



# wwPDB EM Validation Summary Report ⓘ

Aug 4, 2025 – 08:52 PM JST

PDB ID : 8Y5N / pdb\_00008y5n  
EMDB ID : EMD-38943  
Title : E.coli transcription translation coupling complex in TTC-A state 3 containing mRNA with 21-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and viomycin  
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.  
Deposited on : 2024-01-31  
Resolution : 4.50 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev126  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

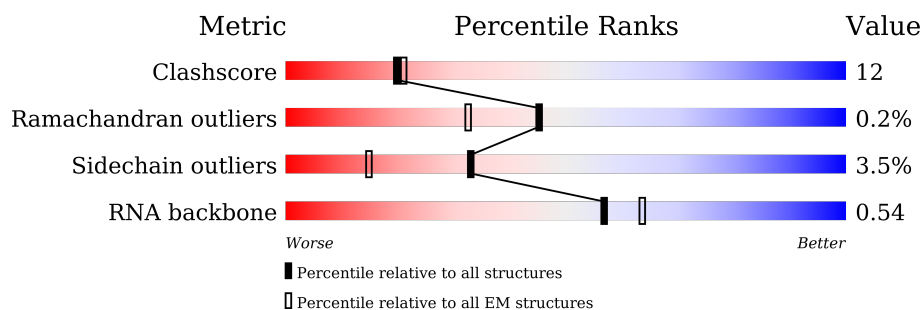
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.50 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.









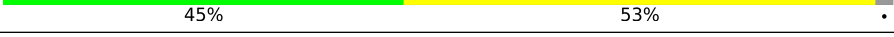

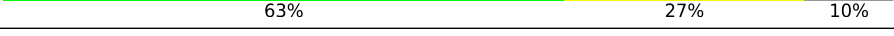

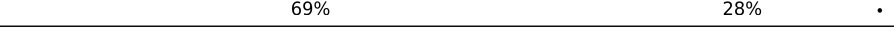
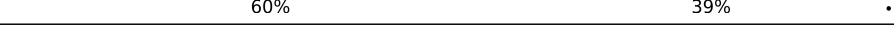

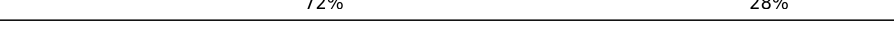


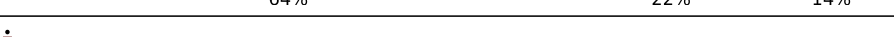

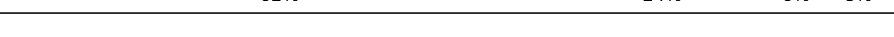






Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	A	70	<div> <div>50%</div> <div>16%</div> <div>34%</div> </div>
2	B	57	<div> <div>67%</div> <div>30%</div> <div>••</div> </div>
3	C	55	<div> <div>49%</div> <div>42%</div> <div>9%</div> </div>
4	D	46	<div> <div>59%</div> <div>37%</div> <div>•</div> </div>
5	E	65	<div> <div>66%</div> <div>31%</div> <div>••</div> </div>
6	F	38	<div> <div>61%</div> <div>39%</div> </div>
7	G	241	<div> <div>64%</div> <div>25%</div> <div>• 10%</div> </div>








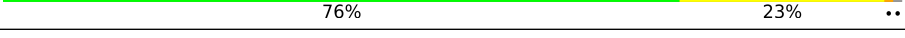
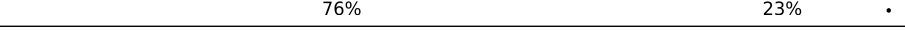

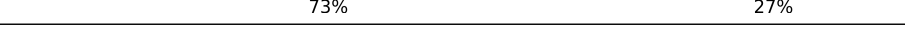

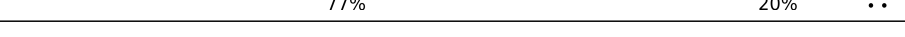
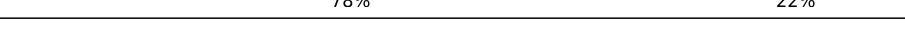

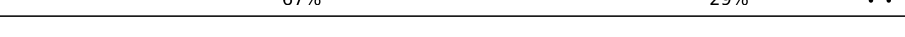
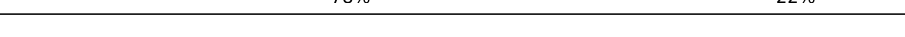
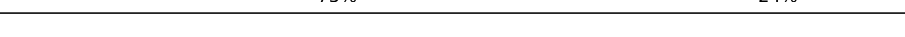
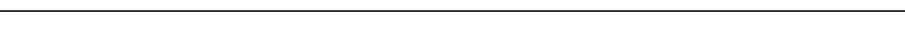


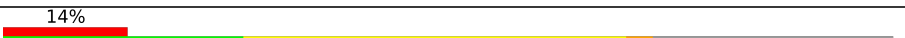



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Mol	Chain	Length	Quality of chain
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	
27	b	273	
28	c	209	
29	d	201	
30	e	179	
31	f	177	
32	g	149	

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Mol	Chain	Length	Quality of chain
33	i	142	
34	j	142	
35	k	123	
36	l	144	
37	m	136	
38	n	127	
39	o	117	
40	p	115	
41	q	118	
42	r	103	
43	s	110	
44	t	100	
45	u	104	
46	v	94	
47	w	85	
48	x	78	
49	y	63	
50	z	59	
51	1	2904	
52	2	120	
53	3	1542	
54	4	38	
55	8	37	
56	9	37	
57	A1	329	

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Mol	Chain	Length	Quality of chain
57	A2	329	
58	B1	1407	
59	B2	1342	
60	W0	91	
61	NG	181	
62	5	76	
63	6	77	
64	a	234	
65	0	716	
66	h	6	

## 2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 179711 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 L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	46	Total	C	N	O	S	0	0
			355	221	62	66	6		

- Molecule 2 is a protein called 50S ribosomal protein L32.

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

- Molecule 3 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 4 is a protein called 50S ribosomal protein L34.

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

- Molecule 5 is a protein called 50S ribosomal protein L35.

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

- Molecule 6 is a protein called 50S ribosomal protein L36.

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

- Molecule 7 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 8 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 9 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1637	1023	312	298	4		

- Molecule 10 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 11 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 12 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 13 is a protein called 30S ribosomal protein S8.

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

- Molecule 14 is a protein called 30S ribosomal protein S9.

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

- Molecule 15 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 16 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 17 is a protein called 30S ribosomal protein S12.

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

- Molecule 18 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 19 is a protein called 30S ribosomal protein S14.

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

- Molecule 20 is a protein called 30S ribosomal protein S15.

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

- Molecule 21 is a protein called 30S ribosomal protein S16.

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

- Molecule 22 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 23 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 24 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 25 is a protein called 30S ribosomal protein S20.

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

- Molecule 26 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 28 is a protein called 50S ribosomal protein L3.

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

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L9.

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

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	u	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

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

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

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

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

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

- Molecule 51 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	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 1929590828

- Molecule 52 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	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	U	conflict	GB NR_103249

- Molecule 53 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	22	Total	C	N	O	P	0	0
			467	208	76	161	22		

- Molecule 55 is a DNA chain called templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	27	Total	C	N	O	P	0	0
			539	257	88	167	27		

- Molecule 56 is a DNA chain called non-templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	9	20	Total	C	N	O	P	0	0
			417	195	84	118	20		

- Molecule 57 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A1	218	Total	C	N	O	S	0	0
			1677	1048	297	326	6		
57	A2	221	Total	C	N	O	S	0	0
			1698	1060	299	333	6		

- Molecule 58 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	B1	1335	Total	C	N	O	S	0	0
			10353	6509	1842	1955	47		

- Molecule 59 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B2	1340	Total	C	N	O	S	0	0
			10546	6616	1839	2048	43		

- Molecule 60 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	W0	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 61 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	NG	88	Total	C	N	O	0	0
			433	257	88	88		

- Molecule 62 is a RNA chain called tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
62	5	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 63 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
63	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 64 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	a	132	Total	C	N	O	S	0	0
			1013	638	183	190	2		

- Molecule 65 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	0	697	Total	C	N	O	S	0	0
			5399	3403	929	1042	25		

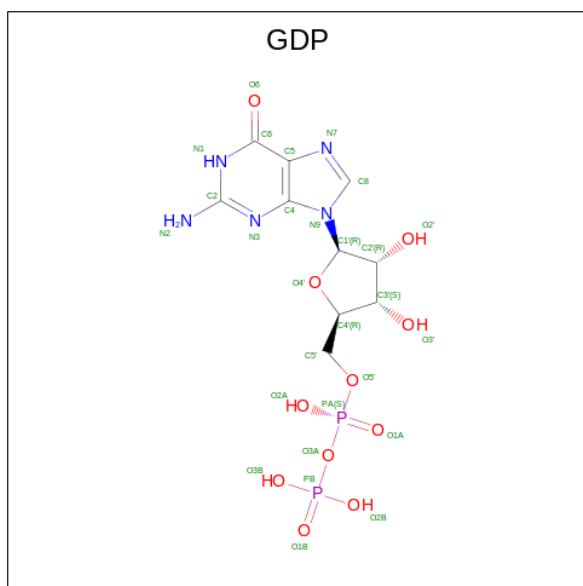
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	705	GLY	-	expression tag	UNP P0A6M8
0	706	SER	-	expression tag	UNP P0A6M8
0	707	SER	-	expression tag	UNP P0A6M8
0	708	GLY	-	expression tag	UNP P0A6M8
0	709	HIS	-	expression tag	UNP P0A6M8
0	710	HIS	-	expression tag	UNP P0A6M8
0	711	HIS	-	expression tag	UNP P0A6M8
0	712	HIS	-	expression tag	UNP P0A6M8
0	713	HIS	-	expression tag	UNP P0A6M8
0	714	HIS	-	expression tag	UNP P0A6M8
0	715	HIS	-	expression tag	UNP P0A6M8
0	716	HIS	-	expression tag	UNP P0A6M8

- Molecule 66 is a protein (with D amino acids) called Viomycin.

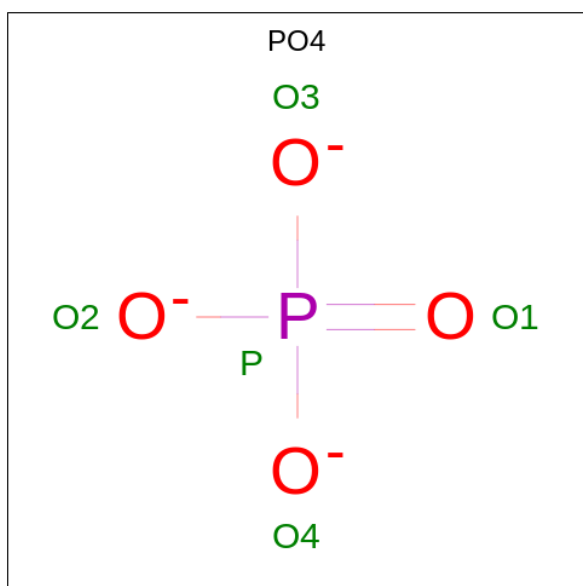
Mol	Chain	Residues	Atoms				AltConf	Trace
66	h	6	Total	C	N	O	0	0
			48	25	13	10		

- Molecule 67 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ).



Mol	Chain	Residues	Atoms					AltConf
67	0	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 68 is PHOSPHATE ION (CCD ID: PO4) (formula:  $O_4P$ ).

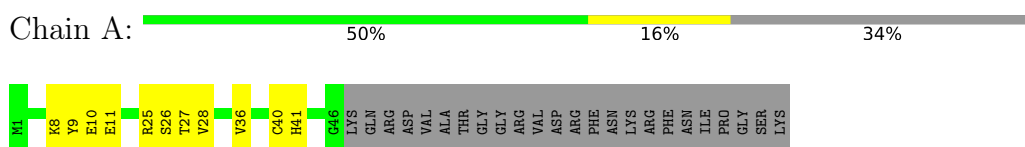


Mol	Chain	Residues	Atoms			AltConf
68	0	1	Total	O	P	0
			5	4	1	

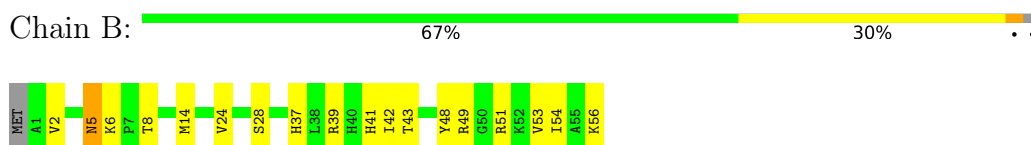
### 3 Residue-property plots [i](#)

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.

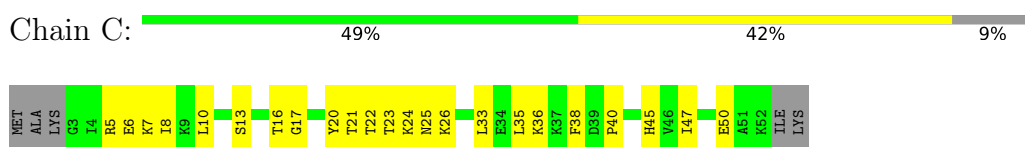
- Molecule 1: 50S ribosomal protein L31



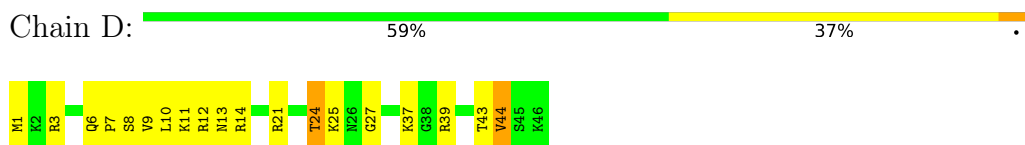
- Molecule 2: 50S ribosomal protein L32



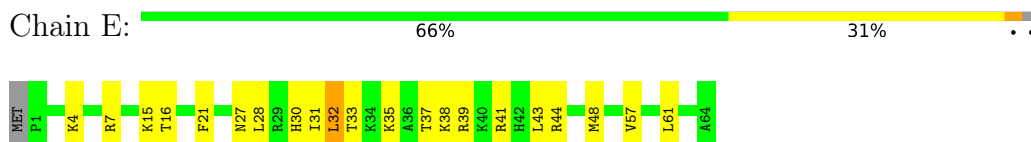
- Molecule 3: 50S ribosomal protein L33



- Molecule 4: 50S ribosomal protein L34



- Molecule 5: 50S ribosomal protein L35



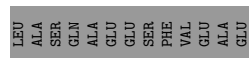
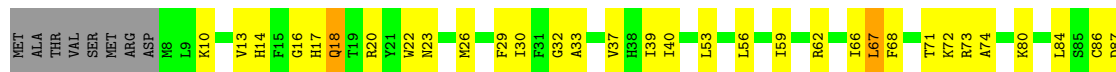
- Molecule 6: 50S ribosomal protein L36

Chain F:  61% 39%



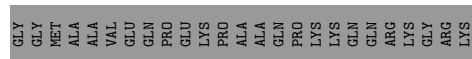
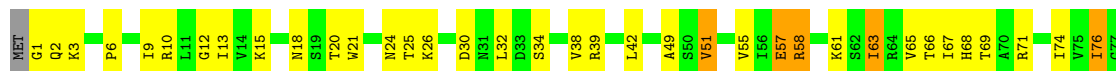
• Molecule 7: 30S ribosomal protein S2

Chain G:  64% 25% 10%



• Molecule 8: 30S ribosomal protein S3

Chain H:  58% 27% 12%



• Molecule 9: 30S ribosomal protein S4

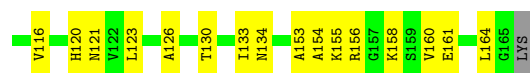
Chain I:  70% 28% 2%



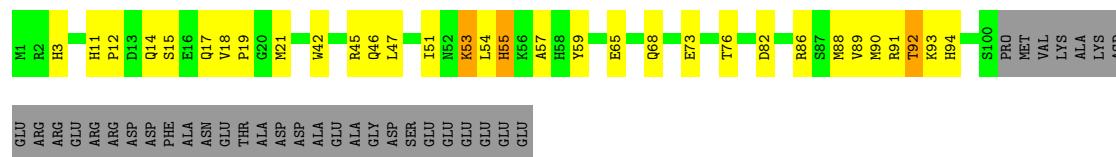
• Molecule 10: 30S ribosomal protein S5

Chain J:  65% 29% 6%

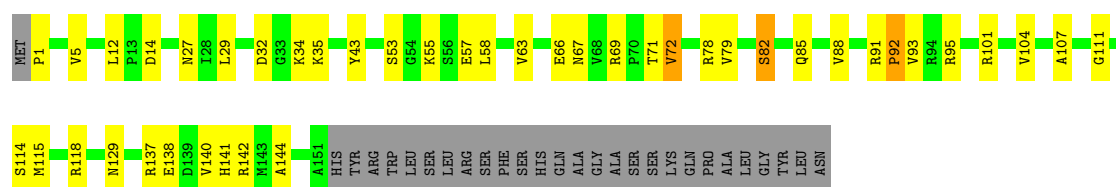




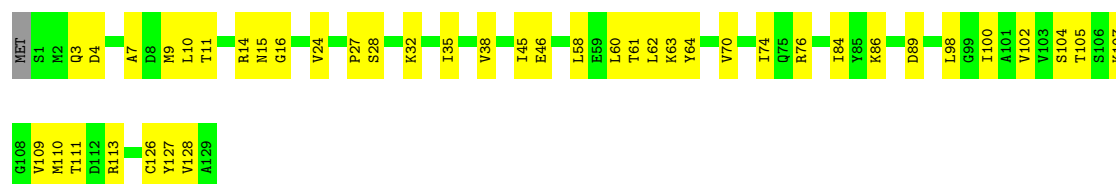
- Molecule 11: 30S ribosomal protein S6, fully modified isoform



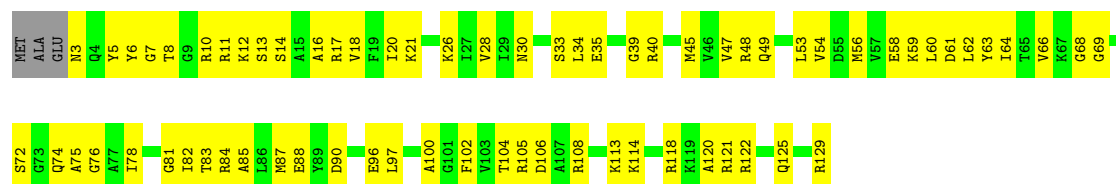
- Molecule 12: 30S ribosomal protein S7



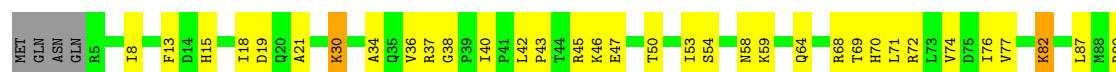
- Molecule 13: 30S ribosomal protein S8



- Molecule 14: 30S ribosomal protein S9



- Molecule 15: 30S ribosomal protein S10





- Molecule 16: 30S ribosomal protein S11

Chain P: 63% 27% 10%



- Molecule 17: 30S ribosomal protein S12

Chain Q: 73% 26% 1%



- Molecule 18: 30S ribosomal protein S13

Chain R: 69% 28% 3%



- Molecule 19: 30S ribosomal protein S14

Chain S: 60% 39% 1%



- Molecule 20: 30S ribosomal protein S15

Chain T: 78% 21% 1%



- Molecule 21: 30S ribosomal protein S16

Chain U: 72% 28% 0%



- Molecule 22: 30S ribosomal protein S17



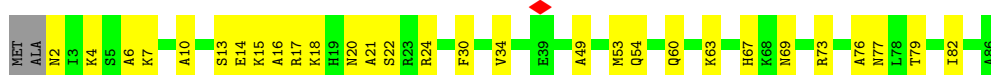
- Molecule 23: 30S ribosomal protein S18



- Molecule 24: 30S ribosomal protein S19



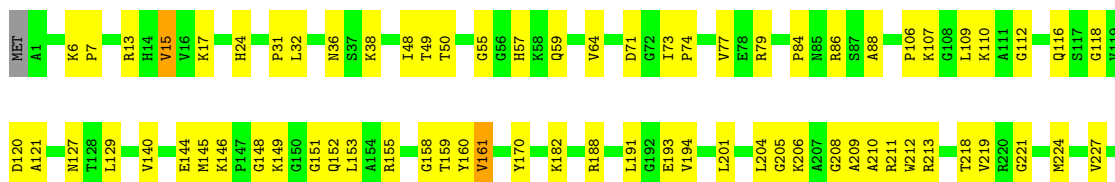
- Molecule 25: 30S ribosomal protein S20



- Molecule 26: 30S ribosomal protein S21



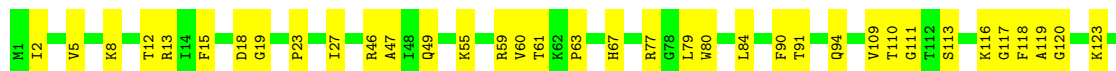
- Molecule 27: 50S ribosomal protein L2





- Molecule 28: 50S ribosomal protein L3

Chain c: 68% 32%



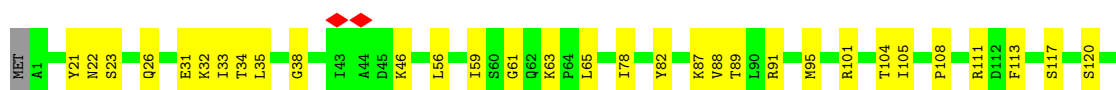
- Molecule 29: 50S ribosomal protein L4

Chain d: 65% 34%



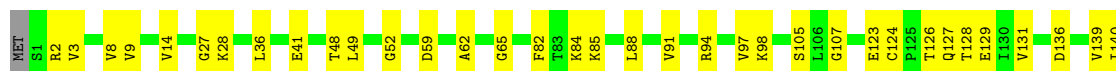
- Molecule 30: 50S ribosomal protein L5

Chain e: 72% 26%



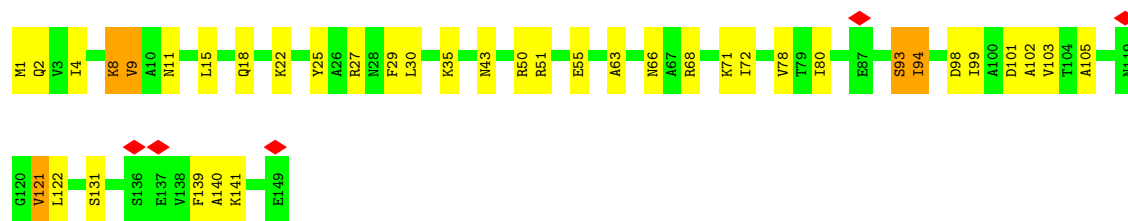
- Molecule 31: 50S ribosomal protein L6

Chain f: 78% 21%

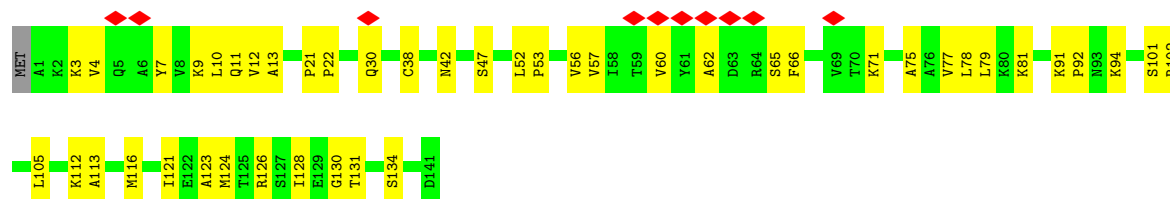


- Molecule 32: 50S ribosomal protein L9

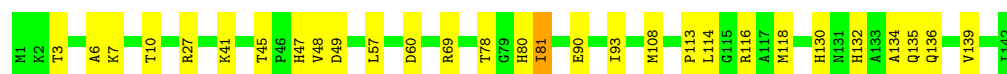
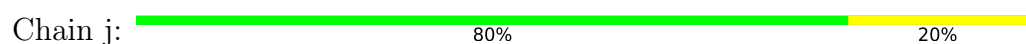
Chain g: 74% 23%



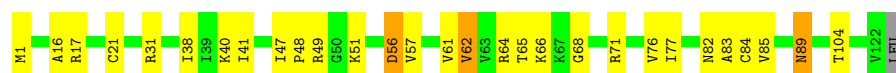
- Molecule 33: 50S ribosomal protein L11



- Molecule 34: 50S ribosomal protein L13



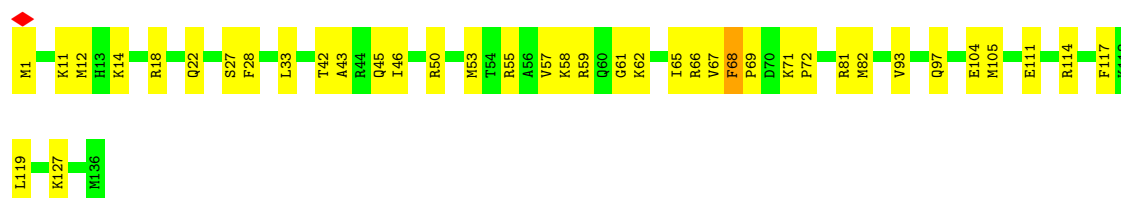
- Molecule 35: 50S ribosomal protein L14



- Molecule 36: 50S ribosomal protein L15

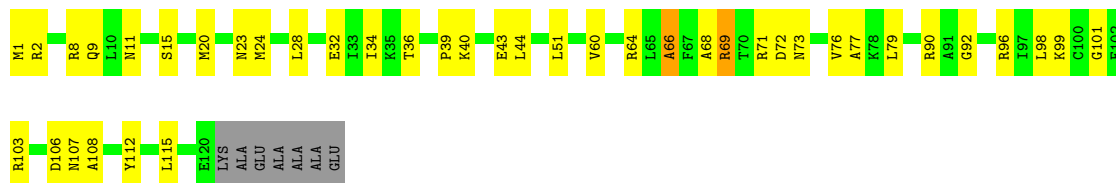


- Molecule 37: 50S ribosomal protein L16



- Molecule 38: 50S ribosomal protein L17

Chain n:  62% 31% 6%



- Molecule 39: 50S ribosomal protein L18

Chain o:  71% 28%




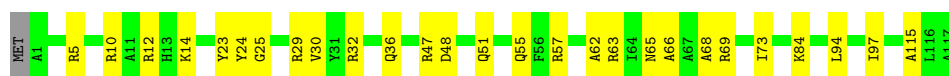
- Molecule 40: 50S ribosomal protein L19

Chain p:  76% 23%



- Molecule 41: 50S ribosomal protein L20

Chain q:  76% 23%



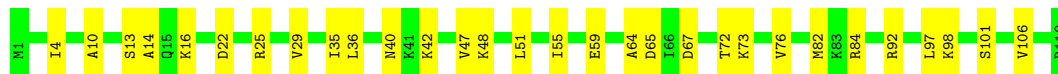
- Molecule 42: 50S ribosomal protein L21

Chain r:  71% 29%



- Molecule 43: 50S ribosomal protein L22

Chain s:  73% 27%



- Molecule 44: 50S ribosomal protein L23

Chain t:  65% 27% 7%



- Molecule 45: 50S ribosomal protein L24

Chain u: 77% 20% ..



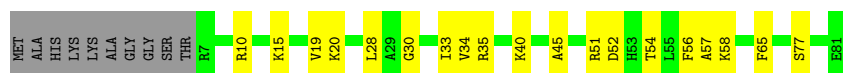
- Molecule 46: 50S ribosomal protein L25

Chain v: 78% 22%



- Molecule 47: 50S ribosomal protein L27

Chain w: 66% 22% 12%



- Molecule 48: 50S ribosomal protein L28

Chain x: 67% 29% ..



- Molecule 49: 50S ribosomal protein L29

Chain y: 78% 22%



- Molecule 50: 50S ribosomal protein L30

Chain z: 75% 24% .

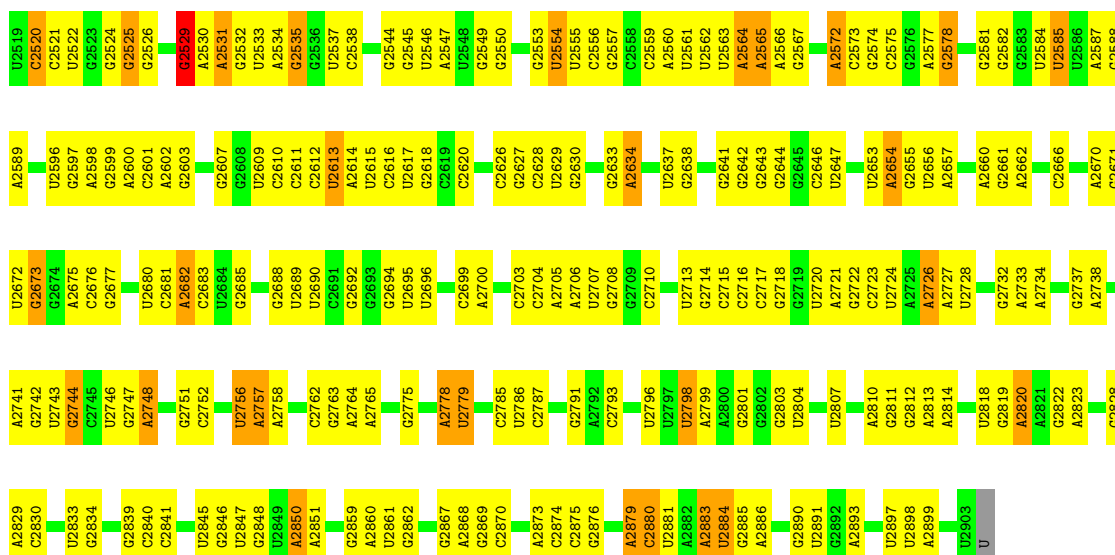


- Molecule 51: 23S rRNA

Chain 1: 44% 48% 8%

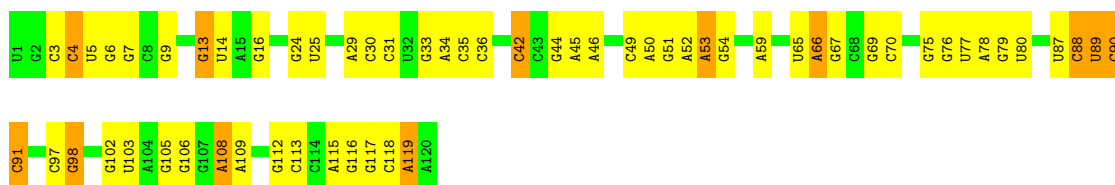
U1198	A1126	G1053	A975	A986	G818	C747	U667	A590	A513	G424	A330	G230	U154	A84	G1
A1127	A1127	A1054	G976	U887	A819	G748	C671	U593	A514	G424	C331	A231	A155	G85	G2
G1128	A1129	G1055	A980	C890	A820	A751	C674	U594	A515	U431	G338	A232	A156	U90	U3
G1205	G1130	A1056	A981	G891	A821	A752	A675	C595	A516	A432	U339	A233	C157	U158	U4
A1206	G1131	U1057	A982	C892	G822	A753	A676	U596	C517	C433	U340	U234	G159	A91	A5
U1209	U1132	G1058	A983	U895	C823	A754	A677	C597	U519	U434	C341	G242	U162	U92	G7
G1210	A1133	U1059	A984	A896	U824	U756	A678	U598	G524	U435	A342	U243	C163	G93	C8
A1134	G1135	A1060	C985	C897	A825	A755	C678	A599	U525	C436	C343	A244	U166	A94	G9
G1136	U1136	G1062	C986	U898	U827	G757	C680	C601	A526	U441	A344	G245	U167	A95	A10
G1212	G1137	G1063	C987	A899	U828	G757	C680	G600	A527	G442	C351	G246	U166	C96	C11
U1216	G1138	C1064	A988	A900	A829	G760	U683	A602	C527	G443	A352	G247	A167	U12	U12
G1236	G1139	U1065	G989	C901	G830	U764	U683	A603	A528	C444	A352	G248	U170	A13	A13
U1219	C1140	A1067	A990	C902	G831	A765	U686	G605	A532	C445	U355	G252	U171	G15	G15
G1220	U1141	G1068	C994	A910	U832	C766	C687	G605	A533	G446	U355	G253	U172	U102	
C1225	A1142	A1069	C995	A911	A833	U767	U688	A608	G533	G446	G361	G254	A173	A103	
A1226	A1143	C912	A996	C912	G834	U767	U688	A609	U534	G450	U365	A255	U174	G107	A21
C1229	A1144	U913	U999	U913	C837	G770	G690	C610	G536	U451	U366	G259	A175	G108	G22
A1230	C1145	G916	A1000	G916	C838	G771	C691	C611	G537	C455	C366	G260	A176	C109	G23
U1148	U1147	A918	C1005	A918	U839	C772	C692	G612	A538	C456	U368	G261	G177	G110	G24
G1236	U1148	G918	C1006	A918	G840	G773	U694	A613	G539	A457	U369	G266	C179	A111	U25
A1246	C1153	U923	G923	G923	U842	G774	G695	U615	G543	U458	G370	A272	G189	U112	G26
A1247	G1154	G924	G924	G924	G843	G775	G696	G697	G544	U459	A371	G273	A190	U113	G27
G1248	A1155	A845	A927	A927	A846	G776	G697	A621	G548	A460	G372	G273	A191	A118	A28
U1249	U1156	U847	A928	A928	U847	G777	G704	G622	G549	G465	G375	U276	A192	A119	U34
G1158	G1157	C848	U929	U929	U848	G778	G704	G623	C550	G466	G376	U277	U193	G120	G35
C1251	C1158	A849	U929	U929	U849	G779	G705	G624	C551	G467	G377	A278	U194	G121	G36
G1252	C1161	U850	A933	A933	U850	A782	U709	A627	U554	G469	C378	U286	A195	G122	C37
A1253	G1162	C851	A1020	A1020	G851	A783	G710	A631	G555	A470	C379	U287	A196	G123	A38
U1254	C1162	U852	G1022	G1022	G852	G785	G711	A632	U556	A471	G380	G287	A197	G124	G39
U1255	A1169	G857	U1023	U1023	G857	G786	G712	A633	C560	A472	A382	A294	C198	A125	U40
G1256	C1170	G858	G1024	G1024	G858	G787	U714	C634	A563	C475	G386	G297	A203	A127	G43
C1257	G1171	G859	G1025	G1025	G859	C787	U715	C635	A564	A478	U387	G298	A204	A44	A44
U1258	C1172	G860	G1026	G1026	G860	A788	A716	C636	A565	A479	G388	A299	G205	A131	G45
G1259	U1173	G861	A1027	A1027	G861	A789	C717	A637	U566	A480	G389	A300	U206	G132	G46
A1262	U1174	G862	A1028	A1028	G862	A790	A718	U639	U567	G481	U390	C305	A207	U133	G51
A1265	A1175	G863	C944	C944	G863	A791	G726	U642	U568	C486	C393	U306	C209	A53	A53
G1267	G1177	G864	A945	A945	G864	A792	G727	A643	U571	C487	C394	G315	C210	U137	
A1268	C1178	G865	C946	C946	G865	A793	G728	A644	A572	C488	U395	G316	C211	U138	U62
A1269	G1179	G866	A947	A947	G866	A794	G729	U645	A573	C489	G396	A311	G212	U139	A63
U1270	U1180	G867	C948	C948	G867	A795	G730	U646	A574	G491	U397	G317	G213	C140	
C1271	G1181	G868	A949	A949	G868	A796	G731	U647	A575	G492	A402	G318	A216	A142	C66
G1271	U1182	G869	G952	G952	G869	A797	G732	U648	U576	C493	A403	G319	A217	C143	A71
A1272	U1183	G870	G953	G953	G870	A798	G733	U649	A577	C494	U404	A320	A218	A144	U72
U1273	U1184	G871	G954	G954	G871	A799	G734	A654	U578	C495	U405	A321	A219	C145	A73
G1185	G1185	U872	U955	U955	U872	C806	C736	A655	U579	C496	A406	A322	A220	A146	A74
A1275	C1186	A877	U956	U956	A877	G807	C737	A656	A580	C497	U407	A323	A221	C147	A75
A1276	U1187	A878	A959	A959	A878	G808	G738	A657	A581	C498	U408	A324	A222	U224	G76
G1277	G1188	A879	A960	A960	A879	A799	A739	A658	A582	C499	U409	A325	A223	C225	C77
C1278	U1191	G880	C961	C961	G880	U811	U741	U658	G583	C500	A409	G326	A224	A149	G77
G1279	G1192	G881	G971	G971	G881	U812	A742	G663	A586	C501	U410	G327	A225	U150	U78
A1287	C1193	C812	A972	A972	C812	U813	A743	G664	C587	C502	U411	U328	A226	C151	G79
G1288	U1196	U883	A973	A973	U883	C814	U744	U665	U588	C503	U412	U329	A227	A152	G80
C1289	G1197	C815	G974	G974	C815	U814	U745	U666	U589	C504	U413	G329	A228	U153	G81





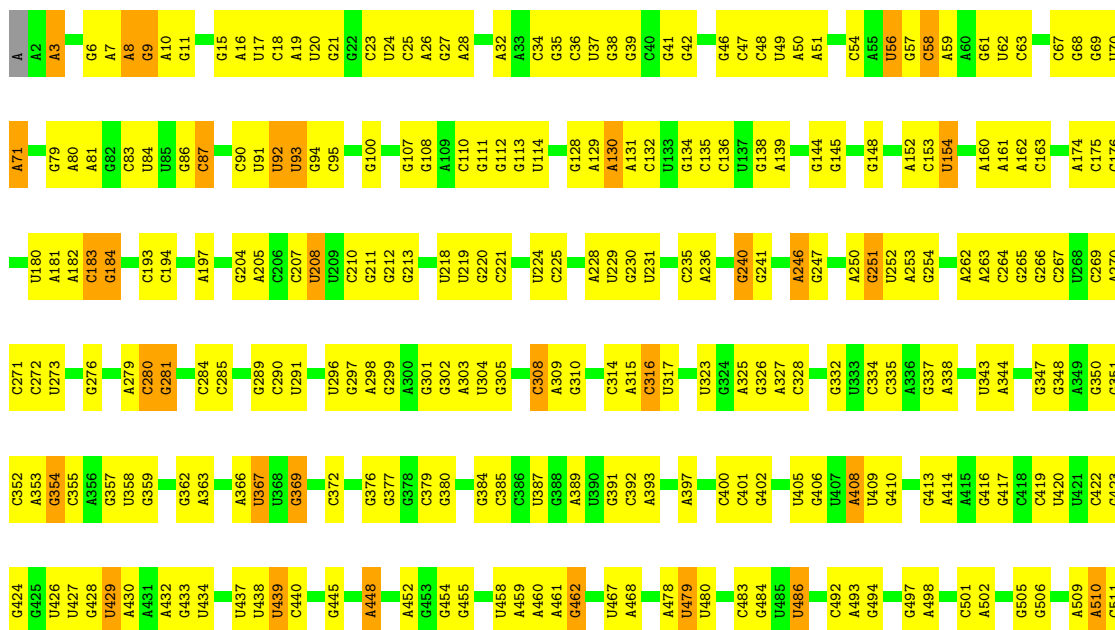
### • Molecule 52: 5S rRNA

Chain 2: 50% 40% 10%

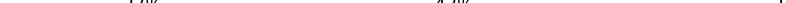


### • Molecule 53: 16S rRNA

Chain 3: 45% 49% 6%



U512	C513	U514	C515	U516	C517	U518	C519	U520	C521	U522	C523	U524	C525	U526	C527	U528	C529	U530	C531	U532	C533	U534	C535	U536	C537	U538	C539	U540	C541	U542	C543	U544	C545	U546	C547	U548	C549	U550	C551	U552	C553	U554	C555	U556	C557	U558	C559	U560	C561	U562	C563	U564	C565	U566	C567	U568	C569	U570	C571	U572	C573	U574	C575	U576	C577	U578	C579	U580	C581	U582	C583	U584	C585	U586	C587	U588	C589	U590	C591	U592	C593	U594	C595	U596	C597	U598	C599	U600	C601	U602	C603	U604	C605	U606	C607	U608	C609	U610	C611	U612	C613	U614	C615	U616	C617	U618	C619	U620	C621	U622	C623	U624	C625	U626	C627	U628	C629	U630	C631	U632	C633	U634	C635	U636	C637	U638	C639	U640	C641	U642	C643	U644	C645	U646	C647	U648	C649	U650	C651	U652	C653	U654	C655	U656	C657	U658	C659	U660	C661	U662	C663	U664	C665	U666	C667	U668	C669	U670	C671	U672	C673	U674	C675	U676	C677	U678	C679	U680	C681	U682	C683	U684	C685	U686	C687	U688	C689	U690	C691	U692	C693	U694	C695	U696	C697	U698	C699	U700	C701	U702	C703	U704	C705	U706	C707	U708	C709	U710	C711	U712	C713	U714	C715	U716	C717	U718	C719	U720	C721	U722	C723	U724	C725	U726	C727	U728	C729	U730	C731	U732	C733	U734	C735	U736	C737	U738	C739	U740	C741	U742	C743	U744	C745	U746	C747	U748	C749	U750	C751	U752	C753	U754	C755	U756	C757	U758	C759	U760	C761	U762	C763	U764	C765	U766	C767	U768	C769	U770	C771	U772	C773	U774	C775	U776	C777	U778	C779	U780	C781	U782	C783	U784	C785	U786	C787	U788	C789	U790	C791	U792	C793	U794	C795	U796	C797	U798	C799	U800	C801	U802	C803	U804	C805	U806	C807	U808	C809	U810	C811	U812	C813	U814	C815	U816	C817	U818	C819	U820	C821	U822	C823	U824	C825	U826	C827	U828	C829	U830	C831	U832	C833	U834	C835	U836	C837	U838	C839	U840	C841	U842	C843	U844	C845	U846	C847	U848	C849	U850	C851	U852	C853	U854	C855	U856	C857	U858	C859	U860	C861	U862	C863	U864	C865	U866	C867	U868	C869	U870	C871	U872	C873	U874	C875	U876	C877	U878	C879	U880	C881	U882	C883	U884	C885	U886	C887	U888	C889	U890	C891	U892	C893	U894	C895	U896	C897	U898	C899	U900	C901	U902	C903	U904	C905	U906	C907	U908	C909	U910	C911	U912	C913	U914	C915	U916	C917	U918	C919	U920	C921	U922	C923	U924	C925	U926	C927	U928	C929	U930	C931	U932	C933	U934	C935	U936	C937	U938	C939	U940	C941	U942	C943	U944	C945	U946	C947	U948	C949	U950	C951	U952	C953	U954	C955	U956	C957	U958	C959	U960	C961	U962	C963	U964	C965	U966	C967	U968	C969	U970	C971	U972	C973	U974	C975	U976	C977	U978	C979	U980	C981	U982	C983	U984	C985	U986	C987	U988	C989	U990	C991	U992	C993	U994	C995	U996	C997	U998	C999	U1000	C1001	U1002	C1003	U1004	C1005	U1006	C1007	U1008	C1009	U1010	C1011	U1012	C1013	U1014	C1015	U1016	C1017	U1018	C1019	U1020	C1021	U1022	C1023	U1024	C1025	U1026	C1027	U1028	C1029	U1030	C1031	U1032	C1033	U1034	C1035	U1036	C1037	U1038	C1039	U1040	C1041	U1042	C1043	U1044	C1045	U1046	C1047	U1048	C1049	U1050	C1051	U1052	C1053	U1054	C1055	U1056	C1057	U1058	C1059	U1060	C1061	U1062	C1063	U1064	C1065	U1066	C1067	U1068	C1069	U1070	C1071	U1072	C1073	U1074	C1075	U1076	C1077	U1078	C1079	U1080	C1081	U1082	C1083	U1084	C1085	U1086	C1087	U1088	C1089	U1090	C1091	U1092	C1093	U1094	C1095	U1096	C1097	U1098	C1099	U1100	C1101	U1102	C1103	U1104	C1105	U1106	C1107	U1108	C1109	U1110	C1111	U1112	C1113	U1114	C1115	U1116	C1117	U1118	C1119	U1120	C1121	U1122	C1123	U1124	C1125	U1126	C1127	U1128	C1129	U1130	C1131	U1132	C1133	U1134	C1135	U1136	C1137	U1138	C1139	U1140	C1141	U1142	C1143	U1144	C1145	U1146	C1147	U1148	C1149	U1150	C1151	U1152	C1153	U1154	C1155	U1156	C1157	U1158	C1159	U1160	C1161	U1162	U1168	C1169	U1170	C1171	U1172	C1173	U1174	C1175	U1176	C1177	U1178	C1179	U1180	C1181	U1182	C1183	U1184	C1185	U1186	C1187	U1188	C1189	U1190	C1191	U1192	C1193	U1194	C1195	U1196	C1197	U1198	C1199	U1200	C1201	U1202	C1203	U1204	C1205	U1206	C1207	U1208	C1209	U1210	C1211	U1212	C1213	U1214	C1215	U1216	C1217	U1218	C1219	U1220	C1221	U1222	C1223	U1224	C1225	U1226	C1227	U1228	C1229	U1230	C1231	U1232	C1233	U1234	C1235	U1236	C1237	U1238	C1239	U1240	C1241	U1242	C1243	U1244	C1245	U1246	C1247	U1248	C1249	U1250	C1251	U1252	C1253	U1254	C1255	U1256	C1257	U1258	C1259	U1260	C1261	U1262	C1263	U1264	C1265	U1266	C1267	U1268	C1269	U1270	C1271	U1272	C1273	U1274	C1275	U1276	C1277	U1278	C1279	U1280	C1281	U1282	C1283	U1284	C1285	U1286	C1287	U1288	C1289	U1290	C1291	U1292	C1293	U1294	C1295	U1296	C1297	U1298	C1299	U1300	C1301	U1302	C1303	U1304	C1305	U1306	C1307	U1308	C1309	U1310	C1311	U1312	C1313	U1314	C1315	U1316	C1317	U1318	C1319	U1320	C1321	U1322	C1323	U1324	C1325	U1326	C1327	U1328	C1329	U1330	C1331	U1332	C1333	U1334	C1335	U1336	C1337	U1338	C1339	U1340	C1341	U1342	C1343	U1344	C1345	U1346	C1347	U1348	C1349	U1350	C1351	U1352	C1353	U1354	C1355	U1356	C1357	U1358	C1359	U1360	C1361	U1362	C1363	U1364	C1365	U1366	C1367	U1368	C1369	U1370	C1371	U1372	C1373	U1374	C1375	U1376	C1377	U1378	C1379	U1380	C1381	U1382	C1383	U1384	C1385	U1386	C1387	U1388	C1389	U1390	C1391	U1392	C1393	U1394	C1395	U1396	C1397	U1398	C1399	U1400	C1401	U1402	C1403	U1404	C1405	U1406	C1407	U1408	C1409	U1410	C1411	U1412	C1413	U1414	C1415	U1416	C1417	U1418	C1419	U1420	C1421	U1422	C1423	U1424	C1425	U1426	C1427	U1428	C1429	U1430	C143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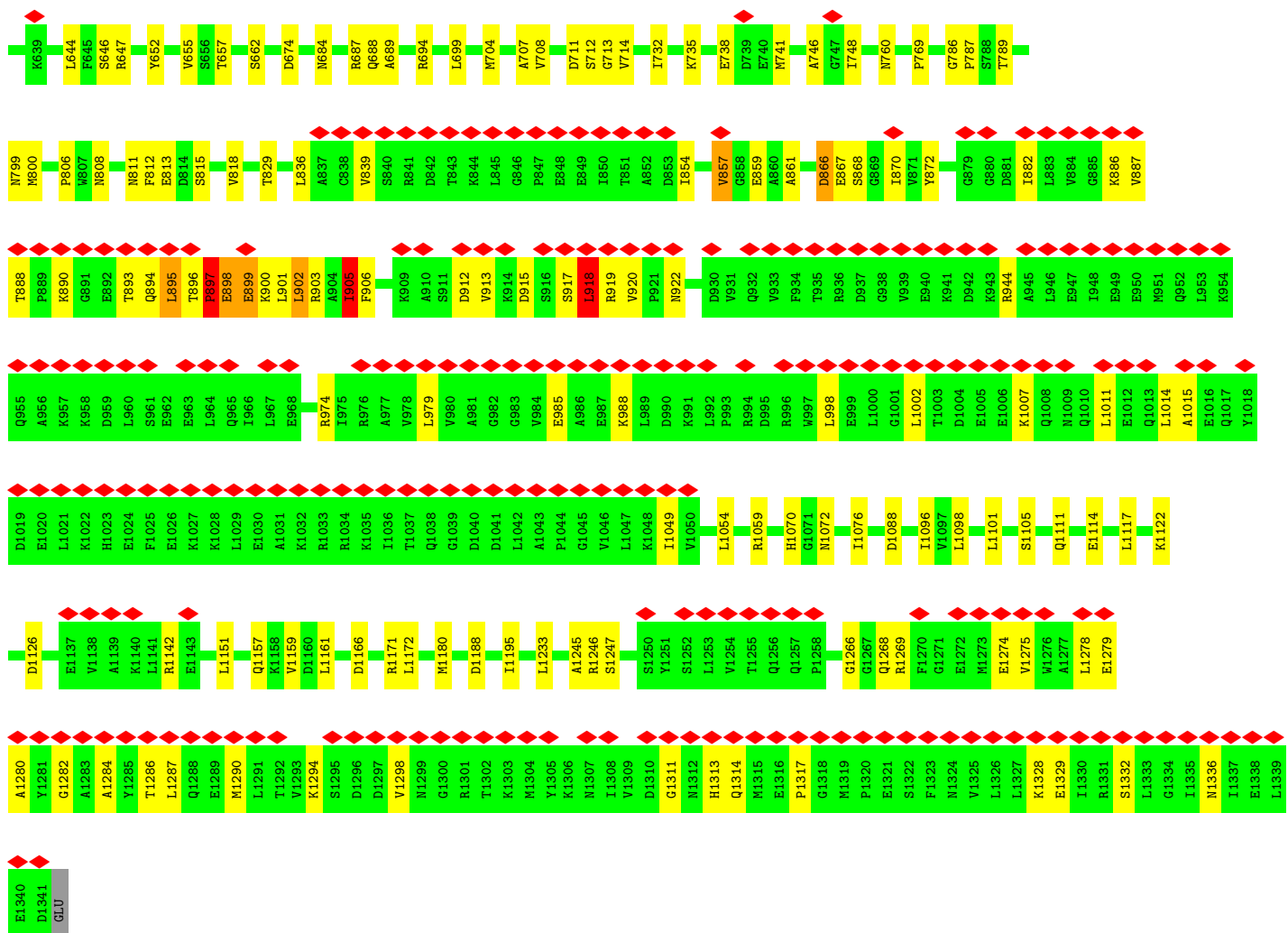
- Chain 8: 



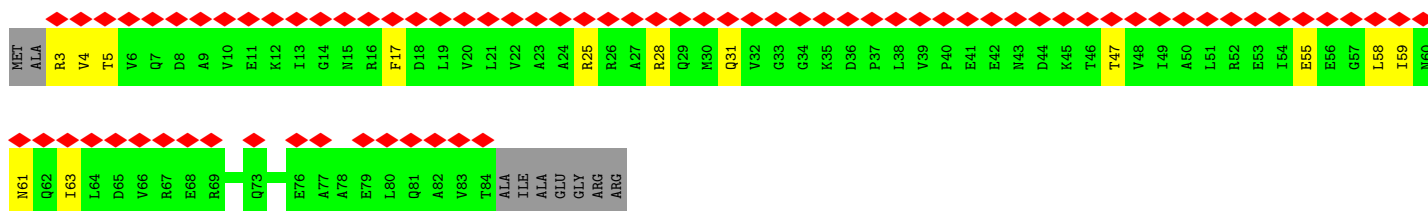
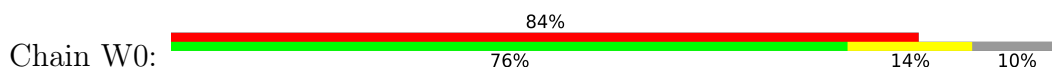
Chain B1:



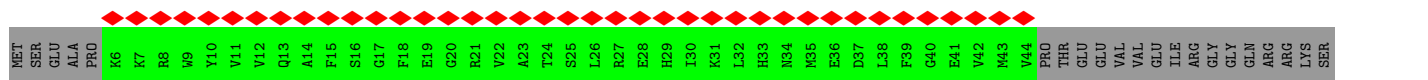


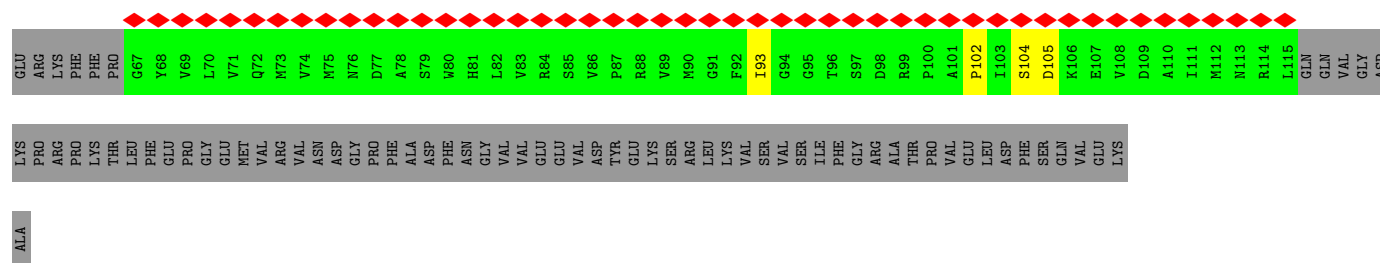


- Molecule 60: DNA-directed RNA polymerase subunit omega

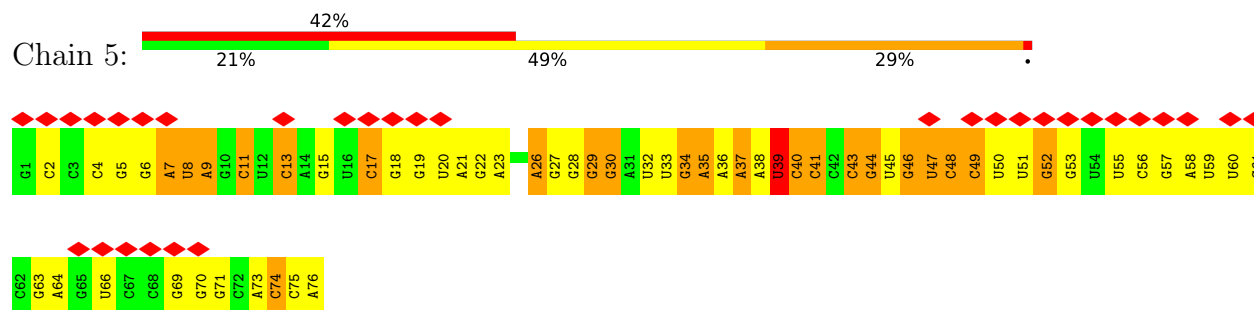


- Molecule 61: Transcription termination/antitermination protein NusG

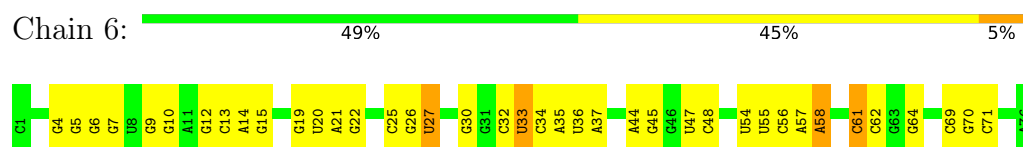




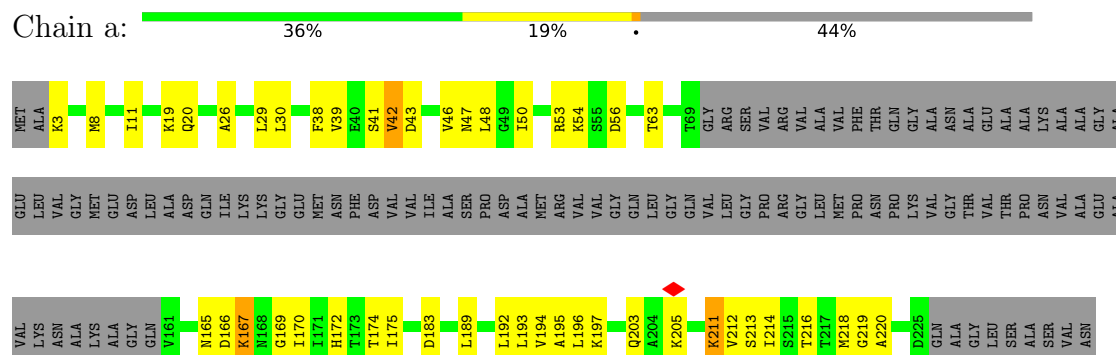
### • Molecule 62: tRNA(Phe)



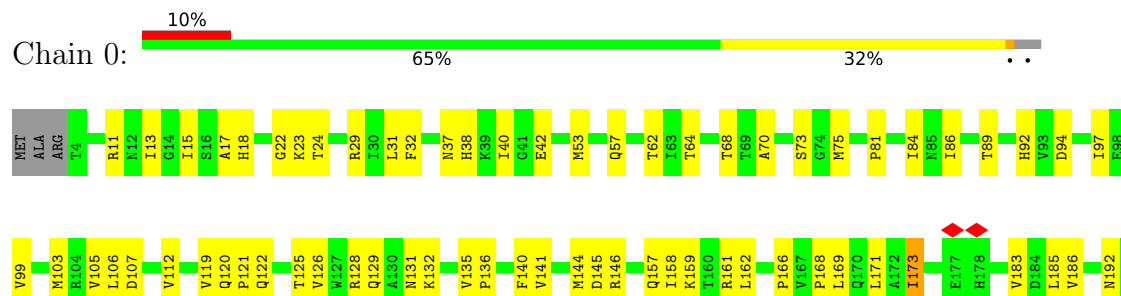
### • Molecule 63: tRNA(fMet)

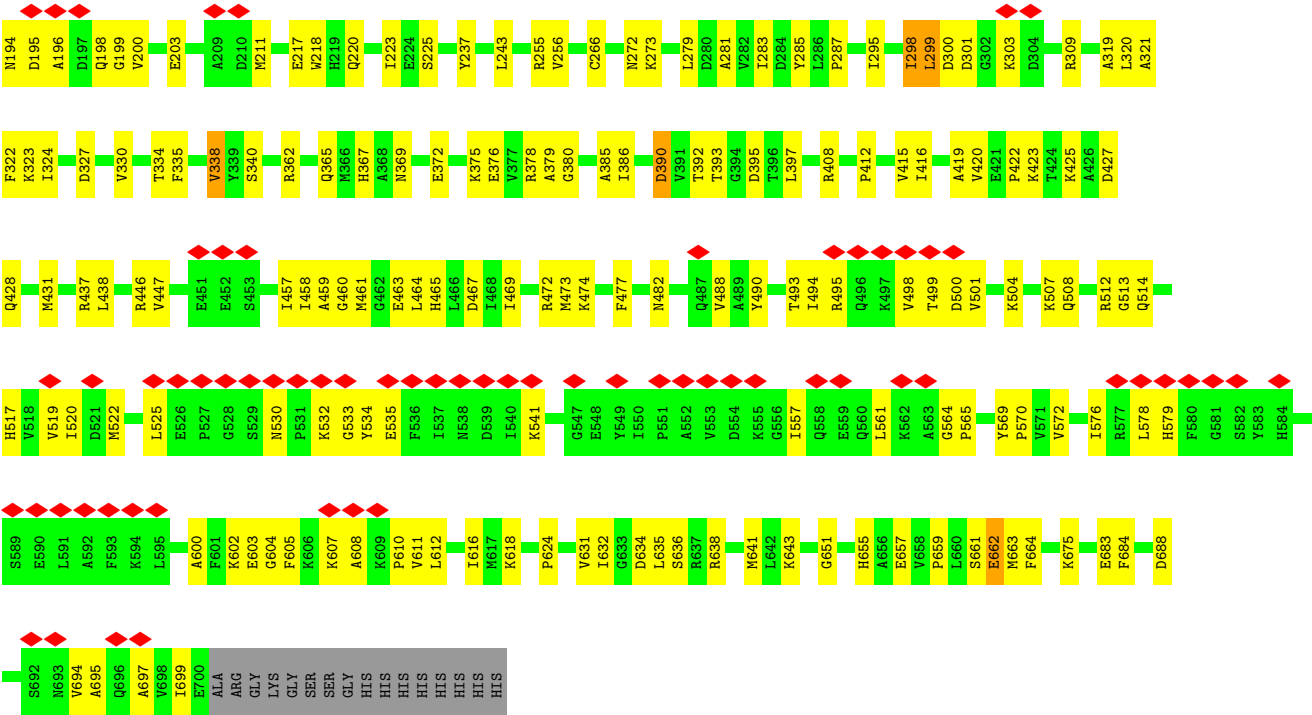


### • Molecule 64: Large ribosomal subunit protein uL1



### • Molecule 65: Elongation factor G





● Molecule 66: Viomycin



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35002	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	47	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.088	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.006	Depositor
Map size ( $\text{\AA}$ )	753.60004, 753.60004, 753.60004	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.57, 1.57, 1.57	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: UAL, 5OH, DPP, GDP, PO4, KBE

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	A	0.25	0/362	0.72	0/485
2	B	0.37	0/450	0.80	2/599 (0.3%)
3	C	0.32	0/416	0.61	0/554
4	D	0.47	0/380	0.95	0/498
5	E	0.46	0/513	0.80	0/676
6	F	0.41	0/303	0.79	0/397
7	G	0.39	0/1735	0.83	0/2338
8	H	0.47	0/1651	0.83	0/2225
9	I	0.32	0/1659	0.77	1/2220 (0.0%)
10	J	0.47	0/1169	0.81	0/1573
11	K	0.44	0/835	0.86	0/1128
12	L	0.41	0/1195	0.82	2/1602 (0.1%)
13	M	0.31	0/989	0.75	0/1326
14	N	0.29	0/1034	0.74	0/1375
15	O	0.59	0/796	0.86	0/1077
16	P	0.42	0/885	0.76	0/1195
17	Q	0.43	0/969	0.80	0/1300
18	R	0.29	0/892	0.68	0/1193
19	S	0.28	0/817	0.68	1/1088 (0.1%)
20	T	0.37	0/722	0.74	0/964
21	U	0.30	0/659	0.64	0/884
22	V	0.33	0/657	0.72	0/881
23	W	0.28	0/544	0.69	0/731
24	X	0.28	0/652	0.64	0/877
25	Y	0.26	0/671	0.64	2/888 (0.2%)
26	Z	0.56	0/550	1.09	1/728 (0.1%)
27	b	0.49	0/2121	0.82	0/2852
28	c	0.45	0/1586	0.77	0/2134
29	d	0.40	0/1571	0.80	3/2113 (0.1%)
30	e	0.30	0/1434	0.66	0/1926
31	f	0.29	0/1343	0.61	0/1816
32	g	0.34	0/1122	0.77	3/1515 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	i	0.39	0/1046	0.80	1/1410 (0.1%)
34	j	0.46	0/1152	0.72	0/1551
35	k	0.42	0/947	0.91	1/1268 (0.1%)
36	l	0.41	0/1054	0.80	2/1403 (0.1%)
37	m	0.40	0/1093	0.81	2/1460 (0.1%)
38	n	0.54	1/973 (0.1%)	0.87	0/1301
39	o	0.32	0/902	0.68	0/1209
40	p	0.39	0/929	0.72	2/1242 (0.2%)
41	q	0.43	0/960	0.72	0/1278
42	r	0.38	0/829	0.78	1/1107 (0.1%)
43	s	0.52	0/864	0.83	0/1156
44	t	0.48	0/744	0.81	1/994 (0.1%)
45	u	0.33	0/787	0.74	2/1051 (0.2%)
46	v	0.35	0/766	0.66	0/1025
47	w	0.40	0/582	0.80	2/769 (0.3%)
48	x	0.62	0/635	1.16	5/848 (0.6%)
49	y	0.28	0/510	0.71	0/677
50	z	0.36	0/453	0.76	1/605 (0.2%)
51	1	0.59	0/69796	0.60	17/108888 (0.0%)
52	2	0.60	0/2872	0.55	1/4479 (0.0%)
53	3	0.60	0/36963	0.57	5/57662 (0.0%)
54	4	0.57	0/519	0.69	0/804
55	8	0.56	0/599	0.71	1/919 (0.1%)
56	9	0.48	0/468	0.53	0/719
57	A1	0.48	0/1696	0.69	0/2298
57	A2	0.47	0/1718	0.67	0/2328
58	B1	0.56	4/10510 (0.0%)	0.74	8/14196 (0.1%)
59	B2	0.46	0/10714	0.68	2/14459 (0.0%)
60	W0	0.30	0/652	0.61	0/879
61	NG	0.56	0/431	0.79	0/596
62	5	0.58	0/1812	0.90	3/2823 (0.1%)
63	6	0.59	0/1832	0.59	0/2855
64	a	0.49	0/1020	0.81	0/1370
65	0	0.39	0/5501	0.72	3/7446 (0.0%)
66	h	3.21	2/11 (18.2%)	0.75	0/13
All	All	0.53	7/193022 (0.0%)	0.66	75/284246 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
8	H	0	1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	h	3	SER	CA-C	-6.76	1.38	1.52
66	h	4	SER	CA-C	-6.29	1.39	1.52
38	n	66	ALA	CA-C	-5.95	1.44	1.52
58	B1	1350	ASN	CG-ND2	-5.26	1.22	1.33
58	B1	424	ASN	CG-ND2	-5.18	1.22	1.33

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	92	PRO	N-CA-C	-10.49	98.47	113.47
51	1	1020	A	C2'-C3'-O3'	7.36	120.54	109.50
48	x	11	PRO	N-CA-C	-7.33	99.53	111.77
51	1	2425	A	O3'-P-O5'	-6.94	93.58	104.00
12	L	82	SER	N-CA-C	6.90	116.42	108.49

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	H	71	ARG	Sidechain

## 5.2 Too-close contacts [i](#)

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	A	355	0	353	10	0
2	B	444	0	461	15	0
3	C	409	0	440	19	0
4	D	377	0	418	17	0
5	E	504	0	574	15	0
6	F	302	0	341	14	0
7	G	1704	0	1732	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	1624	0	1699	55	0
9	I	1637	0	1699	48	0
10	J	1156	0	1199	40	0
11	K	817	0	808	23	0
12	L	1181	0	1240	43	0
13	M	979	0	1034	32	0
14	N	1022	0	1070	56	0
15	O	786	0	828	33	0
16	P	869	0	878	27	0
17	Q	955	0	1019	32	0
18	R	883	0	944	25	0
19	S	805	0	847	34	0
20	T	714	0	737	17	0
21	U	649	0	666	21	0
22	V	648	0	691	17	0
23	W	535	0	552	16	0
24	X	637	0	665	17	0
25	Y	665	0	714	21	0
26	Z	544	0	579	15	0
27	b	2082	0	2157	72	0
28	c	1565	0	1616	55	0
29	d	1552	0	1619	51	0
30	e	1410	0	1447	40	0
31	f	1323	0	1374	31	0
32	g	1111	0	1148	28	0
33	i	1032	0	1088	35	0
34	j	1129	0	1162	30	0
35	k	938	0	1012	22	0
36	l	1045	0	1117	29	0
37	m	1074	0	1157	29	0
38	n	960	0	1000	35	0
39	o	892	0	923	21	0
40	p	917	0	965	24	0
41	q	947	0	1022	24	0
42	r	816	0	839	22	0
43	s	857	0	922	18	0
44	t	738	0	807	15	0
45	u	779	0	834	18	0
46	v	753	0	780	14	0
47	w	575	0	592	20	0
48	x	625	0	655	22	0
49	y	509	0	543	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	z	449	0	491	10	0
51	1	62317	0	31346	1367	0
52	2	2568	0	1303	59	0
53	3	33012	0	16618	727	0
54	4	467	0	234	5	0
55	8	539	0	305	28	0
56	9	417	0	224	1	0
57	A1	1677	0	1713	27	0
57	A2	1698	0	1718	17	0
58	B1	10353	0	10548	321	0
59	B2	10546	0	10550	173	0
60	W0	650	0	658	10	0
61	NG	433	0	193	8	0
62	5	1622	0	821	28	0
63	6	1640	0	837	28	0
64	a	1013	0	1081	38	0
65	0	5399	0	5363	151	0
66	h	48	0	40	8	0
67	0	28	0	12	1	0
68	0	5	0	0	0	0
All	All	179711	0	131022	3773	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 3773 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)
12:L:92:PRO:HA	12:L:95:ARG:HE	1.12	1.12
51:1:1060:U:H4'	51:1:1061:U:H5'	1.32	1.11
53:3:112:G:H21	53:3:354:G:H5'	1.16	1.10
51:1:2061:G:H2'	51:1:2501:C:O2'	1.52	1.09
50:z:37:ARG:HH12	51:1:929:U:H5'	1.12	1.06

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	A	44/70 (63%)	38 (86%)	6 (14%)	0	100	100
2	B	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
3	C	48/55 (87%)	37 (77%)	11 (23%)	0	100	100
4	D	44/46 (96%)	35 (80%)	9 (20%)	0	100	100
5	E	62/65 (95%)	48 (77%)	13 (21%)	1 (2%)	8	37
6	F	36/38 (95%)	29 (81%)	7 (19%)	0	100	100
7	G	216/241 (90%)	182 (84%)	34 (16%)	0	100	100
8	H	204/233 (88%)	186 (91%)	18 (9%)	0	100	100
9	I	203/206 (98%)	171 (84%)	31 (15%)	1 (0%)	25	64
10	J	155/167 (93%)	129 (83%)	26 (17%)	0	100	100
11	K	98/135 (73%)	81 (83%)	17 (17%)	0	100	100
12	L	149/179 (83%)	130 (87%)	19 (13%)	0	100	100
13	M	127/130 (98%)	110 (87%)	17 (13%)	0	100	100
14	N	125/130 (96%)	110 (88%)	15 (12%)	0	100	100
15	O	96/103 (93%)	81 (84%)	15 (16%)	0	100	100
16	P	114/129 (88%)	104 (91%)	10 (9%)	0	100	100
17	Q	121/124 (98%)	97 (80%)	23 (19%)	1 (1%)	16	54
18	R	112/118 (95%)	99 (88%)	13 (12%)	0	100	100
19	S	98/101 (97%)	86 (88%)	12 (12%)	0	100	100
20	T	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
21	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
22	V	78/84 (93%)	69 (88%)	9 (12%)	0	100	100
23	W	63/75 (84%)	59 (94%)	4 (6%)	0	100	100
24	X	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
25	Y	83/87 (95%)	77 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	Z	63/71 (89%)	47 (75%)	16 (25%)	0	100	100
27	b	269/273 (98%)	227 (84%)	42 (16%)	0	100	100
28	c	207/209 (99%)	177 (86%)	30 (14%)	0	100	100
29	d	199/201 (99%)	182 (92%)	17 (8%)	0	100	100
30	e	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
31	f	174/177 (98%)	157 (90%)	17 (10%)	0	100	100
32	g	147/149 (99%)	124 (84%)	23 (16%)	0	100	100
33	i	139/142 (98%)	124 (89%)	15 (11%)	0	100	100
34	j	140/142 (99%)	120 (86%)	20 (14%)	0	100	100
35	k	120/123 (98%)	98 (82%)	22 (18%)	0	100	100
36	l	141/144 (98%)	117 (83%)	24 (17%)	0	100	100
37	m	134/136 (98%)	116 (87%)	18 (13%)	0	100	100
38	n	118/127 (93%)	104 (88%)	14 (12%)	0	100	100
39	o	114/117 (97%)	103 (90%)	11 (10%)	0	100	100
40	p	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
41	q	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
42	r	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
43	s	108/110 (98%)	92 (85%)	16 (15%)	0	100	100
44	t	91/100 (91%)	77 (85%)	14 (15%)	0	100	100
45	u	100/104 (96%)	83 (83%)	17 (17%)	0	100	100
46	v	92/94 (98%)	79 (86%)	13 (14%)	0	100	100
47	w	73/85 (86%)	63 (86%)	10 (14%)	0	100	100
48	x	75/78 (96%)	66 (88%)	9 (12%)	0	100	100
49	y	61/63 (97%)	61 (100%)	0	0	100	100
50	z	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
57	A1	214/329 (65%)	195 (91%)	19 (9%)	0	100	100
57	A2	217/329 (66%)	207 (95%)	10 (5%)	0	100	100
58	B1	1329/1407 (94%)	1205 (91%)	120 (9%)	4 (0%)	37	72
59	B2	1338/1342 (100%)	1206 (90%)	126 (9%)	6 (0%)	30	68
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NG	84/181 (46%)	77 (92%)	6 (7%)	1 (1%)	11	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	a	128/234 (55%)	105 (82%)	23 (18%)	0	100	100
65	0	695/716 (97%)	618 (89%)	72 (10%)	5 (1%)	19	56
66	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	9784/10690 (92%)	8648 (88%)	1117 (11%)	19 (0%)	45	78

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
58	B1	121	PRO
59	B2	897	PRO
59	B2	43	PRO
59	B2	918	LEU
61	NG	102	PRO

### 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	A	42/62 (68%)	42 (100%)	0	100	100
2	B	47/48 (98%)	47 (100%)	0	100	100
3	C	45/49 (92%)	44 (98%)	1 (2%)	47	65
4	D	38/38 (100%)	35 (92%)	3 (8%)	10	29
5	E	51/52 (98%)	46 (90%)	5 (10%)	6	22
6	F	34/34 (100%)	33 (97%)	1 (3%)	37	58
7	G	180/199 (90%)	172 (96%)	8 (4%)	24	46
8	H	170/190 (90%)	158 (93%)	12 (7%)	12	32
9	I	171/173 (99%)	166 (97%)	5 (3%)	37	58
10	J	119/126 (94%)	113 (95%)	6 (5%)	20	42
11	K	87/116 (75%)	82 (94%)	5 (6%)	17	39
12	L	124/147 (84%)	121 (98%)	3 (2%)	44	63
13	M	104/105 (99%)	102 (98%)	2 (2%)	52	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	105/107 (98%)	105 (100%)	0	100	100
15	O	86/90 (96%)	77 (90%)	9 (10%)	5	20
16	P	89/99 (90%)	88 (99%)	1 (1%)	70	80
17	Q	103/104 (99%)	101 (98%)	2 (2%)	52	69
18	R	92/96 (96%)	91 (99%)	1 (1%)	70	80
19	S	83/84 (99%)	82 (99%)	1 (1%)	67	79
20	T	76/77 (99%)	76 (100%)	0	100	100
21	U	65/65 (100%)	65 (100%)	0	100	100
22	V	74/78 (95%)	74 (100%)	0	100	100
23	W	56/65 (86%)	56 (100%)	0	100	100
24	X	70/79 (89%)	70 (100%)	0	100	100
25	Y	65/66 (98%)	65 (100%)	0	100	100
26	Z	55/61 (90%)	46 (84%)	9 (16%)	2	11
27	b	216/218 (99%)	212 (98%)	4 (2%)	52	69
28	c	164/164 (100%)	163 (99%)	1 (1%)	84	88
29	d	165/165 (100%)	160 (97%)	5 (3%)	36	56
30	e	148/150 (99%)	146 (99%)	2 (1%)	62	75
31	f	137/138 (99%)	136 (99%)	1 (1%)	81	87
32	g	114/114 (100%)	111 (97%)	3 (3%)	41	61
33	i	109/110 (99%)	109 (100%)	0	100	100
34	j	116/116 (100%)	113 (97%)	3 (3%)	41	61
35	k	103/104 (99%)	100 (97%)	3 (3%)	37	58
36	l	102/103 (99%)	100 (98%)	2 (2%)	50	68
37	m	109/109 (100%)	108 (99%)	1 (1%)	75	83
38	n	100/103 (97%)	98 (98%)	2 (2%)	50	68
39	o	86/87 (99%)	86 (100%)	0	100	100
40	p	99/100 (99%)	99 (100%)	0	100	100
41	q	89/90 (99%)	89 (100%)	0	100	100
42	r	84/84 (100%)	84 (100%)	0	100	100
43	s	93/93 (100%)	87 (94%)	6 (6%)	14	35
44	t	80/84 (95%)	77 (96%)	3 (4%)	28	50

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	u	83/85 (98%)	82 (99%)	1 (1%)	67	79
46	v	78/78 (100%)	77 (99%)	1 (1%)	65	77
47	w	57/63 (90%)	57 (100%)	0	100	100
48	x	67/68 (98%)	65 (97%)	2 (3%)	36	56
49	y	55/55 (100%)	55 (100%)	0	100	100
50	z	48/49 (98%)	47 (98%)	1 (2%)	48	67
57	A1	185/286 (65%)	174 (94%)	11 (6%)	16	38
57	A2	186/286 (65%)	182 (98%)	4 (2%)	47	65
58	B1	1110/1168 (95%)	1020 (92%)	90 (8%)	9	29
59	B2	1150/1157 (99%)	1115 (97%)	35 (3%)	36	56
60	W0	70/75 (93%)	68 (97%)	2 (3%)	37	58
64	a	109/181 (60%)	98 (90%)	11 (10%)	6	21
65	0	574/588 (98%)	554 (96%)	20 (4%)	31	52
66	h	2/2 (100%)	2 (100%)	0	100	100
All	All	8119/8683 (94%)	7831 (96%)	288 (4%)	33	52

5 of 288 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	B2	615	VAL
65	0	662	GLU
59	B2	895	LEU
64	a	165	ASN
36	l	85	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 157 such sidechains are listed below:

Mol	Chain	Res	Type
58	B1	196	GLN
64	a	172	HIS
58	B1	469	HIS
59	B2	554	HIS
65	0	276	GLN

### 5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	439 (15%)	6 (0%)
52	2	119/120 (99%)	18 (15%)	0
53	3	1538/1542 (99%)	193 (12%)	1 (0%)
54	4	20/38 (52%)	9 (45%)	1 (5%)
62	5	75/76 (98%)	45 (60%)	10 (13%)
63	6	76/77 (98%)	14 (18%)	0
All	All	4730/4757 (99%)	718 (15%)	18 (0%)

5 of 718 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	1	10	A
51	1	12	U
51	1	23	G
51	1	34	U
51	1	35	G

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
62	5	57	G
62	5	75	C
62	5	73	A
62	5	7	A
62	5	48	C

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

4 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
66	KBE	h	1	66	8,8,9	0.62	0	7,8,10	1.21	1 (14%)
66	DPP	h	2	66	3,5,6	0.57	0	1,5,7	0.07	0
66	UAL	h	5	66	7,8,9	2.28	3 (42%)	5,9,11	2.90	2 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
66	5OH	h	6	66	8,12,13	0.80	0	3,16,18	1.52	1 (33%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
66	KBE	h	1	66	-	0/7/7/8	-
66	DPP	h	2	66	-	0/2/4/6	-
66	UAL	h	5	66	-	0/3/7/9	-
66	5OH	h	6	66	-	0/2/18/20	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	h	5	UAL	C1-N1	-4.80	1.32	1.40
66	h	5	UAL	C-CA	-2.86	1.40	1.45
66	h	5	UAL	CA-N	2.05	1.40	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
66	h	5	UAL	CA-CB-N1	-5.28	115.64	125.60
66	h	5	UAL	O-C-CA	-3.24	121.27	125.39
66	h	6	5OH	CR-CB-CA	-2.39	110.03	112.61
66	h	1	KBE	CB-CA-C	-2.08	109.20	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	h	2	DPP	2	0
66	h	5	UAL	2	0
66	h	6	5OH	5	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 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	$\# Z  > 2$
67	GDP	0	801	-	24,30,30	0.96	1 (4%)	30,47,47	1.34	4 (13%)
68	PO4	0	802	-	4,4,4	0.96	0	6,6,6	0.47	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
67	GDP	0	801	-	-	2/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	0	801	GDP	C6-N1	-2.64	1.33	1.37

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	0	801	GDP	PA-O3A-PB	-3.54	120.68	132.83
67	0	801	GDP	C5-C6-N1	2.53	118.43	113.95
67	0	801	GDP	C8-N7-C5	2.53	107.81	102.99
67	0	801	GDP	C3'-C2'-C1'	2.53	104.78	100.98

There are no chirality outliers.

All (2) torsion outliers are listed below:

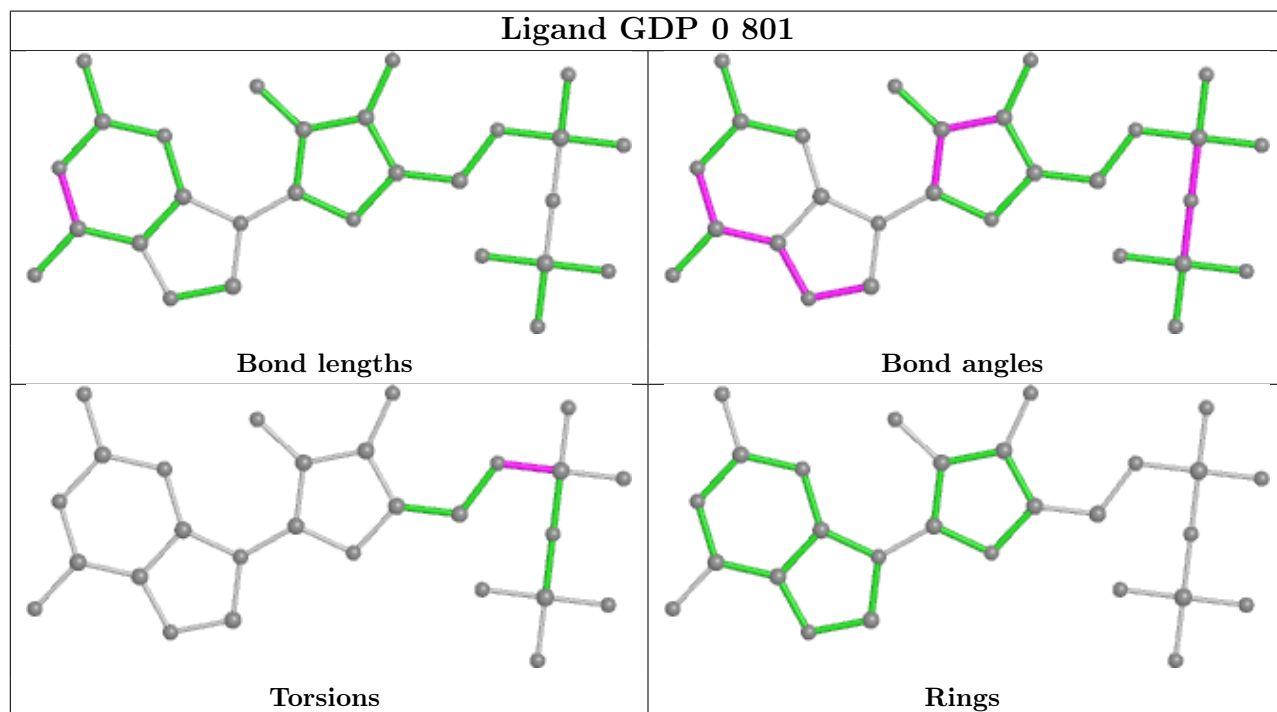
Mol	Chain	Res	Type	Atoms
67	0	801	GDP	C5'-O5'-PA-O3A
67	0	801	GDP	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
67	0	801	GDP	1	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.

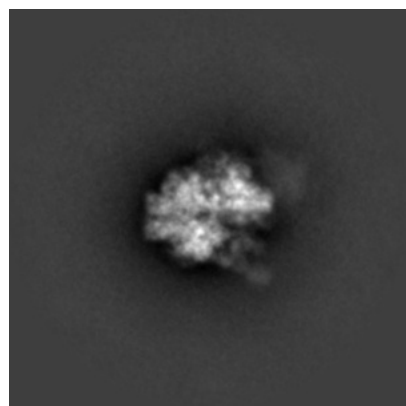
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38943. These allow visual inspection of the internal detail of the map and identification of artifacts.

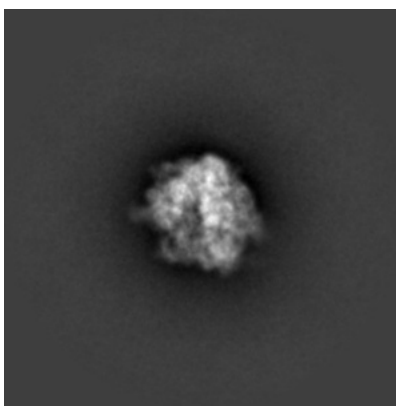
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

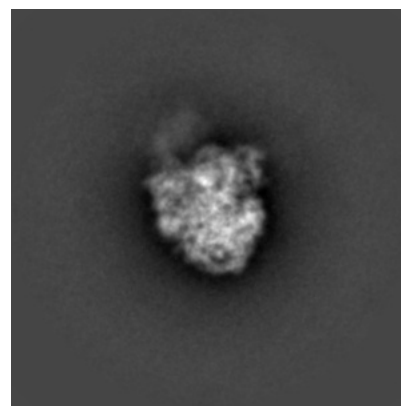
#### 6.1.1 Primary map



X

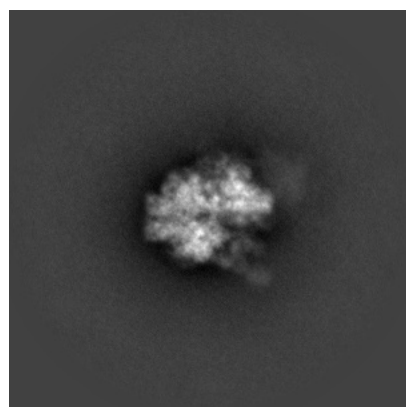


Y

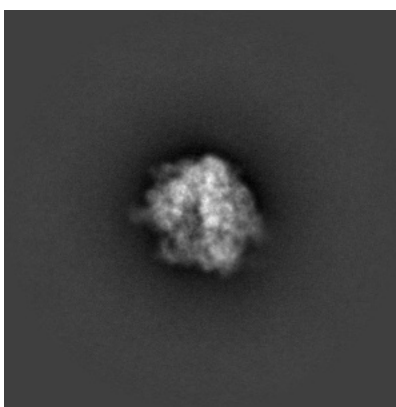


Z

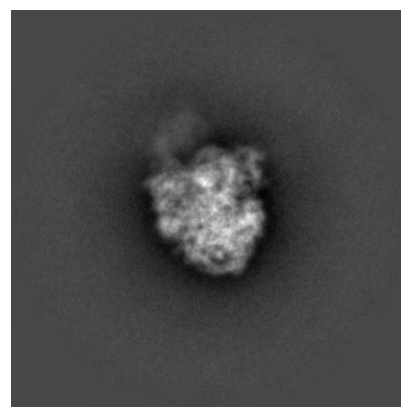
#### 6.1.2 Raw map



X



Y

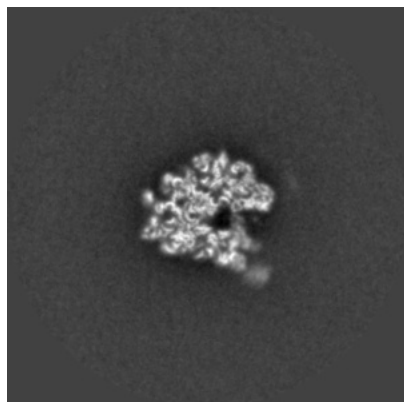


Z

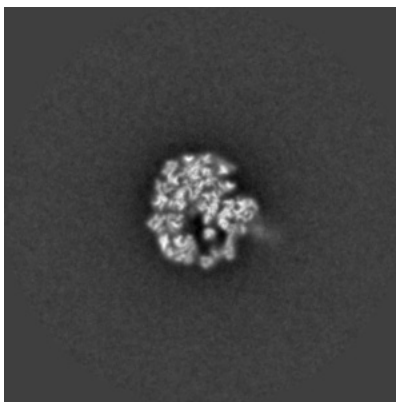
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

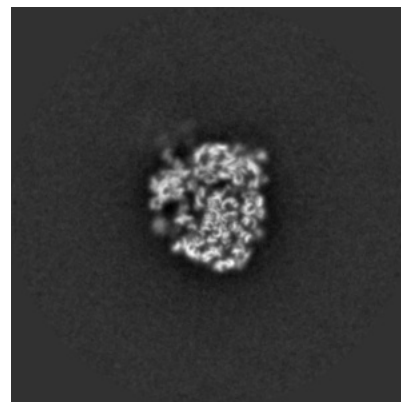
### 6.2.1 Primary map



X Index: 240

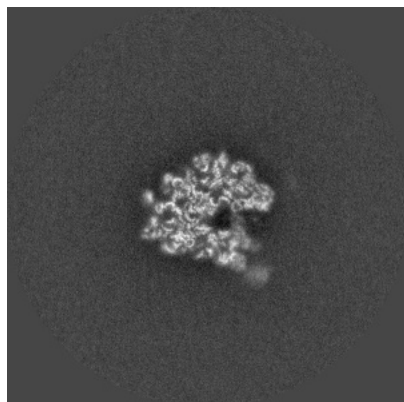


Y Index: 240

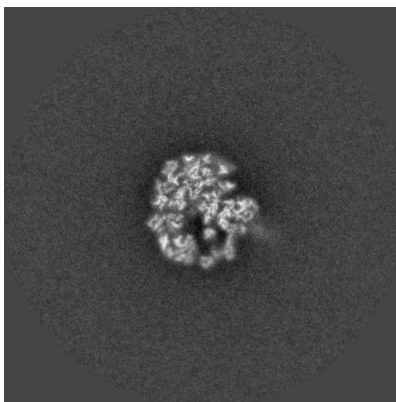


Z Index: 240

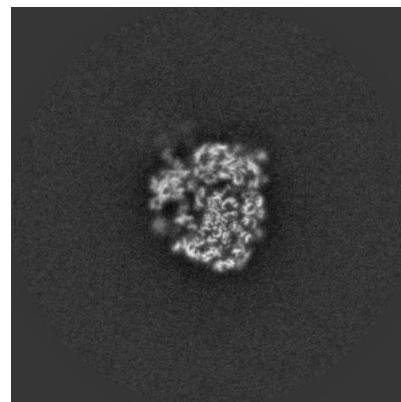
### 6.2.2 Raw map



X Index: 240



Y Index: 240

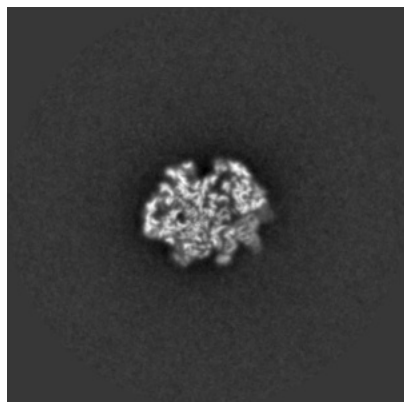


Z Index: 240

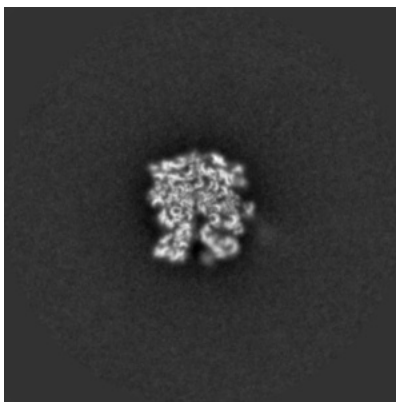
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

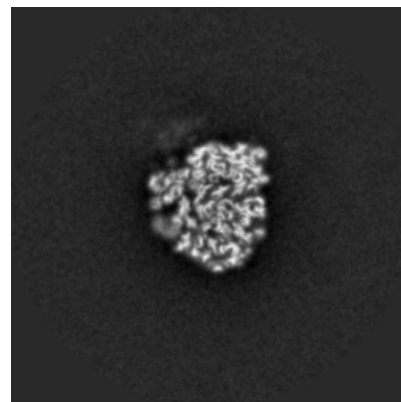
### 6.3.1 Primary map



X Index: 263

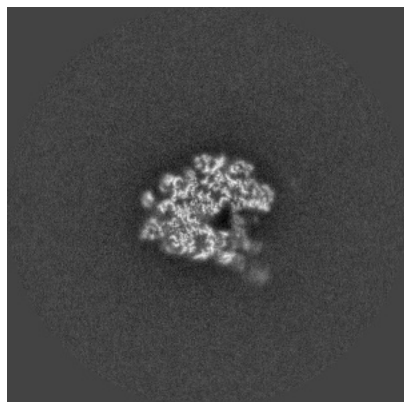


Y Index: 225

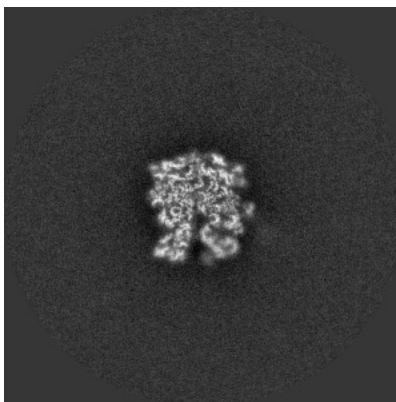


Z Index: 245

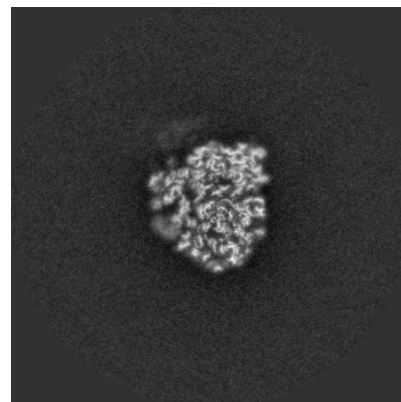
### 6.3.2 Raw map



X Index: 243



Y Index: 225

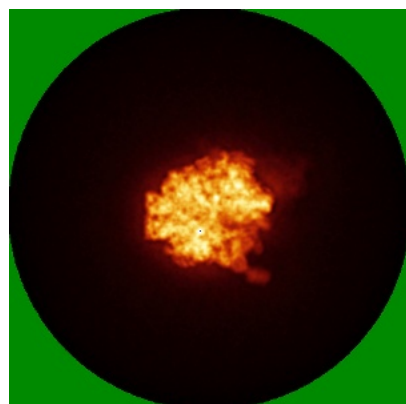


Z Index: 246

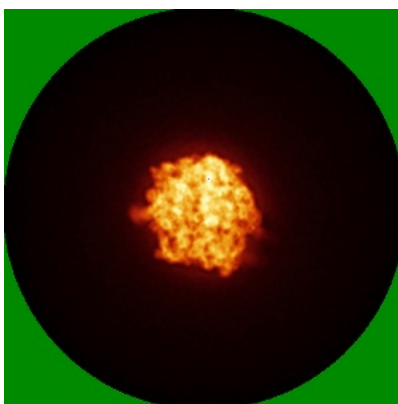
The images above show the largest variance slices of the map in three orthogonal directions.

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

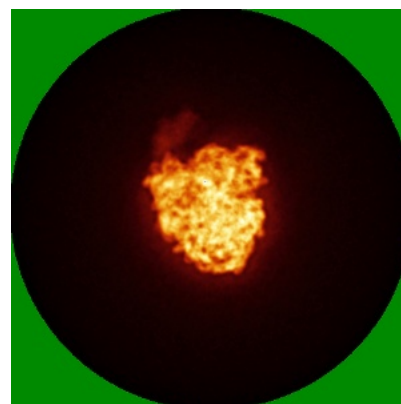
### 6.4.1 Primary map



X

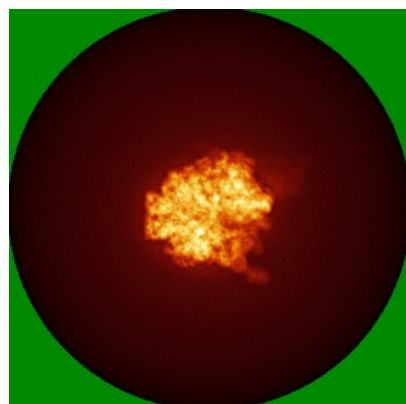


Y

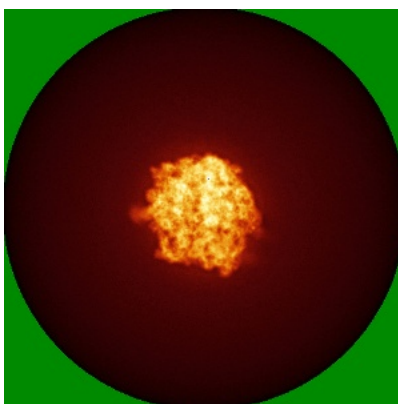


Z

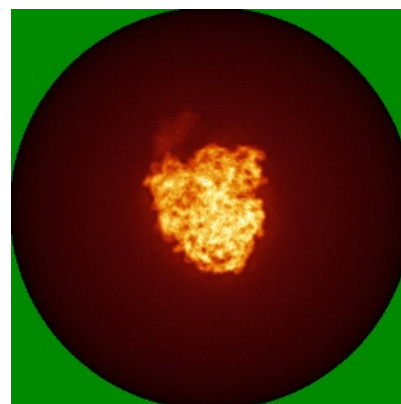
### 6.4.2 Raw map



X



Y

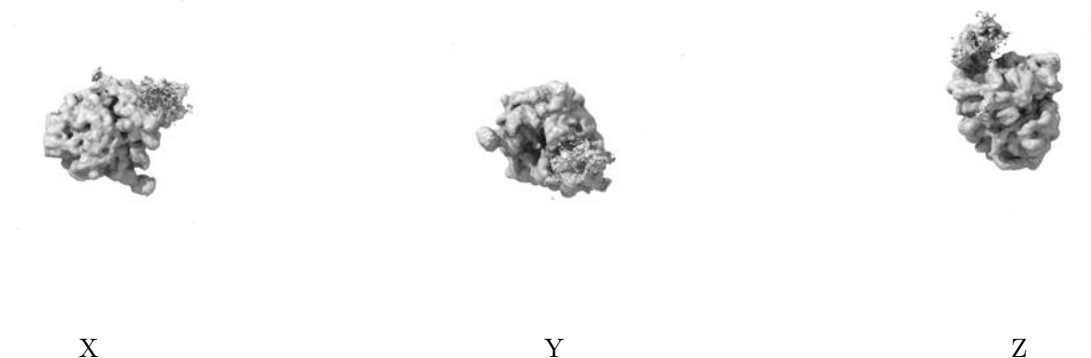


Z

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

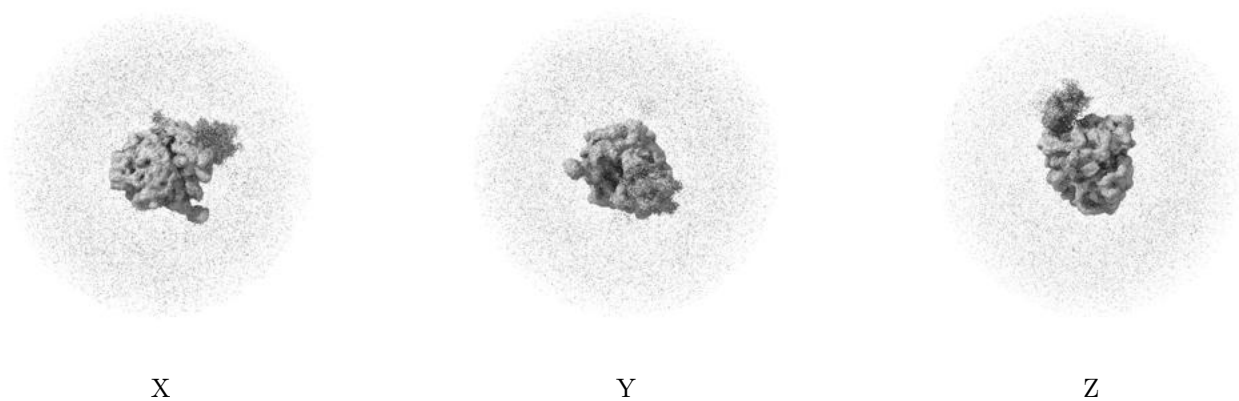
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. 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.

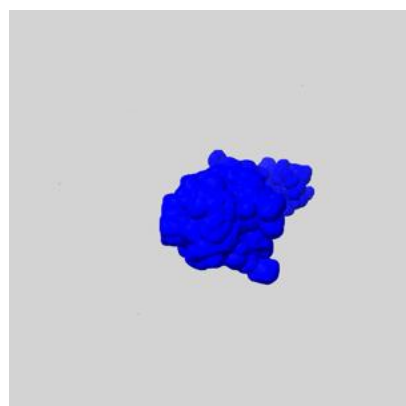
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

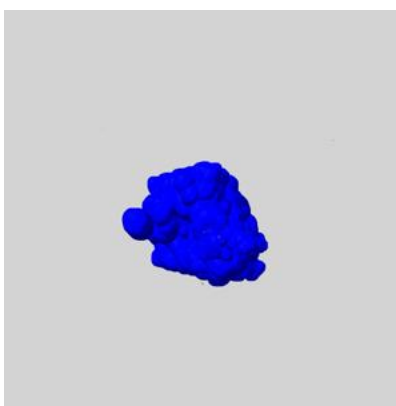
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

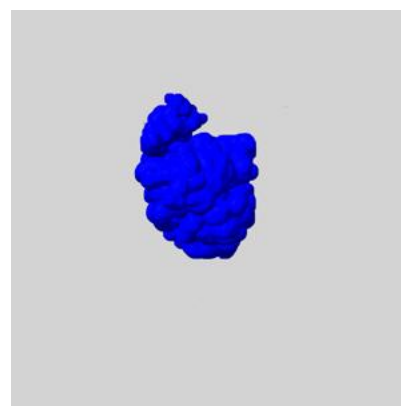
### 6.6.1 emd\_38943\_msk\_1.map [i](#)



X



Y

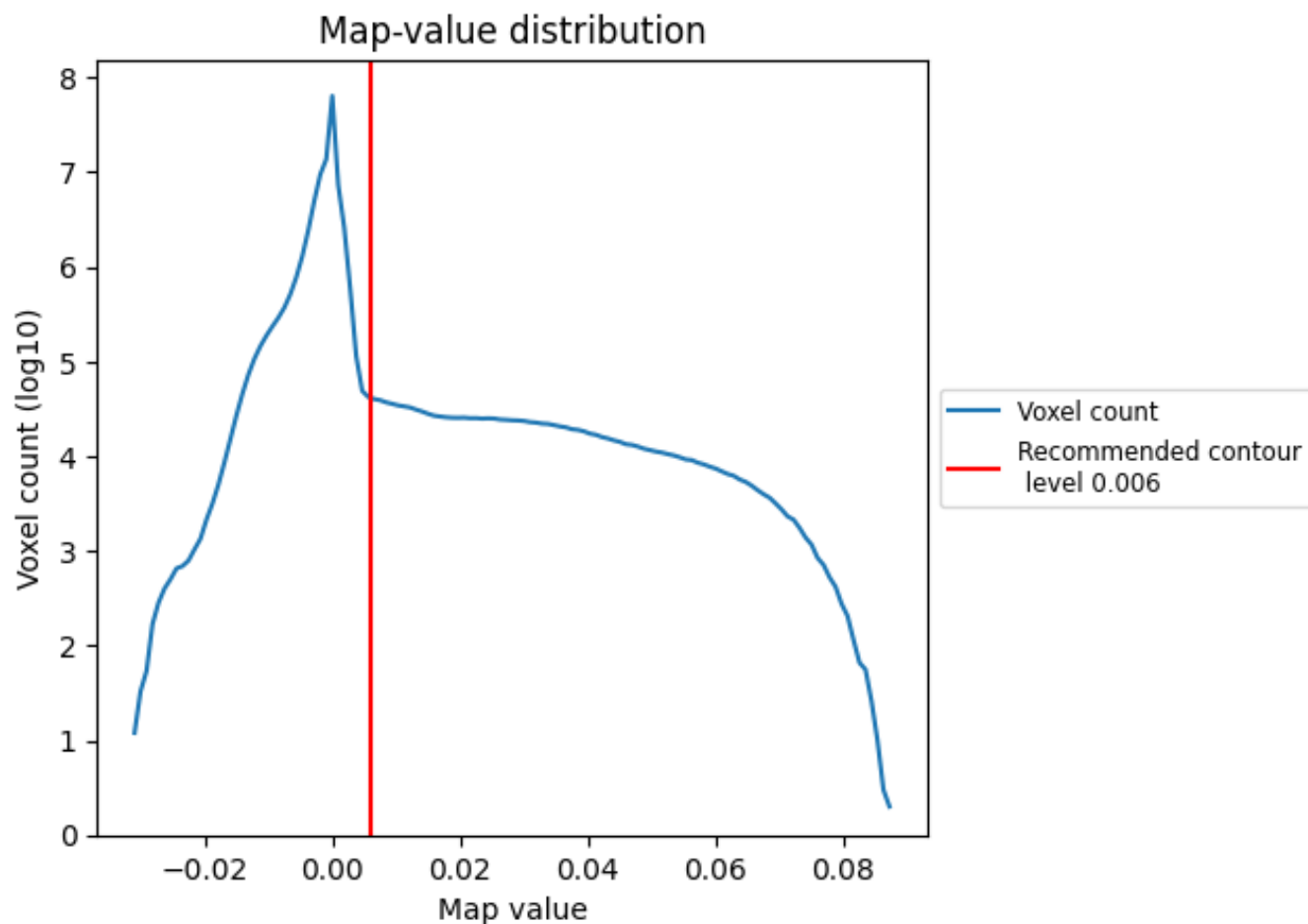


Z

## 7 Map analysis [i](#)

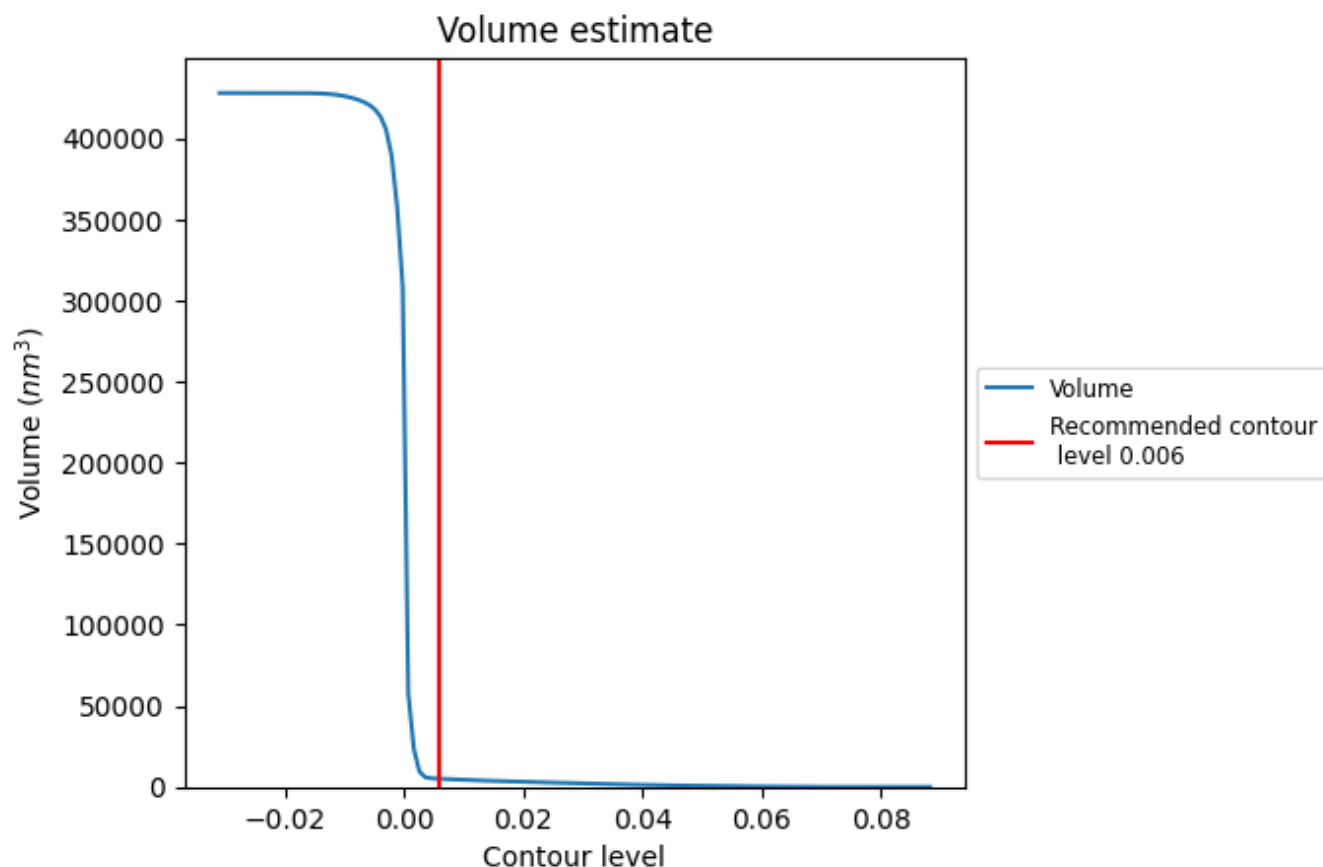
This section contains the results of statistical analysis of the map.

### 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.

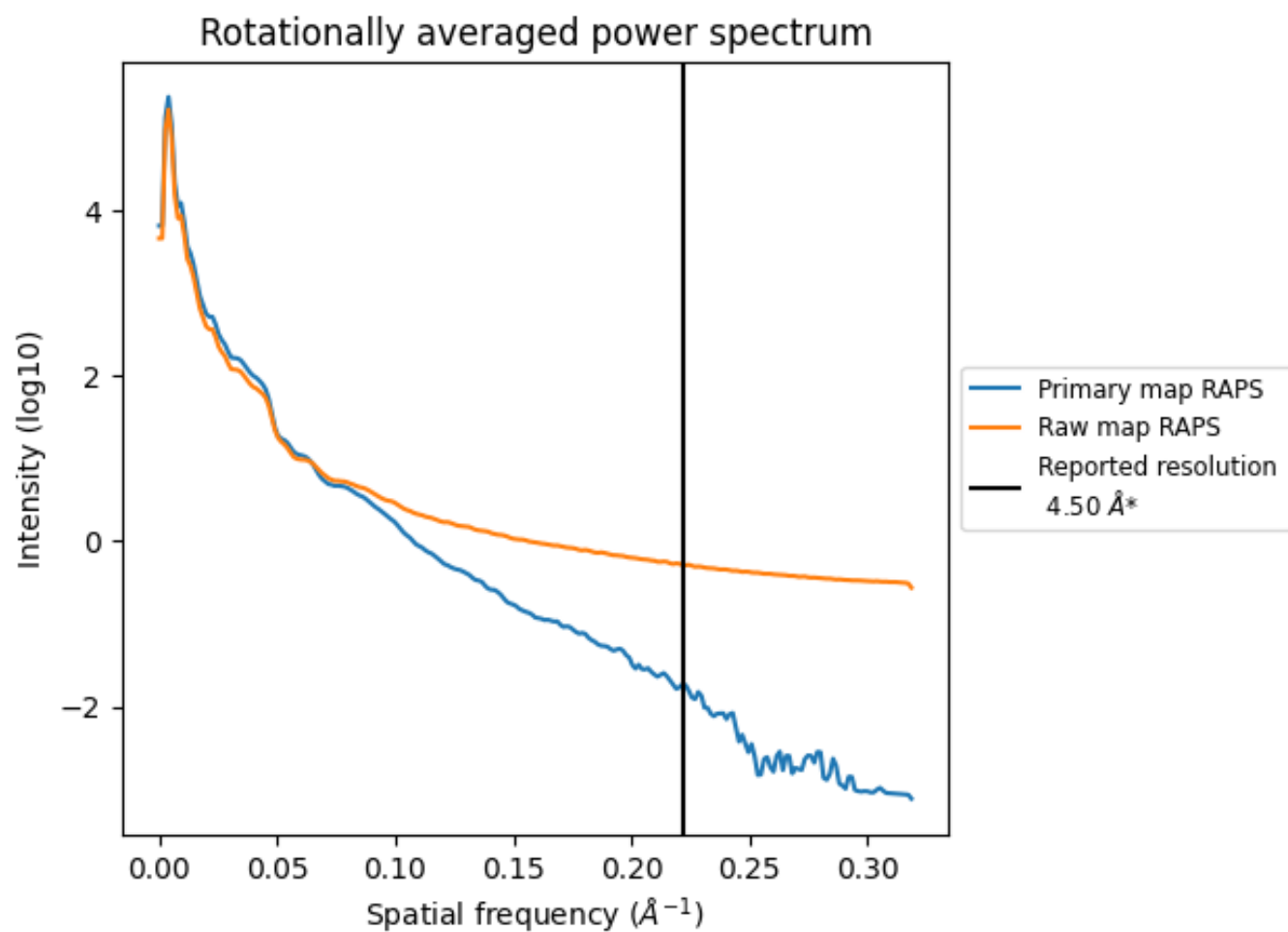
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5051  $\text{nm}^3$ ; this corresponds to an approximate mass of 4562 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 ⓘ

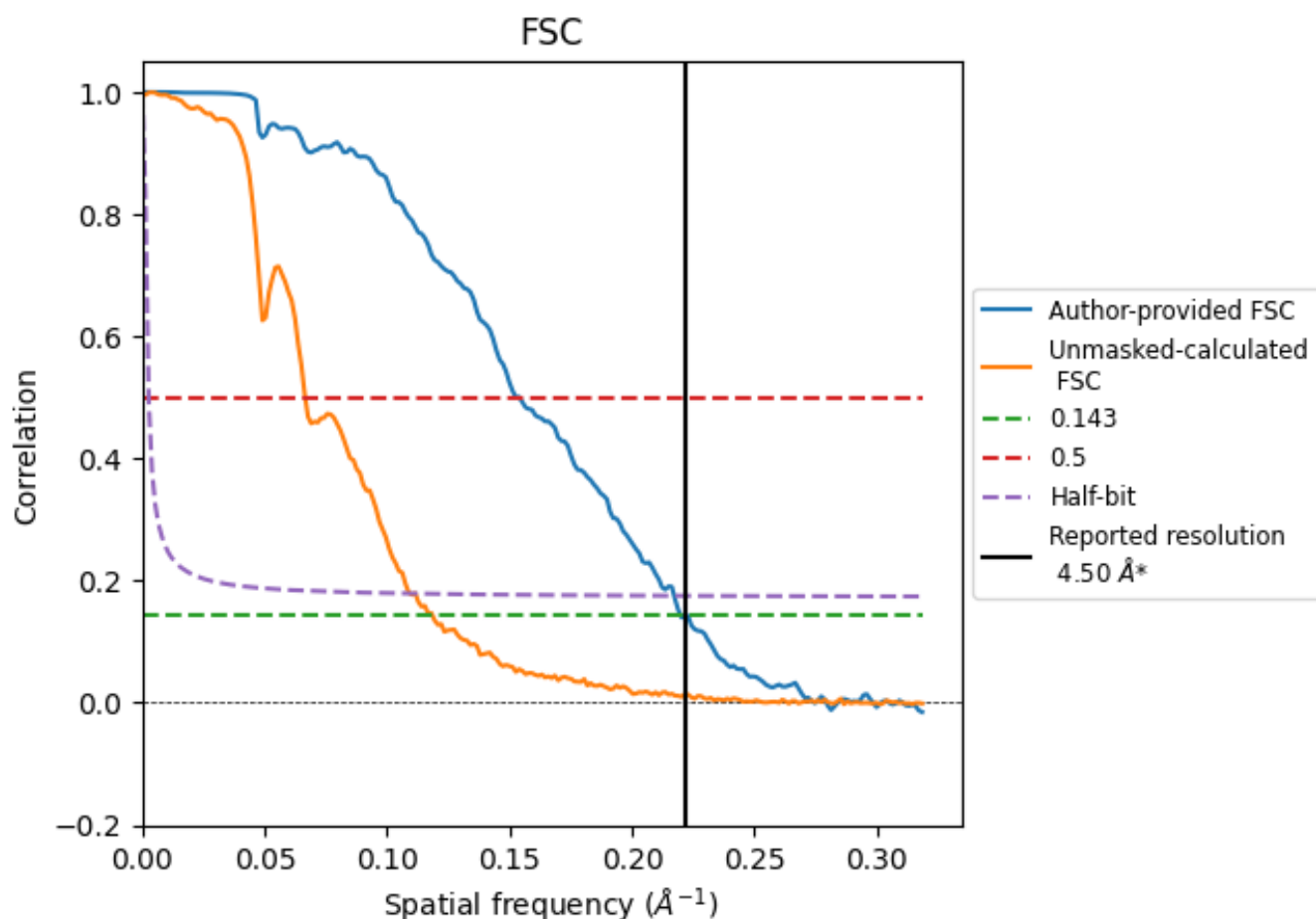


\*Reported resolution corresponds to spatial frequency of 0.222 Å<sup>-1</sup>

## 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  $0.222 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

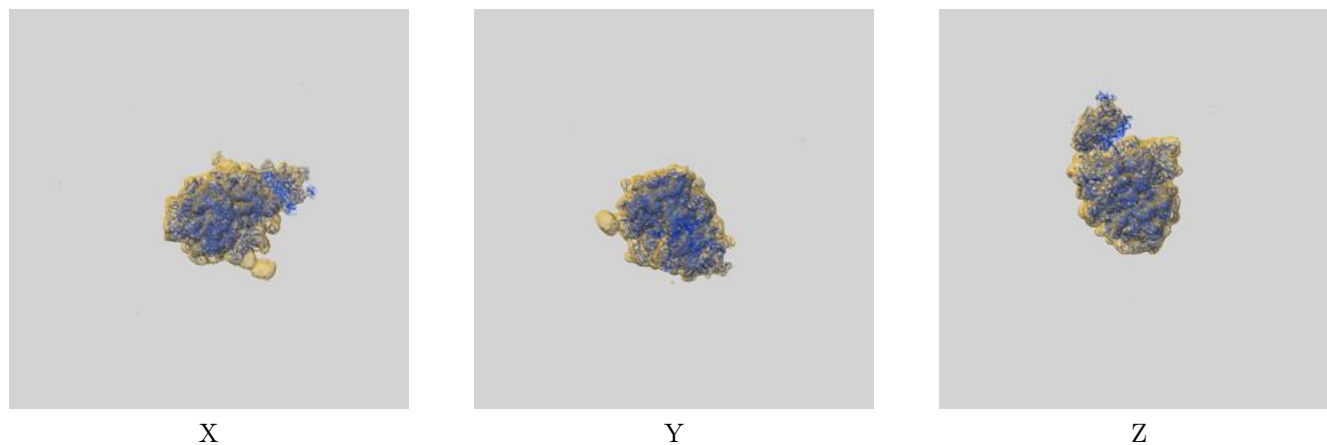
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.55	6.49	4.60
Unmasked-calculated*	8.44	15.02	9.13

\*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 8.44 differs from the reported value 4.5 by more than 10 %

## 9 Map-model fit [i](#)

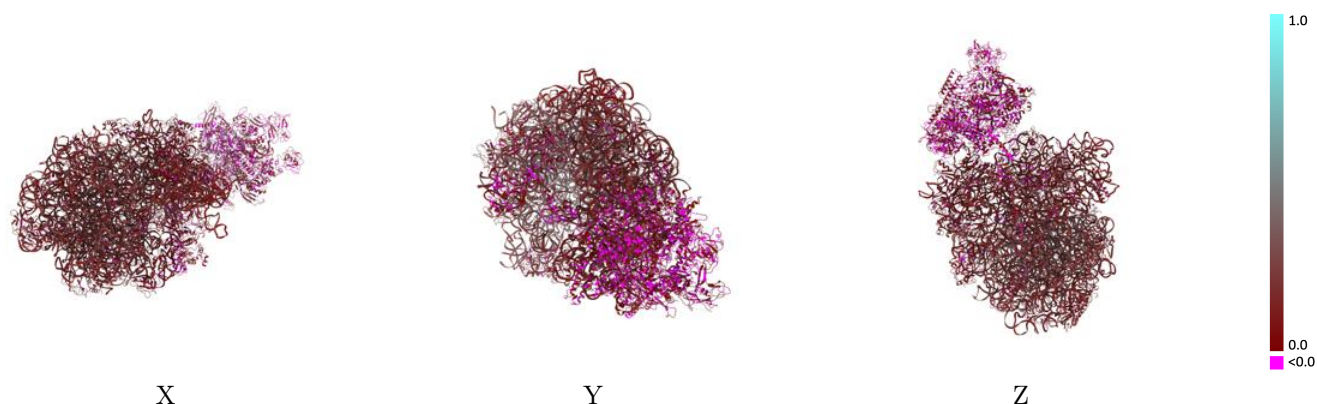
This section contains information regarding the fit between EMDB map EMD-38943 and PDB model 8Y5N. Per-residue inclusion information can be found in section [3](#) on page [18](#).

### 9.1 Map-model overlay [i](#)



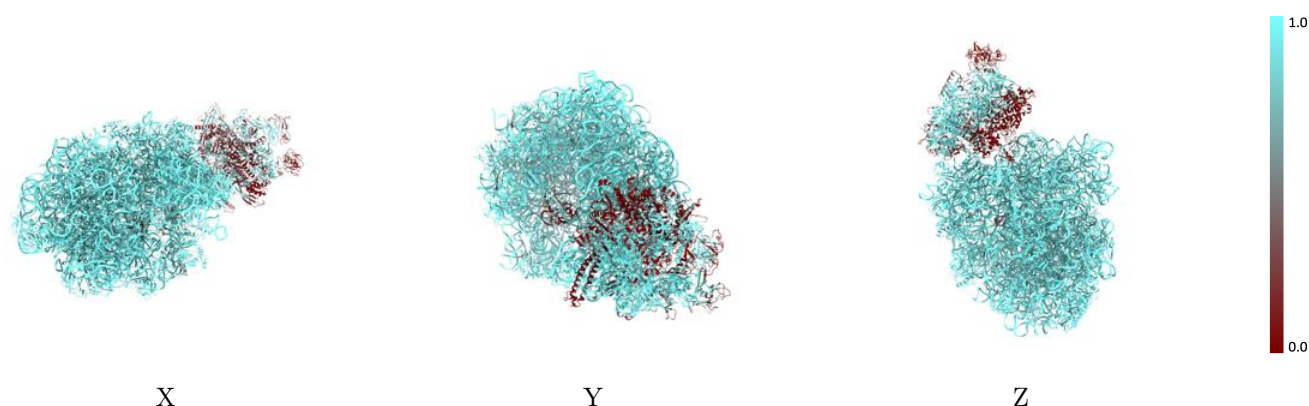
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



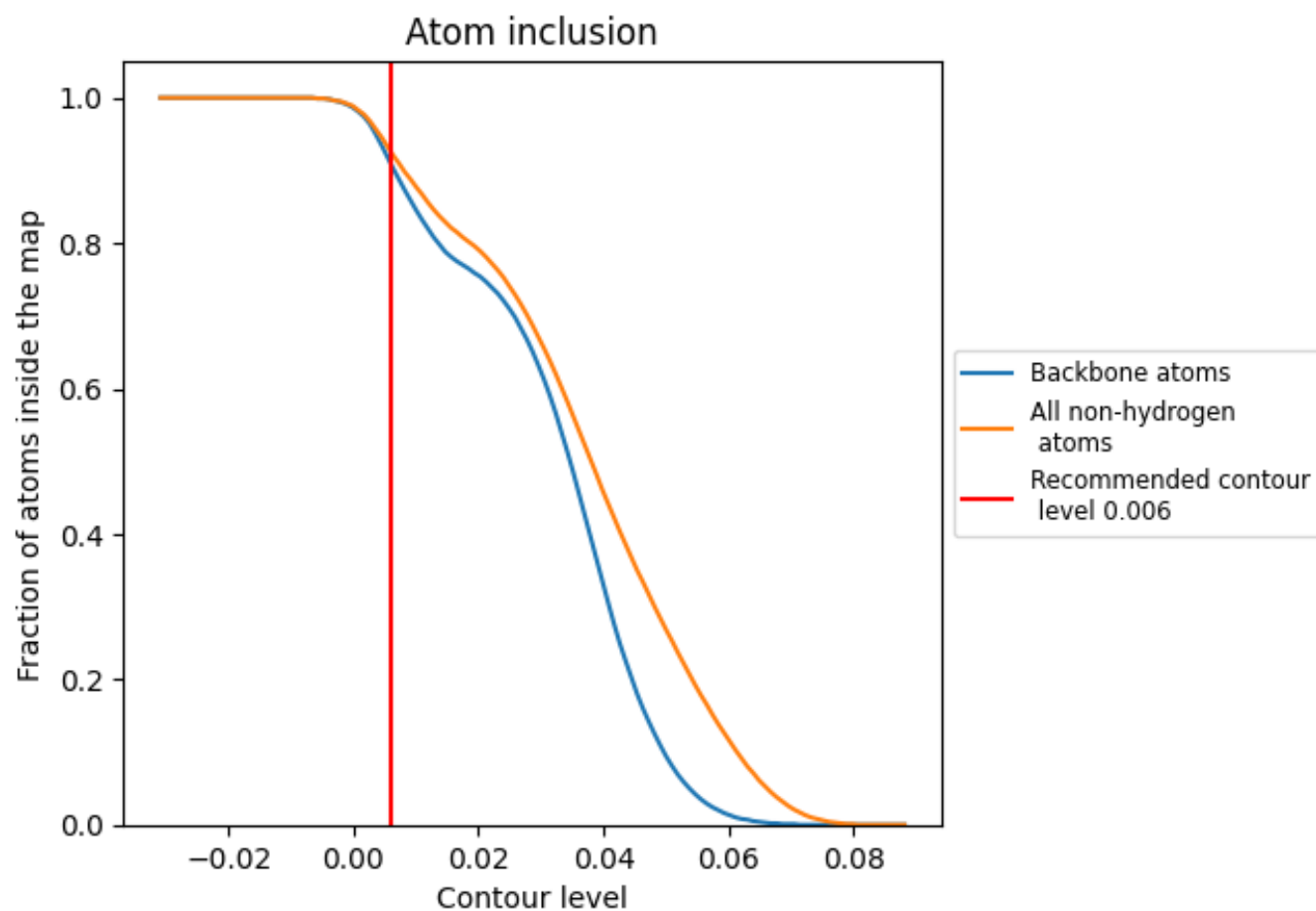
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.006).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ



































































The table lists the average atom inclusion at the recommended contour level (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9250	 0.1580
0	 0.8730	 0.0920
1	 1.0000	 0.2110
2	 1.0000	 0.1580
3	 1.0000	 0.1800
4	 0.9380	 0.1350
5	 0.5650	 0.0810
6	 0.9960	 0.1750
8	 0.8160	 0.0890
9	 0.7410	 0.0960
A	 0.9970	 0.1060
A1	 0.5740	 0.0740
A2	 0.6060	 0.0320
B	 0.9950	 0.1630
B1	 0.4920	 0.0580
B2	 0.6440	 0.0520
C	 0.9750	 0.1480
D	 0.9920	 0.1470
E	 1.0000	 0.1420
F	 1.0000	 0.1290
G	 0.9950	 0.1450
H	 0.9980	 0.1450
I	 0.9970	 0.1280
J	 1.0000	 0.1360
K	 0.9950	 0.1540
L	 0.9900	 0.1350
M	 0.9880	 0.1100
N	 0.9880	 0.1030
NG	 0.0230	 0.1060
O	 0.9990	 0.1210
P	 0.9950	 0.1590
Q	 0.9700	 0.1500
R	 0.9910	 0.1360
S	 1.0000	 0.1200
T	 0.9990	 0.1430



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Chain	Atom inclusion	Q-score
U	 1.0000	 0.1030
V	 0.9970	 0.1060
W	 1.0000	 0.1440
W0	 0.0680	 0.0080
X	 1.0000	 0.1200
Y	 0.9830	 0.1080
Z	 0.9540	 0.1430
a	 0.9890	 0.1000
b	 0.9930	 0.1830
c	 0.9970	 0.1710
d	 0.9970	 0.1500
e	 0.9700	 0.1160
f	 0.9950	 0.1360
g	 0.9380	 0.1300
h	 1.0000	 0.1970
i	 0.9090	 0.0490
j	 1.0000	 0.1690
k	 0.9810	 0.1920
l	 0.9990	 0.1440
m	 0.9800	 0.1540
n	 1.0000	 0.1640
o	 1.0000	 0.1020
p	 0.9940	 0.1790
q	 0.9990	 0.1360
r	 0.9990	 0.1520
s	 0.9950	 0.1750
t	 0.9990	 0.1480
u	 0.9920	 0.1380
v	 0.9970	 0.1450
w	 0.9960	 0.1140
x	 1.0000	 0.1720
y	 0.9980	 0.1500
z	 0.9930	 0.1490