



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 06:21 PM UTC

PDB ID : 6WD8 / pdb_00006wd8
EMDB ID : EMD-21627
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure III-A)
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:

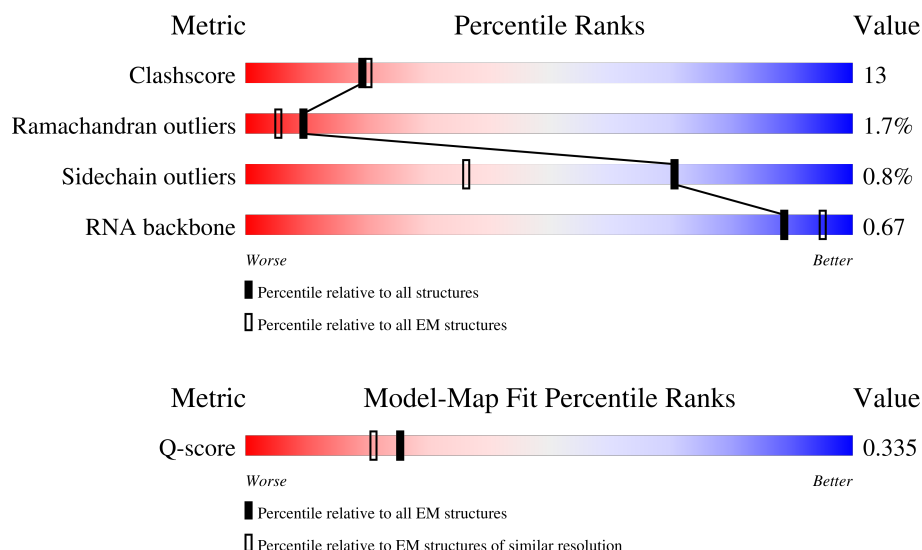
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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.



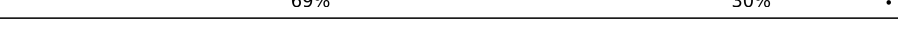
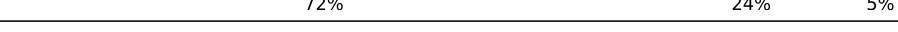
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	

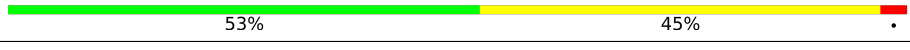
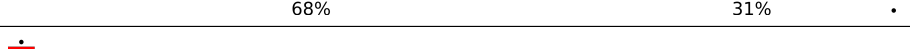
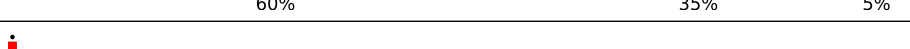
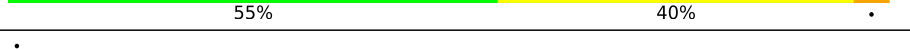
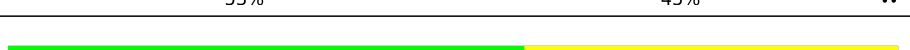
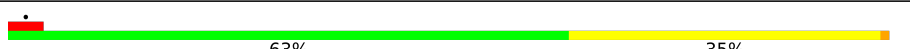
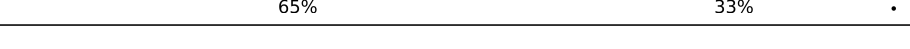
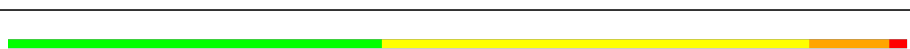
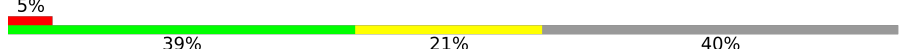
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
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	59%36%5%
55	5	77	65%32%.
55	6	77	5% 39%61%
56	4	18	6% 67%28%6%
57	7	76	. 43%49%8%
58	8	400	6% 53%40%. .

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 153212 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

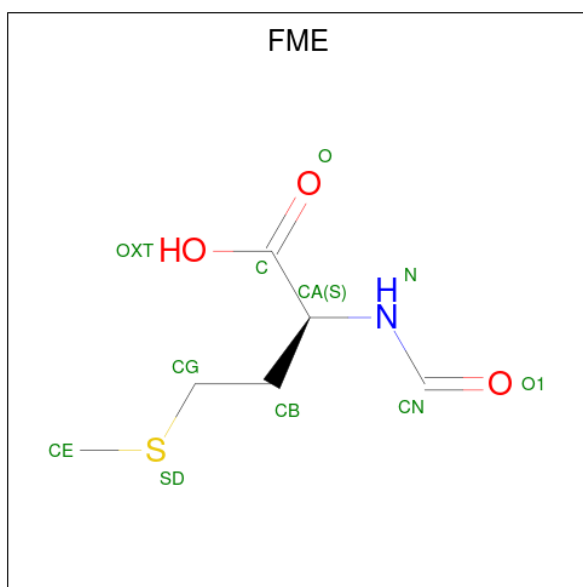
- Molecule 58 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	384	Total	C	N	O	S	0	0
			2958	1871	509	565	13		

There are 7 discrepancies between the modelled and reference sequences:

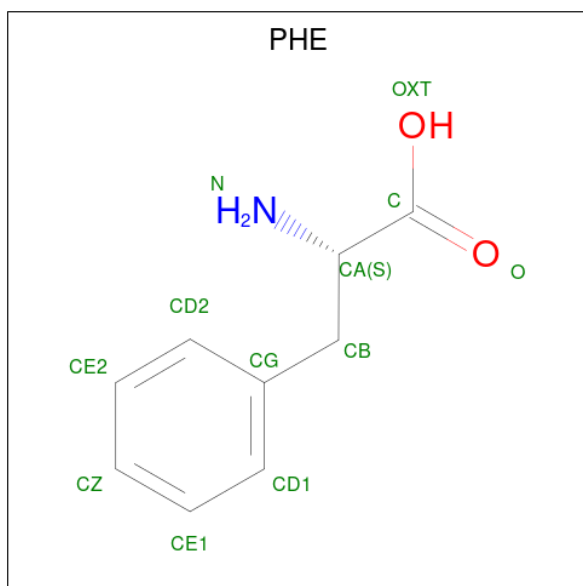
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag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

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



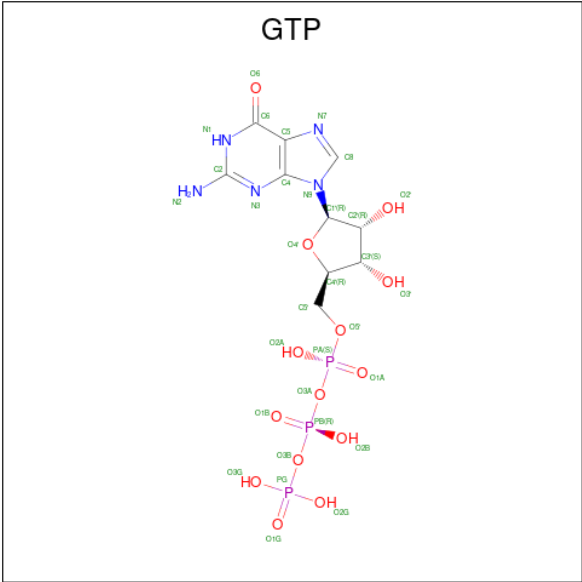
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

- 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'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



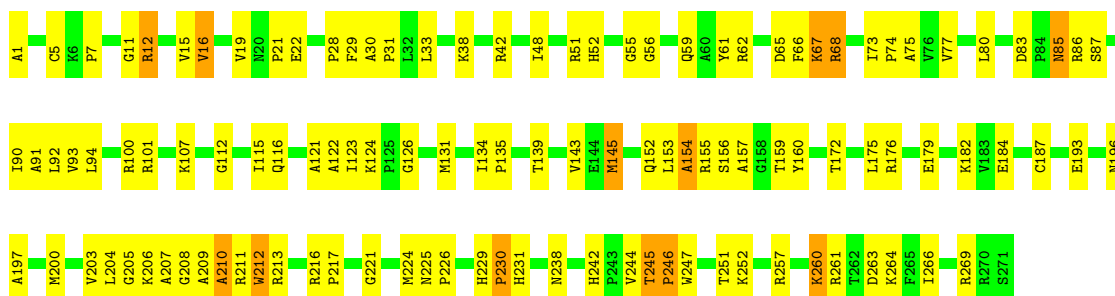
Mol	Chain	Residues	Atoms					AltConf
61	8	1	Total	C	N	O	P	0
			32	10	5	14	3	

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.

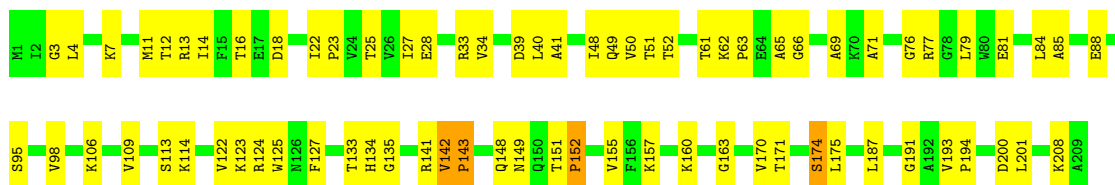
- Molecule 1: 50S ribosomal protein L2

Chain b: 



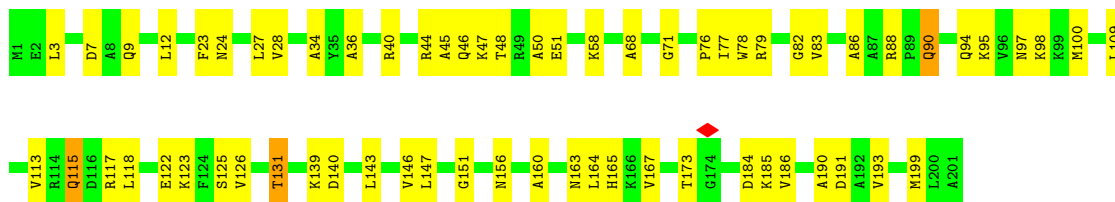
- Molecule 2: 50S ribosomal protein L3

Chain c: 



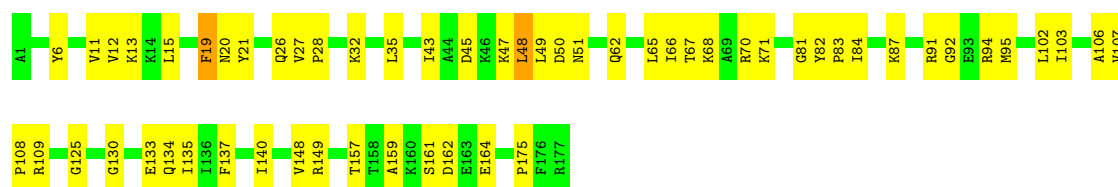
- Molecule 3: 50S ribosomal protein L4

Chain d: 

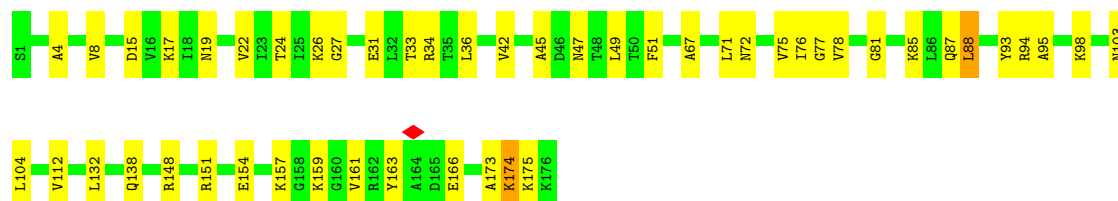


- Molecule 4: 50S ribosomal protein L5

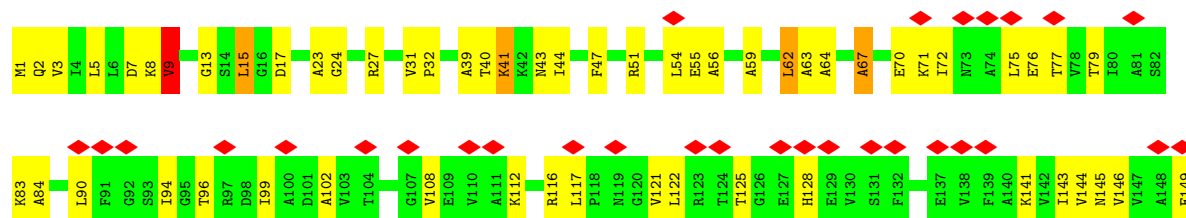
Chain e: 



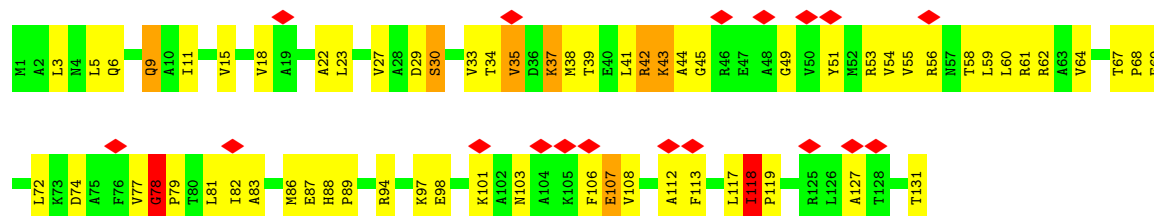
• Molecule 5: 50S ribosomal protein L6



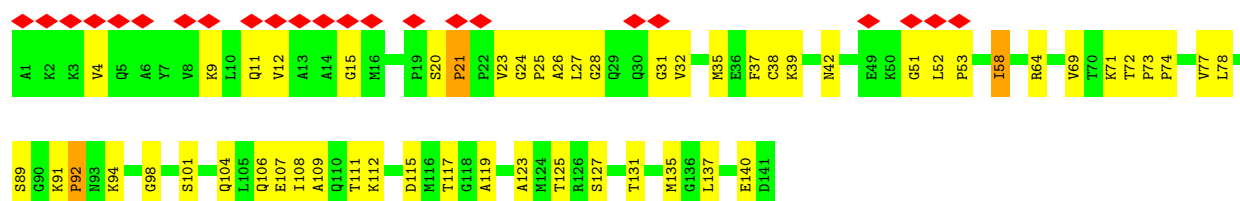
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L10

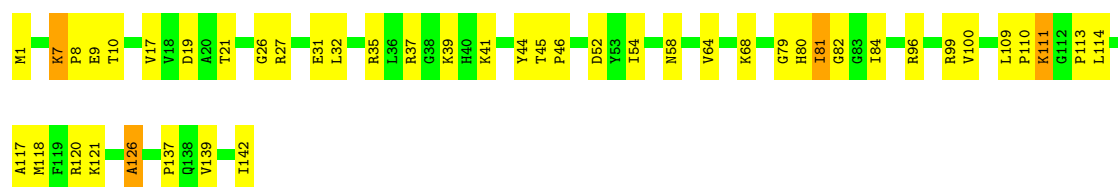


• Molecule 8: 50S ribosomal protein L11



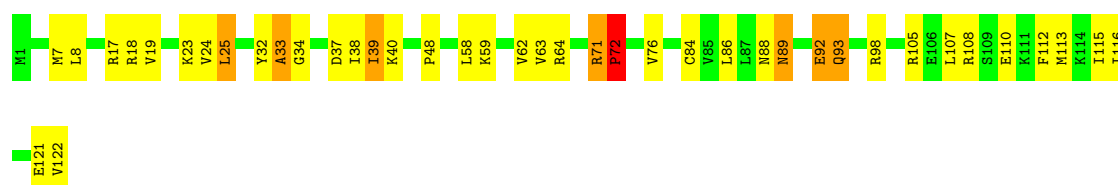
- Molecule 9: 50S ribosomal protein L13

Chain j:  68% 29% .



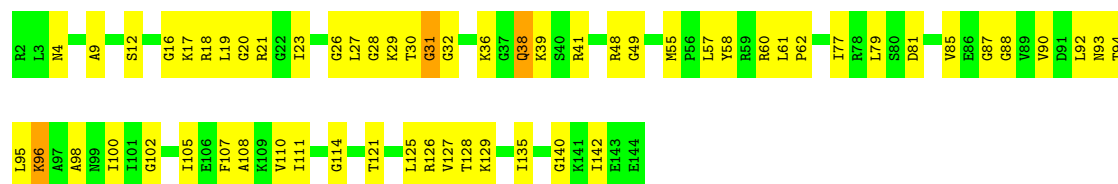
- Molecule 10: 50S ribosomal protein L14

Chain k:  66% 27% 6% .



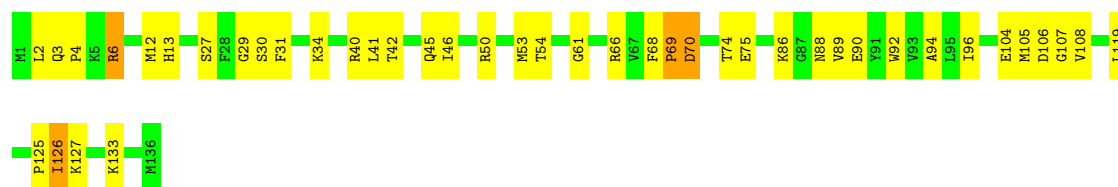
- Molecule 11: 50S ribosomal protein L15

Chain l:  59% 39% .



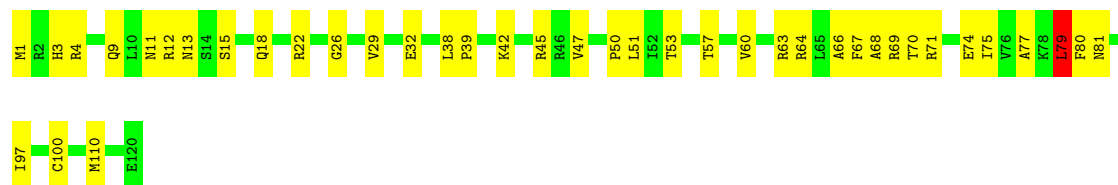
- Molecule 12: 50S ribosomal protein L16

Chain m:  68% 29% .

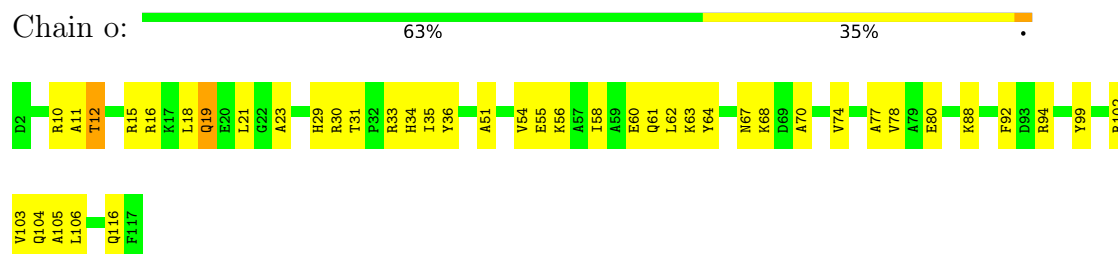


- Molecule 13: 50S ribosomal protein L17

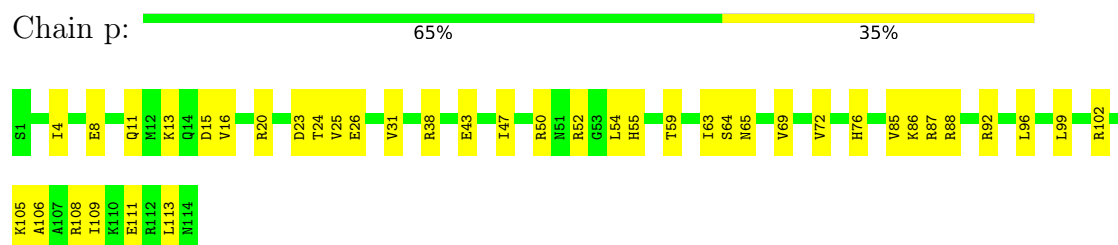
Chain n:  67% 32% .



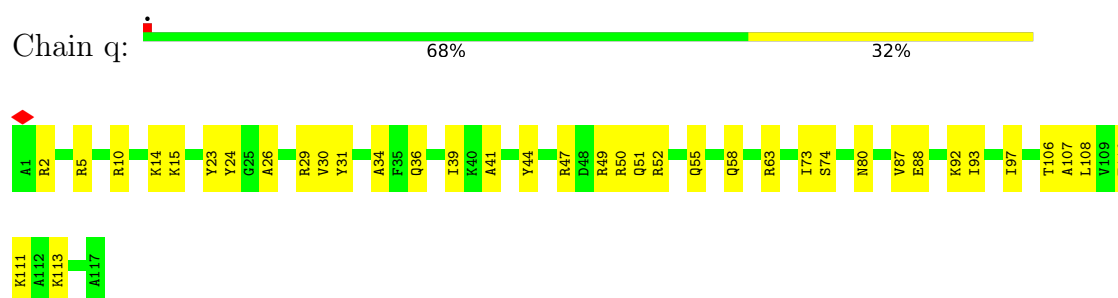
- Molecule 14: 50S ribosomal protein L18



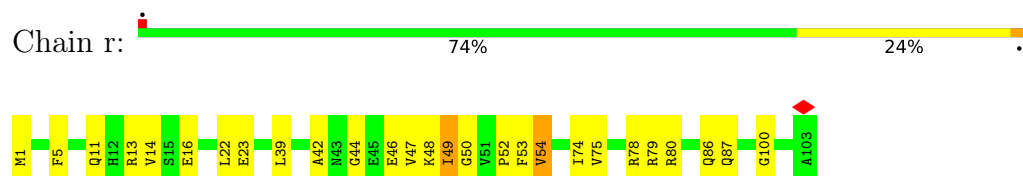
- Molecule 15: 50S ribosomal protein L19



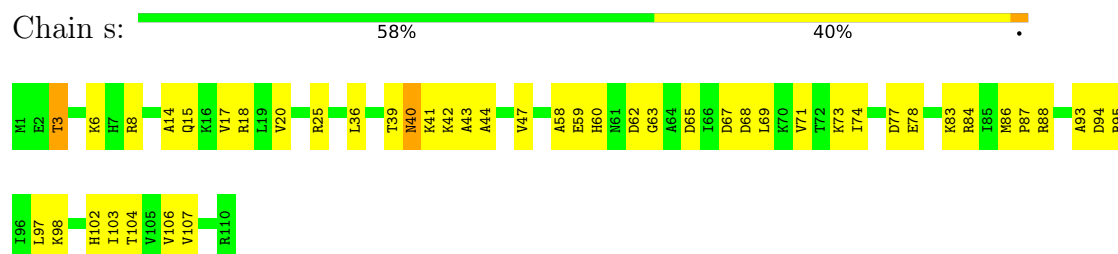
- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23

Chain t:  69% 30%



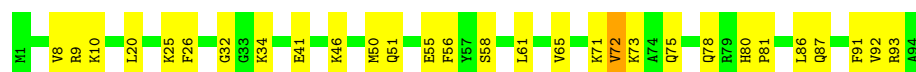
- Molecule 20: 50S ribosomal protein L24

Chain u:  72% 24% 5%



- Molecule 21: 50S ribosomal protein L25

Chain v:  69% 30%



- Molecule 22: 50S ribosomal protein L27

Chain w:  69% 31%



- Molecule 23: 50S ribosomal protein L28

Chain x:  69% 30%



- Molecule 24: 50S ribosomal protein L29

Chain y:  63% 35%



- Molecule 25: 50S ribosomal protein L30

Chain z:  72% 28%



- Molecule 26: 50S ribosomal protein L32

Chain B:  61% 39%



- Molecule 27: 50S ribosomal protein L33

Chain C:  68% 32%



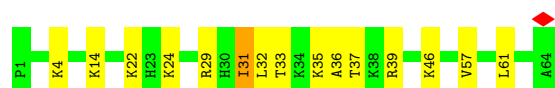
- Molecule 28: 50S ribosomal protein L34

Chain D:  61% 39%



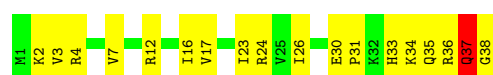
- Molecule 29: 50S ribosomal protein L35

Chain E:  77% 22%



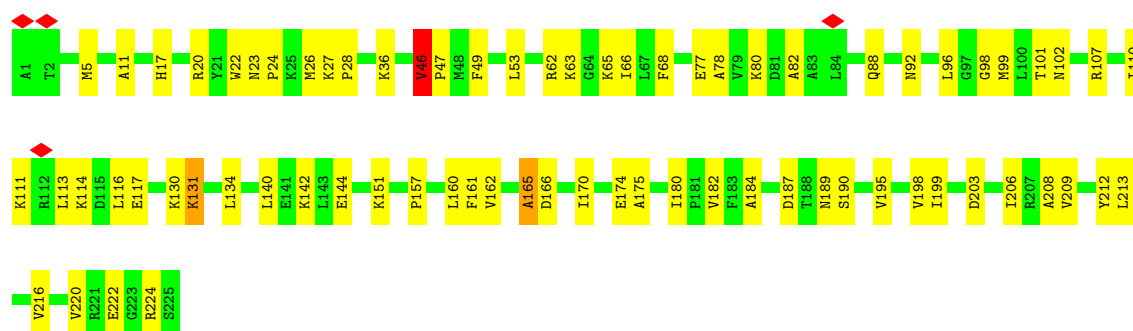
- Molecule 30: 50S ribosomal protein L36

Chain F:  53% 45%

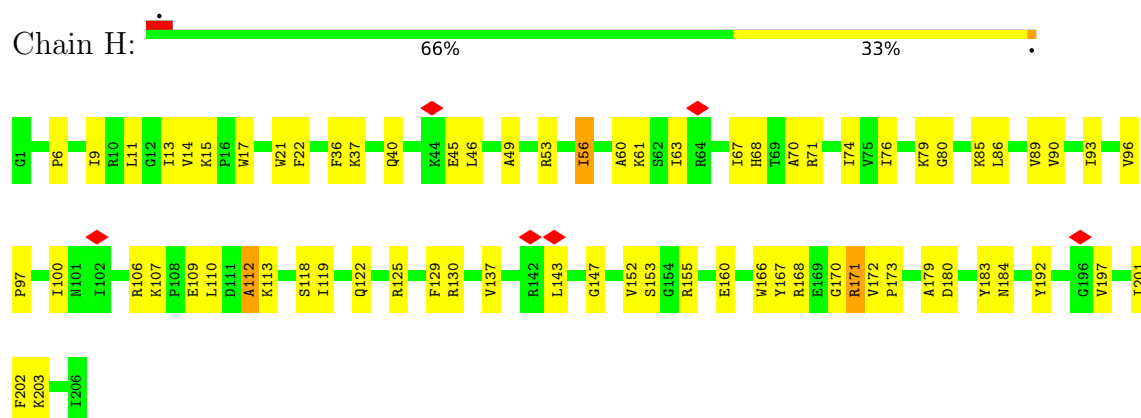


- Molecule 31: 30S ribosomal protein S2

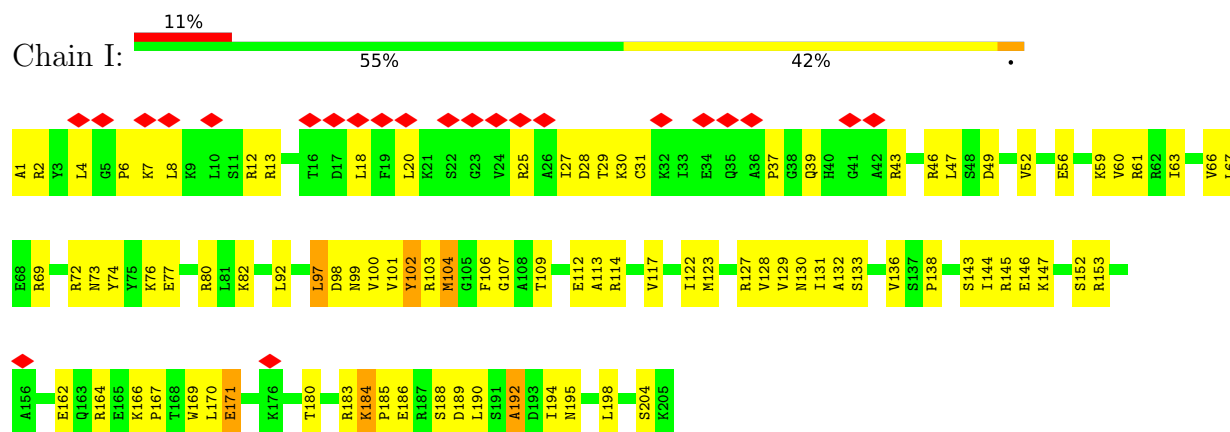
Chain G:  68% 31%



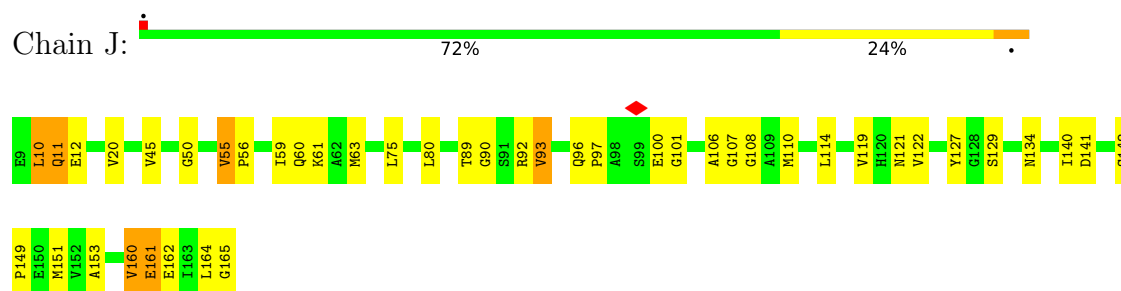
- Molecule 32: 30S ribosomal protein S3



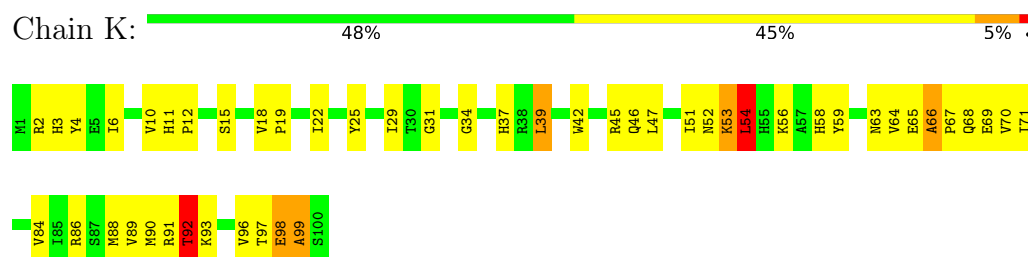
• Molecule 33: 30S ribosomal protein S4



• Molecule 34: 30S ribosomal protein S5

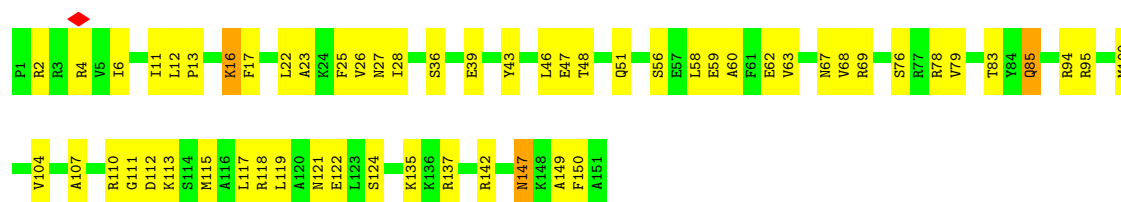


• Molecule 35: 30S ribosomal protein S6



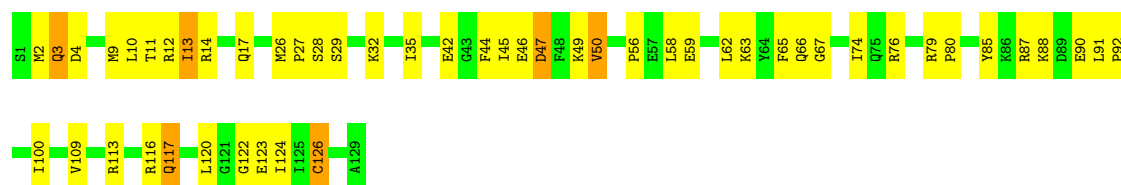
• Molecule 36: 30S ribosomal protein S7

Chain L: 



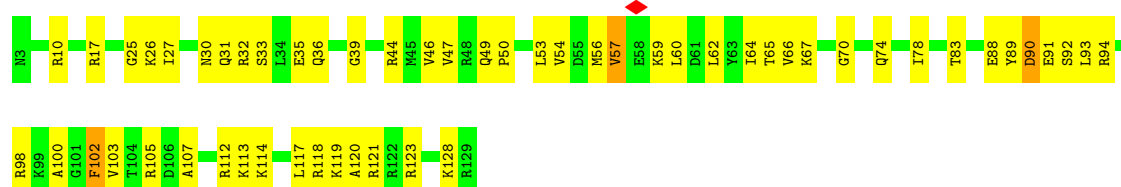
- Molecule 37: 30S ribosomal protein S8

Chain M: 



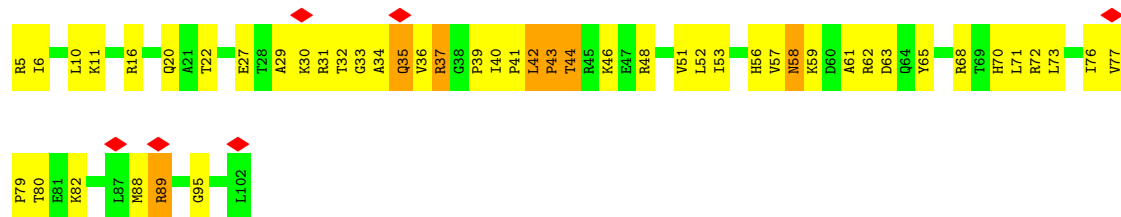
- Molecule 38: 30S ribosomal protein S9

Chain N: 



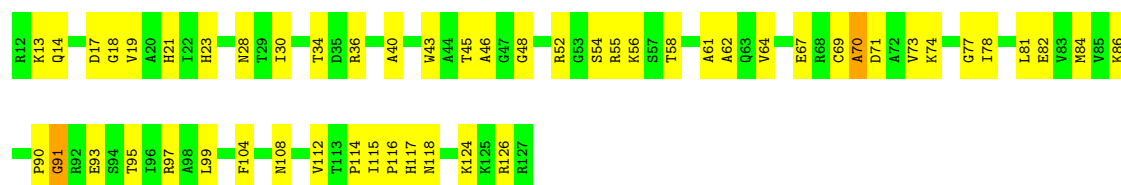
- Molecule 39: 30S ribosomal protein S10

Chain O: 

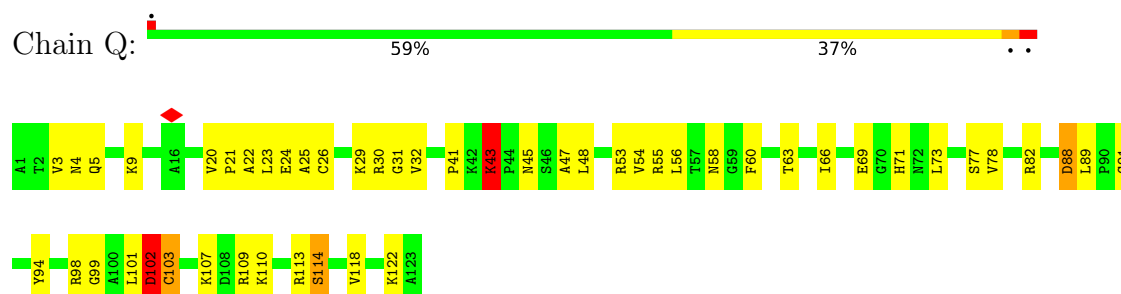


- Molecule 40: 30S ribosomal protein S11

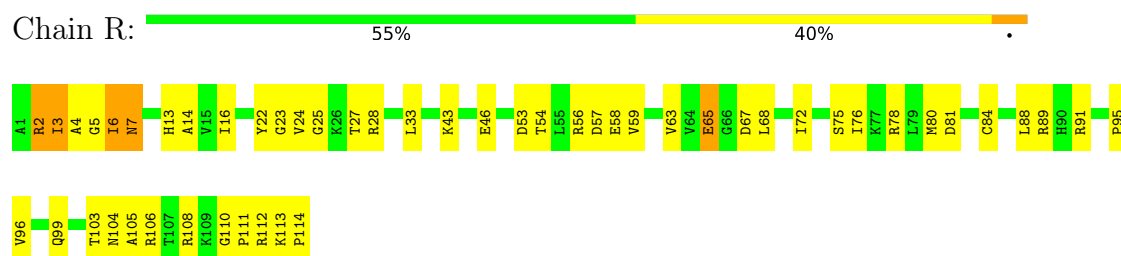
Chain P: 



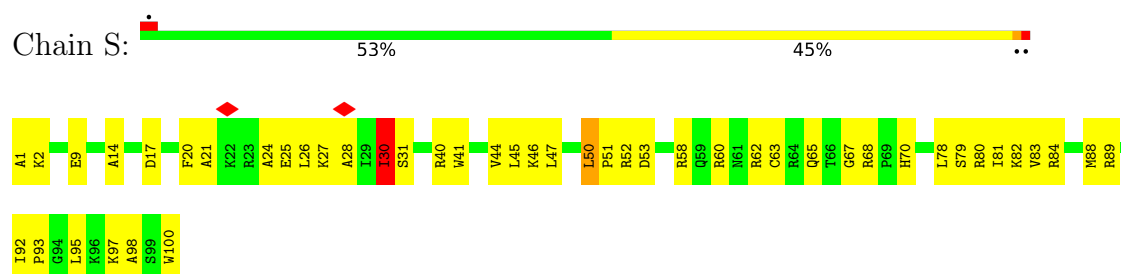
- Molecule 41: 30S ribosomal protein S12



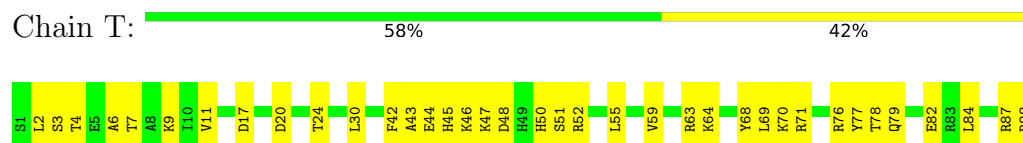
- Molecule 42: 30S ribosomal protein S13



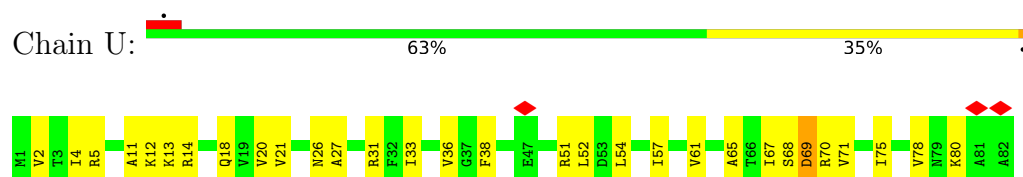
- Molecule 43: 30S ribosomal protein S14



- Molecule 44: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S16

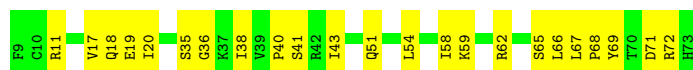


- Molecule 46: 30S ribosomal protein S17





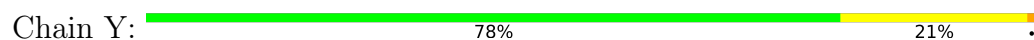
- Molecule 47: 30S ribosomal protein S18



- Molecule 48: 30S ribosomal protein S19



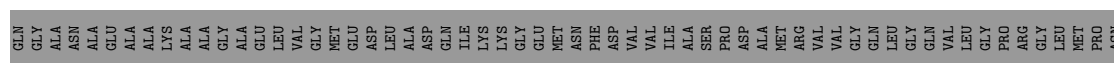
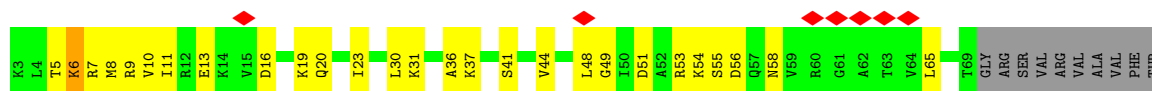
- Molecule 49: 30S ribosomal protein S20



- Molecule 50: 30S ribosomal protein S21



- Molecule 51: 50S ribosomal protein L1



- Molecule 52: 16S ribosomal RNA

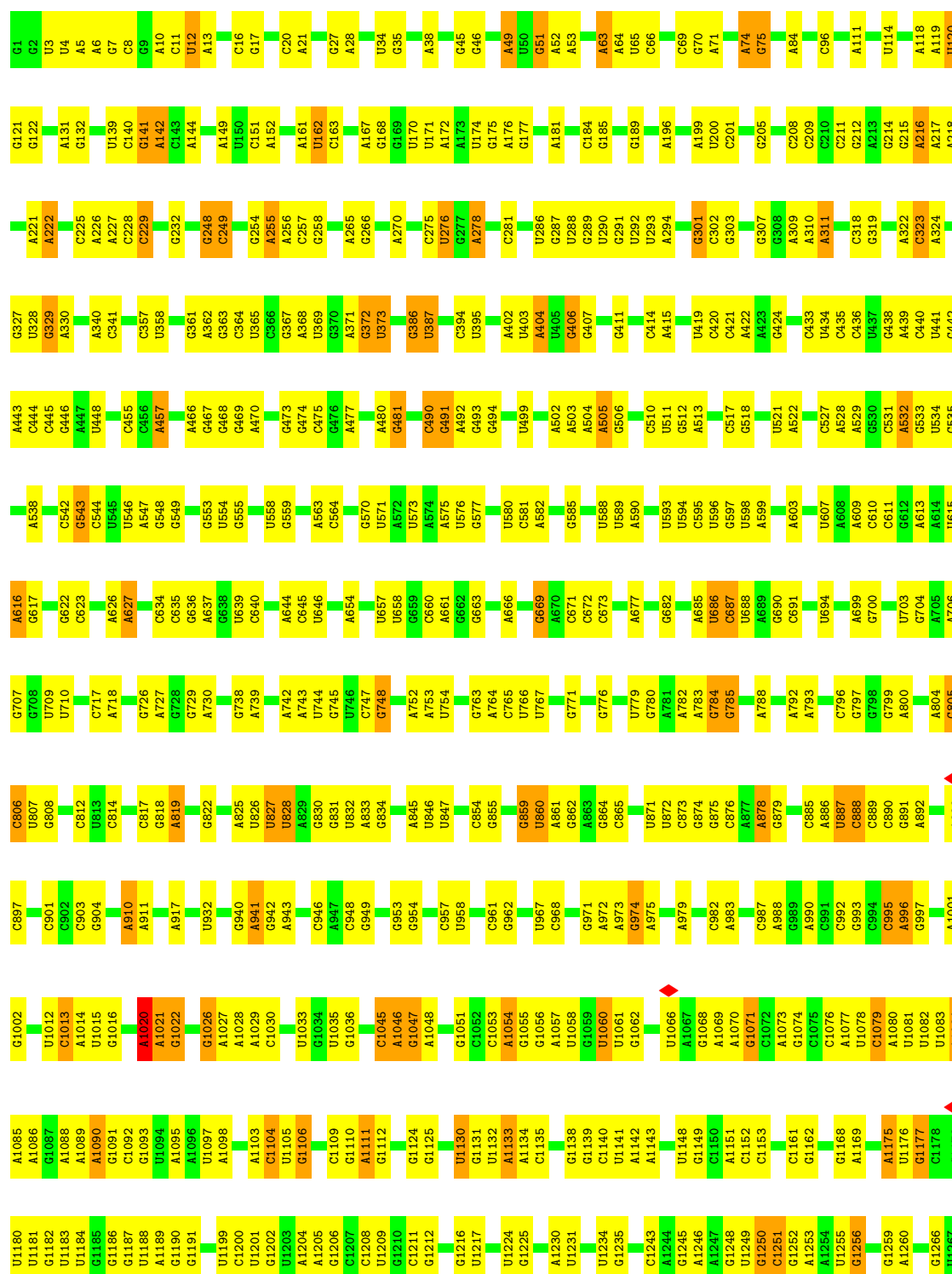
Chain 3:  55% 41% .

A2	C87	G211	C311	C400	A520	U598	G691	G773	C980	A977	U1083	A1179	A1275	G1370
U5	C95	G212	C312	C401	G521	C599	U692	G777	C981	A978	G1088	G1182	G1278	G1371
G6	G100	G213	A321	C403	A523	A600	G693	G778	C982	C979	G1089	G1183	G1279	A1374
G9	C106	U216	A327	U405	C526	G605	A694	C779	C983	U981	G1094	G1184	A1280	A1375
A10	G107	C217	A329	U406	G527	G606	A695	A780	C984	U982	U1095	G1185	C1281	G1379
A16	C110	U224	A330	U407	C528	C613	U701	A784	C985	C985	C1096	G1187	U1286	U1380
C18	G111	C225	A331	U408	G529	C614	A702	G785	C986	U986	C1097	A1188	A1287	U1381
A19	G112	G226	G331	U409	C530	C615	G703	A794	C987	U987	A1101	A1189	A1288	C1384
U20	G113	U229	G332	U410	U531	C616	A706	A815	C988	G993	G1106	A1191	C1296	C1385
G21	U114	U231	U333	A411	A532	C620	A709	A816	C989	G1001	C1107	G1192	G1300	U1390
G22	G115	G232	C334	A412	A533	A621	U710	C817	C990	G1002	C1108	G1193	U1301	U1391
U24	G122	C233	C335	C418	C536	A622	G710	C818	C991	G1003	C1109	G1194	G1302	U1392
C25	U123	C234	G337	C419	G537	C623	G711	C819	C992	A1004	U1115	A1195	C1303	G1392
A26	G128	U236	A338	C422	A538	U626	A712	U820	G902	A1005	U1116	G1197	A1306	C1395
U29	A129	G237	U340	C423	G540	G627	A715	U821	C909	G1006	A1117	U1199	A1307	A1396
U30	A130	A243	C345	C424	G541	U628	A716	C824	C910	C1011	C1120	A1200	G1312	C1402
G31	A131	U244	G346	C425	G542	A629	U717	C825	U911	A1012	C1121	A1201	U1313	C1403
A32	C132	U245	C347	C426	A546	A630	A718	C826	C912	G1013	U1122	U1202	C1314	G1404
A33	U133	A246	G347	A430	A547	G633	A719	U827	U916	A1014	U1123	C1203	U1315	G1405
C34	G142	G247	G350	U439	U552	U634	U723	U828	C917	G1015	G1124	U1211	G1317	C1409
G35	G143	G251	C351	U438	U553	U635	G724	C829	C924	G1020	C1125	U1212	A1318	A1410
U37	G144	U252	A352	U439	U554	C637	G725	A831	C925	G1021	C1126	A1213	A1319	A1411
C38	G149	G255	C353	U458	C556	U638	G726	A832	C926	C1022	U1127	C1218	C1320	C1412
G39	U150	G259	C354	U459	G557	A642	A729	C833	G927	C1023	G1128	C1219	A1130	C1413
G45	A151	G262	A355	A459	G558	C651	G730	U834	C928	U1030	C1136	G1220	G1323	A1414
G46	A152	A263	C356	U467	A559	U652	G731	U835	G929	C1031	C1137	G1221	A1324	U1415
C47	C156	G264	A357	U467	A560	U653	C732	C836	G933	G1032	G1138	A1225	C1325	G1415
C48	U157	G265	C358	U467	A561	U654	C733	U837	C934	G1033	C1139	C1226	U1326	G1422
A50	C163	G267	A363	C483	G564	C659	C734	A844	A935	G1034	C1140	C1227	A1327	U1425
A51	G164	C267	U367	C484	G565	U661	C735	C845	A936	U1049	C1141	C1228	U1328	U1426
C58	C183	U273	G369	C486	G566	U662	C736	C846	C939	U1052	A1146	C1229	A1329	A1429
A59	G184	A274	A371	C490	G567	U663	C737	C847	C940	U1053	C1147	A1238	U1330	A1430
G61	U185	G279	C372	C491	A573	U664	C744	C848	A949	A1055	C1148	U1239	C1331	A1431
U62	C186	A279	C372	C492	A574	U665	C745	C849	A950	U1056	C1149	U1240	G1332	G1432
C63	G187	G281	U375	C497	G575	U666	C746	C850	A951	G1057	A1151	G1241	A1333	A1433
U70	C188	G289	C381	C501	G576	U667	C747	C851	A952	G1058	A1152	G1242	A1334	G1434
A71	A189	U304	A382	C502	G577	U668	C748	C852	A953	C1059	G1156	A1251	A1335	U1435
A77	C194	A298	U387	C503	G578	U669	C749	C853	A954	U1060	A1157	G1252	G1336	U1436
A78	A195	G299	C388	C504	G579	U670	C750	C854	A955	G1061	C1158	G1253	U1337	A1437
G79	A197	U304	A393	C511	G580	U671	C751	C855	A956	U1062	U1159	A1254	A1338	G1438
A80	A205	G305	C396	C512	G581	U672	C752	C856	A957	C1063	G1160	G1255	A1339	A1445
G81	C206	A306	C397	C513	G582	U673	C753	C857	A958	U1064	C1161	G1256	U1340	A1447
C83	C207	C307	U398	C514	G583	U674	C754	C858	A959	U1065	G1162	G1257	A1341	C1448
U84	U208	G308	A399	C515	G584	U675	C755	C859	A960	U1066	A1163	C1258	A1342	C1449
U85	U209	C309	U399	C516	G585	U676	C756	C860	A961	U1067	C1164	G1259	G1343	A1446
C86	C210	G310	C400	C517	G586	U677	C757	C861	A962	U1068	A1165	G1260	U1344	A1447
				C518	G587	U678	C758	C862	A963	U1069	C1166	G1261	G1345	A1448
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								C864	A965	U1071	A1168	G1263	G1347	C1453
								C865	A966	U1072	A1169	G1264	U1348	G1458
								C866	A967	U1073	A1170	G1265	C1349	
								C867	A968	U1074	A1171	G1266	A1353	
								C868	A969	U1075	A1172	G1267	U1354	
								C869	A970	U1076	A1173	G1268	G1355	
								C870	A971	U1077	A1174	G1269	U1356	
								C871	A972	U1078	A1175	G1270	G1357	
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								C873	A974	U1080	A1177	G1272	U1359	
								C874	A975	U1081	A1178	G1273	A1363	
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								C876	A977		A1180	G1275	G1365	
								C877	A978		A1181	G1276	U1366	
								C878	A979		A1182	G1277	C1367	
								C879	A980		A1183	G1278	U1368	
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								C881	A982		A1185	G1280	U1369	
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								C883	A984		A1187	G1282	U1371	
								C884	A985		A1188	G1283	A1430	
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								C886	A987		A1190	G1285	A1432	
								C887	A988		A1191	G1286	A1433	
								C888	A989		A1192	G1287	A1434	
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								C890	A991		A1194	G1289	A1436	
								C891	A992		A1195	G1290	A1437	
								C892	A993		A1196	G1291	A1438	
								C893	A994		A1197	G1292	A1439	
								C894	A995		A1198	G1293	A1440	
								C895	A996		A1199	G1294	A1441	
								C896	A997		A1200	G1295	A1442	
								C897	A998		A1201	G1296	A1443	
								C898	A999		A1202	G1297	A1444	
								C899	A1000		A1203	G1298	A1445	
								C900	A1001		A1204	G1299	A1446	
								C901	A1002		A1205	G1300	A1447	
								C902	A1003		A1206	G1301	A1448	
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								C907	A1008		A1211	G1306	A1453	
								C908	A1009		A1212	G1307	A1454	
								C909	A1010		A1213	G1308	A1455	
								C910	A1011		A1214	G1309	A1456	
								C911	A1012		A1215	G1310	A1457	
								C912	A1013		A1216	G1311	A1458	
								C913	A1014		A1217	G1312	A1459	
								C914	A1015		A1218	G1313	A1460	
								C915	A1016		A1219	G1314	A1461	
								C916	A1017		A1220	G1315	A1462	
								C917	A1018		A1221	G1316	A1463	
								C918	A1019		A1222	G1317	A1464	
								C919	A1020		A1223	G1318	A1465	
								C920	A1021		A1224	G1319	A1466	
								C921	A1022		A1225	G1320	A1467	
								C922	A1023		A1226	G1321	A1468	
								C923	A1024		A1227	G1322	A1469	
								C924	A1025		A1228	G1323	A1470	
								C925	A1026		A1229	G1324	A1471	
								C926	A1027		A1230	G1325	A1472	
								C927	A1028		A1231	G1326	A1473	
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								C929	A1030		A1233	G1328	A1475	

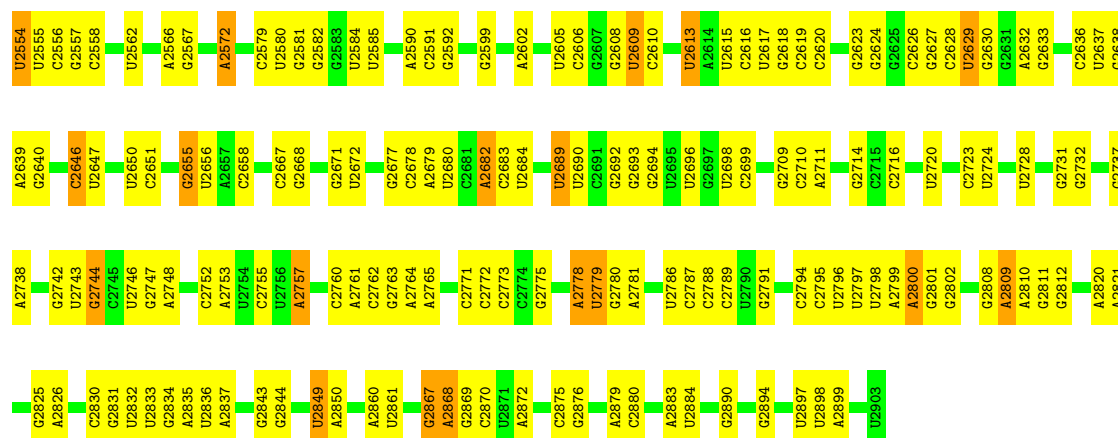


● Molecule 53: 23S ribosomal RNA

Chain 1: 54% 40% 6%

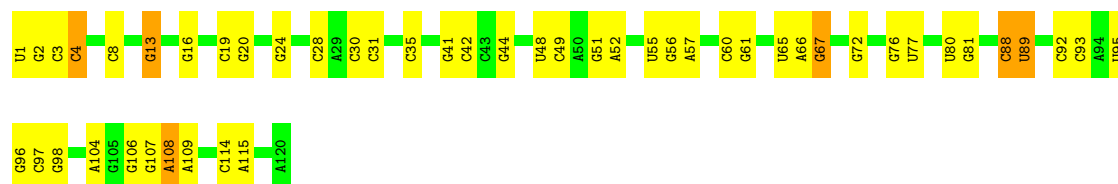


C2466	G2389	U2299	G2226	U2132	G2046	C1958	U1855	A1780	A1664	A1551	G1445	C1357	A1268
C2467	G2390	U2305	A2227	G2133	C2055	U1963	U1856	A1783	A1665	G1555	C1446	G1358	A1269
A2468	G2391	C2309	G2230	A2134	C2056	G1964	A1857	A1784	G1667	G1555	G1447	G1359	C1270
A2469	U2392	G2310	U2233	U2139	A2060	C1965	A1858	A1785	G1670	C1558	G1448	G1360	G1271
G2470	C2393	A2311	G2234	G2140	G2061	A1966	U1859	A1786	U1671	U1559	C1454	G1361	A1272
A2471	C2394	G2312	G2235	G2146	A2062	C1967	G1860	G1786	U1671	G1560	G1455	C1362	A1275
G2472	U2398	U2313	G2238	A2147	G2066	A1970	C1870	C1790	G1674	U1563	U1458	A1365	A1278
A2475	G2399	A2314	G2239	G2156	G2067	U1971	A1871	A1791	G1674	A1566	G1459	A1366	C1278
C2476	G2402	G2315	U2240	G2157	C2068	G1972	A1872	A1794	A1678	C1564	U1460	G1367	G1280
G2480	U2403	G2318	G2241	G2157	G2069	G1973	G1873	U1796	A1679	G1565	C1461	G1368	
G2481	U2404	G2319	G2242	C2161	A2070	U1979	G1874	G1797	U1680	G1566	G1462	C1369	
G2485	G2405	A2322	U2243	G2161	C2071	G1980	G1875	U1798	G1681	G1567	C1463	C1370	G1283
G2486	U2406	G2323	U2244	A2162	C2072	U1981	U1881	U1798	G1682	A1570	G1464	G1371	A1284
G2487	U2407	G2324	G2245	A2163	C2073	U1982	U1882	G1799	U1683	A1571	U1468	U1372	A1285
G2488	G2408	G2325	G2246	C2164	U2074	U1983	U1883	A1801	G1684	A1572	U1468	A1373	A1286
G2489	G2409	C2326	U2247	U2172	C2078	U1991	G1884	A1801	G1684	A1572	U1468	A1373	
G2490	A2412	A2327	G2250	A2173	G2082	U1992	A1885	A1805	G1685	G1573	U1476	U1379	C1297
U2491	G2413	U2328	U2251	C2174	A2083	U1993	U1888	C1806	G1695	G1581	G1482	U1383	C1298
U2492	G2414	U2329	G2252	C2175	G2086	C1996	C1908	G1807	U1709	U1584	G1482	A1386	G1299
U2493	G2415	G2330	C2258	A2176	A2087	C1997	A1899	A1808	G1710	U1584	G1482	A1387	A1301
G2494	C2416	G2331	G2259	U2180	G2088	A1998	A1900	A1809	A1713	U1589	A1490	G1388	A1308
G2495	C2417	C2332	G2260	G2186	G2088	C1999	A1901	A1810	U1714	A1590	G1491	G1389	G1309
C2498	A2418	A2333	U2261	G2187	G2089	C2000	G1906	G1811	G1715	U1593	C1498	U1394	G1310
C2499	U2419	U2334	U2262	A2183	G2093	C2001	C1907	U1812	U1720	A1597	G1499	U1395	G1311
G2502	G2420	A2335	G2263	A2184	G2096	C2008	C1908	G1813	U1721	A1598	G1501	C1398	U1316
G2503	C2421	G2340	U2264	U2185	C2096	A2009	C1909	C1816	U1725	U1601	U1506	U1412	U1326
U2504	G2422	G2341	G2265	G2186	C2096	G2010	G1910	C1817	U1726	U1602	C1507	U1413	A1327
G2505	C2423	C2342	A2267	U2189	C2096	G2011	U1911	U1818	G1726	U1603	A1508	A1419	U1328
G2506	U2424	U2343	G2268	G2190	C2096	G2012	A1912	U1819	U1729	A1603	A1509	G1423	A1329
G2508	A2425	G2344	G2269	U2191	C2096	A2013	C1913	A1821	G1730	U1603	G1524	G1424	G1330
G2509	C2426	U2345	G2270	U2192	C2096	A2014	C1914	C1822	U1730	U1603	A1525	G1424	G1331
G2510	G2427	G2346	G2271	U2193	C2096	A2015	C1915	C1823	A1735	U1603	G1526	G1424	G1332
G2511	C2428	U2347	G2272	U2194	C2096	A2016	C1916	G1824	U1735	U1603	C1527	G1424	G1333
G2512	G2429	G2348	G2273	U2195	C2096	A2017	C1917	U1825	U1735	U1603	G1527	G1424	G1334
G2513	A2430	U2349	A2274	U2196	C2096	A2018	C1918	U1826	U1735	U1603	G1527	G1424	G1335
G2514	U2431	C2350	G2275	U2197	C2096	A2019	C1919	U1827	U1735	U1603	G1527	G1424	G1336
G2515	A2432	G2351	G2276	U2198	C2096	A2020	C1920	U1828	U1735	U1603	G1527	G1424	G1337
G2516	G2433	G2352	G2277	U2199	C2096	A2021	C1921	U1829	U1735	U1603	G1527	G1424	G1338
G2517	C2434	G2353	G2278	U2200	C2096	A2022	C1922	U1830	U1735	U1603	G1527	G1424	G1339
G2518	U2435	G2354	G2279	U2201	C2096	A2023	C1923	U1831	U1735	U1603	G1527	G1424	G1340
G2519	G2436	G2355	G2280	U2202	C2096	A2024	C1924	U1832	U1735	U1603	G1527	G1424	G1341
G2520	U2437	G2356	G2281	U2203	C2096	A2025	C1925	U1833	U1735	U1603	G1527	G1424	G1342
G2521	G2438	G2357	G2282	U2204	C2096	A2026	C1926	U1834	U1735	U1603	G1527	G1424	G1343
G2522	U2439	G2358	G2283	U2205	C2096	A2027	C1927	U1835	U1735	U1603	G1527	G1424	G1344
G2523	G2440	G2359	G2284	U2206	C2096	A2028	C1928	U1836	U1735	U1603	G1527	G1424	G1345
G2524	U2441	G2360	G2285	U2207	C2096	A2029	C1929	U1837	U1735	U1603	G1527	G1424	G1346
G2525	C2442	G2361	G2286	U2208	C2096	A2030	C1930	U1838	U1735	U1603	G1527	G1424	G1347
G2526	U2443	G2362	G2287	U2209	C2096	A2031	C1931	U1839	U1735	U1603	G1527	G1424	G1348
G2527	G2444	G2363	G2288	U2210	C2096	A2032	C1932	U1840	U1735	U1603	G1527	G1424	G1349
G2528	U2445	G2364	G2289	U2211	C2096	A2033	C1933	U1841	U1735	U1603	G1527	G1424	G1350
G2529	G2446	G2365	G2290	U2212	C2096	A2034	C1934	U1842	U1735	U1603	G1527	G1424	G1351
G2530	U2447	G2366	G2291	U2213	C2096	A2035	C1935	U1843	U1735	U1603	G1527	G1424	G1352
G2531	G2448	G2367	G2292	U2214	C2096	A2036	C1936	U1844	U1735	U1603	G1527	G1424	G1353
G2532	U2449	G2368	G2293	U2215	C2096	A2037	C1937	U1845	U1735	U1603	G1527	G1424	G1354
G2533	G2450	G2369	G2294	U2216	C2096	A2038	C1938	U1846	U1735	U1603	G1527	G1424	G1355
G2534	U2451	G2370	G2295	U2217	C2096	A2039	C1939	U1847	U1735	U1603	G1527	G1424	G1356
G2535	G2452	G2371	G2296	U2218	C2096	A2040	C1940	U1848	U1735	U1603	G1527	G1424	G1357
G2536	U2453	G2372	G2297	U2219	C2096	A2041	C1941	U1849	U1735	U1603	G1527	G1424	G1358
G2537	G2454	G2373	G2298	U2220	C2096	A2042	C1942	U1850	U1735	U1603	G1527	G1424	G1359
G2538	U2455	G2374	G2299	U2221	C2096	A2043	C1943	U1851	U1735	U1603	G1527	G1424	G1360
G2539	G2456	G2375	G2300	U2222	C2096	A2044	C1944	U1852	U1735	U1603	G1527	G1424	G1361
G2540	U2457	G2376	G2301	U2223	C2096	A2045	C1945	U1853	U1735	U1603	G1527	G1424	G1362
G2541	G2458	G2377	G2302	U2224	C2096	A2046	C1946	U1854	U1735	U1603	G1527	G1424	G1363
G2542	U2459	G2378	G2303	U2225	C2096	A2047	C1947	U1855	U1735	U1603	G1527	G1424	G1364
G2543	G2460	G2379	G2304	U2226	C2096	A2048	C1948	U1856	U1735	U1603	G1527	G1424	G1365
G2544	U2461	G2380	G2305	U2227	C2096	A2049	C1949	U1857	U1735	U1603	G1527	G1424	G1366
G2545	G2462	G2381	G2306	U2228	C2096	A2050	C1950	U1858	U1735	U1603	G1527	G1424	G1367
G2546	U2463	G2382	G2307	U2229	C2096	A2051	C1951	U1859	U1735	U1603	G1527	G1424	G1368
G2547	G2464	G2383	G2308	U2230	C2096	A2052	C1952	U1860	U1735	U1603	G1527	G1424	G1369
G2548	U2465	G2384	G2309	U2231	C2096	A2053	C1953	U1861	U1735	U1603	G1527	G1424	G1370
G2549	G2466	G2385	G2310	U2232	C2096	A2054	C1954	U1862	U1735	U1603	G1527	G1424	G1371
G2550	U2467	G2386	G2311	U2233	C2096	A2055	C1955	U1863	U1735	U1603	G1527	G1424	G1372
G2551	G2468	G2387	G2312	U2234	C2096	A2056	C1956	U1864	U1735	U1603	G1527	G1424	G1373
G2552	U2469	G2388	G2313	U2235	C2096	A2057	C1957	U1865	U1735	U1603	G1527	G1424	G1374
G2553	G2470	G2389	G2314	U2236	C2096	A2058	C1958	U1866	U1735	U1603	G1527	G1424	G1375
G2554	U2471	G2390	G2315	U2237	C2096	A2059	C1959	U1867	U1735	U1603	G1527	G1424	G1376
G2555	G2472	G2391	G2316	U2238	C2096	A2060	C1960	U1868	U1735	U1603	G1527	G1424	G1377



• Molecule 54: 5S ribosomal RNA

Chain 2: 59% 36% 5%



• Molecule 55: tRNA^{fMet}

Chain 5: 65% 32% 3%



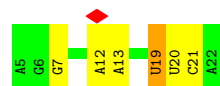
• Molecule 55: tRNA^{fMet}

Chain 6: 5% 39% 56%



• Molecule 56: mRNA

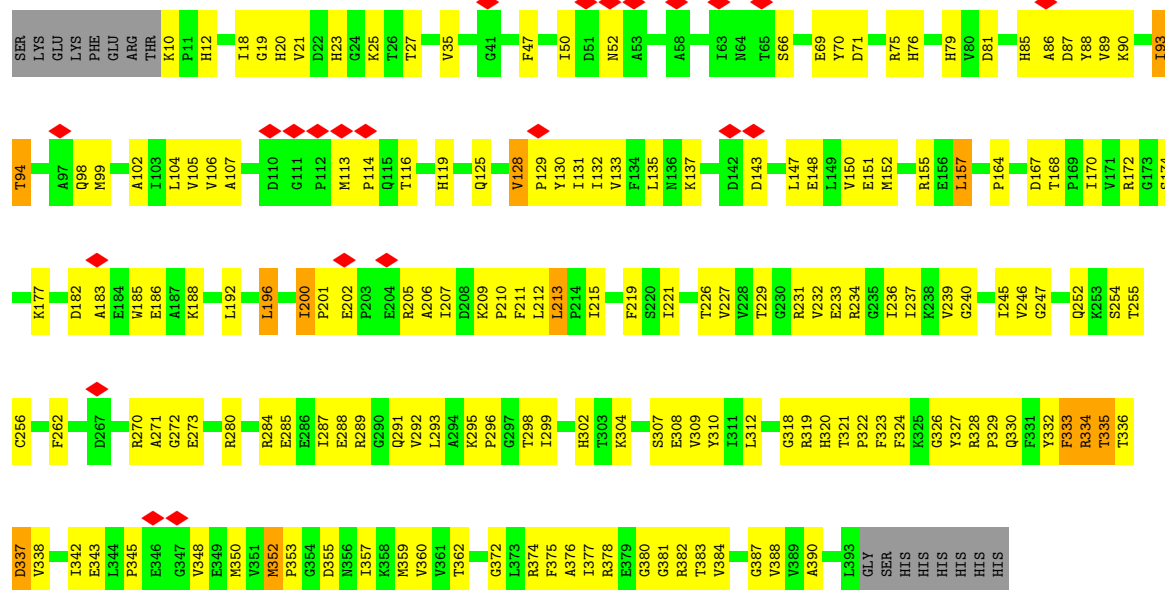
Chain 4: 6% 67% 28% 6%



• Molecule 57: tRNA^{Phe}



• Molecule 58: Elongation factor Tu



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	7269	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	17.471	Depositor
Minimum map value	-9.094	Depositor
Average map value	0.116	Depositor
Map value standard deviation	0.814	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: GTP, 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	1.02	12/2852 (0.4%)
2	c	0.30	0/1586	0.86	5/2134 (0.2%)
3	d	0.29	0/1571	0.92	6/2113 (0.3%)
4	e	0.29	0/1435	0.95	4/1926 (0.2%)
5	f	0.31	0/1343	0.90	4/1816 (0.2%)
6	g	0.33	0/1122	0.97	5/1515 (0.3%)
7	h	0.35	0/1002	1.13	14/1350 (1.0%)
8	i	0.36	0/1046	1.01	6/1410 (0.4%)
9	j	0.29	0/1152	0.96	8/1551 (0.5%)
10	k	0.29	0/948	1.00	7/1268 (0.6%)
11	l	0.30	0/1054	0.93	4/1403 (0.3%)
12	m	0.29	0/1093	0.90	3/1460 (0.2%)
13	n	0.30	0/974	0.94	4/1301 (0.3%)
14	o	0.29	0/902	1.03	5/1209 (0.4%)
15	p	0.31	0/929	0.91	1/1242 (0.1%)
16	q	0.29	0/960	0.97	6/1278 (0.5%)
17	r	0.30	0/829	0.89	4/1107 (0.4%)
18	s	0.28	0/864	0.87	2/1156 (0.2%)
19	t	0.29	0/745	0.86	2/994 (0.2%)
20	u	0.28	0/788	1.00	8/1051 (0.8%)
21	v	0.30	0/766	0.90	2/1025 (0.2%)
22	w	0.28	0/582	0.90	0/769
23	x	0.29	0/635	0.88	3/848 (0.4%)
24	y	0.28	0/510	0.88	1/677 (0.1%)
25	z	0.28	0/453	0.85	1/605 (0.2%)
26	B	0.29	0/450	0.93	1/599 (0.2%)
27	C	0.32	0/417	0.78	0/554
28	D	0.29	0/380	0.84	1/498 (0.2%)
29	E	0.30	0/513	0.96	3/676 (0.4%)
30	F	0.31	0/303	0.83	0/397
31	G	0.30	0/1788	0.92	8/2408 (0.3%)
32	H	0.32	0/1652	0.91	4/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	1.00	14/2227 (0.6%)
34	J	0.32	0/1170	0.90	4/1573 (0.3%)
35	K	0.31	0/836	1.05	5/1128 (0.4%)
36	L	0.29	0/1196	0.94	7/1602 (0.4%)
37	M	0.30	0/989	0.95	5/1326 (0.4%)
38	N	0.29	0/1034	0.94	5/1375 (0.4%)
39	O	0.33	0/797	1.01	5/1077 (0.5%)
40	P	0.33	0/886	1.00	4/1195 (0.3%)
41	Q	0.33	0/969	1.11	10/1300 (0.8%)
42	R	0.32	0/893	0.98	2/1193 (0.2%)
43	S	0.30	0/817	0.93	1/1088 (0.1%)
44	T	0.28	0/722	0.85	2/964 (0.2%)
45	U	0.32	0/659	0.95	3/884 (0.3%)
46	V	0.30	0/658	0.93	0/881
47	W	0.33	0/545	1.02	2/731 (0.3%)
48	X	0.32	0/653	0.92	3/877 (0.3%)
49	Y	0.29	0/671	1.04	4/888 (0.5%)
50	Z	0.34	0/551	1.00	3/728 (0.4%)
51	a	0.32	0/1034	0.83	1/1387 (0.1%)
52	3	0.41	0/36963	0.47	1/57662 (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	0.39	0/1832	0.45	0/2855
55	6	0.42	0/1832	0.48	0/2855
56	4	0.42	0/436	0.50	0/679
57	7	0.41	0/1809	0.49	0/2819
58	8	0.32	0/3013	0.97	16/4081 (0.4%)
All	All	0.38	0/166212	0.64	232/248159 (0.1%)

There are no bond length outliers.

The worst 5 of 232 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	Q	20	VAL	N-CA-C	9.69	117.74	108.15
12	m	53	MET	N-CA-C	-9.28	102.47	113.88
1	b	87	SER	N-CA-C	-9.15	101.91	113.43
26	B	53	VAL	N-CA-C	9.13	120.95	111.00
42	R	3	ILE	N-CA-C	8.50	120.06	108.84

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	96	0
2	c	1565	0	1616	59	0
3	d	1552	0	1619	50	0
4	e	1411	0	1447	48	0
5	f	1323	0	1374	36	0
6	g	1111	0	1148	42	0
7	h	989	0	1025	57	0
8	i	1032	0	1088	40	0
9	j	1129	0	1162	38	0
10	k	939	0	1012	33	0
11	l	1045	0	1117	47	0
12	m	1074	0	1157	35	0
13	n	961	0	1000	26	0
14	o	892	0	923	30	0
15	p	917	0	965	34	0
16	q	947	0	1022	33	0
17	r	816	0	839	23	0
18	s	857	0	922	43	0
19	t	739	0	807	27	0
20	u	780	0	834	18	0
21	v	753	0	780	23	0
22	w	575	0	592	18	0
23	x	625	0	655	16	0
24	y	509	0	543	24	0
25	z	449	0	491	11	0
26	B	444	0	461	20	0
27	C	410	0	440	11	0
28	D	377	0	418	20	0
29	E	504	0	574	12	0
30	F	302	0	343	23	0
31	G	1757	0	1787	62	0
32	H	1625	0	1699	63	0
33	I	1643	0	1710	78	0
34	J	1157	0	1199	35	0
35	K	818	0	808	47	0
36	L	1182	0	1240	43	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	53	0
39	O	787	0	828	46	0
40	P	870	0	878	49	0
41	Q	955	0	1019	39	0
42	R	884	0	944	48	0
43	S	805	0	847	42	0
44	T	714	0	737	28	0
45	U	649	0	666	29	0
46	V	649	0	691	34	0
47	W	536	0	552	17	0
48	X	638	0	665	21	0
49	Y	665	0	714	14	0
50	Z	545	0	579	35	0
51	a	1027	0	1092	39	0
52	3	33012	0	16618	601	0
53	1	62317	0	31346	1008	0
54	2	2568	0	1303	44	0
55	5	1640	0	836	24	0
55	6	1640	0	837	36	0
56	4	388	0	196	4	0
57	7	1619	0	821	57	0
58	8	2958	0	2972	127	0
59	5	10	0	10	0	0
60	7	11	0	8	3	0
61	8	32	0	12	2	0
All	All	153212	0	104249	3255	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 13.

The worst 5 of 3255 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''	1.26	1.13
38:N:98:ARG:HD2	38:N:103:VAL:HG21	1.30	1.08
1:b:216:ARG:HD3	1:b:217:PRO:HD2	1.40	1.04
53:1:45:G:H5''	53:1:46:G:H5'	1.39	1.02
32:H:171:ARG:HG2	32:H:173:PRO:HD3	1.40	1.01

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%)	223 (83%)	41 (15%)	5 (2%)	6	33
2	c	207/209 (99%)	181 (87%)	24 (12%)	2 (1%)	12	43
3	d	199/201 (99%)	175 (88%)	23 (12%)	1 (0%)	24	56
4	e	175/177 (99%)	153 (87%)	20 (11%)	2 (1%)	11	42
5	f	174/176 (99%)	155 (89%)	16 (9%)	3 (2%)	7	34
6	g	147/149 (99%)	127 (86%)	17 (12%)	3 (2%)	6	32
7	h	129/131 (98%)	96 (74%)	28 (22%)	5 (4%)	2	21
8	i	139/141 (99%)	120 (86%)	18 (13%)	1 (1%)	18	50
9	j	140/142 (99%)	128 (91%)	8 (6%)	4 (3%)	3	26
10	k	120/122 (98%)	98 (82%)	18 (15%)	4 (3%)	3	25
11	l	141/143 (99%)	114 (81%)	20 (14%)	7 (5%)	1	17
12	m	134/136 (98%)	113 (84%)	18 (13%)	3 (2%)	5	31
13	n	118/120 (98%)	105 (89%)	12 (10%)	1 (1%)	16	48
14	o	114/116 (98%)	103 (90%)	10 (9%)	1 (1%)	14	45
15	p	112/114 (98%)	98 (88%)	14 (12%)	0	100	100
16	q	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
17	r	101/103 (98%)	85 (84%)	15 (15%)	1 (1%)	12	43
18	s	108/110 (98%)	92 (85%)	14 (13%)	2 (2%)	6	33
19	t	91/93 (98%)	77 (85%)	14 (15%)	0	100	100
20	u	100/102 (98%)	88 (88%)	11 (11%)	1 (1%)	12	43
21	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
22	w	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
23	x	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
24	y	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
25	z	56/58 (97%)	50 (89%)	6 (11%)	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%)	43 (90%)	5 (10%)	0	100	100
28	D	44/46 (96%)	36 (82%)	7 (16%)	1 (2%)	5	30
29	E	62/64 (97%)	49 (79%)	12 (19%)	1 (2%)	7	35
30	F	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	4	27
31	G	223/225 (99%)	210 (94%)	13 (6%)	0	100	100
32	H	204/206 (99%)	186 (91%)	18 (9%)	0	100	100
33	I	203/205 (99%)	177 (87%)	23 (11%)	3 (2%)	8	36
34	J	155/157 (99%)	128 (83%)	22 (14%)	5 (3%)	3	25
35	K	98/100 (98%)	76 (78%)	16 (16%)	6 (6%)	1	14
36	L	149/151 (99%)	135 (91%)	14 (9%)	0	100	100
37	M	127/129 (98%)	114 (90%)	11 (9%)	2 (2%)	7	35
38	N	125/127 (98%)	106 (85%)	15 (12%)	4 (3%)	3	25
39	O	96/98 (98%)	81 (84%)	9 (9%)	6 (6%)	1	14
40	P	114/116 (98%)	95 (83%)	15 (13%)	4 (4%)	3	24
41	Q	121/123 (98%)	96 (79%)	20 (16%)	5 (4%)	2	20
42	R	112/114 (98%)	97 (87%)	11 (10%)	4 (4%)	2	23
43	S	98/100 (98%)	79 (81%)	17 (17%)	2 (2%)	6	32
44	T	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	40
45	U	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
46	V	78/80 (98%)	63 (81%)	9 (12%)	6 (8%)	1	10
47	W	63/65 (97%)	53 (84%)	10 (16%)	0	100	100
48	X	77/79 (98%)	70 (91%)	7 (9%)	0	100	100
49	Y	83/85 (98%)	78 (94%)	5 (6%)	0	100	100
50	Z	63/65 (97%)	43 (68%)	13 (21%)	7 (11%)	0	5
51	a	130/223 (58%)	121 (93%)	7 (5%)	2 (2%)	8	36
58	8	382/400 (96%)	342 (90%)	37 (10%)	3 (1%)	16	48
All	All	6301/6512 (97%)	5475 (87%)	717 (11%)	109 (2%)	9	34

5 of 109 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL

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Mol	Chain	Res	Type
5	f	174	LYS
6	g	9	VAL
6	g	41	LYS
7	h	107	GLU

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%)	163 (99%)	1 (1%)	78	79
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	77
6	g	114/114 (100%)	112 (98%)	2 (2%)	51	67
7	h	100/100 (100%)	99 (99%)	1 (1%)	68	74
8	i	109/109 (100%)	107 (98%)	2 (2%)	51	67
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	75
10	k	103/103 (100%)	103 (100%)	0	100	100
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	107 (98%)	2 (2%)	51	67
13	n	100/100 (100%)	98 (98%)	2 (2%)	48	64
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%)	88 (99%)	1 (1%)	65	73
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	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%)	76 (97%)	2 (3%)	40	60
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%)	54 (98%)	1 (2%)	51	67
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%)	33 (97%)	1 (3%)	37	57
31	G	186/186 (100%)	184 (99%)	2 (1%)	65	73
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	79
33	I	172/172 (100%)	171 (99%)	1 (1%)	78	79
34	J	119/119 (100%)	117 (98%)	2 (2%)	53	67
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%)	105 (100%)	0	100	100
39	O	86/86 (100%)	85 (99%)	1 (1%)	63	72
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%)	81 (98%)	2 (2%)	43	61
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%)	73 (99%)	1 (1%)	59	70
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	52 (94%)	3 (6%)	19	46
51	a	110/174 (63%)	109 (99%)	1 (1%)	70	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
58	8	317/332 (96%)	312 (98%)	5 (2%)	55 68
All	All	5225/5304 (98%)	5183 (99%)	42 (1%)	70 76

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	M	120	LEU
50	Z	40	PRO
39	O	89	ARG
46	V	54	ILE
58	8	157	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 123 such sidechains are listed below:

Mol	Chain	Res	Type
24	y	15	ASN
47	W	30	ASN
32	H	40	GLN
46	V	50	ASN
58	8	20	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	146 (9%)	2 (0%)
53	1	2902/2903 (99%)	327 (11%)	11 (0%)
54	2	119/120 (99%)	9 (7%)	1 (0%)
55	5	76/77 (98%)	7 (9%)	0
55	6	76/77 (98%)	7 (9%)	0
56	4	17/18 (94%)	3 (17%)	0
57	7	75/76 (98%)	15 (20%)	0
All	All	4803/4810 (99%)	514 (10%)	14 (0%)

5 of 514 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 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	1475	G
53	1	1930	G
54	2	88	C
53	1	2326	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	$\# Z > 2$
60	PHE	7	101	57	10,11,12	0.66	0	8,13,15	0.28	0
61	GTP	8	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.53	9 (18%)
59	FME	5	101	55	8,9,10	0.50	0	8,9,11	0.90	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	PHE	7	101	57	-	0/5/6/8	0/1/1/1
61	GTP	8	501	-	-	5/22/38/38	0/3/3/3
59	FME	5	101	55	-	2/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GTP	C2-N3	2.00	1.38	1.33

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GTP	C5-C4-N3	-4.76	120.81	128.39
61	8	501	GTP	C2-N3-C4	4.20	119.53	112.30
61	8	501	GTP	C2-N1-C6	-2.99	119.69	125.11
61	8	501	GTP	N9-C4-N3	2.97	131.90	125.95
61	8	501	GTP	N9-C8-N7	-2.56	108.65	113.40

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA
59	5	101	FME	O-C-CA-CB
61	8	501	GTP	O4'-C4'-C5'-O5'
61	8	501	GTP	C3'-C4'-C5'-O5'
61	8	501	GTP	PG-O3B-PB-O2B

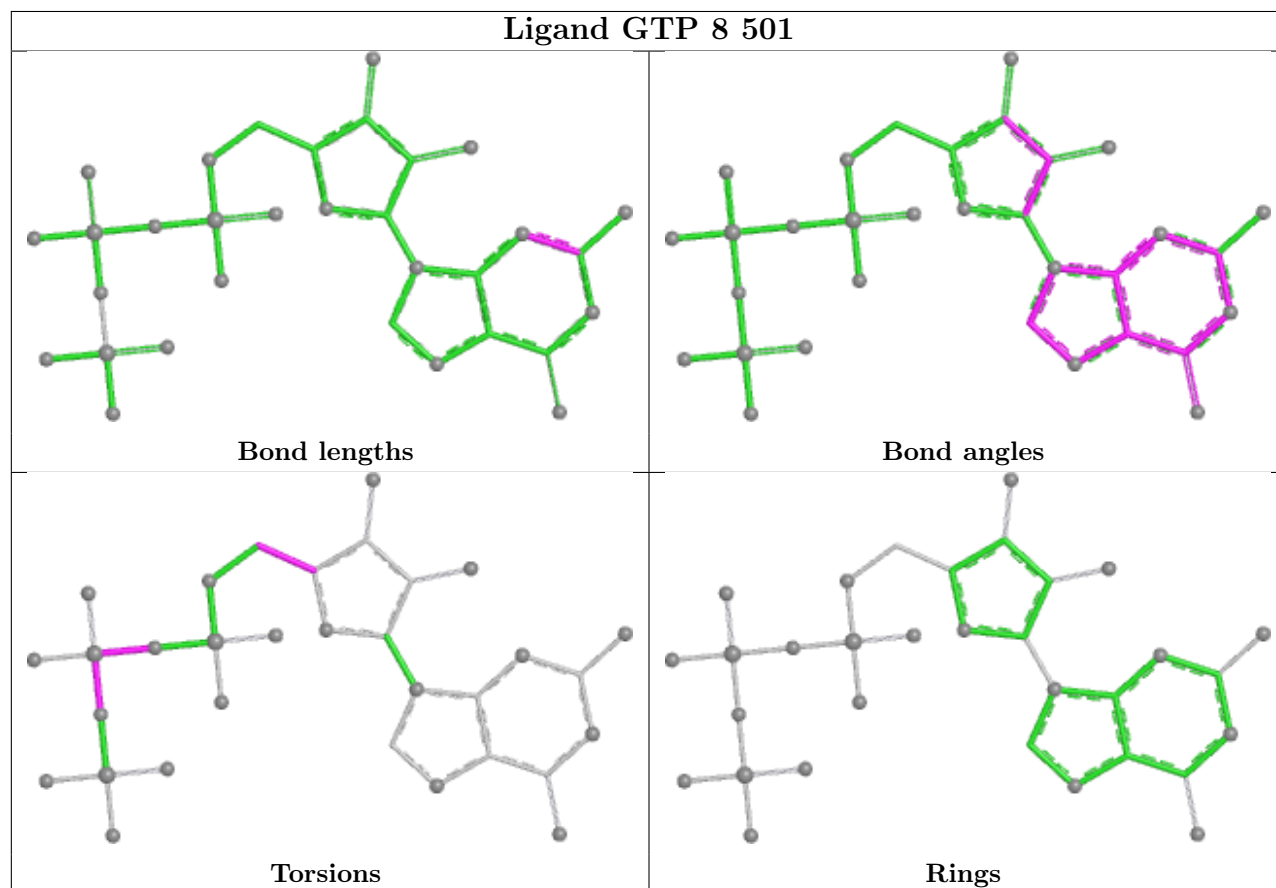
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	7	101	PHE	3	0
61	8	501	GTP	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.

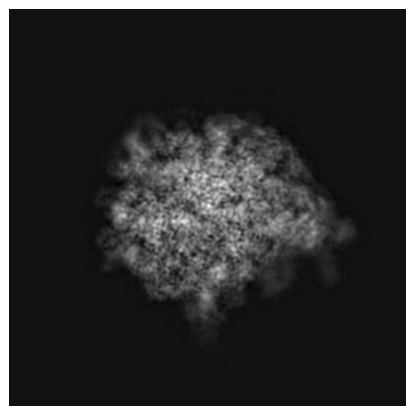
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21627. These allow visual inspection of the internal detail of the map and identification of artifacts.

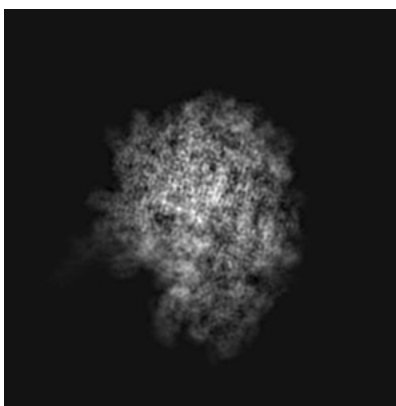
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

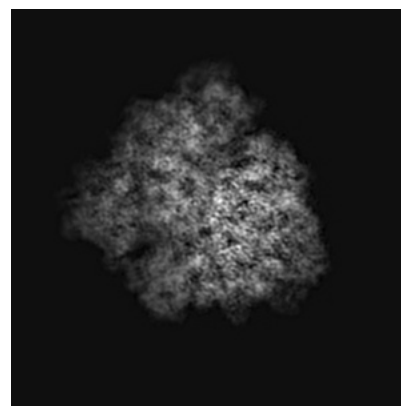
6.1.1 Primary map



X

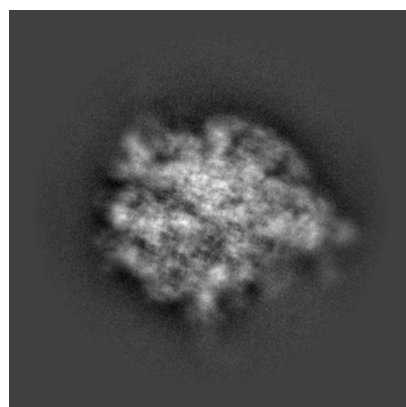


Y

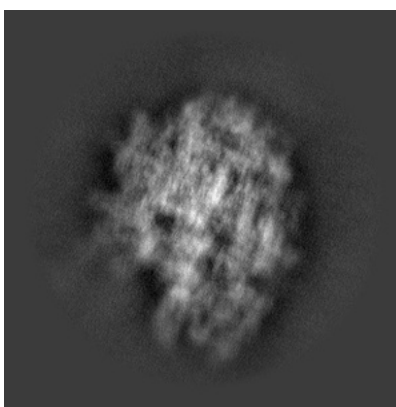


Z

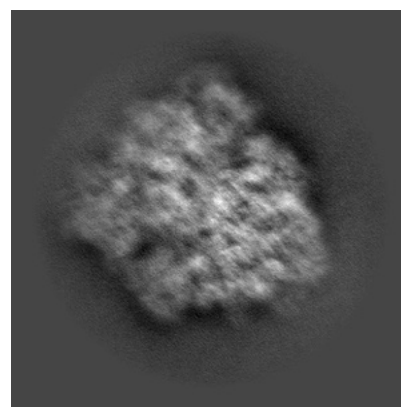
6.1.2 Raw map



X



Y

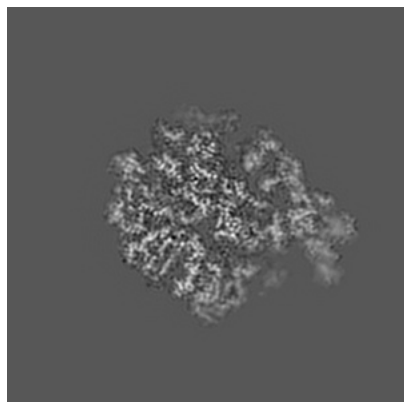


Z

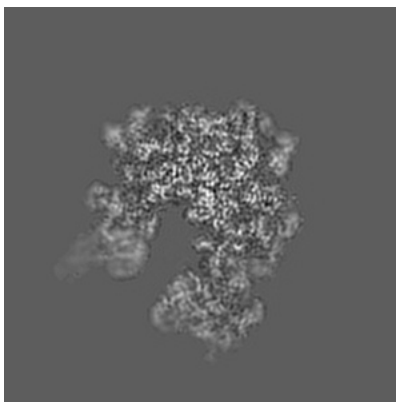
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

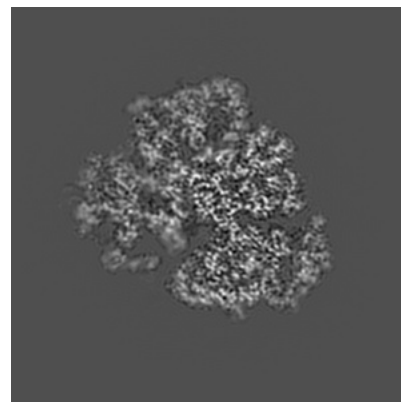
6.2.1 Primary map



X Index: 144

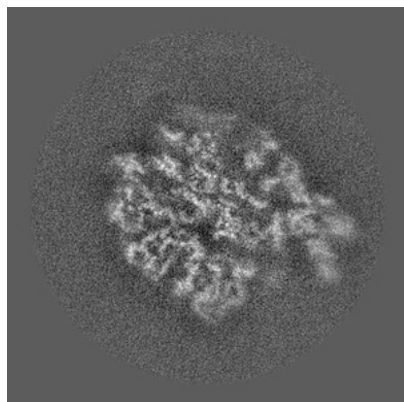


Y Index: 144

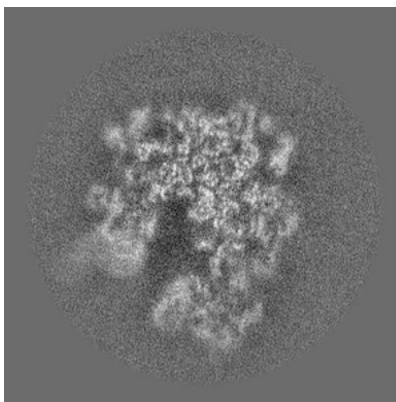


Z Index: 144

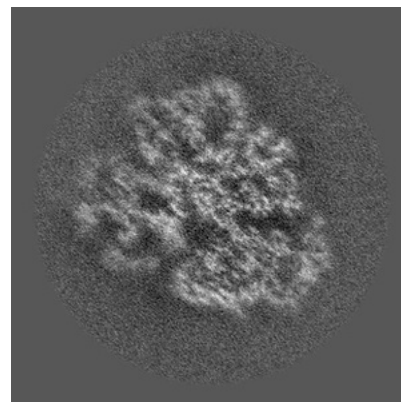
6.2.2 Raw map



X Index: 144



Y Index: 144

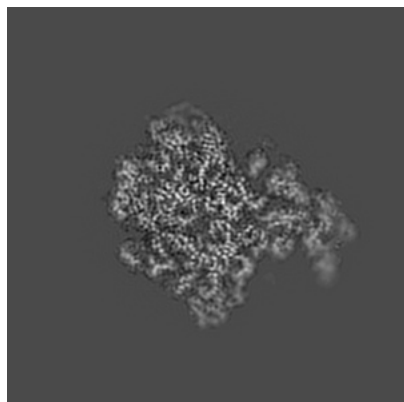


Z Index: 144

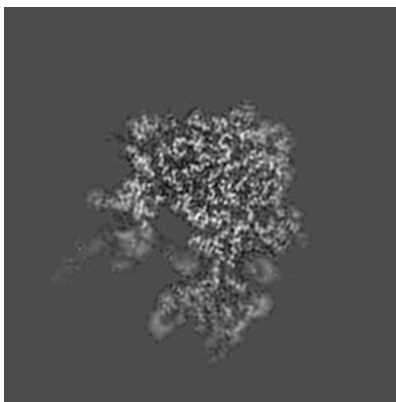
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

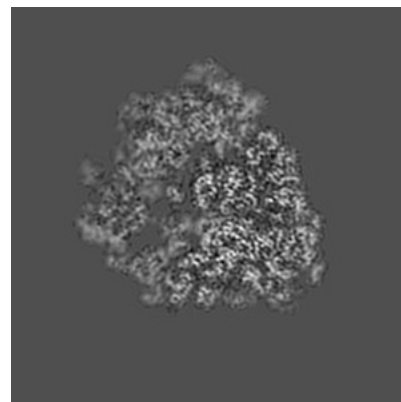
6.3.1 Primary map



X Index: 149

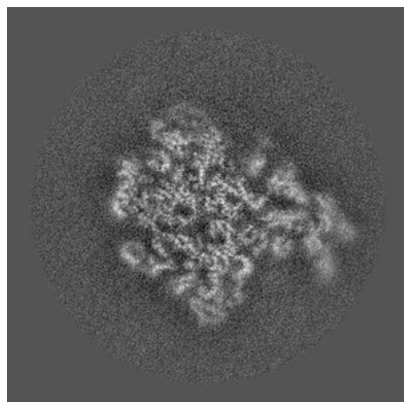


Y Index: 151

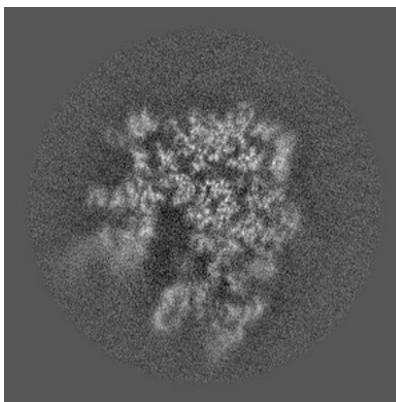


Z Index: 135

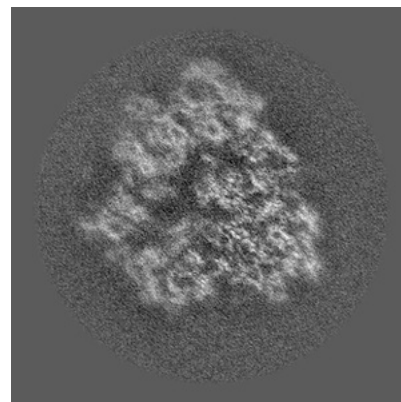
6.3.2 Raw map



X Index: 149



Y Index: 148

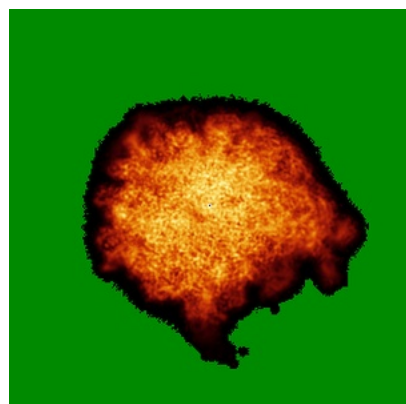


Z Index: 132

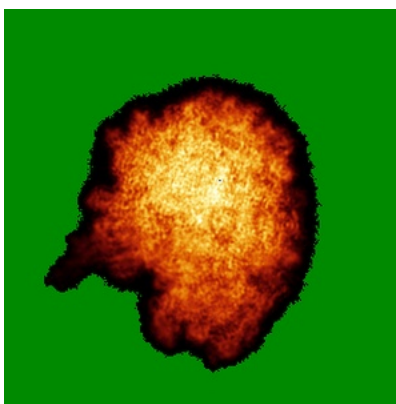
The images above show the largest variance slices of the map in three orthogonal directions.

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

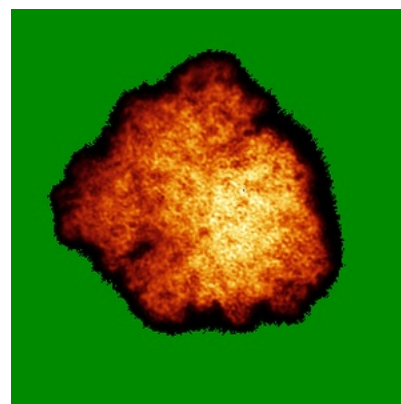
6.4.1 Primary map



X

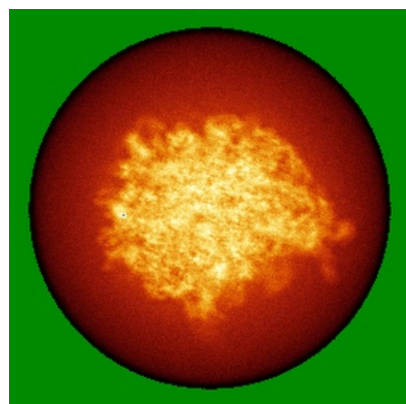


Y

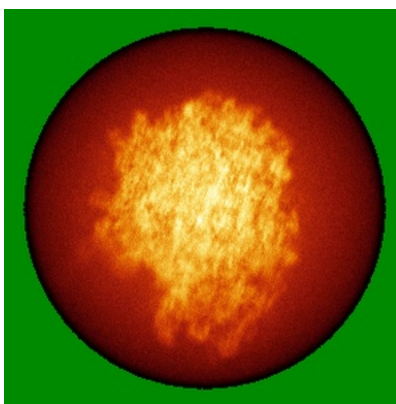


Z

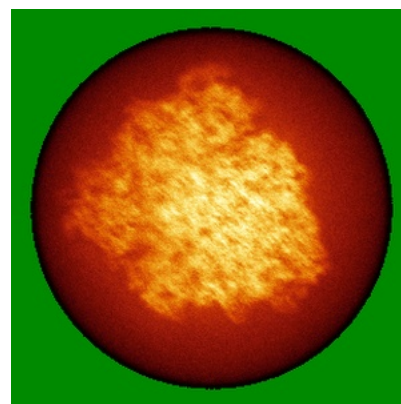
6.4.2 Raw map



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.

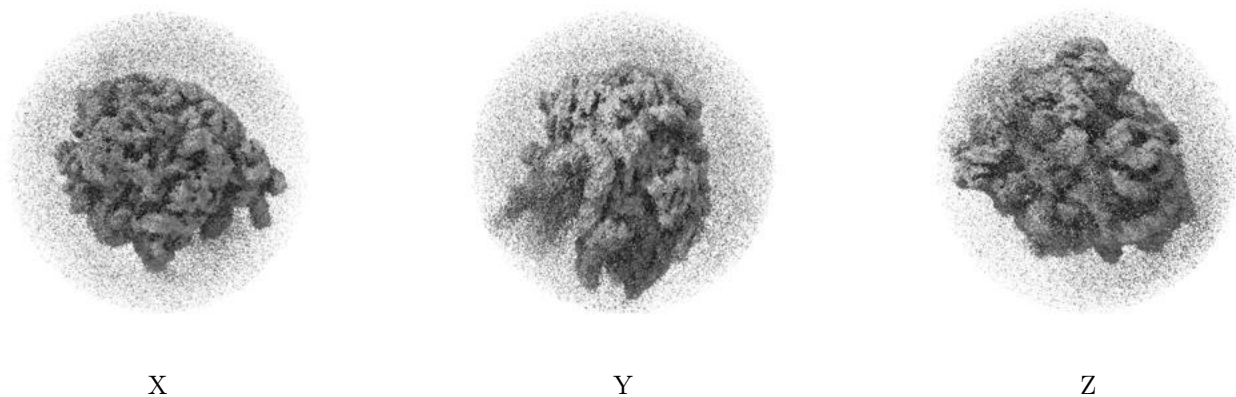
6.5 Orthogonal surface views [i](#)

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.

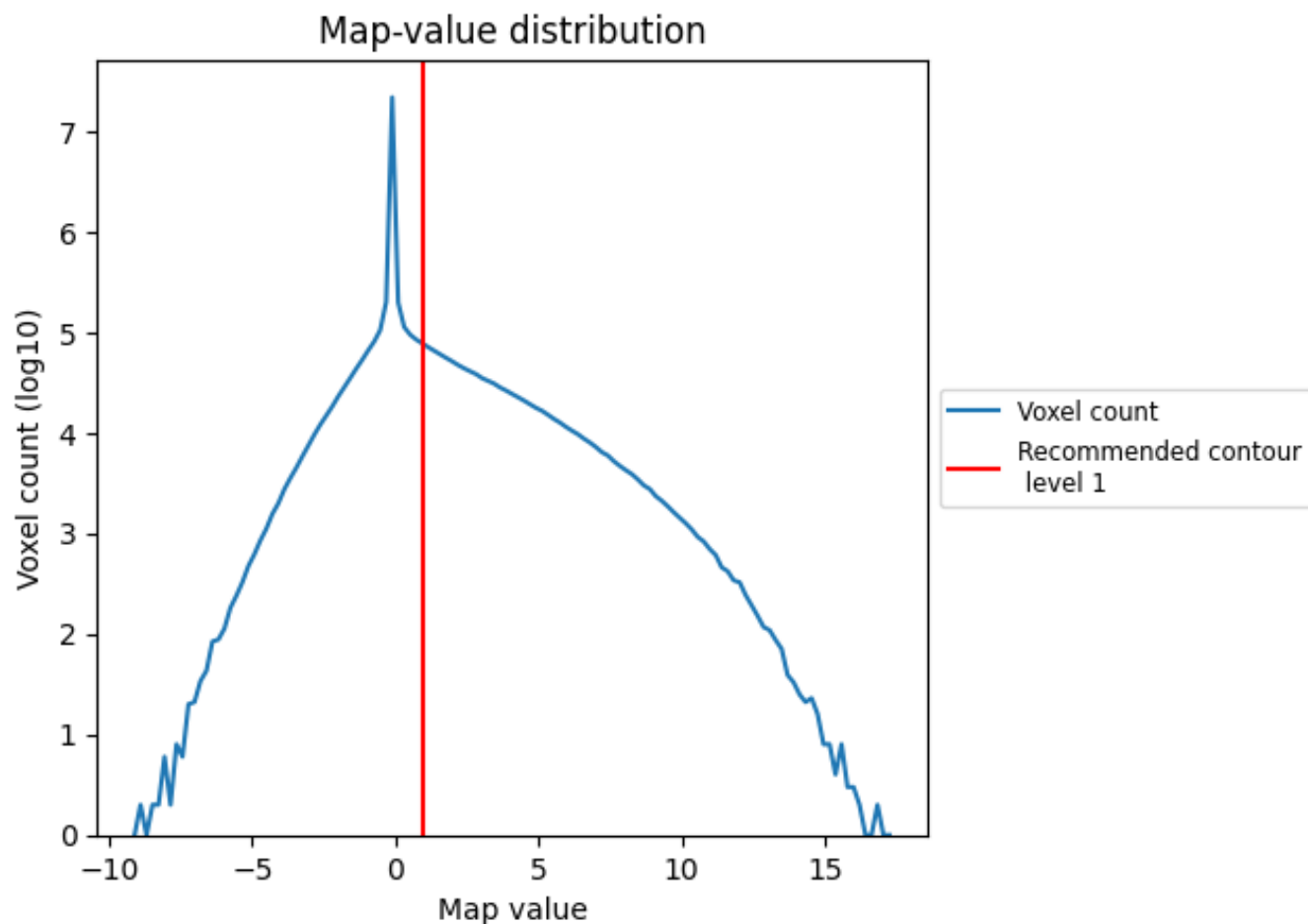
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

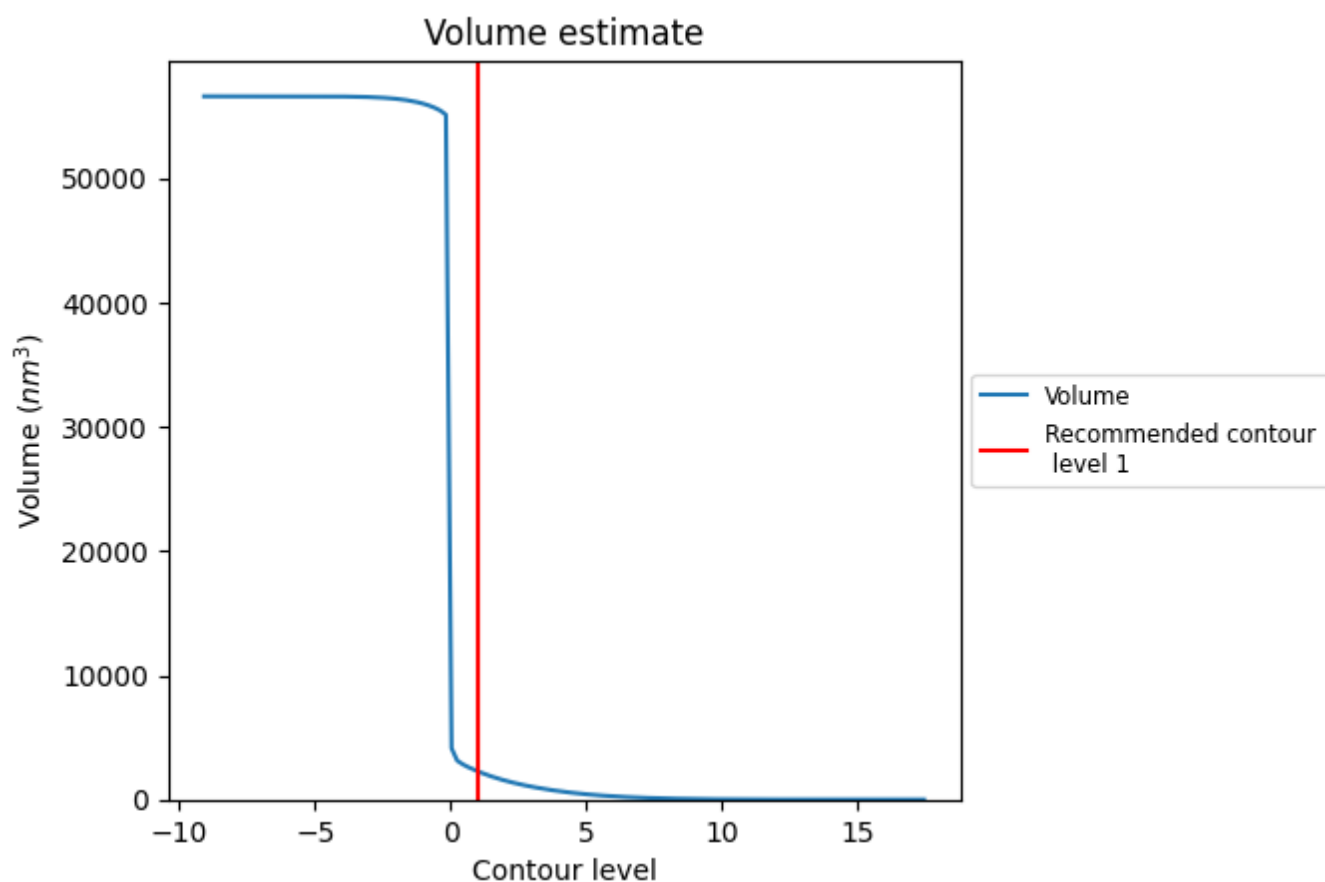
This section contains the results of statistical analysis of the map.

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.

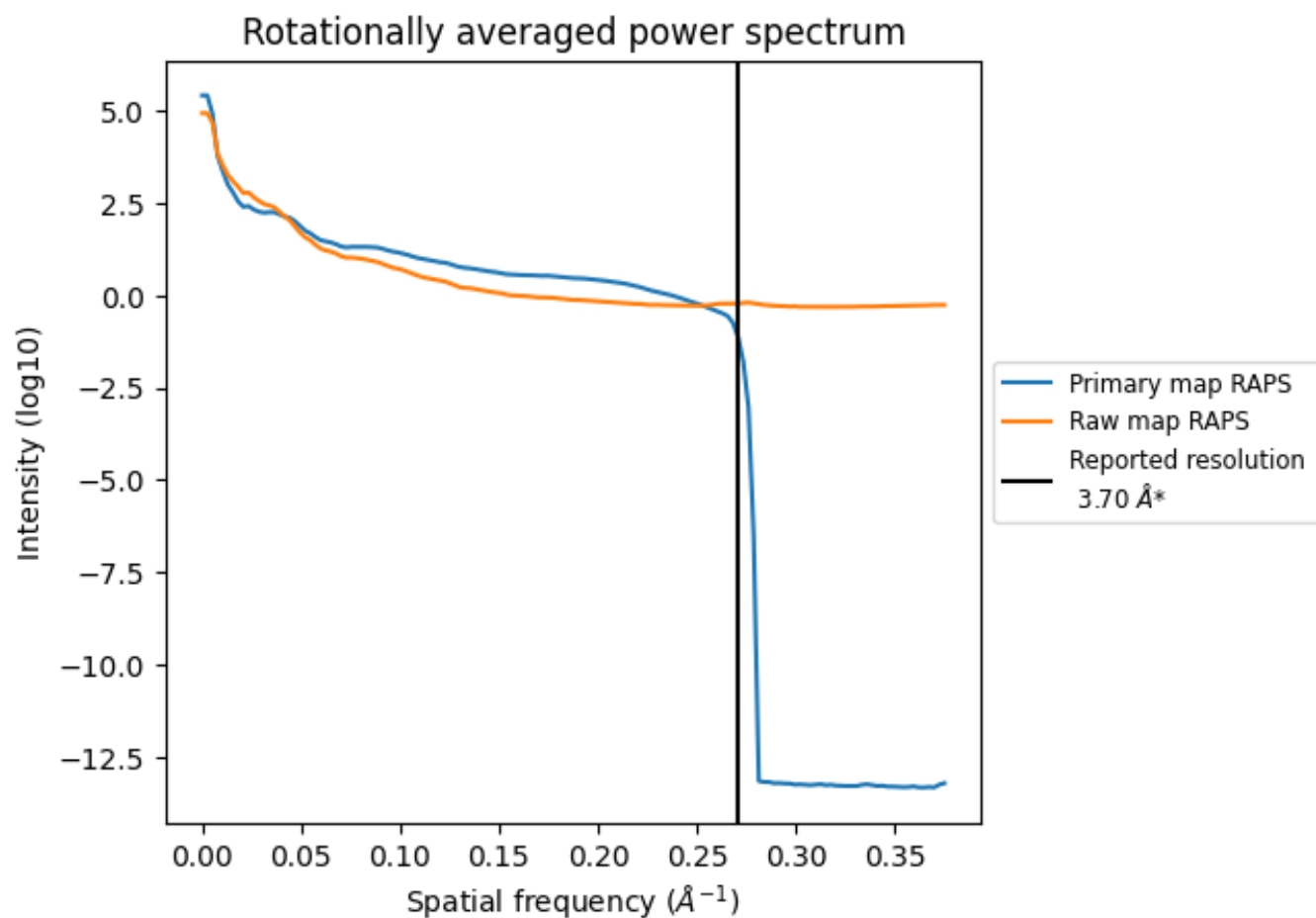
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2276 nm³; this corresponds to an approximate mass of 2056 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

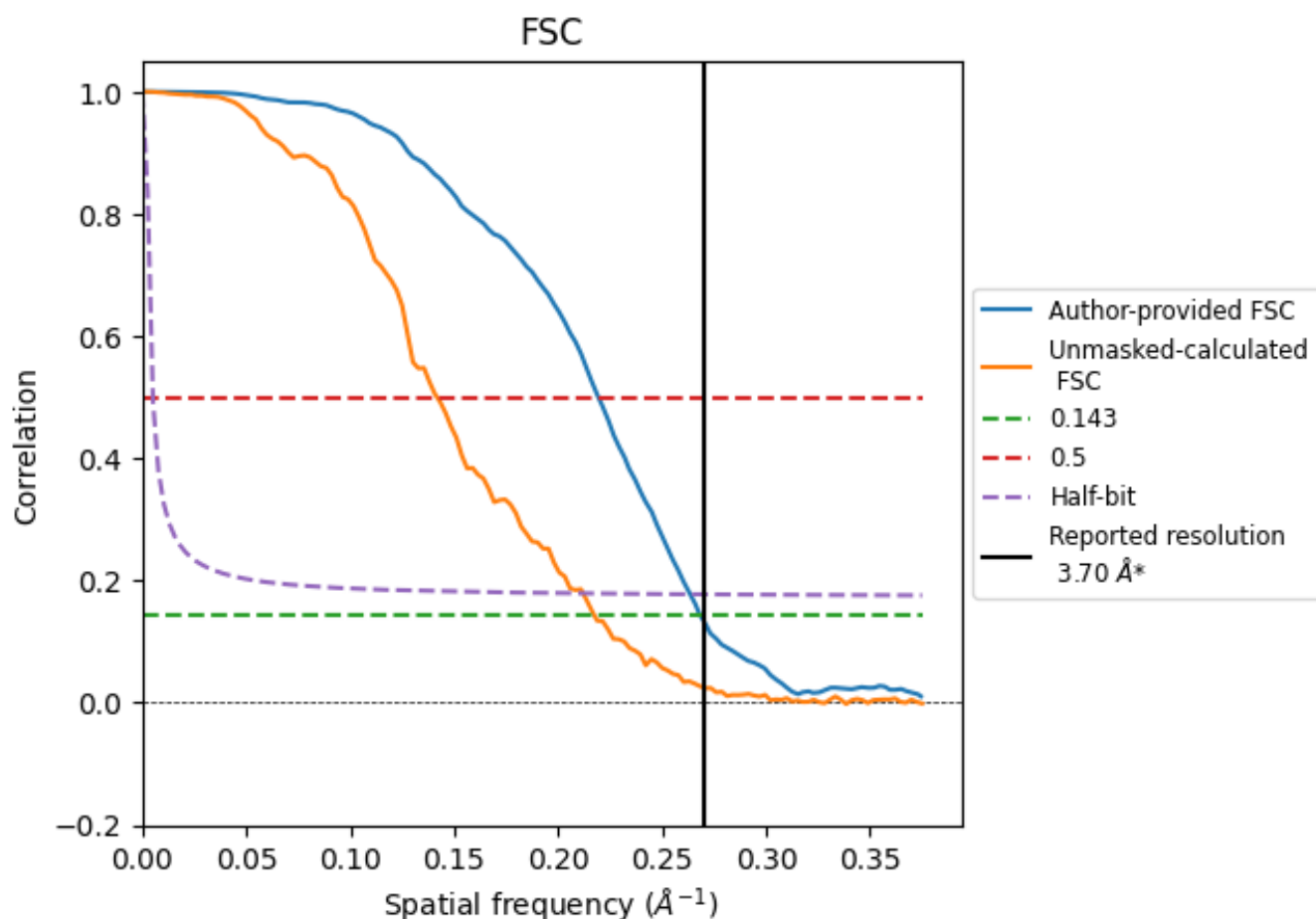


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

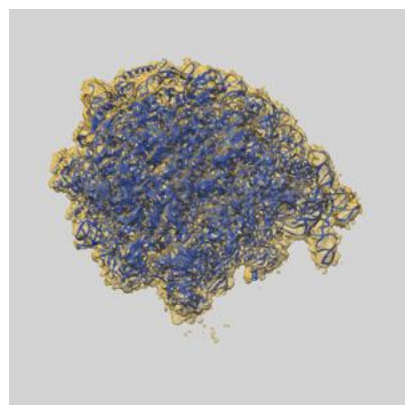
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.73	4.56	3.80
Unmasked-calculated*	4.60	7.06	4.72

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

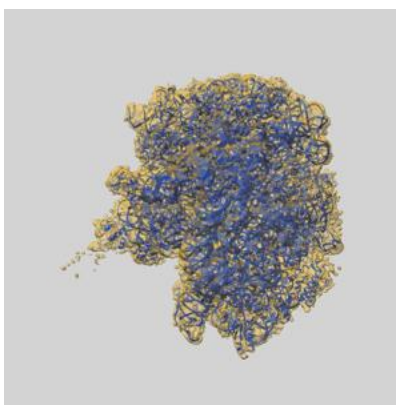
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21627 and PDB model 6WD8. Per-residue inclusion information can be found in section [3](#) on page [17](#).

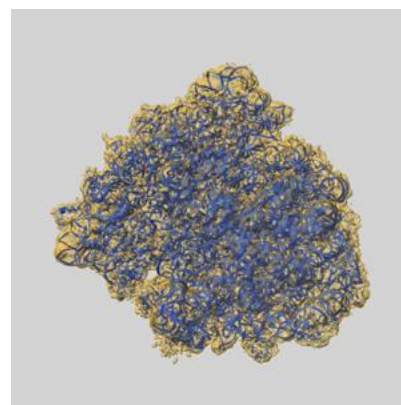
9.1 Map-model overlay [i](#)



X



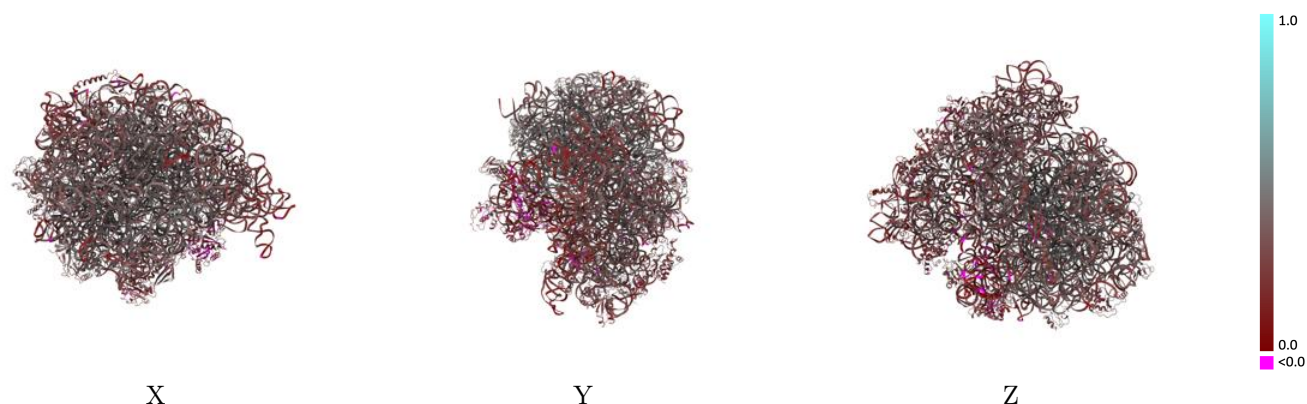
Y



Z

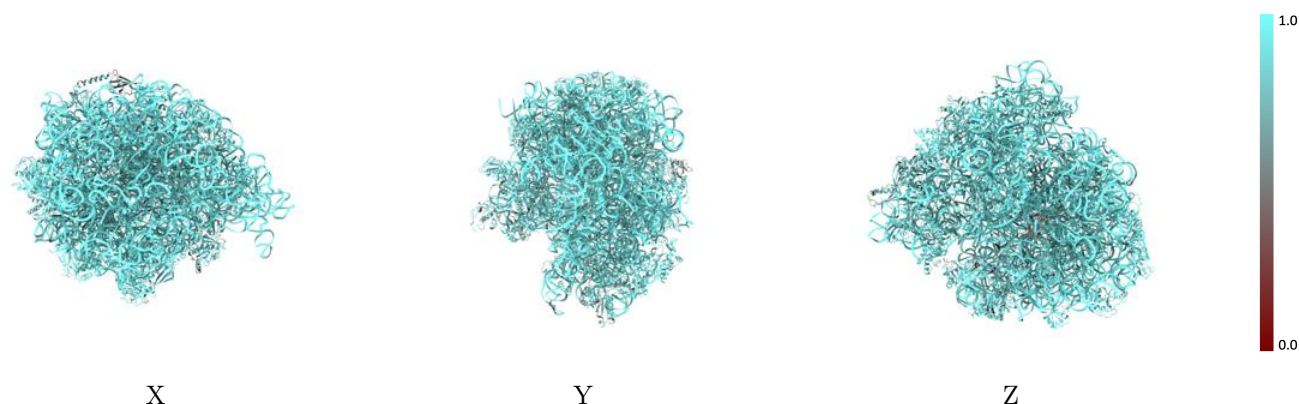
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



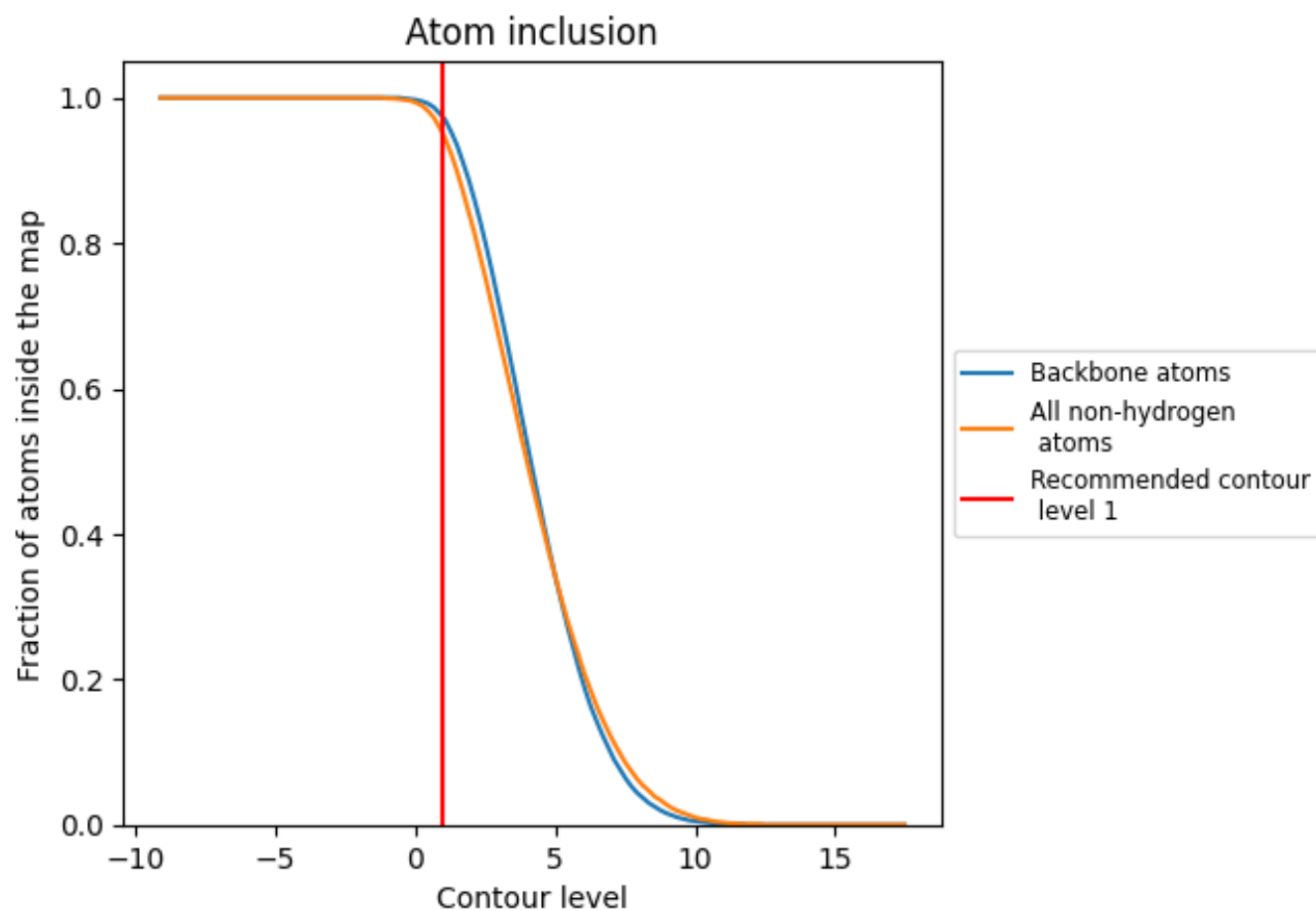
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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, 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	 0.3350
1	 0.9800	 0.3620
2	 0.9810	 0.3170
3	 0.9770	 0.3110
4	 0.8810	 0.2270
5	 0.9680	 0.2730
6	 0.7770	 0.1260
7	 0.9130	 0.1430
8	 0.8720	 0.1580
B	 0.9510	 0.4160
C	 0.8210	 0.3360
D	 0.9320	 0.4410
E	 0.9330	 0.4430
F	 0.8290	 0.3810
G	 0.8820	 0.2930
H	 0.8140	 0.3320
I	 0.7990	 0.2390
J	 0.9260	 0.3660
K	 0.9540	 0.3420
L	 0.9180	 0.2950
M	 0.9410	 0.3800
N	 0.8850	 0.2940
O	 0.7240	 0.2800
P	 0.9400	 0.3620
Q	 0.9480	 0.3670
R	 0.9140	 0.2720
S	 0.8200	 0.3020
T	 0.9620	 0.3600
U	 0.8880	 0.3100
V	 0.9420	 0.3510
W	 0.9300	 0.3330
X	 0.9370	 0.2790
Y	 0.9480	 0.3100
Z	 0.8760	 0.2960
a	 0.7900	 0.1530



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Chain	Atom inclusion	Q-score
b	 0.9550	 0.4510
c	 0.9490	 0.4300
d	 0.9310	 0.3780
e	 0.9380	 0.2970
f	 0.9520	 0.2980
g	 0.6740	 0.2550
h	 0.7540	 0.1810
i	 0.7470	 0.1620
j	 0.9430	 0.4310
k	 0.9420	 0.4310
l	 0.9370	 0.4060
m	 0.9130	 0.4080
n	 0.9480	 0.4300
o	 0.9400	 0.3320
p	 0.9490	 0.4160
q	 0.9460	 0.4180
r	 0.9540	 0.3910
s	 0.9290	 0.4170
t	 0.9410	 0.4070
u	 0.9310	 0.3630
v	 0.9420	 0.3620
w	 0.9410	 0.4170
x	 0.9470	 0.4260
y	 0.9190	 0.3210
z	 0.9290	 0.4070