G520	C420	G274	A196	U102
G1449	U1335	U1231	U1107	G1024	A922	U832	U766	A677	U597	G521	A423	G275	A197	A103
C1451	A1336	G1232	U1108	G1025	A923	U833	U767	A678	U598	G522	G424	G276	C198	A104
C1454	G1341	U1236	U1109	C1045	A924	U834	U768	A679	A599	G523	U419	G277	A199	A105
C1461	U1344	A1237	U1110	A1054	A925	U835	U769	A680	A603	G524	U420	G278	U200	C106
A1469	C1345	G1238	U1111	G1055	A926	U836	U770	A681	A609	G525	C433	G279	U201	G107
U1470	U1352	U1248	U1112	G1056	A927	U837	G776	A682	C610	G526	U434	G301	C202	G108
			U1113	U1057	A928	U838	A781	A683	U615	A532	C435	G303	C203	
			C1135	U1058	A929	U839		A684			C436			
			U1134		A930	U840		A685						
			U1135		A931	U841		A686						
			U1136		A932	U842		A687						
			U1137		A933	U843		A688						
			U1138		A934	U844		A689						
			U1139		A935	U845		A690						
			U1140		A936	U846		A691						
			U1141		A937	U847		A692						
			U1142		A938	U848		A693						
			U1143		A939	U849		A694						
			U1144		A940	U850		A695						
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			U1146		A942	U852		A697						
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			U1150		A946	U856		A701						
			U1151		A947	U857		A702						
			U1152		A948	U858		A703						
			U1153		A949	U859		A704						
			U1154		A950	U860		A705						
			U1155		A951	U861		A706						
			U1156		A952	U862		A707						
			U1157		A953	U863		A708						
			U1158		A954	U864		A709						
			U1159		A955	U865		A710						
			U1160		A956	U866		A711						
			U1161		A957	U867		A712						
			U1162		A958	U868		A713						
			U1163		A959	U869		A714						
			U1164		A960	U870		A715						
			U1165		A961	U871		A716						
			U1166		A962	U872		A717						
			U1167		A963	U873		A718						
			U1168		A964	U874		A719						
			U1169		A965	U875		A720						
			U1170		A966	U876		A721						
			U1171		A967	U877		A722						
			U1172		A968	U878		A723						
			U1173		A969	U879		A724						
			U1174		A970	U880		A725						
			U1175		A971	U881		A726						
			U1176		A972	U882		A727						
			U1177		A973	U883		A728						
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			U1179		A975	U885		A730						
			U1180		A976	U886		A731						
			U1181		A977	U887		A732						
			U1182		A978	U888		A733						
			U1183		A979	U889		A734						
			U1184		A980	U890		A735						
			U1185		A981	U891		A736						
			U1186		A982	U892		A737						
			U1187		A983	U893		A738						
			U1188		A984	U894		A739						
			U1189		A985	U895		A740						
			U1190		A986	U896		A741						
			U1191		A987	U897		A742						
			U1192		A988	U898		A743						
			U1193		A989	U899		A744						
			U1194		A990	U900		A745						
			U1195		A991	U901		A746						
			U1196		A992	U902		A747						
			U1197		A993	U903		A748						
			U1198		A994	U904		A749						
			U1199		A995	U905		A750						
			U1200		A996	U906		A751						
			U1201		A997	U907		A752						
			U1202		A998	U908		A753						

A2820	U2724	G2623	C2527	C2442	U2285	U2180	G2087	U1991	A1900	C1806	U1709	C1592	U1474
A2821	A2725	G2624	U2528	C2443	A2266	U2181	A2088	G1992	A1901	G1807	G1710	A1593	G1475
G2825	U2728	G2625	G2529	G2444	A2267	U2182	C2089	U1993	C1902	A1808	G1715	U1594	U1476
A2826	G2731	G2627	A2530	U2448	A2268	A2183	G2093	C1996	G1903	A1809	G1720	C1595	G1482
A2829	G2732	G2628	G2532	A2449	U2272	A2184	C2096	U1997	G1904	G1811	U1720	A1603	A1490
G2830	A2733	G2630	U2533	C2452	A2273	U2187	G2104	C1999	G1905	U1812	G1721	C1606	C1498
G2831	G2742	G2631	U2537	U2457	G2277	U2188	U2105	G2010	G1907	C1816	U1726	C1607	C1499
U2832	U2632	G2632	G2538	G2458	A2278	U2189	U2106	U2011	C1909	U1817	C1725	G1608	G1500
G2834	U2743	G2633	G2539	U2459	G2279	G2190	G2107	G2012	G1910	U1818	U1729	A1609	G1501
A2835	G2744	G2634	C2539	C2462	G2280	G2193	G2110	G2013	U1911	U1819	U1730	A1610	C1611
U2836	G2747	G2636	U2544	C2463	G2282	U2194	G2111	A2014	A1912	U1820	C1730	C1615	U1506
C2840	A2748	G2638	G2547	C2467	C2283	U2195	G2112	A2015	A1913	G1823	U1736	A1614	C1507
C2841	A2749	G2638	A2547	C2467	G2286	U2196	G2113	A2020	U1917	G1824	U1737	C1615	C1507
G2842	A2750	G2641	U2548	A2468	A2287	U2197	U2113	A2021	A1918	U1827	G1738	A1616	A1508
U2845	G2751	C2646	G2549	A2469	A2288	A2198	G2114	U2022	A1919	G1828	A1739	A1509	G1510
U2846	G2755	U2647	G2550	G2470	A2288	C2200	G2115	C2023	G1929	G1829	A1746	C1625	A1515
G2848	U2756	G2653	G2553	C2475	U2292	G2201	G2116	G2023	G1930	C1830	U1747	A1626	G1524
U2849	A2757	U2554	U2554	A2476	G2293	G2204	U2118	G2029	U1931	G1831	C1748	G1627	G1524
A2850	U2758	G2655	G2555	C2480	U2296	U2205	G2119	A2030	G1935	C1832	U1629	U1628	U1629
U2851	G2759	C2656	G2556	G2481	A2297	G2206	G2120	A2031	U1936	C1833	U1758	A1630	A1528
C2853	U2762	U2656	G2557	A2482	A2298	C2208	G2121	G2032	A1937	U1834	A1759	A1637	G1529
G2854	G2763	G2657	U2561	C2483	C2385	U2210	U2122	C2036	A1938	C1837	C1760	C1637	A1535
G2859	A2764	G2658	U2562	G2484	G2389	A2211	G2126	U2039	U1943	U1851	C1761	A1641	C1536
A2860	A2765	G2659	G2563	G2485	G2390	A2212	G2127	G2040	U1944	G1856	G1763	A1642	C1537
U2861	G2772	G2660	U2566	C2486	G2394	U2213	G2128	U2041	G1947	U1857	C1764	G1645	G1538
G2862	C2773	G2661	G2567	G2487	U2305	U2220	C2129	C2042	G1948	G1858	U1765	G1646	U1540
C2863	G2774	G2662	U2568	G2488	A2309	G2225	U2132	C2043	U1951	U1859	G1766	G1647	A1549
G2864	U2775	A2665	A2572	U2489	U2312	A2226	G2133	C2045	A1952	G1860	A1773	U1648	C1560
G2867	G2776	C2666	G2573	G2490	C2313	G2226	A2134	U2045	A1953	G1861	U1775	C1649	A1551
A2868	U2778	G2674	G2574	U2491	U2317	G2230	U2139	A2052	G1954	U1866	G1776	A1650	A1551
G2869	A2779	C2678	U2580	C2498	G2318	U2231	G2140	C2055	U1955	G1867	U1779	U1657	U1554
C2870	U2784	A2679	G2581	C2499	G2319	U2232	G2141	G2056	U1956	A1871	A1781	C1658	G1555
A2872	G2785	U2680	U2582	G2502	G2325	G2233	A2147	A2060	C1957	A1872	U1780	U1662	U1559
A2879	U2786	C2681	U2584	A2503	A2326	U2234	U2151	G2061	U1963	C1873	A1784	G1663	G1560
U2880	G2787	G2682	U2585	A2504	U2329	A2241	G2156	A2062	G1964	C1874	U1785	A1664	U1563
C2884	U2788	C2683	G2588	G2505	G2331	G2242	G2157	C2063	C1965	G1875	A1786	C1665	C1564
U2888	G2789	U2689	A2589	G2508	C2332	U2243	G2162	C2064	C1966	A1876	A1787	G1666	C1565
C2889	A2790	U2690	A2590	G2509	A2333	U2244	A2163	G2067	G1968	G1878	C1788	A1566	A1566
A2893	G2791	G2697	G2592	C2512	U2334	U2245	U2166	U2068	A1969	C1879	C1790	A1669	A1569
U2903	C2794	U2698	A2513	A2514	U2335	C2248	U2166	G2069	A1970	U1880	A1791	C1670	U1569
U2904	G2795	U2699	G2515	C2515	A2336	U2249	U2166	A2070	U1971	C1881	C1795	G1674	A1570
U2905	U2796	U2700	U2516	C2516	U2337	U2250	U2166	A2071	G1972	U1882	U1796	C1685	A1572
U2906	U2797	A2705	U2517	A2518	U2338	U2251	A2170	C2072	A1977	U1883	G1797	C1686	G1581
U2907	U2798	A2706	C2519	C2519	U2339	U2252	A2171	C2073	U1978	A1885	U1798	G1697	U1584
U2908	G2799	G2710	U2520	C2520	A2340	U2253	A2172	U2074	U1979	G1890	G1799	C1697	U1584
U2909	A2800	C2711	G2521	U2522	C2342	C2258	A2173	U2074	G1980	G1891	C1800	C1704	C1585
U2910	G2801	G2712	U2523	U2523	A2343	C2261	A2176	A2080	U1981	A1890	U1801	A1586	G1587
U2911	A2809	G2714	G2524	G2526	U2344	C2264	C2177	U2086	U1982	G1899	A1705	A1705	

- Molecule 54: 5S ribosomal RNA

Chain 2: 



- Molecule 55: tRNA^{fMet}

Chain 5: 



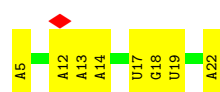
- Molecule 55: tRNA^{fMet}

Chain 6: 



- Molecule 56: mRNA

Chain 4: 



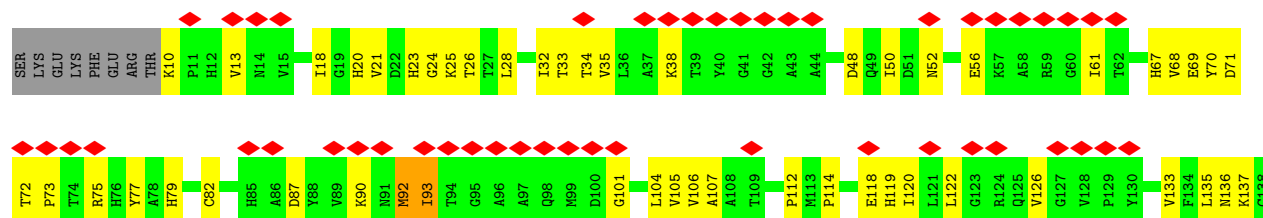
- Molecule 57: tRNA^{Phe}

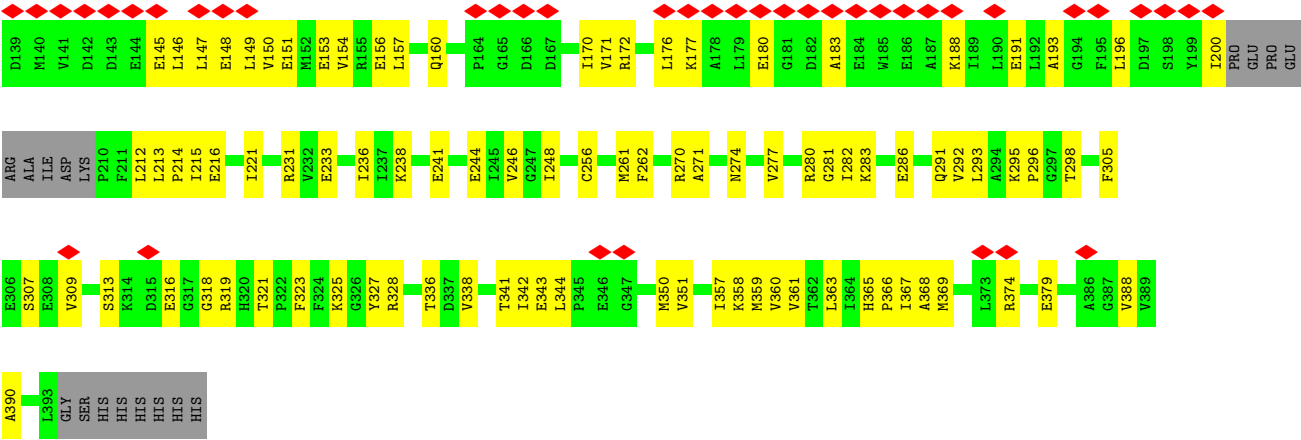
Chain 7: 



- 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	7840	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	18.517	Depositor
Minimum map value	-9.717	Depositor
Average map value	0.113	Depositor
Map value standard deviation	0.863	Depositor
Recommended contour level	1	Depositor
Map size ($\text{\AA}$)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.333, 1.333, 1.333	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	b	0.29	0/2122	0.96	8/2852 (0.3%)
2	c	0.29	0/1586	0.86	1/2134 (0.0%)
3	d	0.28	0/1571	0.87	6/2113 (0.3%)
4	e	0.31	0/1435	0.89	5/1926 (0.3%)
5	f	0.30	0/1343	0.87	4/1816 (0.2%)
6	g	0.31	0/1122	0.94	5/1515 (0.3%)
7	h	0.33	0/1002	1.01	10/1350 (0.7%)
8	i	0.36	0/1046	0.99	6/1410 (0.4%)
9	j	0.30	0/1152	0.94	4/1551 (0.3%)
10	k	0.28	0/948	0.89	3/1268 (0.2%)
11	l	0.30	0/1054	0.98	5/1403 (0.4%)
12	m	0.29	0/1093	0.88	3/1460 (0.2%)
13	n	0.29	0/974	0.96	6/1301 (0.5%)
14	o	0.28	0/902	0.86	2/1209 (0.2%)
15	p	0.29	0/929	0.82	1/1242 (0.1%)
16	q	0.28	0/960	0.97	4/1278 (0.3%)
17	r	0.29	0/829	0.93	3/1107 (0.3%)
18	s	0.29	0/864	0.92	1/1156 (0.1%)
19	t	0.27	0/745	0.88	2/994 (0.2%)
20	u	0.29	0/788	0.88	2/1051 (0.2%)
21	v	0.28	0/766	0.90	2/1025 (0.2%)
22	w	0.29	0/582	0.90	4/769 (0.5%)
23	x	0.28	0/635	0.90	1/848 (0.1%)
24	y	0.28	0/510	0.94	2/677 (0.3%)
25	z	0.30	0/453	0.81	0/605
26	B	0.27	0/450	0.85	1/599 (0.2%)
27	C	0.31	0/417	0.89	2/554 (0.4%)
28	D	0.33	0/380	0.92	0/498
29	E	0.30	0/513	0.94	1/676 (0.1%)
30	F	0.31	0/303	0.88	0/397
31	G	0.29	0/1788	0.90	4/2408 (0.2%)
32	H	0.33	0/1652	0.93	7/2225 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.29	0/1665	0.94	10/2227 (0.4%)
34	J	0.35	0/1170	0.97	5/1573 (0.3%)
35	K	0.32	0/836	0.87	2/1128 (0.2%)
36	L	0.29	0/1196	0.92	4/1602 (0.2%)
37	M	0.29	0/989	0.88	2/1326 (0.2%)
38	N	0.31	0/1034	0.91	0/1375
39	O	0.35	0/797	0.92	3/1077 (0.3%)
40	P	0.30	0/886	0.96	5/1195 (0.4%)
41	Q	0.32	0/969	1.07	10/1300 (0.8%)
42	R	0.30	0/893	0.90	1/1193 (0.1%)
43	S	0.30	0/817	0.93	3/1088 (0.3%)
44	T	0.28	0/722	0.86	2/964 (0.2%)
45	U	0.31	0/659	0.84	0/884
46	V	0.29	0/658	0.92	3/881 (0.3%)
47	W	0.31	0/545	0.94	2/731 (0.3%)
48	X	0.32	0/653	0.94	3/877 (0.3%)
49	Y	0.28	0/671	0.93	1/888 (0.1%)
50	Z	0.33	0/551	1.08	6/728 (0.8%)
51	a	0.31	0/1034	0.80	0/1387
52	3	0.41	0/36963	0.47	3/57662 (0.0%)
53	1	0.40	0/69796	0.48	5/108888 (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	0.47	0/679
57	7	0.40	0/1809	0.48	0/2819
58	8	0.31	0/2937	0.89	6/3975 (0.2%)
All	All	0.37	0/166136	0.63	181/248053 (0.1%)

There are no bond length outliers.

The worst 5 of 181 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R	3	ILE	N-CA-C	9.16	122.18	109.45
17	r	50	GLY	N-CA-C	-8.87	101.76	112.49
44	T	43	ALA	N-CA-C	-8.80	101.61	111.82
33	I	200	VAL	N-CA-C	8.71	119.51	110.36
9	j	120	ARG	N-CA-C	-8.39	102.48	112.89

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	59	0
2	c	1565	0	1616	44	0
3	d	1552	0	1619	47	0
4	e	1411	0	1447	46	0
5	f	1323	0	1374	36	0
6	g	1111	0	1148	39	0
7	h	989	0	1025	55	0
8	i	1032	0	1088	56	0
9	j	1129	0	1162	28	0
10	k	939	0	1012	39	0
11	l	1045	0	1117	34	0
12	m	1074	0	1157	36	0
13	n	961	0	1000	39	0
14	o	892	0	923	25	0
15	p	917	0	965	36	0
16	q	947	0	1022	32	0
17	r	816	0	839	28	0
18	s	857	0	922	19	0
19	t	739	0	807	28	0
20	u	780	0	834	27	0
21	v	753	0	780	22	0
22	w	575	0	592	17	0
23	x	625	0	655	20	0
24	y	509	0	543	19	0
25	z	449	0	491	12	0
26	B	444	0	461	24	0
27	C	410	0	440	8	0
28	D	377	0	418	15	0
29	E	504	0	574	17	0
30	F	302	0	343	13	0
31	G	1757	0	1787	53	0
32	H	1625	0	1699	49	0
33	I	1643	0	1710	56	0
34	J	1157	0	1199	49	0
35	K	818	0	808	45	0
36	L	1182	0	1240	38	0
37	M	979	0	1034	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	52	0
39	O	787	0	828	33	0
40	P	870	0	878	35	0
41	Q	955	0	1019	30	0
42	R	884	0	944	37	0
43	S	805	0	847	45	0
44	T	714	0	737	18	0
45	U	649	0	666	24	0
46	V	649	0	691	30	0
47	W	536	0	552	18	0
48	X	638	0	665	26	0
49	Y	665	0	714	22	0
50	Z	545	0	579	39	0
51	a	1027	0	1092	21	0
52	3	33012	0	16618	599	0
53	1	62317	0	31346	936	0
54	2	2568	0	1303	51	0
55	5	1640	0	836	17	0
55	6	1640	0	837	20	0
56	4	388	0	196	6	0
57	7	1619	0	821	31	0
58	8	2885	0	2900	99	0
59	5	10	0	10	1	0
60	7	11	0	8	2	0
61	8	28	0	12	2	0
All	All	153135	0	104177	2993	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 2993 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''	1.39	1.05
38:N:83:THR:HG21	38:N:102:PHE:HB3	1.36	1.05
34:J:107:GLY:HA3	52:3:9:G:H5'	1.39	1.03
50:Z:66:ARG:HH21	52:3:1099:G:H4'	1.21	1.03
52:3:1197:A:H2'	52:3:1198:G:H5''	1.41	0.99

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	220 (82%)	37 (14%)	12 (4%)	2	17
2	c	207/209 (99%)	183 (88%)	23 (11%)	1 (0%)	24	57
3	d	199/201 (99%)	169 (85%)	27 (14%)	3 (2%)	8	37
4	e	175/177 (99%)	155 (89%)	19 (11%)	1 (1%)	21	54
5	f	174/176 (99%)	156 (90%)	16 (9%)	2 (1%)	11	43
6	g	147/149 (99%)	130 (88%)	16 (11%)	1 (1%)	18	51
7	h	129/131 (98%)	100 (78%)	21 (16%)	8 (6%)	1	12
8	i	139/141 (99%)	121 (87%)	11 (8%)	7 (5%)	1	16
9	j	140/142 (99%)	132 (94%)	7 (5%)	1 (1%)	18	51
10	k	120/122 (98%)	105 (88%)	14 (12%)	1 (1%)	16	49
11	l	141/143 (99%)	118 (84%)	19 (14%)	4 (3%)	4	26
12	m	134/136 (98%)	113 (84%)	17 (13%)	4 (3%)	3	25
13	n	118/120 (98%)	97 (82%)	20 (17%)	1 (1%)	16	49
14	o	114/116 (98%)	106 (93%)	6 (5%)	2 (2%)	6	34
15	p	112/114 (98%)	93 (83%)	18 (16%)	1 (1%)	14	46
16	q	115/117 (98%)	109 (95%)	5 (4%)	1 (1%)	14	46
17	r	101/103 (98%)	83 (82%)	15 (15%)	3 (3%)	3	25
18	s	108/110 (98%)	92 (85%)	11 (10%)	5 (5%)	2	17
19	t	91/93 (98%)	79 (87%)	12 (13%)	0	100	100
20	u	100/102 (98%)	87 (87%)	9 (9%)	4 (4%)	2	20
21	v	92/94 (98%)	84 (91%)	7 (8%)	1 (1%)	11	43
22	w	73/75 (97%)	63 (86%)	10 (14%)	0	100	100
23	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	y	61/63 (97%)	58 (95%)	2 (3%)	1 (2%)	7	36
25	z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	47 (87%)	7 (13%)	0	100	100
27	C	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
28	D	44/46 (96%)	36 (82%)	7 (16%)	1 (2%)	5	30
29	E	62/64 (97%)	54 (87%)	6 (10%)	2 (3%)	3	24
30	F	36/38 (95%)	28 (78%)	7 (19%)	1 (3%)	4	26
31	G	223/225 (99%)	203 (91%)	19 (8%)	1 (0%)	30	61
32	H	204/206 (99%)	185 (91%)	18 (9%)	1 (0%)	24	57
33	I	203/205 (99%)	171 (84%)	30 (15%)	2 (1%)	12	45
34	J	155/157 (99%)	124 (80%)	25 (16%)	6 (4%)	2	20
35	K	98/100 (98%)	77 (79%)	18 (18%)	3 (3%)	3	25
36	L	149/151 (99%)	128 (86%)	20 (13%)	1 (1%)	18	51
37	M	127/129 (98%)	113 (89%)	12 (9%)	2 (2%)	7	36
38	N	125/127 (98%)	99 (79%)	19 (15%)	7 (6%)	1	14
39	O	96/98 (98%)	78 (81%)	15 (16%)	3 (3%)	3	25
40	P	114/116 (98%)	95 (83%)	14 (12%)	5 (4%)	2	18
41	Q	121/123 (98%)	95 (78%)	20 (16%)	6 (5%)	1	16
42	R	112/114 (98%)	97 (87%)	11 (10%)	4 (4%)	2	22
43	S	98/100 (98%)	78 (80%)	19 (19%)	1 (1%)	12	45
44	T	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	10	41
45	U	80/82 (98%)	67 (84%)	12 (15%)	1 (1%)	9	39
46	V	78/80 (98%)	65 (83%)	12 (15%)	1 (1%)	9	39
47	W	63/65 (97%)	56 (89%)	5 (8%)	2 (3%)	3	24
48	X	77/79 (98%)	68 (88%)	9 (12%)	0	100	100
49	Y	83/85 (98%)	76 (92%)	6 (7%)	1 (1%)	10	41
50	Z	63/65 (97%)	42 (67%)	15 (24%)	6 (10%)	0	6
51	a	130/223 (58%)	124 (95%)	5 (4%)	1 (1%)	16	49
58	8	371/400 (93%)	333 (90%)	37 (10%)	1 (0%)	36	65
All	All	6290/6512 (97%)	5438 (86%)	728 (12%)	124 (2%)	8	32

5 of 124 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	56	GLY

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Mol	Chain	Res	Type
2	c	86	GLU
5	f	45	ALA
6	g	9	VAL
7	h	113	PHE

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	76
2	c	164/164 (100%)	164 (100%)	0	100	100
3	d	165/165 (100%)	163 (99%)	2 (1%)	63	73
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	114 (100%)	0	100	100
7	h	100/100 (100%)	98 (98%)	2 (2%)	48	66
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	76
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	75
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	76
13	n	100/100 (100%)	96 (96%)	4 (4%)	28	54
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	73
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	75
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	73
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	74
19	t	80/80 (100%)	78 (98%)	2 (2%)	42	63
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%)	77 (99%)	1 (1%)	61	72
22	w	57/57 (100%)	56 (98%)	1 (2%)	51	68
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%)	44 (98%)	1 (2%)	45	65
28	D	38/38 (100%)	36 (95%)	2 (5%)	20	48
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	33 (97%)	1 (3%)	37	60
31	G	186/186 (100%)	184 (99%)	2 (1%)	65	74
32	H	170/170 (100%)	170 (100%)	0	100	100
33	I	172/172 (100%)	172 (100%)	0	100	100
34	J	119/119 (100%)	119 (100%)	0	100	100
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	74
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	104 (100%)	0	100	100
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	64
40	P	89/89 (100%)	88 (99%)	1 (1%)	65	74
41	Q	103/103 (100%)	102 (99%)	1 (1%)	68	75
42	R	92/92 (100%)	91 (99%)	1 (1%)	65	74
43	S	83/83 (100%)	83 (100%)	0	100	100
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	64 (98%)	1 (2%)	57	70
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	55 (98%)	1 (2%)	51	68
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	52 (94%)	3 (6%)	19	47
51	a	110/174 (63%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	8	309/332 (93%)	308 (100%)	1 (0%)	86	83
All	All	5217/5304 (98%)	5178 (99%)	39 (1%)	73	78

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	O	58	ASN
50	Z	10	PRO
39	O	89	ARG
42	R	64	VAL
50	Z	31	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 136 such sidechains are listed below:

Mol	Chain	Res	Type
41	Q	95	HIS
43	S	48	GLN
58	8	12	HIS
16	q	71	ASN
15	p	114	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	135 (8%)	4 (0%)
53	1	2902/2903 (99%)	321 (11%)	8 (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%)	13 (17%)	0
All	All	4803/4810 (99%)	495 (10%)	14 (0%)

5 of 495 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	7	A
52	3	9	G

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Mol	Chain	Res	Type
52	3	22	G
52	3	31	G

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	1130	U
53	1	2286	G
54	2	88	C
53	1	2391	G
54	2	66	A

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	$\# Z > 2$
60	PHE	7	101	57	10,11,12	0.67	0	8,13,15	0.28	0
59	FME	5	101	55	8,9,10	0.45	0	8,9,11	1.05	0
61	GDP	8	501	-	29,30,30	1.04	1 (3%)	45,47,47	1.92	13 (28%)

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
60	PHE	7	101	57	-	1/5/6/8	0/1/1/1
59	FME	5	101	55	-	2/7/9/11	-
61	GDP	8	501	-	-	5/16/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GDP	PB-O3B	2.03	1.62	1.54

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	C2-N3-C4	5.49	121.76	112.30
61	8	501	GDP	C5-C4-N3	-5.41	119.78	128.39
61	8	501	GDP	N9-C4-N3	4.09	134.13	125.95
61	8	501	GDP	O4'-C4'-C3'	3.18	111.46	105.15
61	8	501	GDP	C8-N7-C5	2.91	109.44	104.26

There are no chirality outliers.

5 of 8 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	C5'-O5'-PA-O3A
61	8	501	GDP	O4'-C4'-C5'-O5'
61	8	501	GDP	C3'-C4'-C5'-O5'

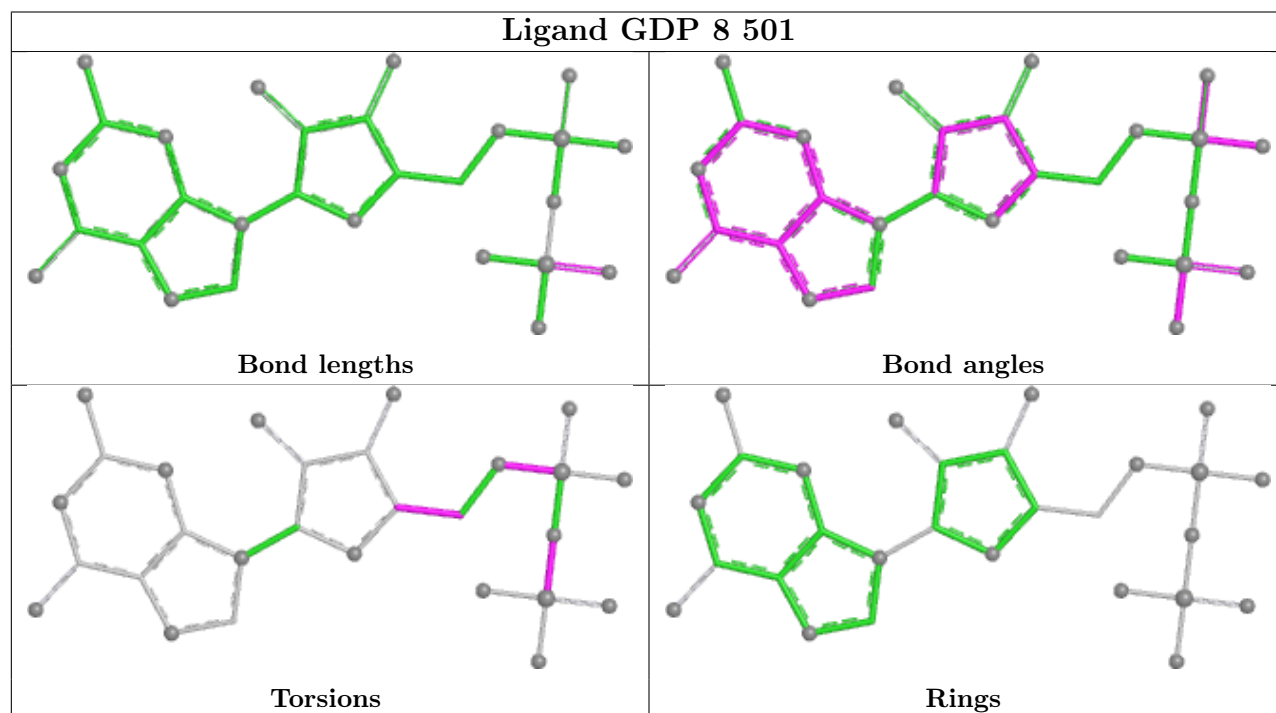
There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	7	101	PHE	2	0
59	5	101	FME	1	0
61	8	501	GDP	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.

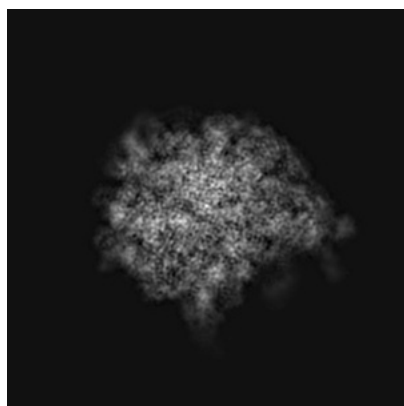
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21624. These allow visual inspection of the internal detail of the map and identification of artifacts.

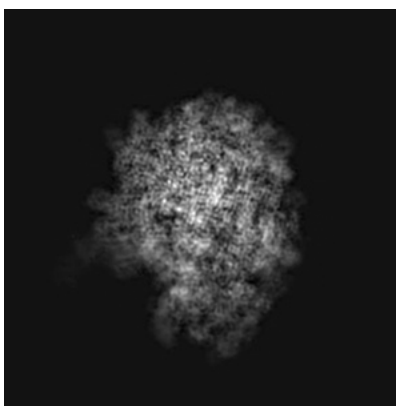
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

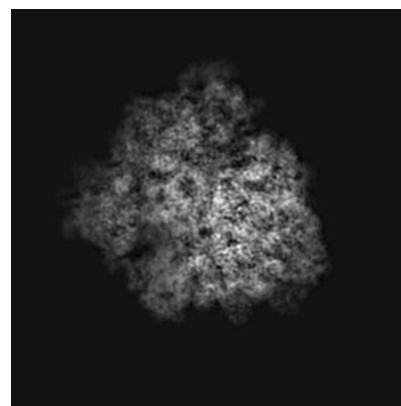
6.1.1 Primary map



X

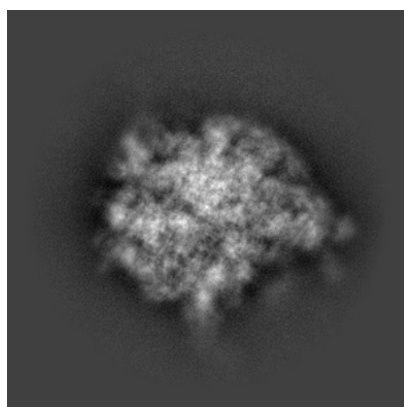


Y

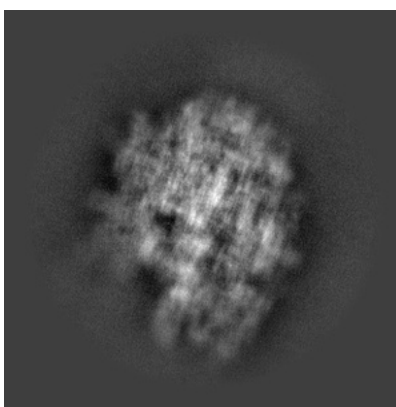


Z

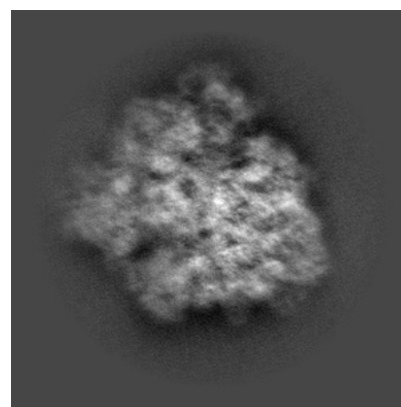
6.1.2 Raw map



X



Y

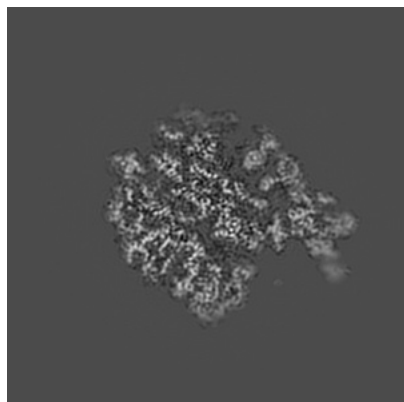


Z

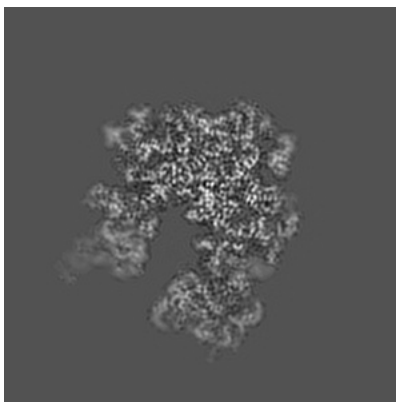
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

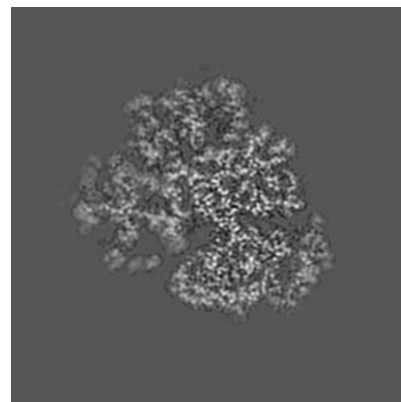
6.2.1 Primary map



X Index: 144

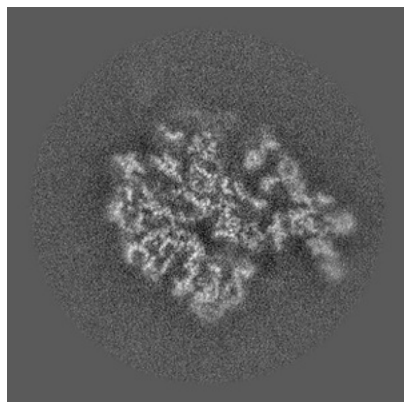


Y Index: 144

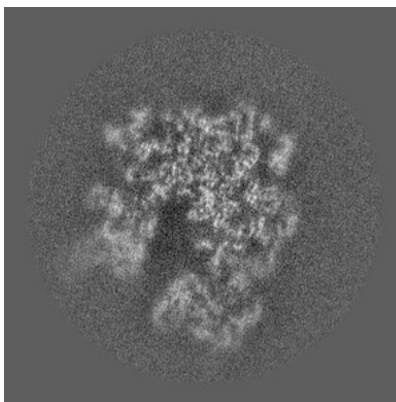


Z Index: 144

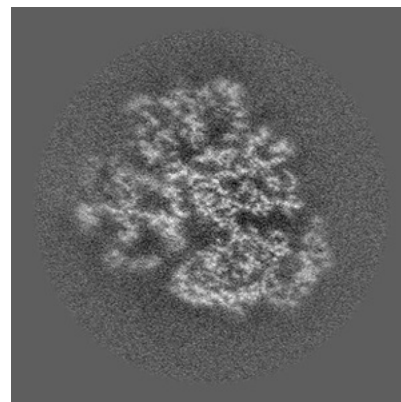
6.2.2 Raw map



X Index: 144



Y Index: 144

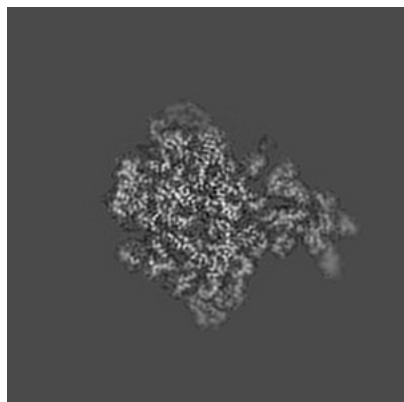


Z Index: 144

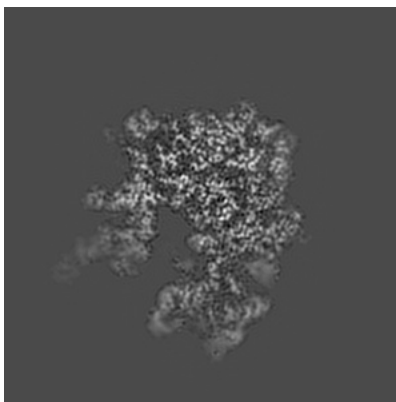
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

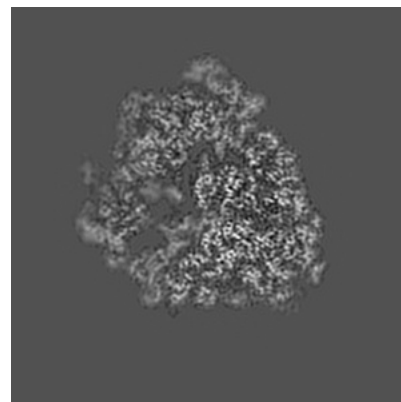
6.3.1 Primary map



X Index: 149

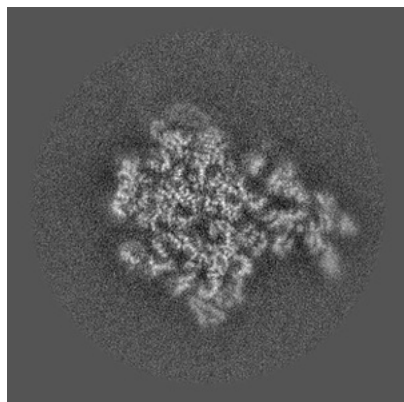


Y Index: 149

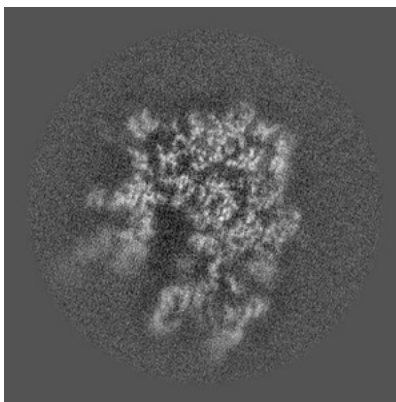


Z Index: 135

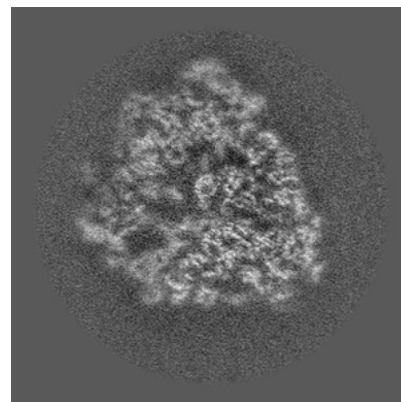
6.3.2 Raw map



X Index: 149



Y Index: 149

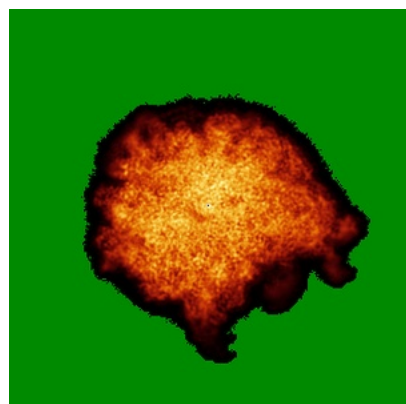


Z Index: 135

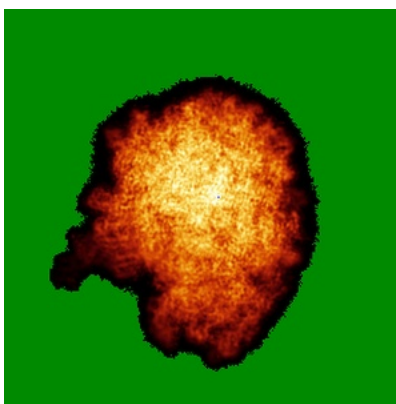
The images above show the largest variance slices of the map in three orthogonal directions.

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

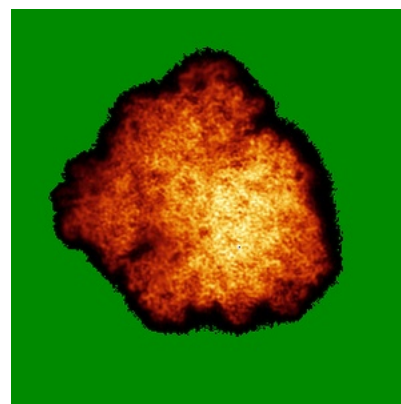
6.4.1 Primary map



X

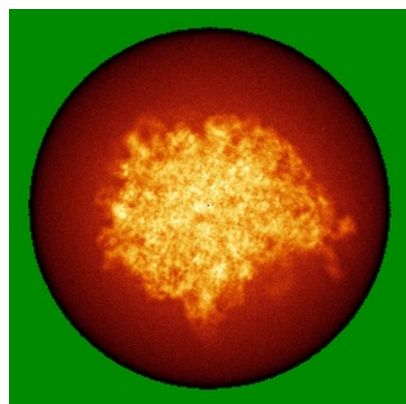


Y

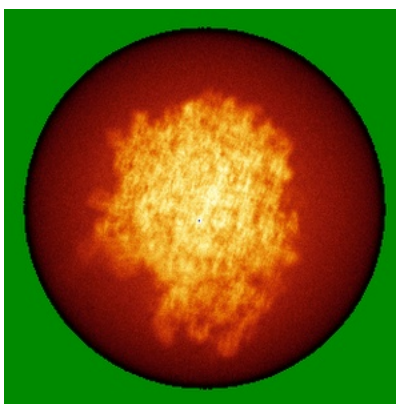


Z

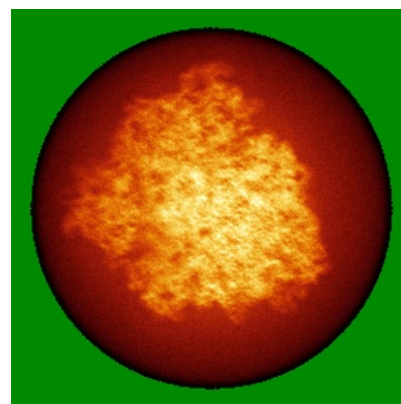
6.4.2 Raw map



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



X



Y



Z

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

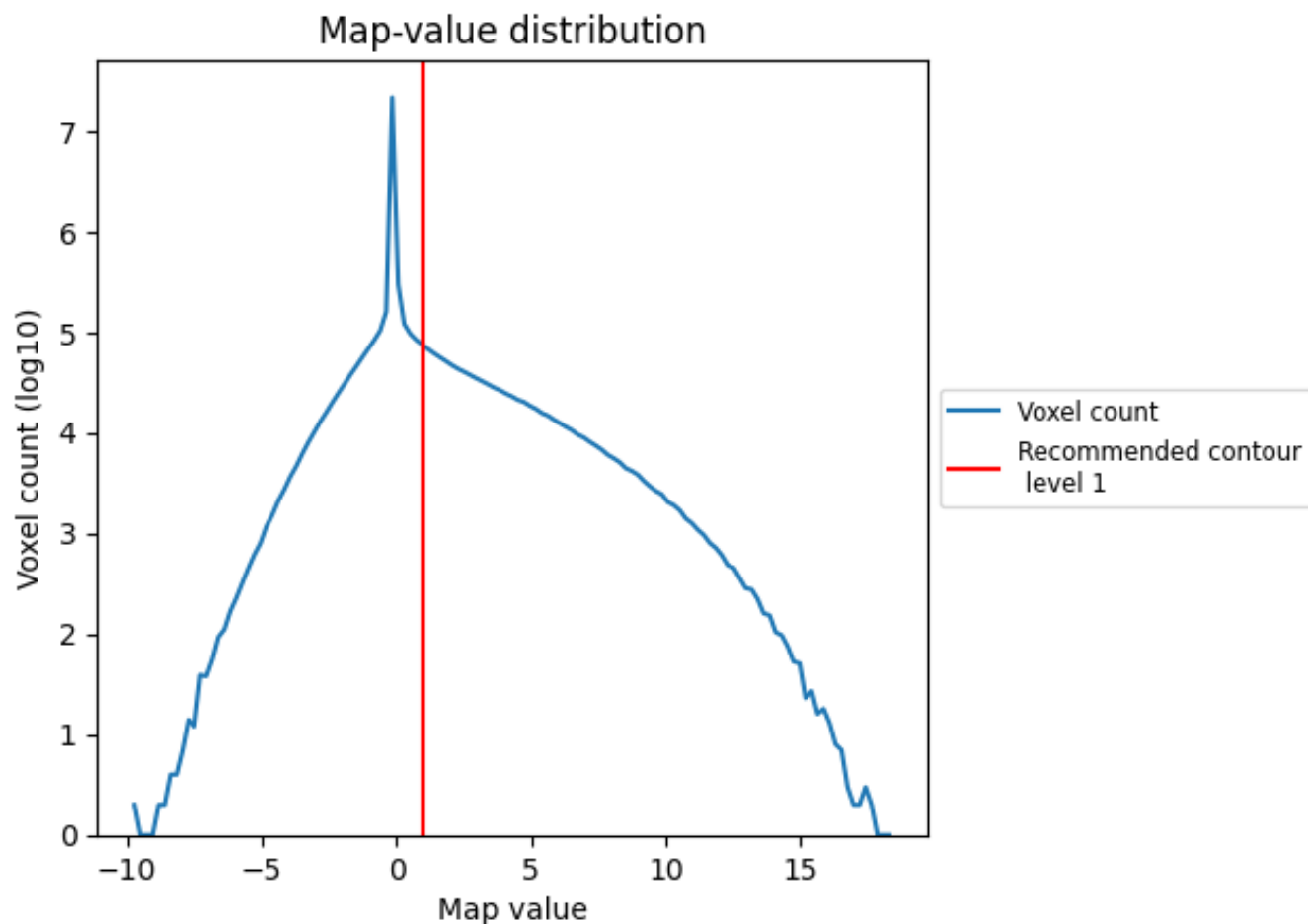
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

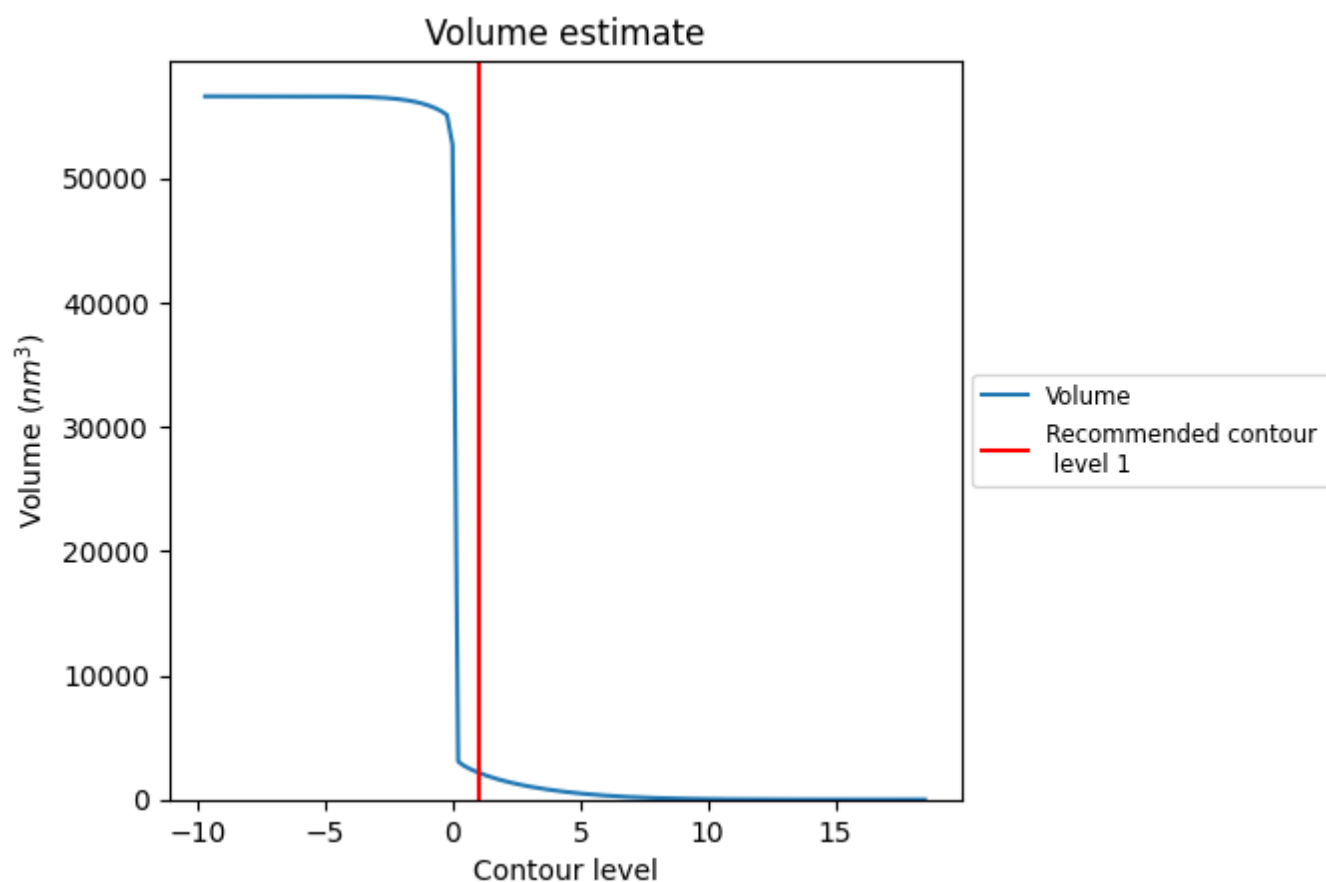
This section contains the results of statistical analysis of the map.

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.

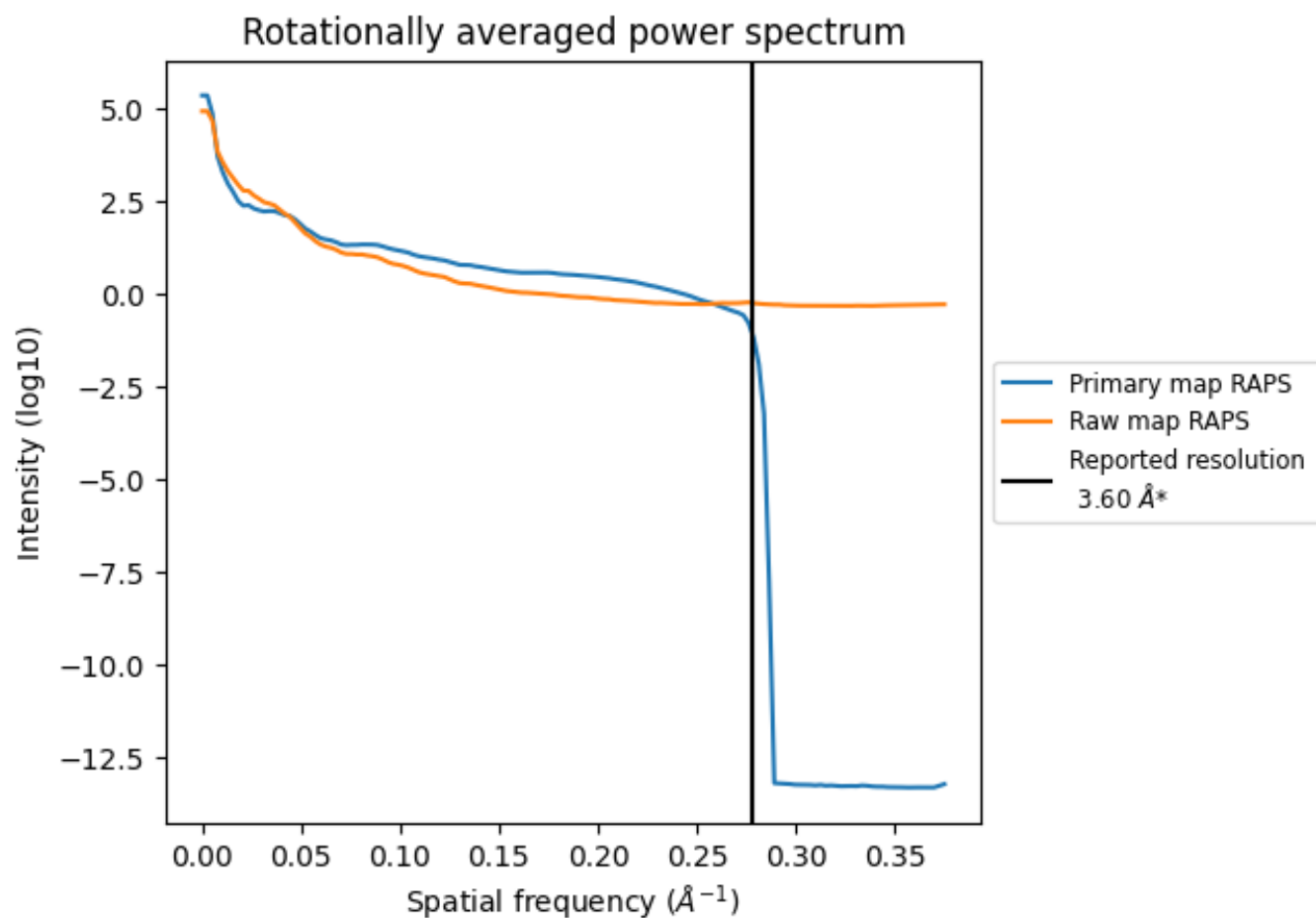
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2173 nm³; this corresponds to an approximate mass of 1963 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 ⓘ

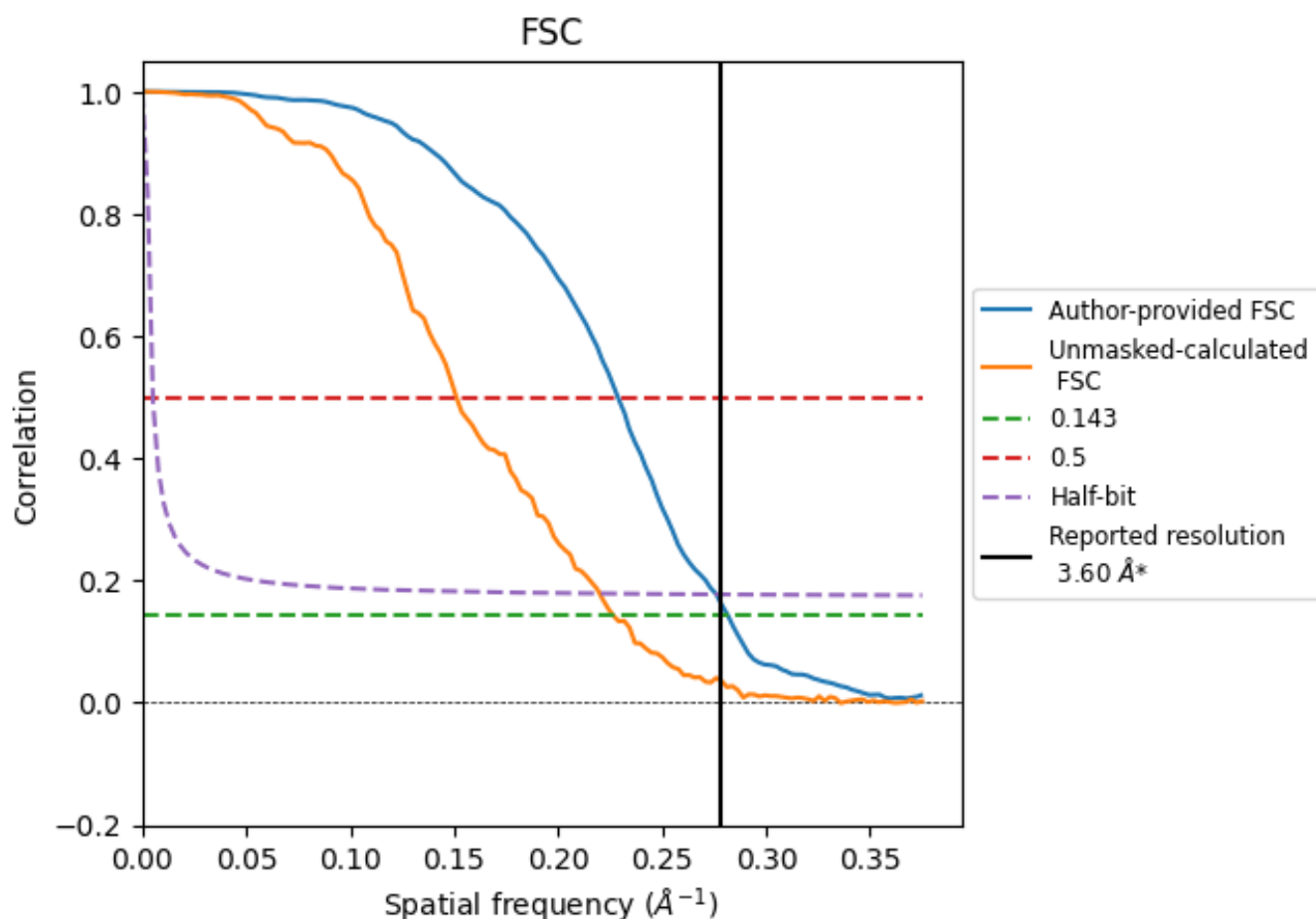


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

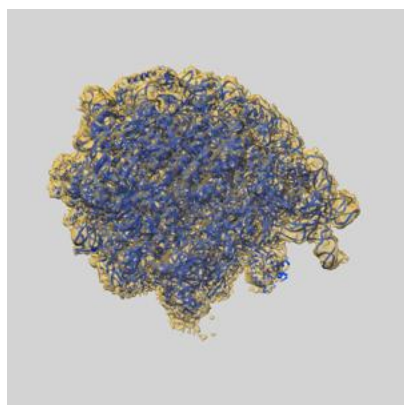
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.55	4.37	3.62
Unmasked-calculated*	4.42	6.62	4.55

*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 4.42 differs from the reported value 3.6 by more than 10 %

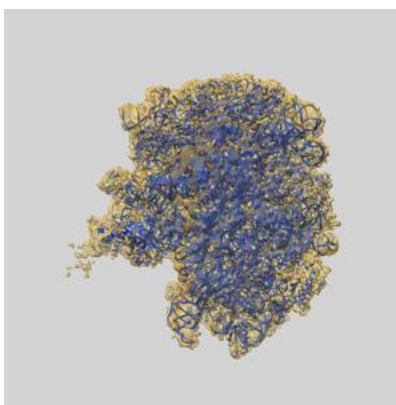
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21624 and PDB model 6WD5. Per-residue inclusion information can be found in section [3](#) on page [17](#).

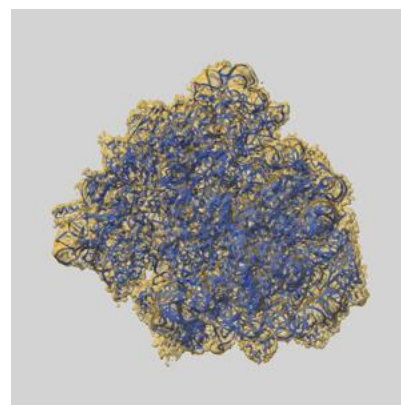
9.1 Map-model overlay [i](#)



X



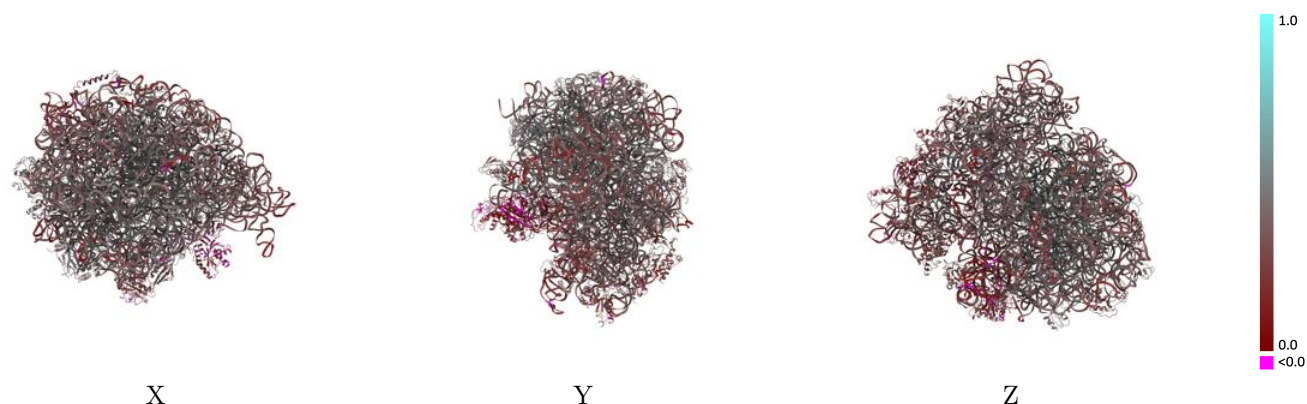
Y



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](#)

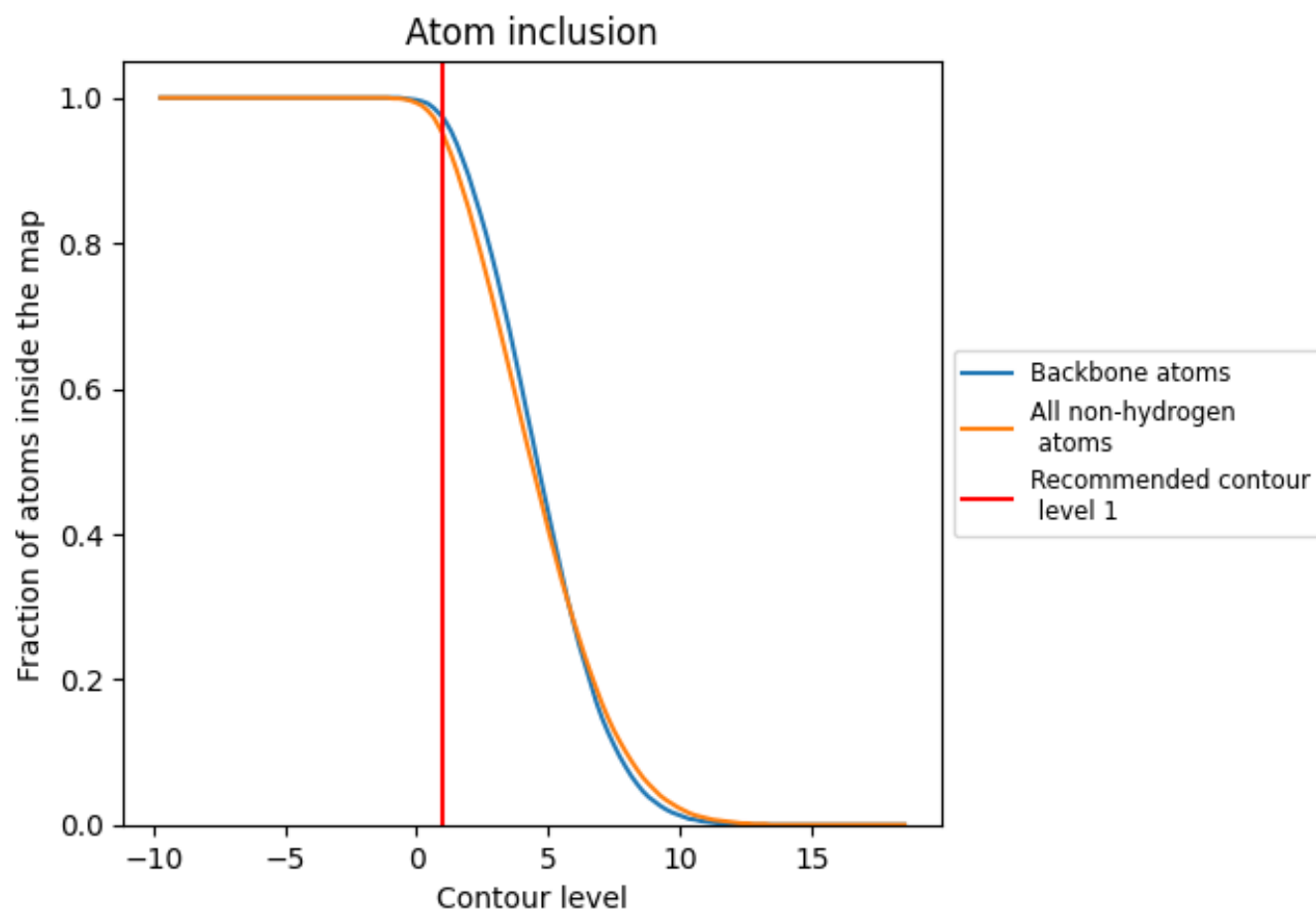


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% 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	 0.9500	 0.3620
1	 0.9840	 0.3860
2	 0.9880	 0.3360
3	 0.9780	 0.3500
4	 0.8810	 0.2410
5	 0.9690	 0.3150
6	 0.8380	 0.1570
7	 0.9420	 0.1960
8	 0.6960	 0.1670
B	 0.9530	 0.4520
C	 0.8680	 0.3840
D	 0.9440	 0.4550
E	 0.9390	 0.4680
F	 0.8970	 0.4250
G	 0.8830	 0.3120
H	 0.6920	 0.3020
I	 0.8770	 0.3180
J	 0.9190	 0.4010
K	 0.9460	 0.3640
L	 0.9370	 0.3240
M	 0.9210	 0.4100
N	 0.8880	 0.3040
O	 0.6610	 0.2650
P	 0.9470	 0.3960
Q	 0.9080	 0.4110
R	 0.9330	 0.3190
S	 0.7440	 0.2990
T	 0.9570	 0.3820
U	 0.9030	 0.4000
V	 0.9340	 0.3730
W	 0.9400	 0.3570
X	 0.9630	 0.3050
Y	 0.9030	 0.3630
Z	 0.8690	 0.2970
a	 0.8160	 0.1700



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Chain	Atom inclusion	Q-score
b	 0.9530	 0.4560
c	 0.9400	 0.4510
d	 0.9380	 0.4020
e	 0.9300	 0.3280
f	 0.9540	 0.3560
g	 0.7770	 0.2720
h	 0.7880	 0.1540
i	 0.7220	 0.1840
j	 0.9440	 0.4430
k	 0.9350	 0.4520
l	 0.9510	 0.4380
m	 0.9260	 0.4360
n	 0.9360	 0.4370
o	 0.9590	 0.3640
p	 0.9380	 0.4390
q	 0.9420	 0.4400
r	 0.9610	 0.4350
s	 0.9510	 0.4410
t	 0.9310	 0.4010
u	 0.9360	 0.3860
v	 0.9570	 0.4050
w	 0.9460	 0.4560
x	 0.9470	 0.4340
y	 0.9360	 0.3380
z	 0.9500	 0.4310