



wwPDB EM Validation Summary Report ⓘ

Aug 4, 2025 – 08:51 PM JST

PDB ID : 8Y5K / pdb_00008y5k
EMDB ID : EMD-38940
Title : E.coli transcription translation coupling complex in TTC-A state 2 containing mRNA with 27-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 : 6.90 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.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

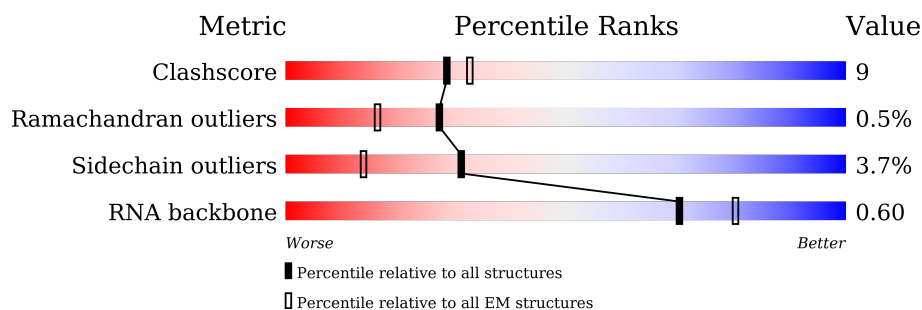
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.90 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 ≥ 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	 64% 29% 6%
2	B	57	 79% 19%
3	C	55	 75% 16% 9%
4	D	46	 67% 30%
5	E	65	 77% 22%
6	F	38	 71% 29%
7	G	241	 70% 18% 10%



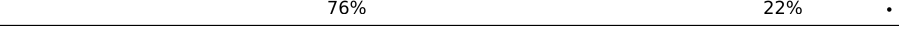
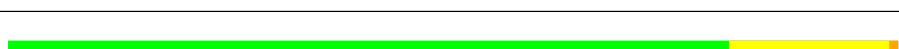



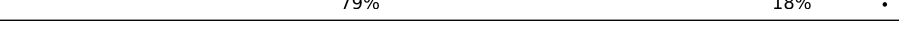



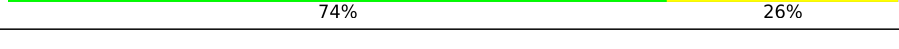

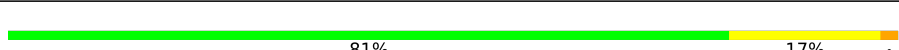


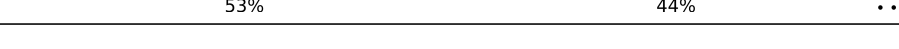
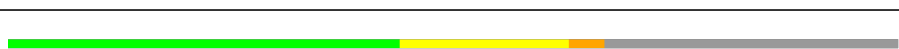
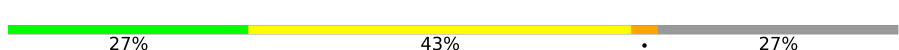
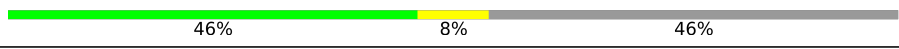




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Mol	Chain	Length	Quality of chain
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	
27	b	273	
28	c	209	
29	d	201	
30	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	27	
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 69 unique types of molecules in this entry. The entry contains 179757 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	66	Total	C	N	O	S	0	0
			522	323	99	94	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
			1620	1025	304	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
			1643	1026	315	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
			1152	717	218	211	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	S	0	0
			776	489	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	18	Total	C	N	O	P	0	0
			387	172	67	130	18		

- 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
			10496	6580	1833	2040	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	134	Total	C	N	O	S	0	0
			1026	645	186	193	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

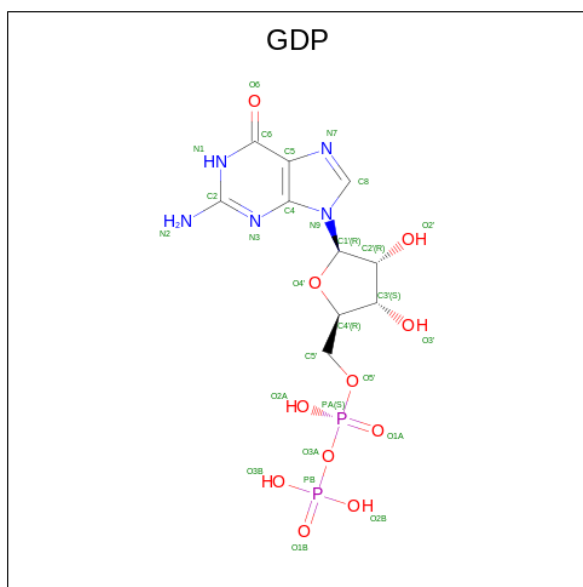
- Molecule 66 is a protein (with D amino acids) called Viomycin.

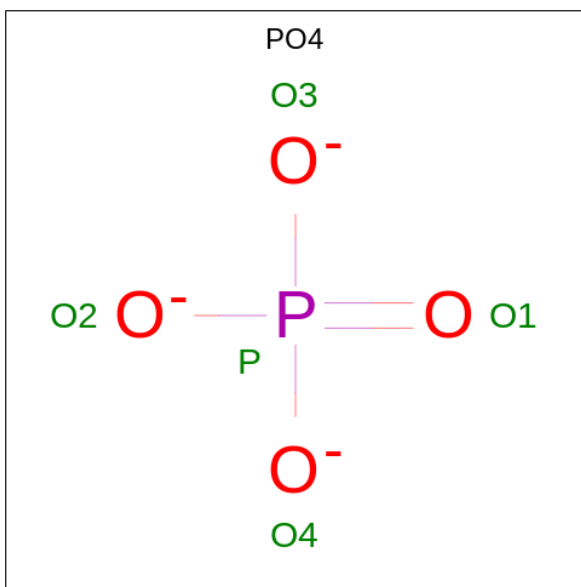
Mol	Chain	Residues	Atoms				AltConf	Trace
66	h	6	Total	C	N	O	0	0
			48	25	13	10		

- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
67	B1	1	Total	Mg	0
			1	1	

- Molecule 68 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).





Mol	Chain	Residues	Atoms			AltConf
			Total	O	P	
69	0	1	5	4	1	0

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

Chain A: 




- Molecule 2: 50S ribosomal protein L32

Chain B: 



- Molecule 3: 50S ribosomal protein L33

Chain C: 



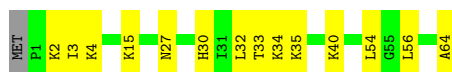
- Molecule 4: 50S ribosomal protein L34

Chain D: 



- Molecule 5: 50S ribosomal protein L35

Chain E: 



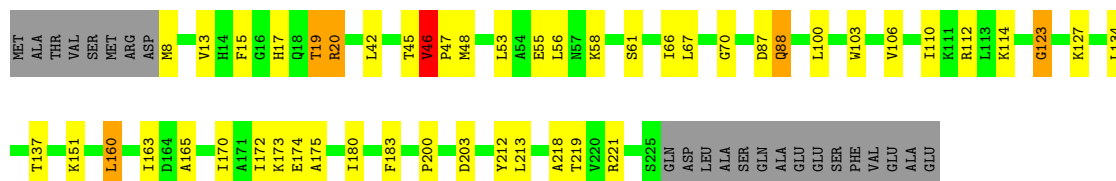
- Molecule 6: 50S ribosomal protein L36

Chain F:  71% 29%



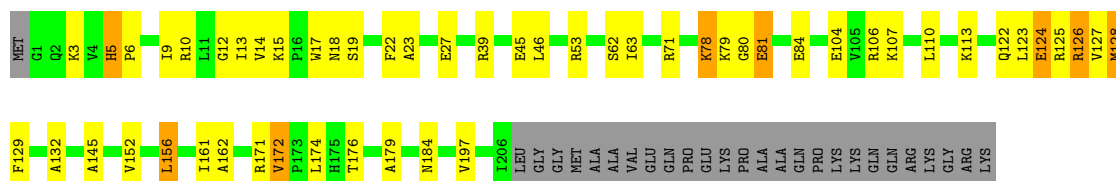
- Molecule 7: 30S ribosomal protein S2

Chain G:  70% 18% 10%



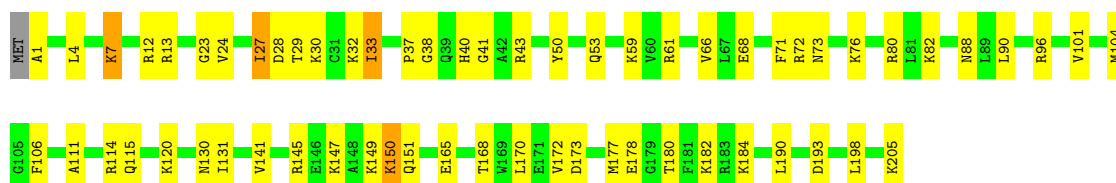
- Molecule 8: 30S ribosomal protein S3

Chain H:  66% 19% 12%



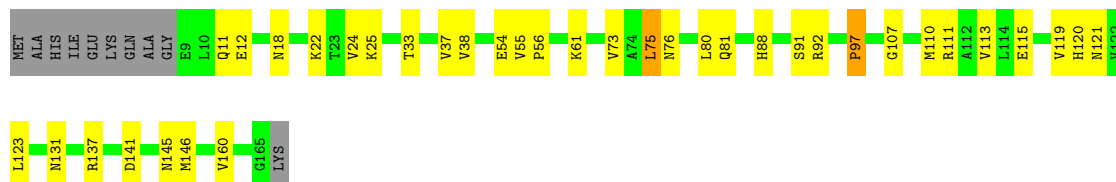
- Molecule 9: 30S ribosomal protein S4

Chain I:  69% 28%



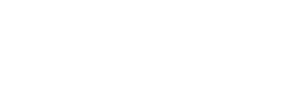
- Molecule 10: 30S ribosomal protein S5

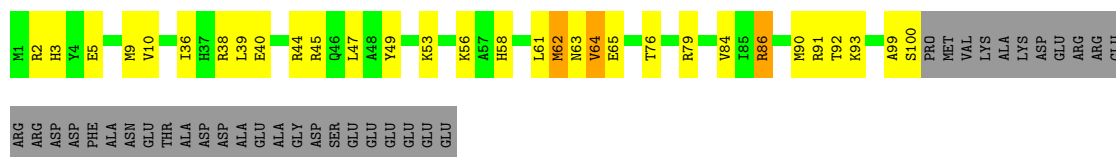
Chain J:  72% 21% 6%



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

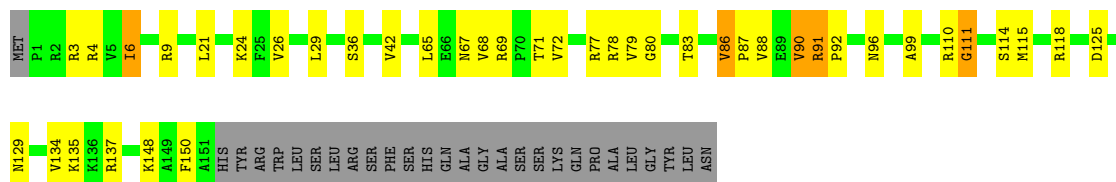
Chain K:  51% 21% 26%





- Molecule 12: 30S ribosomal protein S7

Chain L: 61% 20% 16%



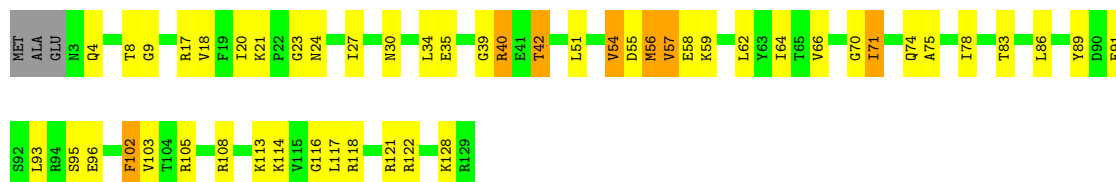
- Molecule 13: 30S ribosomal protein S8

Chain M: 84% 15%



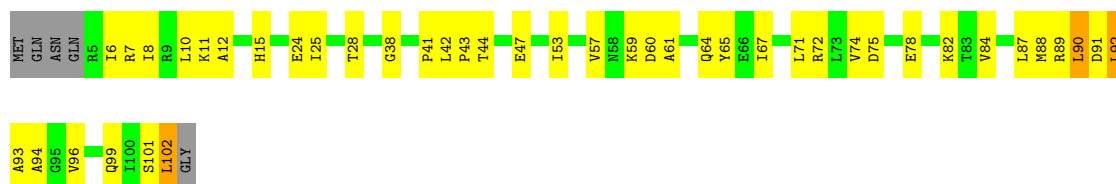
- Molecule 14: 30S ribosomal protein S9

Chain N: 59% 33% 5%



- Molecule 15: 30S ribosomal protein S10

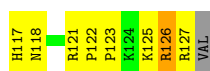
Chain O: 53% 39% 5%



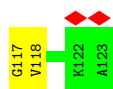
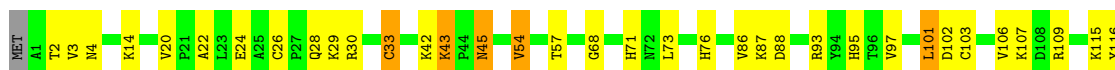
- Molecule 16: 30S ribosomal protein S11

Chain P: 63% 26% 10%





- Molecule 17: 30S ribosomal protein S12



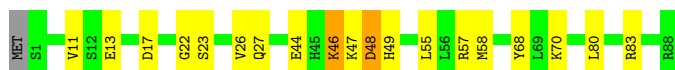
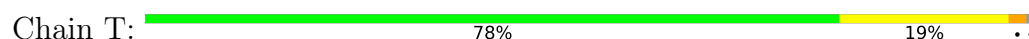
- Molecule 18: 30S ribosomal protein S13



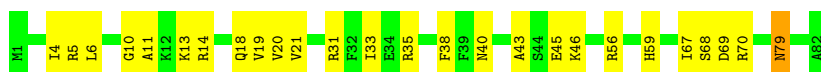
- Molecule 19: 30S ribosomal protein S14



- Molecule 20: 30S ribosomal protein S15



- Molecule 21: 30S ribosomal protein S16

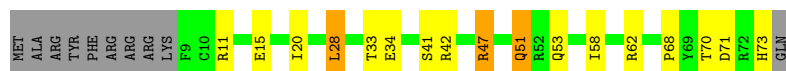


- Molecule 22: 30S ribosomal protein S17



- Molecule 23: 30S ribosomal protein S18

Chain W:  64% 19% 13%



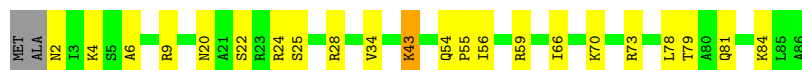
- Molecule 24: 30S ribosomal protein S19

Chain X:  60% 25% 14%



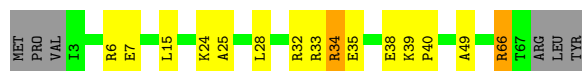
- Molecule 25: 30S ribosomal protein S20

Chain Y:  72% 24% ..



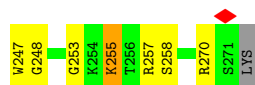
- Molecule 26: 30S ribosomal protein S21

Chain Z:  70% 18% 8%




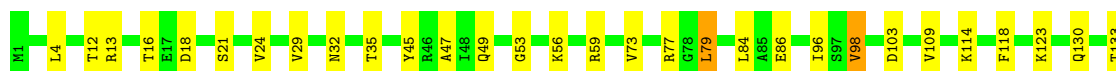
- Molecule 27: 50S ribosomal protein L2

Chain b:  71% 27% ..

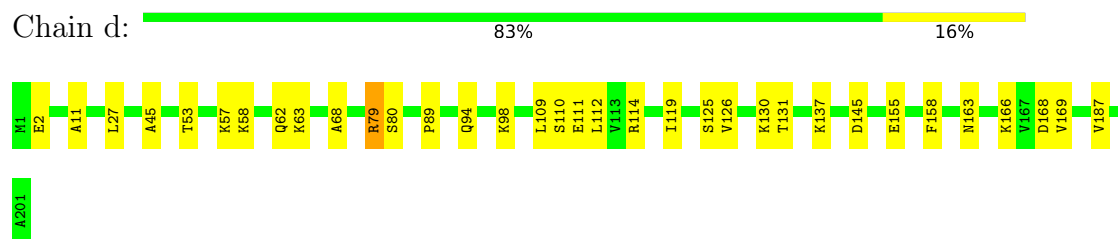


- Molecule 28: 50S ribosomal protein L3

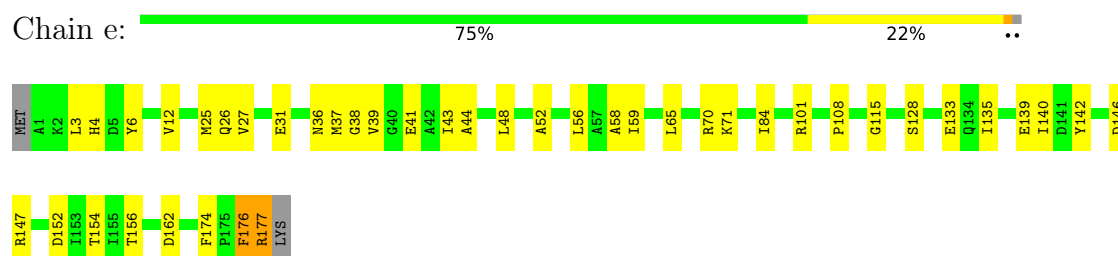
Chain c:  78% 22%



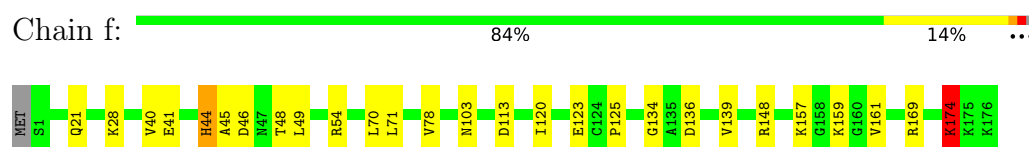
- Molecule 29: 50S ribosomal protein L4



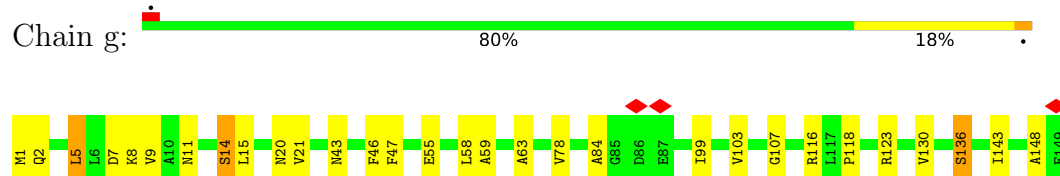
- Molecule 30: 50S ribosomal protein L5



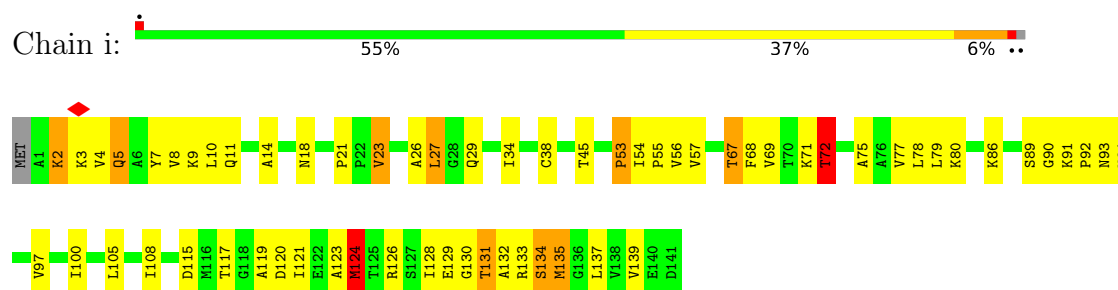
- Molecule 31: 50S ribosomal protein L6



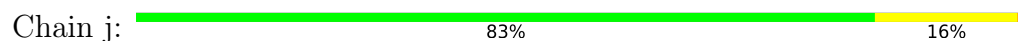
- Molecule 32: 50S ribosomal protein L9



- Molecule 33: 50S ribosomal protein L11



- Molecule 34: 50S ribosomal protein L13

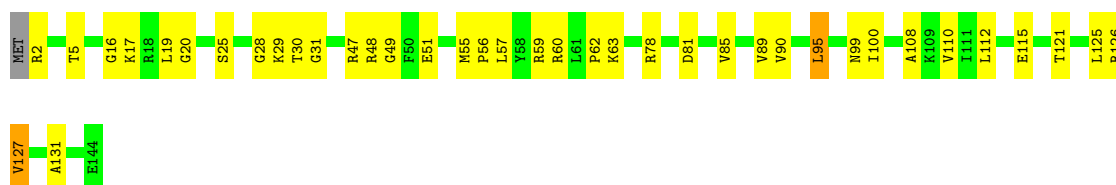




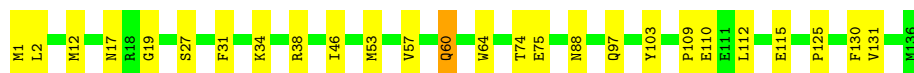
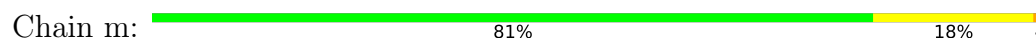
- Molecule 35: 50S ribosomal protein L14



- Molecule 36: 50S ribosomal protein L15



- Molecule 37: 50S ribosomal protein L16



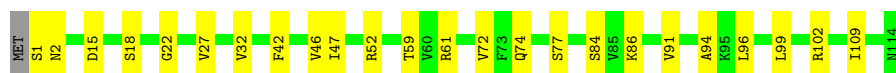
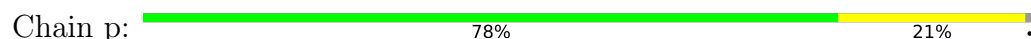
- Molecule 38: 50S ribosomal protein L17




- Molecule 39: 50S ribosomal protein L18



- Molecule 40: 50S ribosomal protein L19




- Molecule 41: 50S ribosomal protein L20

Chain q:  79% 18% ..




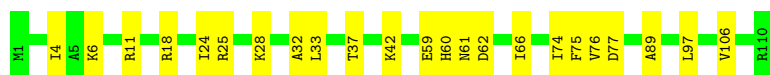
- Molecule 42: 50S ribosomal protein L21

Chain r:  78% 21% .



- Molecule 43: 50S ribosomal protein L22

Chain s:  79% 21%




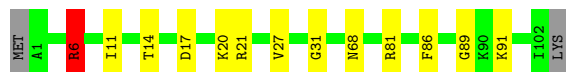
- Molecule 44: 50S ribosomal protein L23

Chain t:  73% 20% 7%



- Molecule 45: 50S ribosomal protein L24

Chain u:  86% 12% ..



- Molecule 46: 50S ribosomal protein L25

Chain v:  74% 26%




- Molecule 47: 50S ribosomal protein L27

Chain w:  69% 18% . 12%




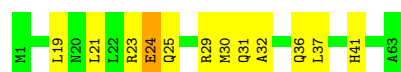
- Molecule 48: 50S ribosomal protein L28

Chain x:  79% 17% ..




- Molecule 49: 50S ribosomal protein L29

Chain y:  81% 17% .



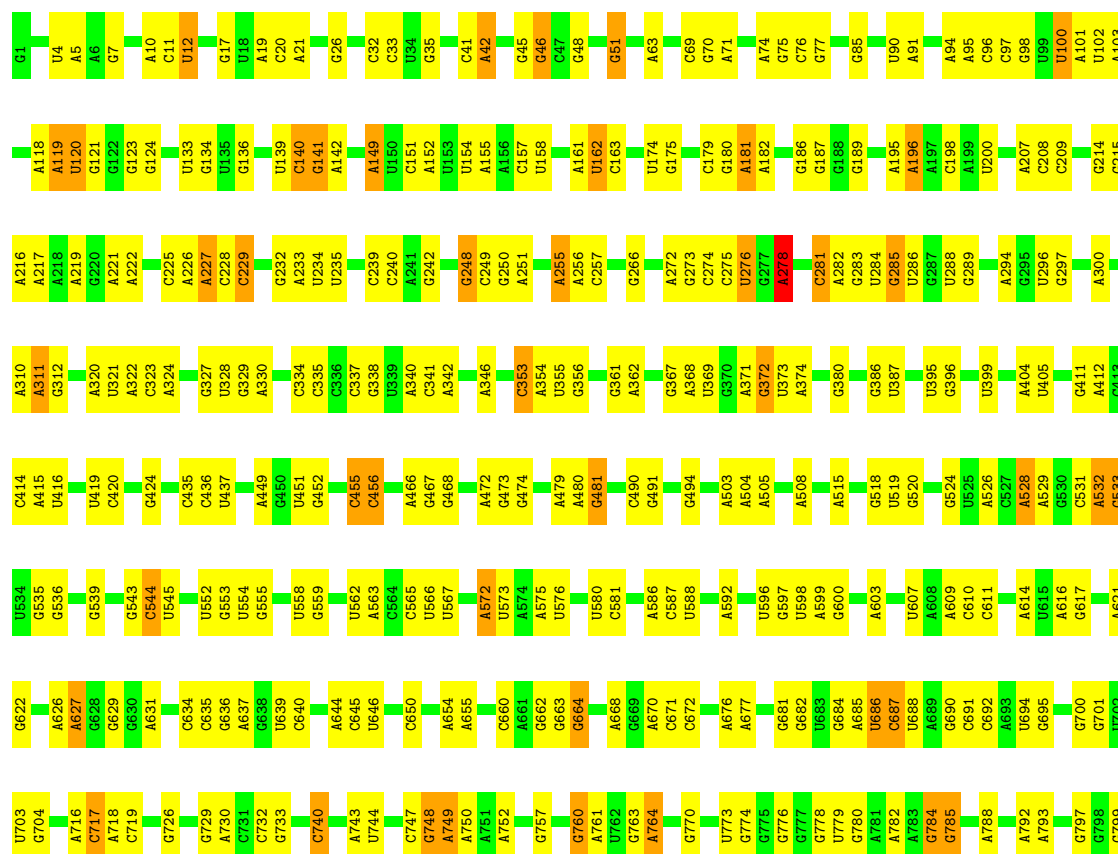
- Molecule 50: 50S ribosomal protein L30

Chain z:  78% 19% ..

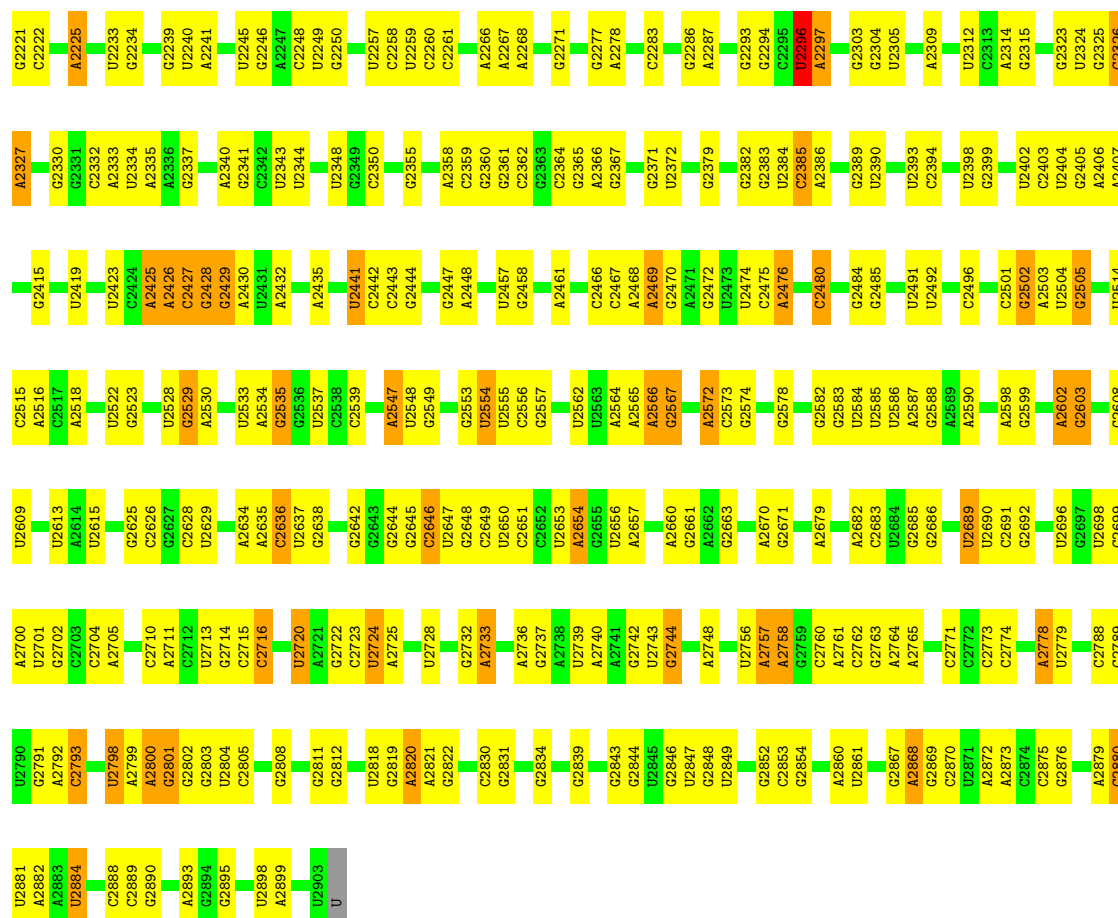


- Molecule 51: 23S rRNA

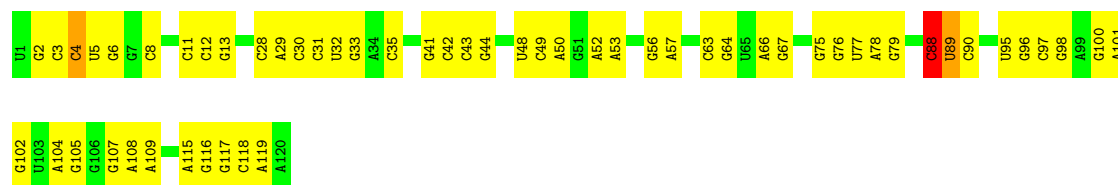
Chain 1:  56% 38% 6%



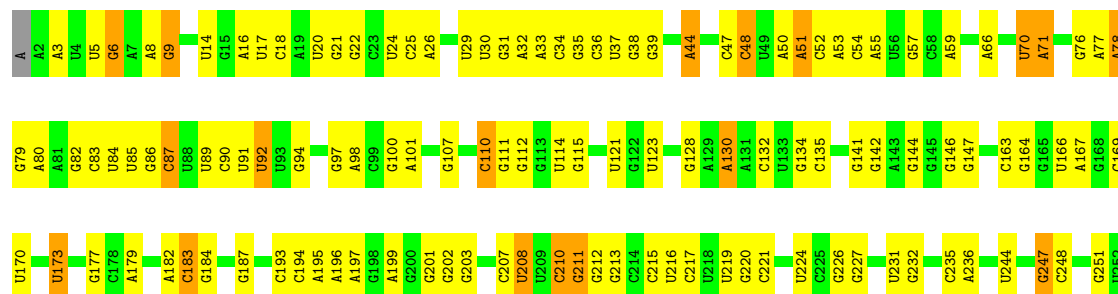
C2146	C2147	U2068	A1970	A1877	U1782	G1674	G1560	U1468	G1364	G1256	U1130	U1061	A983	U887	A800
A2071	C2072	A2077	U1991	C1893	C1790	U1680	G1568	G1473	G1377	U1271	G1137	G1063	A984	A892	G801
C2152	C2153	C2077	C1992	C1894	A1791	G1682	A1589	G1475	A1378	G1272	G1138	U1066	C986	A894	A802
G2156	G2157	A2080	U1993	C1899	A1794	G1697	U1578	G1478	G1380	A1272	G1139	G1069	C987	A896	C806
G2158	G2159	U2081	C1996	A1899	C1795	A1698	U1584	G1482	A1383	A1274	G1140	U1070	C994	G904	U809
C2160	C2161	U2086	C1997	A1901	U1796	G1702	G1587	G1482	C1386	A1275	U1141	C1072	A996	U811	C812
G2162	G2163	G2087	C1998	G1906	U1798	G1709	C1595	A1490	A1387	G1277	A1143	G1074	U999	C908	U813
A2163	C2090	A2090	G1907	C1908	G1799	G1710	A1596	G1491	U1394	C1278	A1155	C1075	A1000	A909	C814
C2165	C2092	U2092	C1909	A1801	U1806	G1715	A1597	G1492	U1397	G1279	A1156	U1077	A1001	A910	C815
U2166	G2093	G2093	G1910	A1809	A1810	C1726	A1598	C1494	C1398	A1287	G1157	U1083	C1006	G914	C816
U2167	A2094	A2094	U1911	A1805	G1811	G1727	A1608	A1494	G1416	G1288	G1158	U1084	C1006	C915	C817
G2168	A2095	A2095	A1912	C1806	G1811	G1728	C1611	A1495	G1417	C1297	U1173	A1085	G1016	G916	C818
A2169	C2096	A2097	A1913	G1807	G1816	G1718	U1601	A1504	U1409	G1300	G1159	U1086	G1011	A917	A819
A2170	C2096	A2097	A1914	A1808	A1819	G1730	U1603	A1505	G1410	A1301	G1160	U1081	U1012	A918	U827
A2171	C2096	A2097	U1915	A1809	G1820	C1731	A1616	A1506	C1293	G1296	C1161	U1082	C1013	A919	U828
A2172	C2096	A2097	U1916	A1810	G1821	C1732	A1617	A1507	G1416	G1297	C1162	U1083	A1014	A920	A829
A2173	C2096	A2097	U1917	A1811	G1822	G1733	C1611	A1508	G1417	G1300	G1163	U1084	U1015	U929	G830
C2174	C2100	G2100	A1918	G1823	G1824	G1734	A1616	A1509	G1418	A1322	U1174	U1085	G1017	U831	C830
C2175	C2100	G2100	A1919	G1825	G1826	G1735	A1617	A1510	G1419	G1322	U1175	U1086	G1017	U832	C831
A2176	C2100	G2100	A1920	G1827	G1828	G1736	A1618	A1511	A1420	G1322	U1176	U1087	G1018	U833	A833
C2177	C2100	G2100	A1921	G1829	G1830	G1737	A1619	A1512	G1421	G1322	U1177	U1088	G1019	U834	U839
C2178	C2100	G2100	A1922	G1831	G1832	G1738	A1620	A1513	G1422	G1322	U1178	U1089	G1020	C935	C840
U2182	A2183	U2183	U1923	G1833	G1834	G1739	A1621	A1514	G1423	G1322	U1179	U1090	G1021	C936	A845
A2184	C2184	A2184	C1925	G1835	G1836	G1740	A1622	A1515	G1424	G1322	U1180	U1091	G1022	C937	U846
U2185	A2185	U2185	U1926	G1837	G1838	G1741	A1623	A1516	G1425	G1322	U1181	U1092	G1023	C938	A846
C2186	C2186	U2186	A1927	G1839	G1840	G1742	A1624	A1517	G1426	G1322	U1182	U1093	G1024	G940	G855
U2187	U2187	U2187	U1928	G1841	G1842	G1743	U1625	A1518	G1427	G1322	U1183	U1094	G1025	A941	G856
U2188	U2188	U2188	U1929	G1843	G1844	G1744	A1626	A1519	G1428	G1322	U1184	U1095	G1026	G942	G857
U2189	C2189	U2189	U1930	G1845	G1846	G1745	A1627	A1520	G1429	G1322	U1185	U1096	G1027	C943	G858
G2190	A2191	G2190	U1931	G1847	G1848	G1746	A1628	A1521	G1430	G1322	U1186	U1097	G1028	C946	U860
U2192	U2192	U2192	U1932	G1849	G1850	G1747	A1629	A1522	G1431	G1322	U1187	U1098	G1029	C947	A861
A2198	A2198	U2198	U1933	G1851	G1852	G1748	A1630	A1523	G1432	G1322	U1188	U1099	G1030	C948	G862
U2203	G2204	A2205	U1934	G1853	G1854	G1749	A1631	A1524	G1433	G1322	U1189	U1100	G1031	C949	G863
A2206	C2206	C2206	U1935	G1855	G1856	G1750	A1632	A1525	G1434	G1322	U1190	U1101	G1032	G949	G864
C2207	C2207	C2207	U1936	G1857	G1858	G1751	A1633	A1526	G1435	G1322	U1191	U1102	G1033	C951	C865
C2208	C2208	C2208	U1937	G1859	G1860	G1752	A1634	A1527	G1436	G1322	U1192	U1103	G1034	U967	G869
G2209	U2210	A2211	U1938	G1861	G1862	G1753	A1635	A1528	G1437	G1322	U1193	U1104	G1035	C968	U870
A2212	A2212	A2212	U1939	G1863	G1864	G1754	A1636	A1529	G1438	G1322	U1194	U1105	G1036	G969	U871
C2215	G2216	C2216	U1940	G1865	G1866	G1755	A1637	A1530	G1439	G1322	U1195	U1106	G1037	U970	C873
U2220	U2220	U2220	U1941	G1867	G1868	G1756	A1638	A1531	G1440	G1322	U1196	U1107	G1038	A972	C876
			U1942	G1869	G1870	G1757	A1639	A1532	G1441	G1322	U1197	U1108	G1039	G974	A878
			U1943	G1871	G1872	G1758	A1640	A1533	G1442	G1322	U1198	U1109	G1040	A975	C879
			U1944	G1873	G1874	G1759	A1641	A1534	G1443	G1322	U1199	U1110	G1041	A979	C885
			U1945	G1875	G1876	G1760	A1642	A1535	G1444	G1322	U1200	U1111	G1042	C982	A886
			U1946	G1877	G1878	G1761	A1643	A1536	G1445	G1322	U1201	U1112	G1043		
			U1947	G1879	G1880	G1762	A1644	A1537	G1446	G1322	U1202	U1113	G1044		
			U1948	G1881	G1882	G1763	A1645	A1538	G1447	G1322	U1203	U1114	G1045		
			U1949	G1883	G1884	G1764	A1646	A1539	G1448	G1322	U1204	U1115	G1046		
			U1950	G1885	G1886	G1765	A1647	A1540	G1449	G1322	U1205	U1116	G1047		
			U1951	G1887	G1888	G1766	A1648	A1541	G1450	G1322	U1206	U1117	G1048		
			U1952	G1889	G1890	G1767	A1649	A1542	G1451	G1322	U1207	U1118	G1049		
			U1953	G1891	G1892	G1768	A1650	A1543	G1452	G1322	U1208	U1119	G1050		
			U1954	G1893	G1894	G1769	A1651	A1544	G1453	G1322	U1209	U1120	G1051		
			U1955	G1895	G1896	G1770	A1652	A1545	G1454	G1322	U1210	U1121	G1052		
			U1956	G1897	G1898	G1771	A1653	A1546	G1455	G1322	U1211	U1122	G1053		
			U1957	G1899	G1900	G1772	A1654	A1547	G1456	G1322	U1212	U1123	G1054		
			U1958	G1901	G1902	G1773	A1655	A1548	G1457	G1322	U1213	U1124	G1055		
			U1959	G1903	G1904	G1774	A1656	A1549	G1458	G1322	U1214	U1125	G1056		
			U1960	G1905	G1906	G1775	A1657	A1550	G1459	G1322	U1215	U1126	G1057		
			U1961	G1907	G1908	G1776	A1658	A1551	G1460	G1322	U1216	U1127	G1058		
			U1962	G1909	G1910	G1777	A1659	A1552	G1461	G1322	U1217	U1128	G1059		
			U1963	G1911	G1912	G1778	A1660	A1553	G1462	G1322	U1218	U1129	G1060		
			U1964	G1913	G1914	G1779	A1661	A1554	G1463	G1322	U1219	U1130	G1061		
			U1965	G1915	G1916	G1780	A1662	A1555	G1464	G1322	U1220	U1131	G1062		
			U1966	G1917	G1918	G1781	A1663	A1556	G1465	G1322	U1221	U1132	G1063		
			U1967	G1919	G1920	G1782	A1664	A1557	G1466	G1322	U1222	U1133	G1064		
			U1968	G1921	G1922	G1783	A1665	A1558	G1467	G1322	U1223	U1134	G1065		
			U1969	G1923	G1924	G1784	A1666	A1559	G1468	G1322	U1224	U1135	G1066		
			U1970	G1925	G1926	G1785	A1667	A1560	G1469	G1322	U1225	U1136	G1067		
			U1971	G1927	G1928	G1786	A1668	A1561	G1470	G1322	U1226	U1137	G1068		
			U1972	G1929	G1930	G1787	A1669	A1562	G1471	G1322	U1227	U1138	G1069		
			U1973	G1931	G1932	G1788	A1670	A1563	G1472	G1322	U1228	U1139	G1070		
			U1974	G1933	G1934	G1789	A1671	A1564	G1473	G1322	U1229	U1140	G1071		
			U1975	G1935	G1936	G1790	A1672	A1565	G1474	G1322	U1230	U1141	G1072		
			U1976	G1937	G1938	G1791	A1673	A1566	G1475	G1322	U1231	U1142	G1073		
			U1977	G1939	G1940	G1792	A1674	A1567	G1476	G1322	U1232	U1143	G1074		
			U1978	G1941	G1942	G1793	A1675	A1568	G1477	G1322	U1233	U1144	G1075		
			U1979	G1943	G1944	G1794	A1676	A1569	G1478	G1322	U1234	U1145	G1076		
			U1980	G1945	G1946	G1795	A1677	A1570	G1479	G1322	U1235	U1146	G1077		
			U1981	G1947	G1948	G1796	A1678	A1571	G1480	G1322	U1236	U1147	G1078		
			U1982	G1949	G1950	G1797	A1679	A1572	G1481	G1322	U1237	U1148	G1079		
			U1983	G1951	G1952	G1798	A1680	A1573	G1482	G1322	U1238	U1149	G1080		
			U1984	G1953	G1954	G1799	A1681	A1574	G1483	G1322	U1239	U1150	G1081		
			U1985	G1955	G1956	G1800	A1682	A1575	G1484	G1322	U1240	U1151	G1082		
			U1986	G1957	G1958	G1801	A1683	A1576	G1485	G1322	U1241	U1152	G1083		
			U1987	G1959	G1960	G1802	A1684	A1577	G1486	G1322	U1242	U1153	G1084		
			U1988	G1961	G1962	G1803	A1685	A1578	G1487	G1322	U1243	U1154	G1085		
			U1989	G1963	G1964	G1804	A1686	A1579	G1488	G1322	U1244	U1155	G1086		
			U1990	G1965	G1966	G1805	A1687	A1580	G1489	G1322	U1245	U1156	G1087		
			U1991	G1967	G1968	G1806	A1688	A							

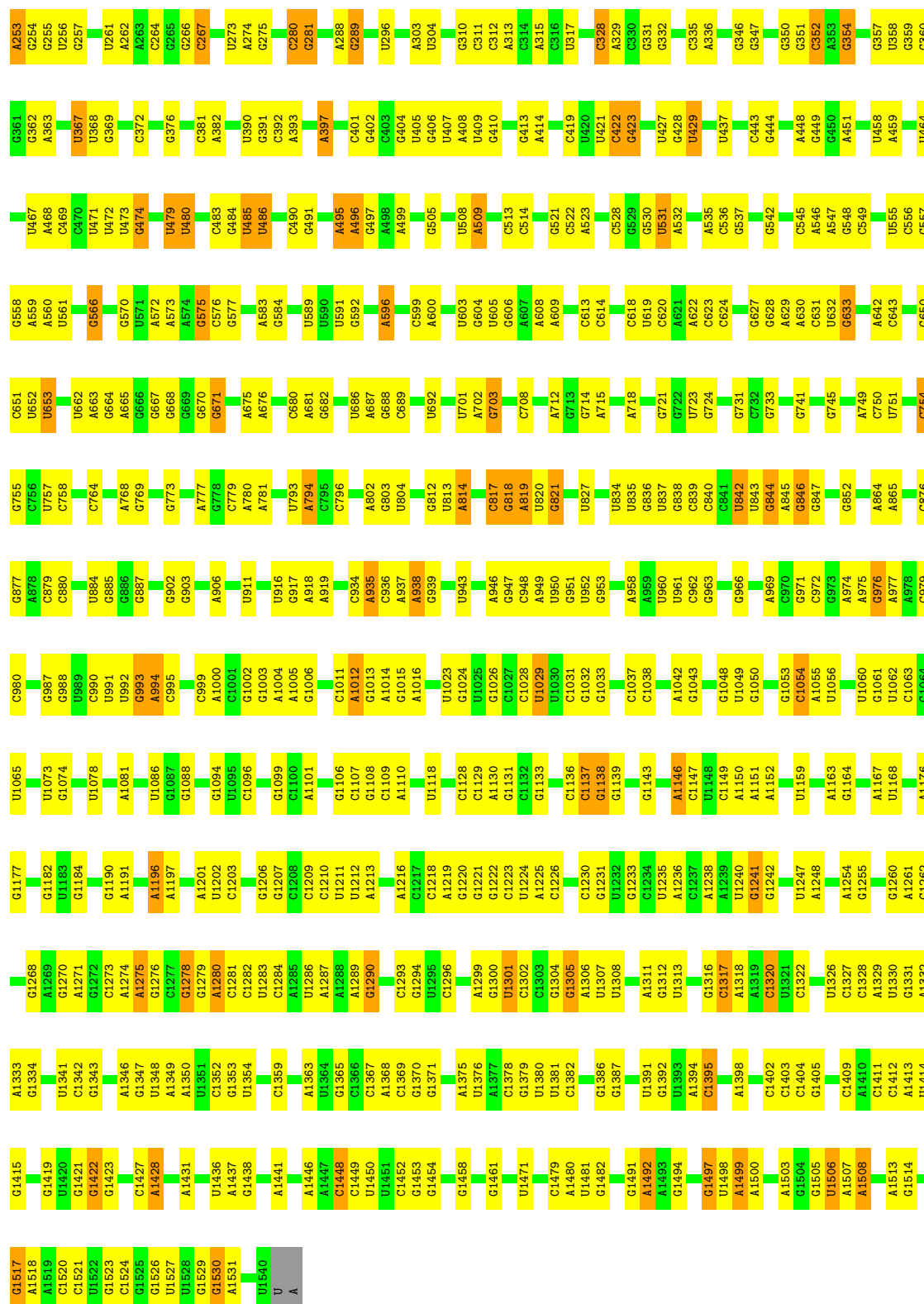


• Molecule 52: 5S rRNA



• Molecule 53: 16S rRNA



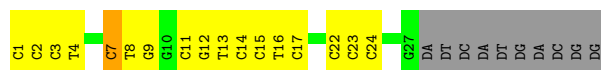


• Molecule 54: mRNA

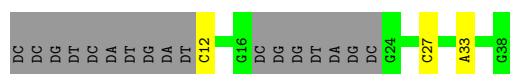
Chain 4: 44% 19% 33%



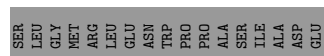
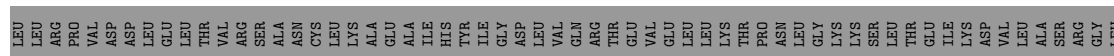
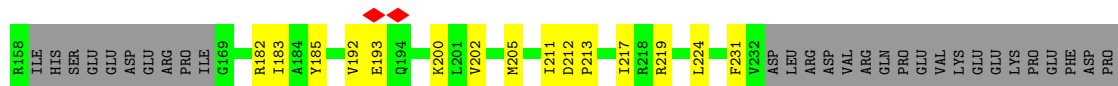
- Molecule 55: template DNA strand



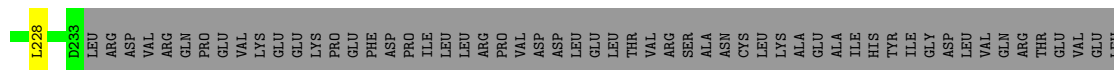
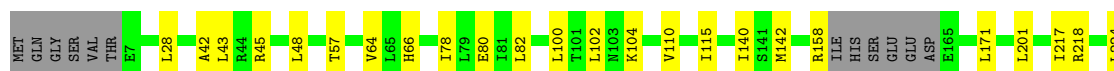
- Molecule 56: non-template DNA strand



- Molecule 57: DNA-directed RNA polymerase subunit alpha



- Molecule 57: DNA-directed RNA polymerase subunit alpha

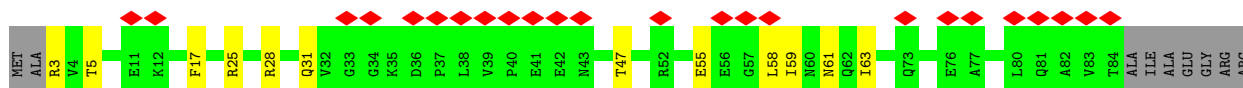
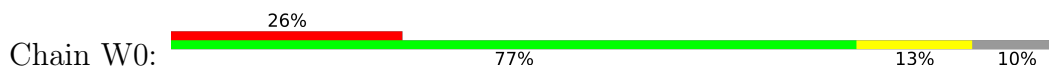


- Molecule 58: DNA-directed RNA polymerase subunit beta'

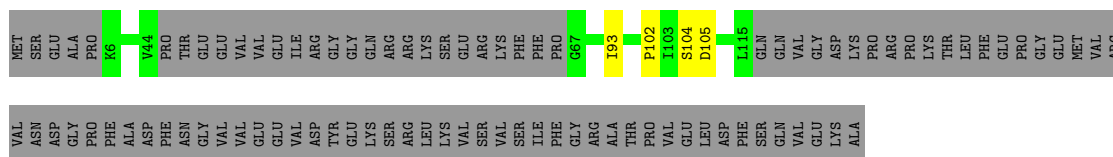




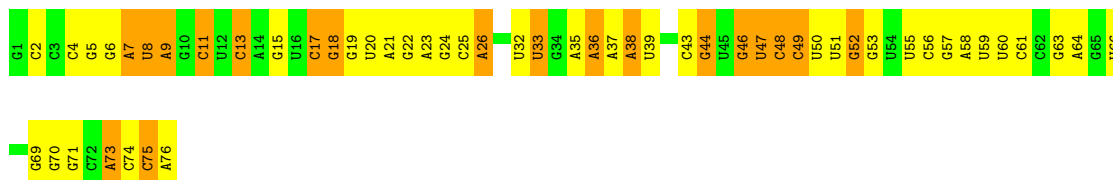
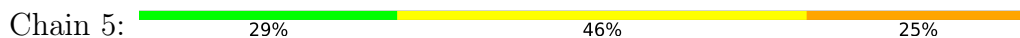
- Molecule 60: DNA-directed RNA polymerase subunit omega



- Molecule 61: Transcription termination/antitermination protein NusG



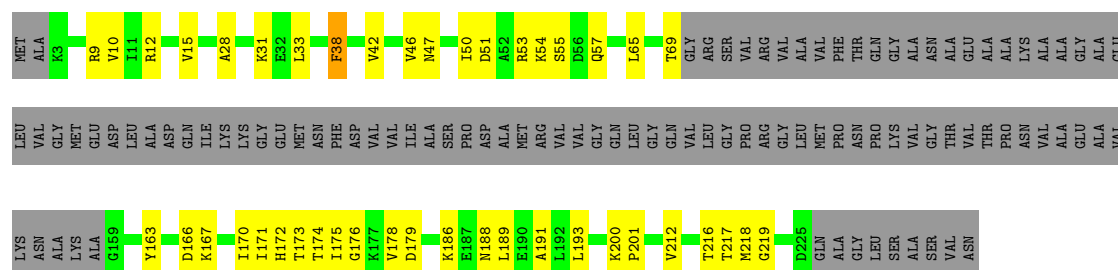
- Molecule 62: tRNA(Phe)



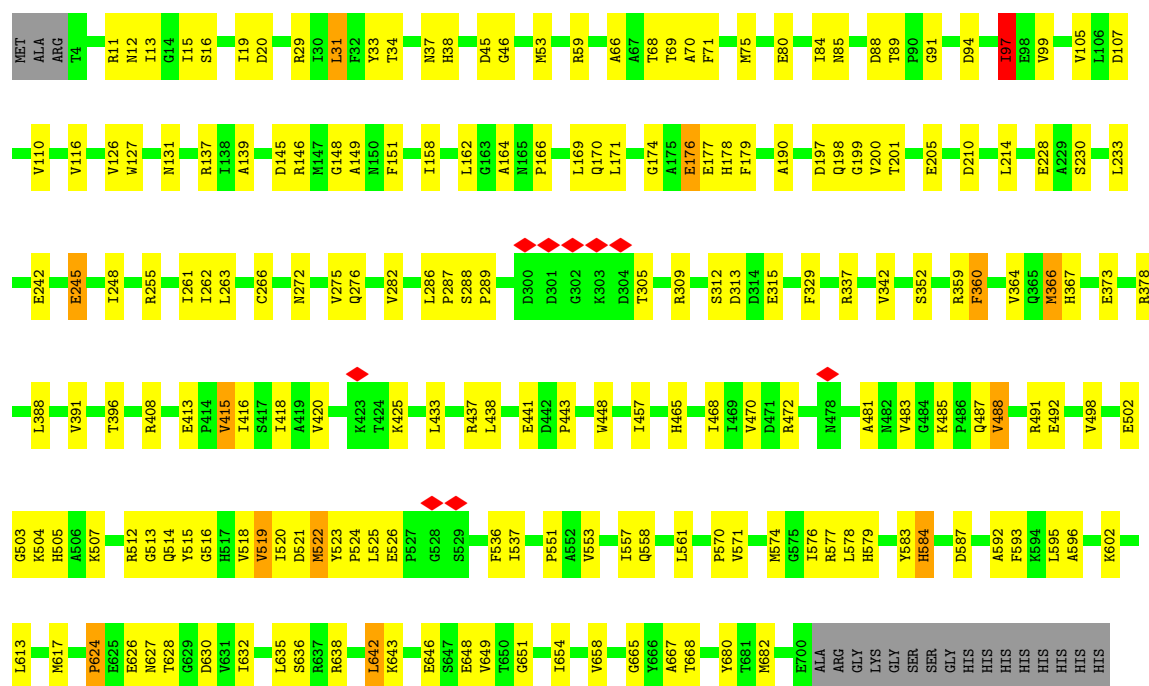
- Molecule 63: tRNA(fMet)



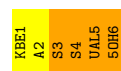
- Chain a: 



- Chain 0: 70% 26% .



- Chain h:  33% 67%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	626298	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	0.082	Depositor
Minimum map value	-0.033	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.005	Depositor
Map size (\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 (\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: 5OH, UAL, PO4, DPP, KBE, MG, GDP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.47	0/531	0.99	4/709 (0.6%)
2	B	0.51	0/450	0.84	0/599
3	C	0.35	0/416	0.73	0/554
4	D	0.41	0/380	0.89	1/498 (0.2%)
5	E	0.49	0/513	0.87	0/676
6	F	0.34	0/303	0.77	0/397
7	G	0.48	0/1735	0.93	8/2338 (0.3%)
8	H	0.51	0/1647	0.94	4/2221 (0.2%)
9	I	0.46	0/1665	0.98	7/2227 (0.3%)
10	J	0.53	0/1165	0.94	5/1568 (0.3%)
11	K	0.58	0/835	1.02	5/1128 (0.4%)
12	L	0.45	0/1195	1.02	8/1602 (0.5%)
13	M	0.38	0/989	0.80	0/1326
14	N	0.55	0/1034	1.09	6/1375 (0.4%)
15	O	0.58	0/796	1.05	3/1077 (0.3%)
16	P	0.41	0/885	0.98	6/1195 (0.5%)
17	Q	0.62	1/969 (0.1%)	1.05	5/1300 (0.4%)
18	R	0.39	0/892	0.87	1/1193 (0.1%)
19	S	0.39	0/817	0.90	2/1088 (0.2%)
20	T	0.41	0/722	0.84	0/964
21	U	0.40	0/659	0.91	2/884 (0.2%)
22	V	0.41	0/657	0.85	2/881 (0.2%)
23	W	0.47	0/544	0.95	2/731 (0.3%)
24	X	0.40	0/652	0.95	1/877 (0.1%)
25	Y	0.38	0/671	0.90	2/888 (0.2%)
26	Z	0.60	0/550	1.12	2/728 (0.3%)
27	b	0.45	0/2121	0.93	6/2852 (0.2%)
28	c	0.39	0/1586	0.84	4/2134 (0.2%)
29	d	0.43	0/1571	0.78	0/2113
30	e	0.43	0/1434	0.87	3/1926 (0.2%)
31	f	0.41	0/1343	0.82	2/1816 (0.1%)
32	g	0.47	0/1122	0.93	3/1515 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.70	1/1046 (0.1%)	1.16	6/1410 (0.4%)
34	j	0.39	0/1152	0.86	4/1551 (0.3%)
35	k	0.50	0/947	0.92	1/1268 (0.1%)
36	l	0.41	0/1054	0.95	4/1403 (0.3%)
37	m	0.39	0/1093	0.85	3/1460 (0.2%)
38	n	0.39	0/973	0.92	3/1301 (0.2%)
39	o	0.39	0/902	0.92	3/1209 (0.2%)
40	p	0.40	0/929	0.85	1/1242 (0.1%)
41	q	0.48	0/960	0.86	1/1278 (0.1%)
42	r	0.49	0/829	0.96	1/1107 (0.1%)
43	s	0.39	0/864	0.84	2/1156 (0.2%)
44	t	0.39	0/744	0.78	0/994
45	u	0.41	0/784	0.92	3/1047 (0.3%)
46	v	0.39	0/766	0.78	0/1025
47	w	0.34	0/582	0.72	0/769
48	x	0.37	0/635	0.85	2/848 (0.2%)
49	y	0.34	0/510	0.87	1/677 (0.1%)
50	z	0.50	0/453	0.75	0/605
51	1	0.44	0/69796	0.54	8/108888 (0.0%)
52	2	0.45	0/2872	0.53	1/4479 (0.0%)
53	3	0.45	0/36963	0.53	3/57662 (0.0%)
54	4	0.56	0/431	0.62	0/668
55	8	0.56	0/599	0.71	1/919 (0.1%)
56	9	0.48	0/468	0.52	0/719
57	A1	0.48	0/1696	0.69	0/2298
57	A2	0.42	0/1718	0.62	0/2328
58	B1	0.56	4/10510 (0.0%)	0.74	8/14196 (0.1%)
59	B2	0.47	0/10663	0.68	2/14396 (0.0%)
60	W0	0.29	0/652	0.61	0/879
61	NG	0.55	0/431	0.79	0/596
62	5	0.56	0/1812	0.88	2/2823 (0.1%)
63	6	0.43	0/1832	0.56	0/2855
64	a	0.47	0/1033	0.98	5/1387 (0.4%)
65	0	0.51	0/5501	0.96	19/7446 (0.3%)
66	h	3.19	2/11 (18.2%)	0.75	0/13
All	All	0.46	8/193060 (0.0%)	0.68	178/284282 (0.1%)

The worst 5 of 8 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	-6.20	1.40	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	B1	1350	ASN	CG-ND2	-5.25	1.22	1.33
33	i	2	LYS	N-CA	5.17	1.49	1.46
58	B1	424	ASN	CG-ND2	-5.14	1.22	1.33

The worst 5 of 178 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	57	VAL	N-CA-C	-10.06	103.67	112.12
65	0	174	GLY	N-CA-C	10.05	123.42	111.35
11	K	99	ALA	N-CA-C	9.92	123.42	111.02
64	a	179	ASP	N-CA-C	-9.71	99.89	114.64
16	P	73	VAL	N-CA-C	-9.11	104.45	113.20

There are no chirality outliers.

There are no planarity outliers.

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	522	0	524	19	0
2	B	444	0	461	10	0
3	C	409	0	440	7	0
4	D	377	0	418	14	0
5	E	504	0	574	9	0
6	F	302	0	341	10	0
7	G	1704	0	1732	25	0
8	H	1620	0	1688	36	0
9	I	1643	0	1710	43	0
10	J	1152	0	1195	21	0
11	K	817	0	808	16	0
12	L	1181	0	1240	27	0
13	M	979	0	1034	13	0
14	N	1022	0	1070	35	0
15	O	786	0	828	28	0
16	P	869	0	878	23	0
17	Q	955	0	1019	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	R	883	0	944	21	0
19	S	805	0	847	21	0
20	T	714	0	737	12	0
21	U	649	0	666	21	0
22	V	648	0	691	20	0
23	W	535	0	552	14	0
24	X	637	0	665	22	0
25	Y	665	0	714	21	0
26	Z	544	0	579	10	0
27	b	2082	0	2157	54	0
28	c	1565	0	1616	36	0
29	d	1552	0	1619	25	0
30	e	1410	0	1447	28	0
31	f	1323	0	1374	20	0
32	g	1111	0	1148	19	0
33	i	1032	0	1088	59	0
34	j	1129	0	1162	21	0
35	k	938	0	1012	19	0
36	l	1045	0	1117	30	0
37	m	1074	0	1157	17	0
38	n	960	0	1000	20	0
39	o	892	0	923	21	0
40	p	917	0	965	21	0
41	q	947	0	1022	18	0
42	r	816	0	839	16	0
43	s	857	0	922	15	0
44	t	738	0	807	12	0
45	u	776	0	825	6	0
46	v	753	0	780	17	0
47	w	575	0	592	16	0
48	x	625	0	655	14	0
49	y	509	0	543	8	0
50	z	449	0	491	9	0
51	1	62317	0	31346	959	0
52	2	2568	0	1303	57	0
53	3	33012	0	16618	566	0
54	4	387	0	192	6	0
55	8	539	0	305	29	0
56	9	417	0	224	6	0
57	A1	1677	0	1713	27	0
57	A2	1698	0	1718	16	0
58	B1	10353	0	10548	330	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	B2	10496	0	10451	173	0
60	W0	650	0	658	10	0
61	NG	433	0	193	8	0
62	5	1622	0	821	23	0
63	6	1640	0	837	19	0
64	a	1026	0	1092	31	0
65	0	5399	0	5363	109	0
66	h	48	0	40	7	0
67	B1	1	0	0	0	0
68	0	28	0	12	2	0
69	0	5	0	0	1	0
All	All	179757	0	131050	2851	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 9.

The worst 5 of 2851 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)
23:W:42:ARG:NH2	53:3:721:G:H5''	1.59	1.17
35:k:48:PRO:HB3	53:3:1423:G:H5''	1.23	1.16
33:i:93:ASN:HB2	51:1:1077:A:H5'	1.12	1.07
51:1:2682:A:H61	51:1:2728:U:H1'	1.17	1.07
51:1:1064:C:H3'	51:1:1065:U:H5''	1.37	1.07

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	64/70 (91%)	54 (84%)	10 (16%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
3	C	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
4	D	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
5	E	62/65 (95%)	53 (86%)	9 (14%)	0	100	100
6	F	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
7	G	216/241 (90%)	187 (87%)	29 (13%)	0	100	100
8	H	204/233 (88%)	181 (89%)	22 (11%)	1 (0%)	25	64
9	I	203/206 (98%)	178 (88%)	25 (12%)	0	100	100
10	J	155/167 (93%)	133 (86%)	21 (14%)	1 (1%)	22	60
11	K	98/135 (73%)	83 (85%)	14 (14%)	1 (1%)	13	49
12	L	149/179 (83%)	130 (87%)	17 (11%)	2 (1%)	10	43
13	M	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
14	N	125/130 (96%)	97 (78%)	26 (21%)	2 (2%)	8	38
15	O	96/103 (93%)	77 (80%)	18 (19%)	1 (1%)	13	49
16	P	114/129 (88%)	90 (79%)	22 (19%)	2 (2%)	7	35
17	Q	121/124 (98%)	100 (83%)	18 (15%)	3 (2%)	4	26
18	R	112/118 (95%)	99 (88%)	12 (11%)	1 (1%)	14	52
19	S	98/101 (97%)	80 (82%)	15 (15%)	3 (3%)	3	22
20	T	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
21	U	80/82 (98%)	69 (86%)	10 (12%)	1 (1%)	10	43
22	V	78/84 (93%)	67 (86%)	10 (13%)	1 (1%)	10	43
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%)	80 (96%)	3 (4%)	0	100	100
26	Z	63/71 (89%)	45 (71%)	18 (29%)	0	100	100
27	b	269/273 (98%)	233 (87%)	31 (12%)	5 (2%)	6	32
28	c	207/209 (99%)	181 (87%)	25 (12%)	1 (0%)	25	64
29	d	199/201 (99%)	186 (94%)	13 (6%)	0	100	100
30	e	175/179 (98%)	159 (91%)	16 (9%)	0	100	100
31	f	174/177 (98%)	152 (87%)	19 (11%)	3 (2%)	7	37
32	g	147/149 (99%)	133 (90%)	13 (9%)	1 (1%)	19	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	i	139/142 (98%)	115 (83%)	23 (16%)	1 (1%)	19	57
34	j	140/142 (99%)	128 (91%)	11 (8%)	1 (1%)	19	57
35	k	120/123 (98%)	100 (83%)	20 (17%)	0	100	100
36	l	141/144 (98%)	121 (86%)	20 (14%)	0	100	100
37	m	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
38	n	118/127 (93%)	101 (86%)	17 (14%)	0	100	100
39	o	114/117 (97%)	103 (90%)	10 (9%)	1 (1%)	14	52
40	p	112/115 (97%)	102 (91%)	10 (9%)	0	100	100
41	q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
42	r	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
43	s	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
44	t	91/100 (91%)	78 (86%)	13 (14%)	0	100	100
45	u	100/104 (96%)	81 (81%)	18 (18%)	1 (1%)	13	49
46	v	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
47	w	73/85 (86%)	68 (93%)	5 (7%)	0	100	100
48	x	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
49	y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	8	38
50	z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
57	A1	214/329 (65%)	195 (91%)	19 (9%)	0	100	100
57	A2	217/329 (66%)	206 (95%)	11 (5%)	0	100	100
58	B1	1329/1407 (94%)	1206 (91%)	119 (9%)	4 (0%)	37	73
59	B2	1338/1342 (100%)	1204 (90%)	129 (10%)	5 (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	45
64	a	130/234 (56%)	112 (86%)	18 (14%)	0	100	100
65	0	695/716 (97%)	621 (89%)	71 (10%)	3 (0%)	30	68
66	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	9806/10690 (92%)	8733 (89%)	1026 (10%)	47 (0%)	27	64

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	Q	87	LYS

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Mol	Chain	Res	Type
31	f	45	ALA
32	g	136	SER
49	y	24	GLU
58	B1	121	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	59/62 (95%)	56 (95%)	3 (5%)	20	41
2	B	47/48 (98%)	45 (96%)	2 (4%)	25	46
3	C	45/49 (92%)	45 (100%)	0	100	100
4	D	38/38 (100%)	37 (97%)	1 (3%)	41	59
5	E	51/52 (98%)	48 (94%)	3 (6%)	16	37
6	F	34/34 (100%)	34 (100%)	0	100	100
7	G	180/199 (90%)	174 (97%)	6 (3%)	33	52
8	H	169/190 (89%)	158 (94%)	11 (6%)	14	35
9	I	172/173 (99%)	165 (96%)	7 (4%)	26	47
10	J	118/126 (94%)	114 (97%)	4 (3%)	32	51
11	K	87/116 (75%)	83 (95%)	4 (5%)	23	44
12	L	124/147 (84%)	122 (98%)	2 (2%)	58	74
13	M	104/105 (99%)	104 (100%)	0	100	100
14	N	105/107 (98%)	95 (90%)	10 (10%)	7	22
15	O	86/90 (96%)	77 (90%)	9 (10%)	5	19
16	P	89/99 (90%)	88 (99%)	1 (1%)	70	80
17	Q	103/104 (99%)	93 (90%)	10 (10%)	6	22
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%)	71 (93%)	5 (7%)	14	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	U	65/65 (100%)	64 (98%)	1 (2%)	60	75
22	V	74/78 (95%)	73 (99%)	1 (1%)	62	75
23	W	56/65 (86%)	54 (96%)	2 (4%)	30	50
24	X	70/79 (89%)	69 (99%)	1 (1%)	62	75
25	Y	65/66 (98%)	65 (100%)	0	100	100
26	Z	55/61 (90%)	52 (94%)	3 (6%)	18	39
27	b	216/218 (99%)	212 (98%)	4 (2%)	52	69
28	c	164/164 (100%)	162 (99%)	2 (1%)	67	79
29	d	165/165 (100%)	163 (99%)	2 (1%)	67	79
30	e	148/150 (99%)	144 (97%)	4 (3%)	40	58
31	f	137/138 (99%)	137 (100%)	0	100	100
32	g	114/114 (100%)	112 (98%)	2 (2%)	54	71
33	i	109/110 (99%)	95 (87%)	14 (13%)	3	14
34	j	116/116 (100%)	115 (99%)	1 (1%)	75	83
35	k	103/104 (99%)	96 (93%)	7 (7%)	13	34
36	l	102/103 (99%)	100 (98%)	2 (2%)	50	68
37	m	109/109 (100%)	109 (100%)	0	100	100
38	n	100/103 (97%)	99 (99%)	1 (1%)	73	82
39	o	86/87 (99%)	86 (100%)	0	100	100
40	p	99/100 (99%)	97 (98%)	2 (2%)	50	68
41	q	89/90 (99%)	84 (94%)	5 (6%)	17	38
42	r	84/84 (100%)	81 (96%)	3 (4%)	30	50
43	s	93/93 (100%)	93 (100%)	0	100	100
44	t	80/84 (95%)	79 (99%)	1 (1%)	65	77
45	u	82/85 (96%)	81 (99%)	1 (1%)	67	79
46	v	78/78 (100%)	77 (99%)	1 (1%)	65	77
47	w	57/63 (90%)	56 (98%)	1 (2%)	54	71
48	x	67/68 (98%)	67 (100%)	0	100	100
49	y	55/55 (100%)	55 (100%)	0	100	100
50	z	48/49 (98%)	46 (96%)	2 (4%)	25	46
57	A1	185/286 (65%)	174 (94%)	11 (6%)	16	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	A2	186/286 (65%)	186 (100%)	0	100	100
58	B1	1110/1168 (95%)	1020 (92%)	90 (8%)	9	28
59	B2	1137/1157 (98%)	1111 (98%)	26 (2%)	45	64
60	W0	70/75 (93%)	69 (99%)	1 (1%)	62	75
64	a	110/181 (61%)	110 (100%)	0	100	100
65	0	574/588 (98%)	546 (95%)	28 (5%)	21	42
66	h	2/2 (100%)	2 (100%)	0	100	100
All	All	8122/8683 (94%)	7823 (96%)	299 (4%)	31	49

5 of 299 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
58	B1	514	THR
65	0	551	PRO
58	B1	1181	ASP
59	B2	872	TYR
30	e	174	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 153 such sidechains are listed below:

Mol	Chain	Res	Type
58	B1	469	HIS
65	0	157	GLN
58	B1	1195	GLN
59	B2	808	ASN
65	0	517	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	419 (14%)	10 (0%)
52	2	119/120 (99%)	12 (10%)	1 (0%)
53	3	1538/1542 (99%)	182 (11%)	6 (0%)
54	4	16/27 (59%)	2 (12%)	0
62	5	75/76 (98%)	38 (50%)	7 (9%)
63	6	76/77 (98%)	18 (23%)	0
All	All	4726/4746 (99%)	671 (14%)	24 (0%)

5 of 671 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	1	10	A
51	1	12	U
51	1	35	G
51	1	42	A
51	1	46	G

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	3	1054	C
62	5	7	A
53	3	1395	C
62	5	35	A
51	1	2296	U

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

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	5OH	h	6	66	8,12,13	0.79	0	3,16,18	1.49	1 (33%)
66	KBE	h	1	66	8,8,9	0.61	0	7,8,10	1.20	1 (14%)
66	UAL	h	5	66	7,8,9	2.29	3 (42%)	5,9,11	2.91	2 (40%)
66	DPP	h	2	66	3,5,6	0.57	0	1,5,7	0.08	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
66	5OH	h	6	66	-	0/2/18/20	0/1/1/1

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	h	5	UAL	C1-N1	-4.83	1.32	1.40
66	h	5	UAL	C-CA	-2.90	1.40	1.45
66	h	5	UAL	CA-N	2.02	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	-5.29	115.63	125.60
66	h	5	UAL	O-C-CA	-3.24	121.27	125.39
66	h	6	5OH	CR-CB-CA	-2.33	110.09	112.61
66	h	1	KBE	CB-CA-C	-2.04	109.25	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	h	6	5OH	4	0
66	h	5	UAL	2	0
66	h	2	DPP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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$
68	GDP	0	801	-	24,30,30	0.93	1 (4%)	30,47,47	1.45	5 (16%)
69	PO4	0	802	-	4,4,4	1.11	0	6,6,6	0.69	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
68	GDP	0	801	-	-	0/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
68	0	801	GDP	C6-N1	-2.51	1.34	1.37

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	0	801	GDP	PA-O3A-PB	-4.36	117.86	132.83
68	0	801	GDP	C3'-C2'-C1'	2.55	104.82	100.98
68	0	801	GDP	C5-C6-N1	2.37	118.14	113.95
68	0	801	GDP	C8-N7-C5	2.24	107.25	102.99
68	0	801	GDP	O6-C6-C5	-2.09	120.29	124.37

There are no chirality outliers.

There are no torsion outliers.

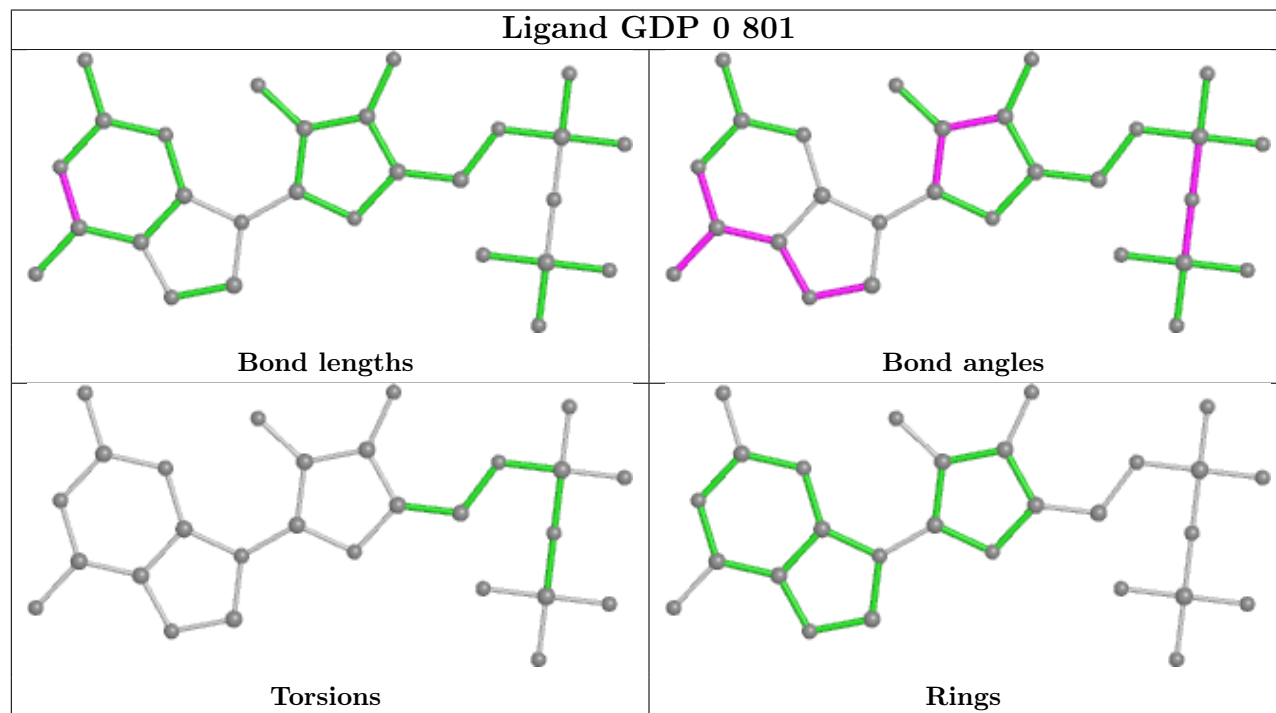
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
68	0	801	GDP	2	0
69	0	802	PO4	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.

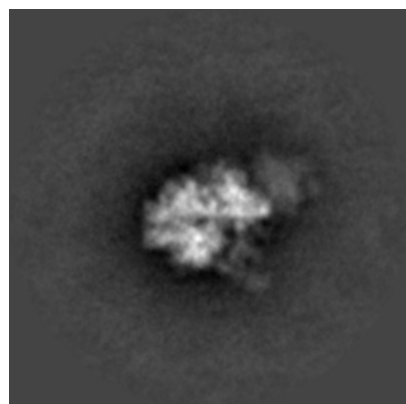
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38940. These allow visual inspection of the internal detail of the map and identification of artifacts.

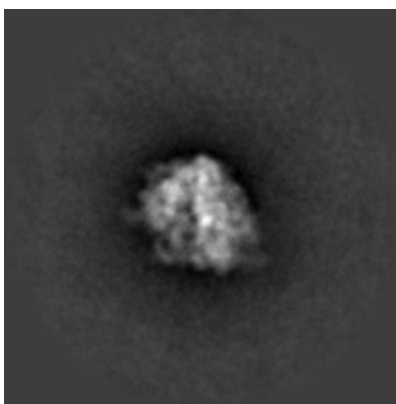
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

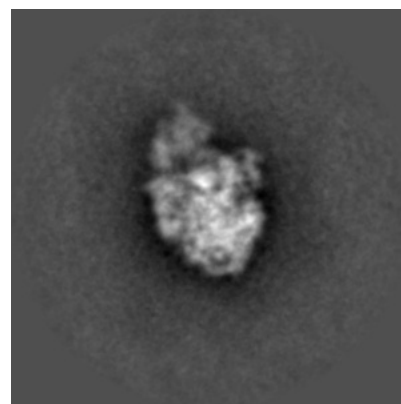
6.1.1 Primary map



X

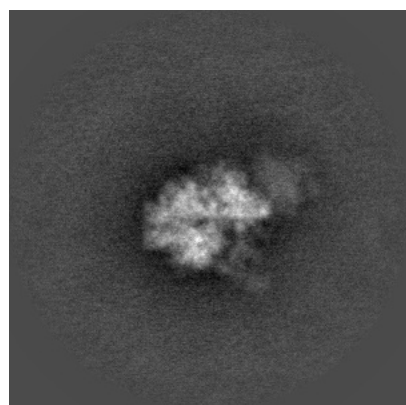


Y

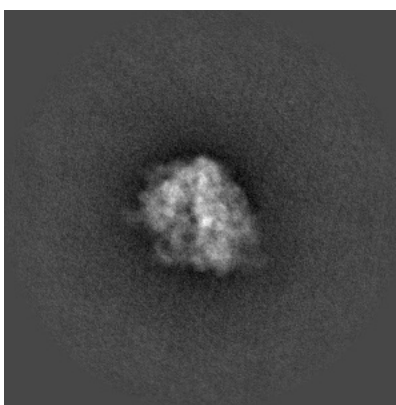


Z

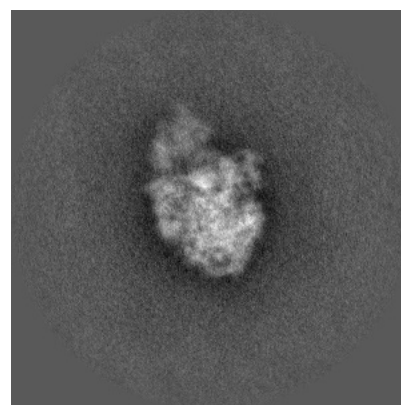
6.1.2 Raw map



X



Y

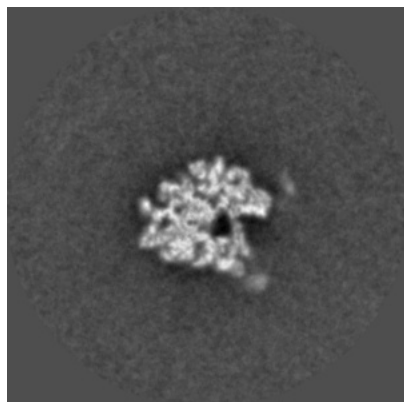


Z

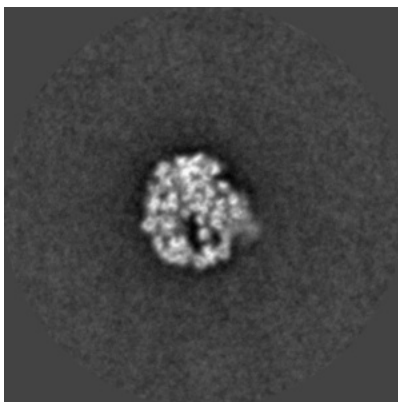
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

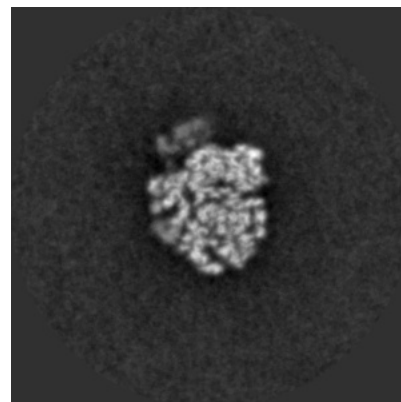
6.2.1 Primary map



X Index: 240

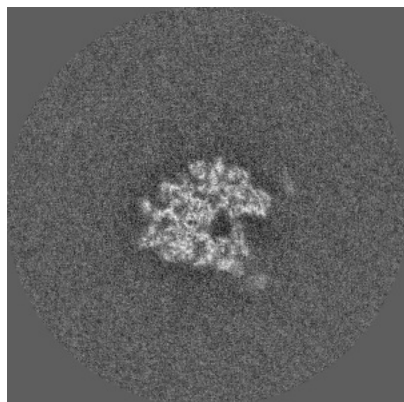


Y Index: 240

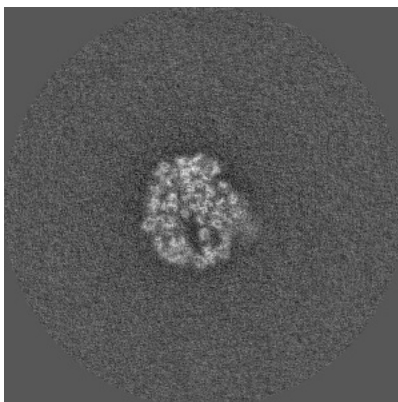


Z Index: 240

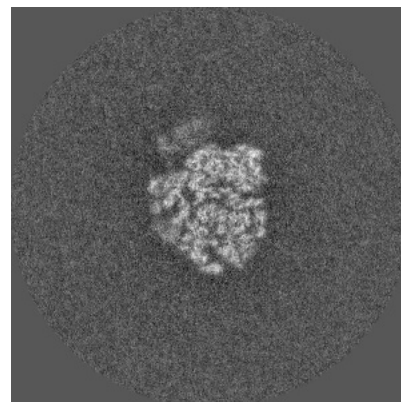
6.2.2 Raw map



X Index: 240



Y Index: 240

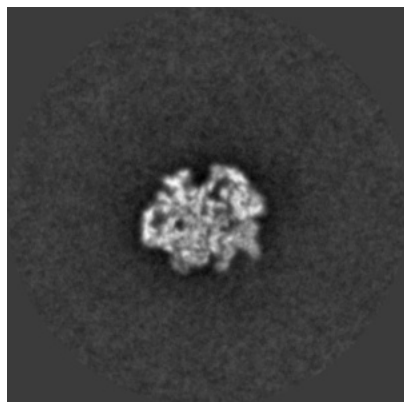


Z Index: 240

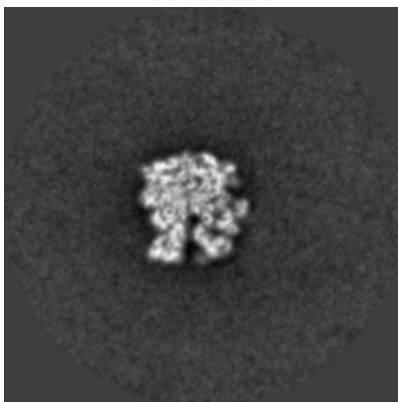
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

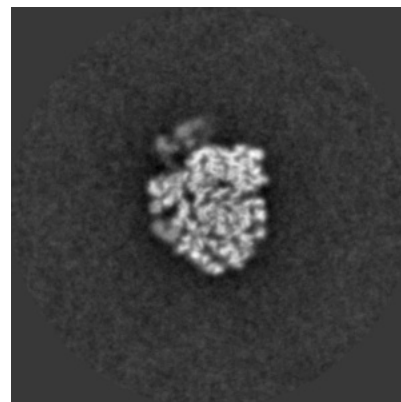
6.3.1 Primary map



X Index: 262

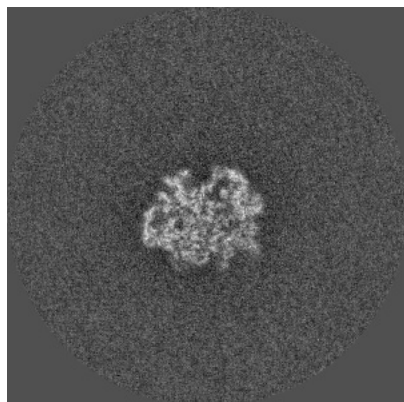


Y Index: 223

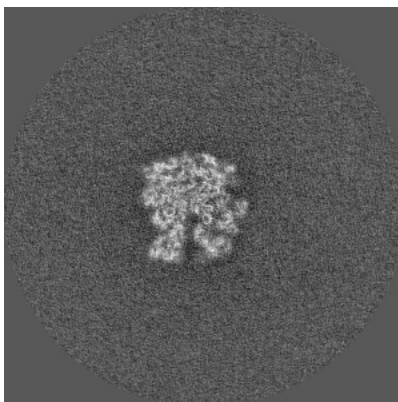


Z Index: 238

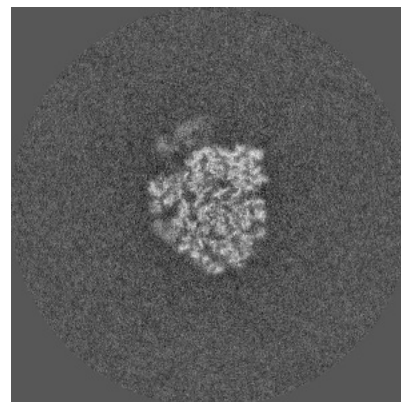
6.3.2 Raw map



X Index: 263



Y Index: 223

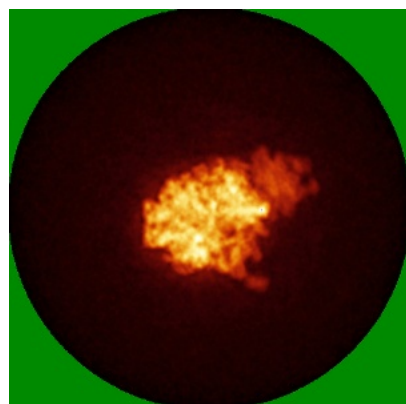


Z Index: 238

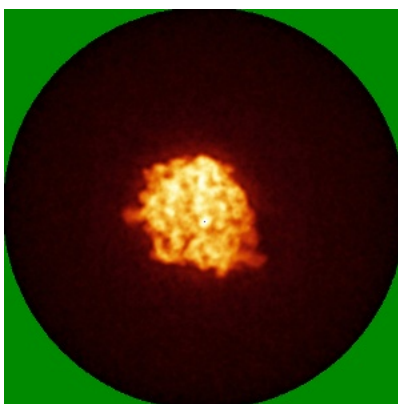
The images above show the largest variance slices of the map in three orthogonal directions.

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

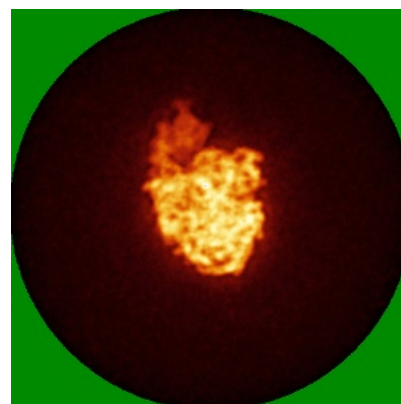
6.4.1 Primary map



X

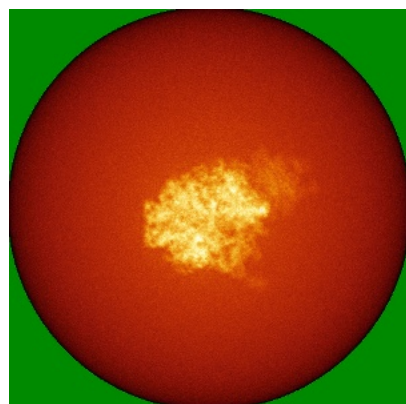


Y

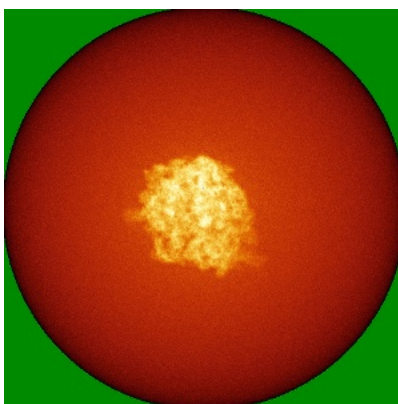


Z

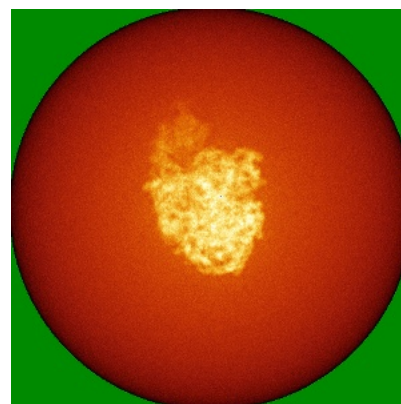
6.4.2 Raw map



X



Y

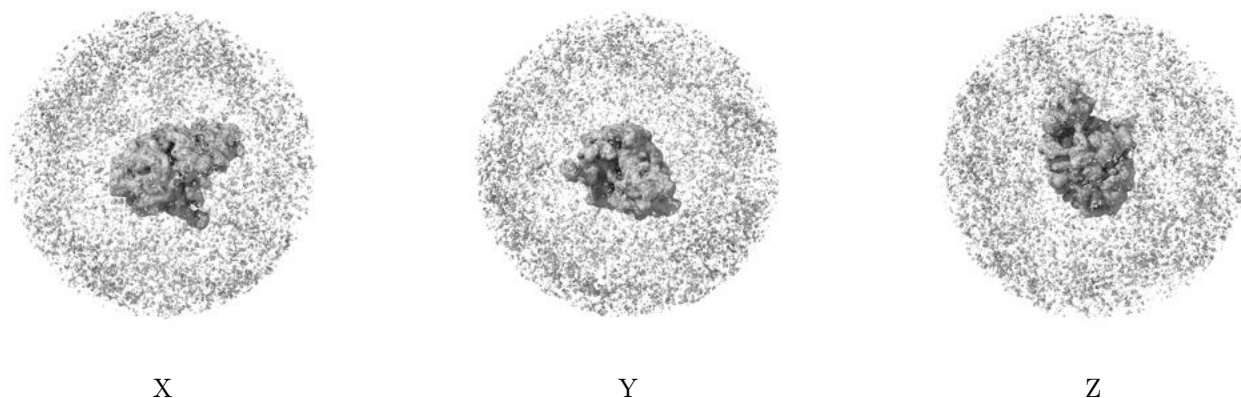


Z

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.

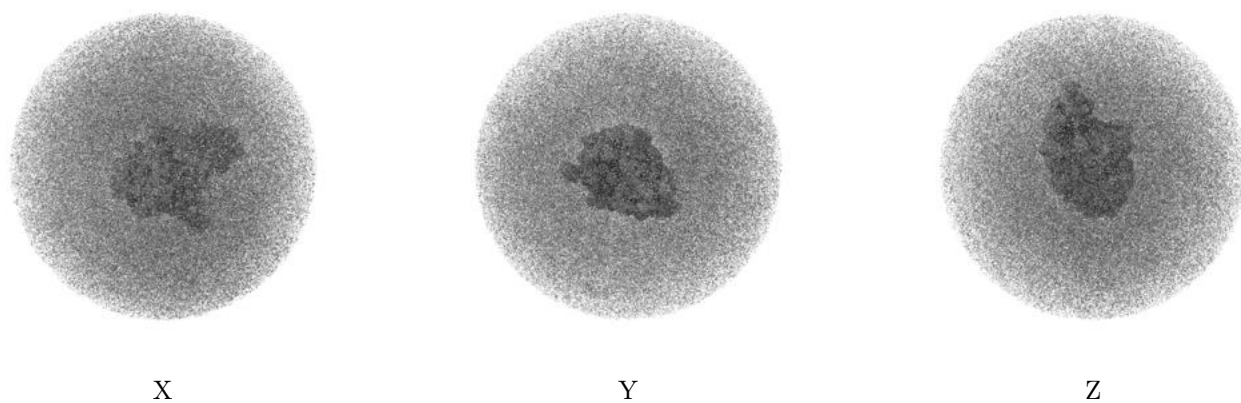
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. 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.

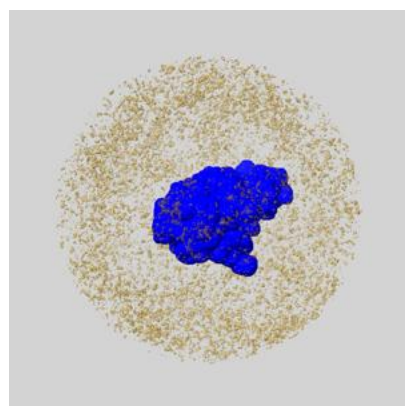
6.6 Mask visualisation [i](#)

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

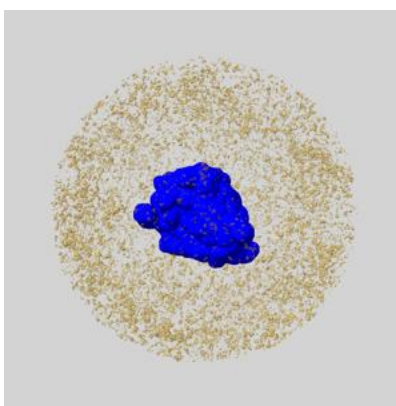
A mask typically either:

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

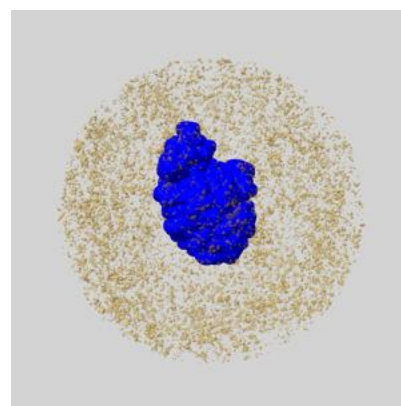
6.6.1 emd_38940_msk_1.map [i](#)



X



Y

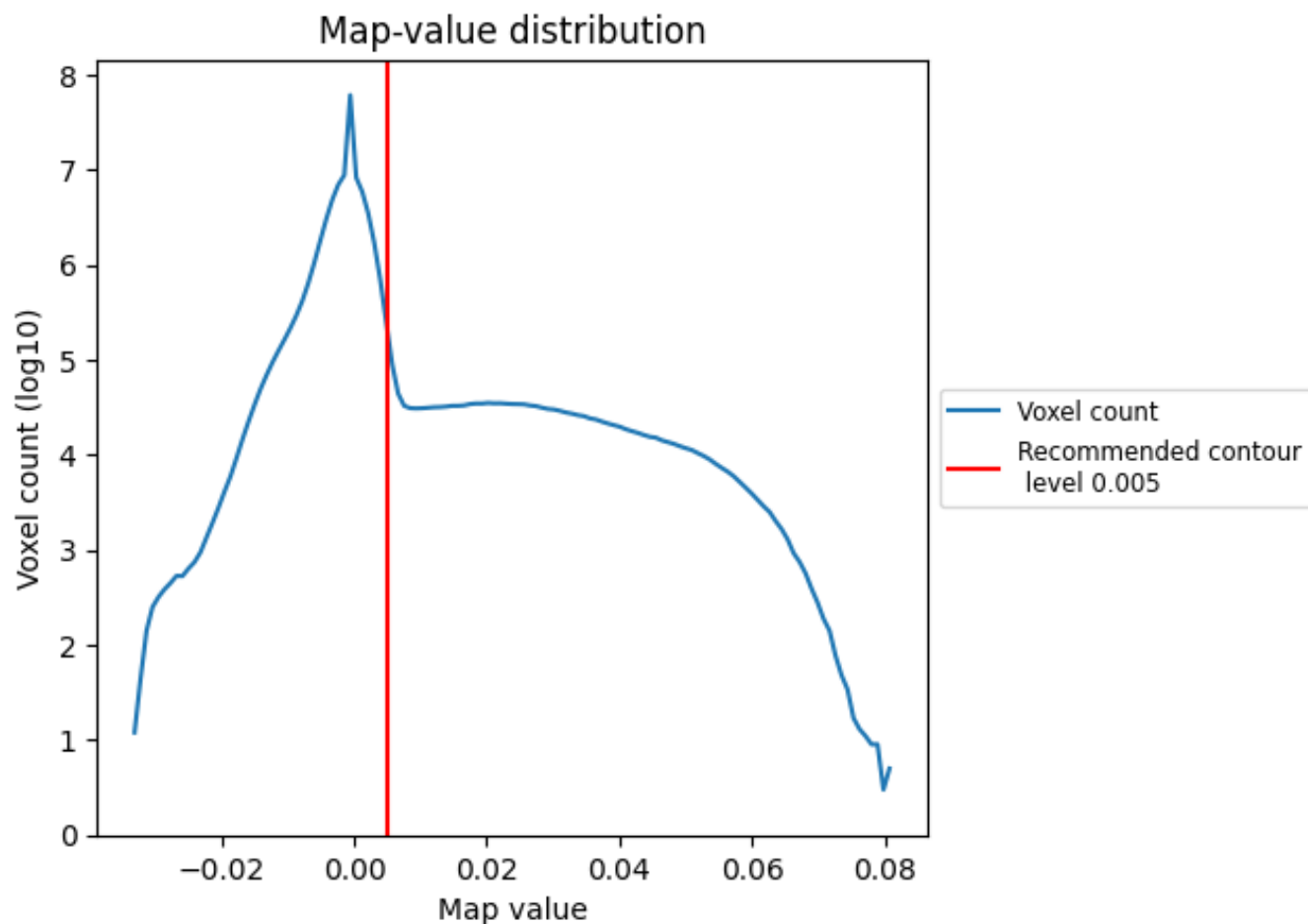


Z

7 Map analysis [i](#)

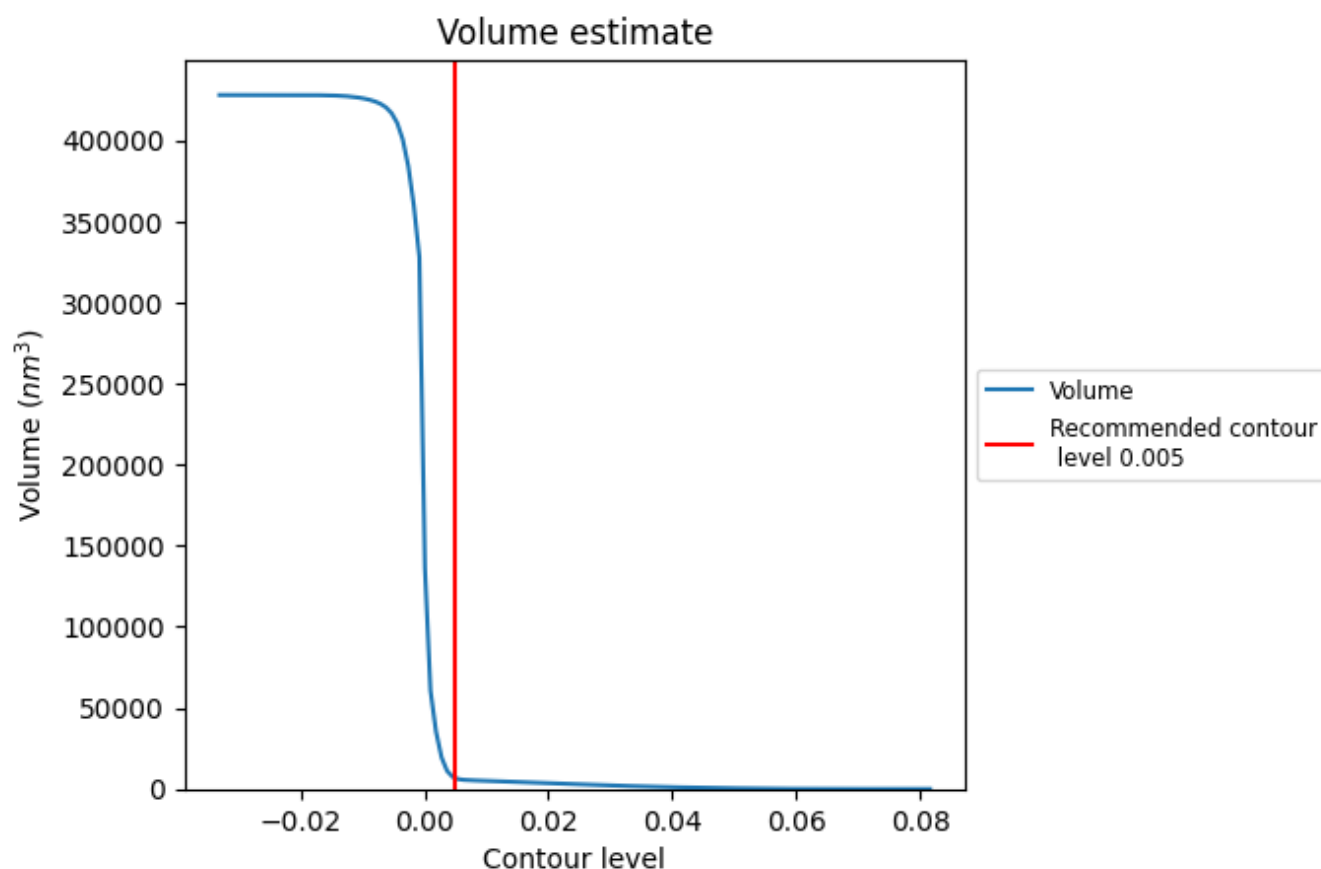
This section contains the results of statistical analysis of the map.

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.

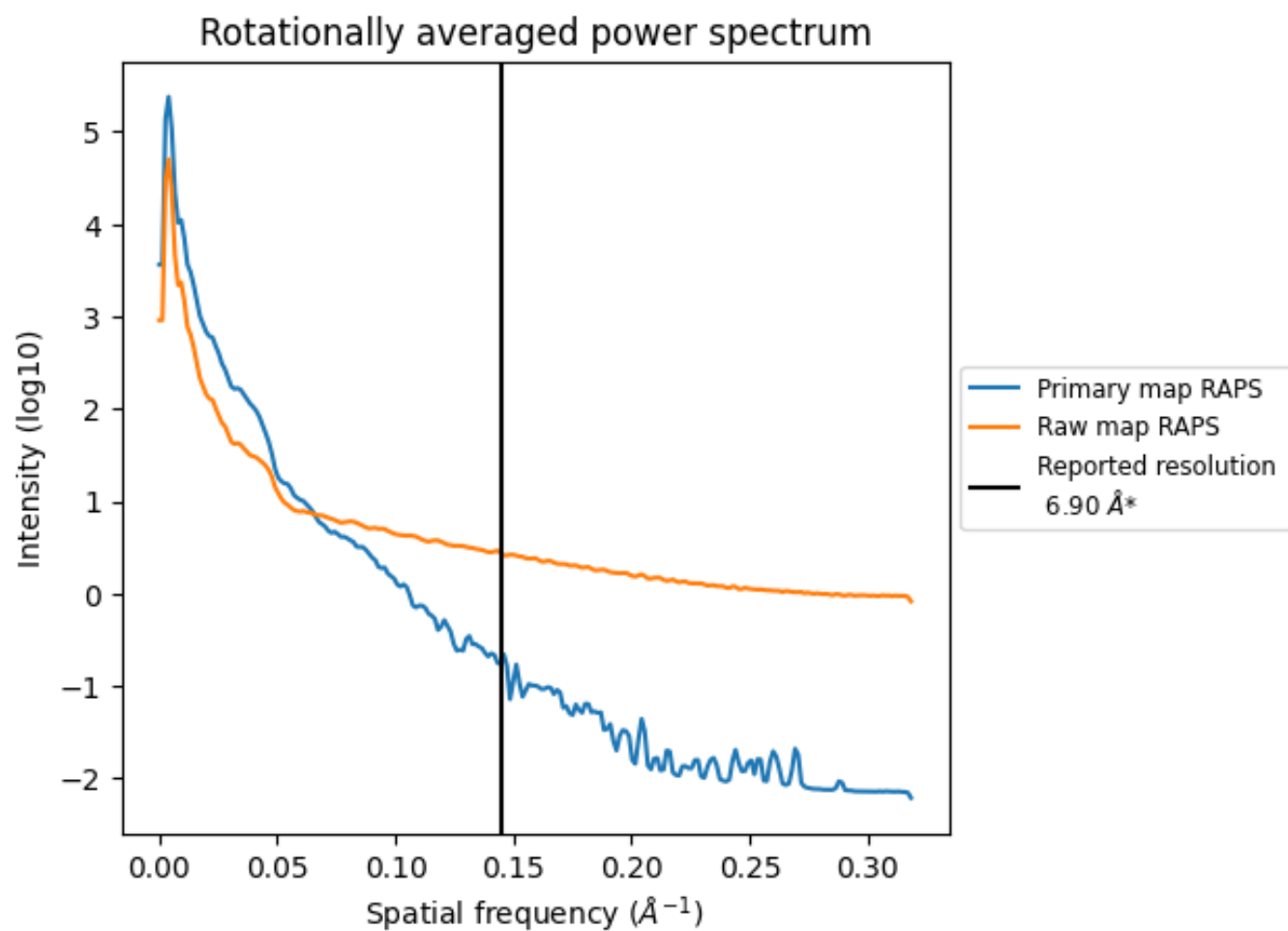
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6757 nm^3 ; this corresponds to an approximate mass of 6104 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 ⓘ

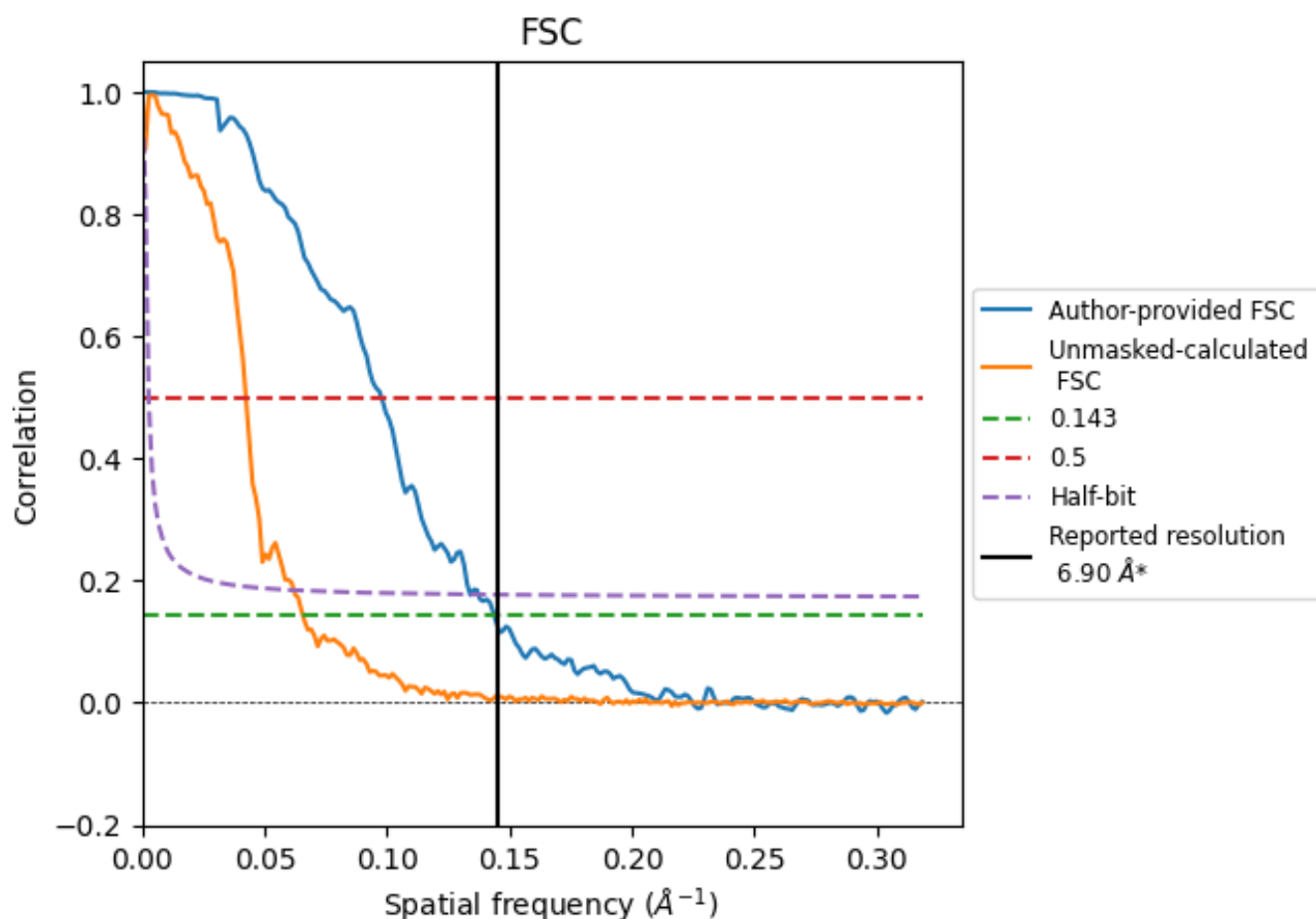


*Reported resolution corresponds to spatial frequency of 0.145 \AA^{-1}

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 0.145 Å⁻¹

8.2 Resolution estimates [i](#)

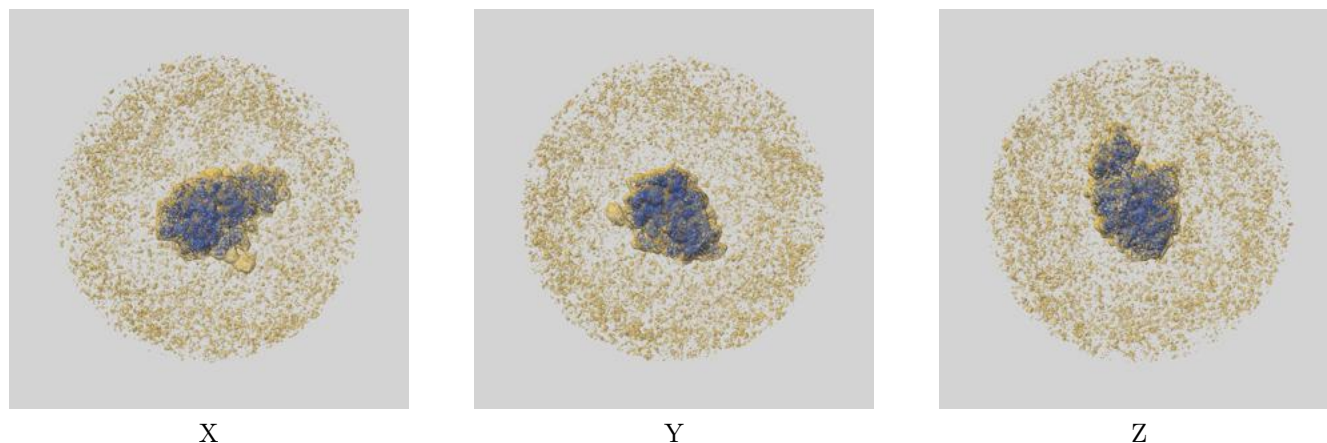
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.90	-	-
Author-provided FSC curve	6.95	10.24	7.46
Unmasked-calculated*	15.22	23.64	16.16

*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 15.22 differs from the reported value 6.9 by more than 10 %

9 Map-model fit [i](#)

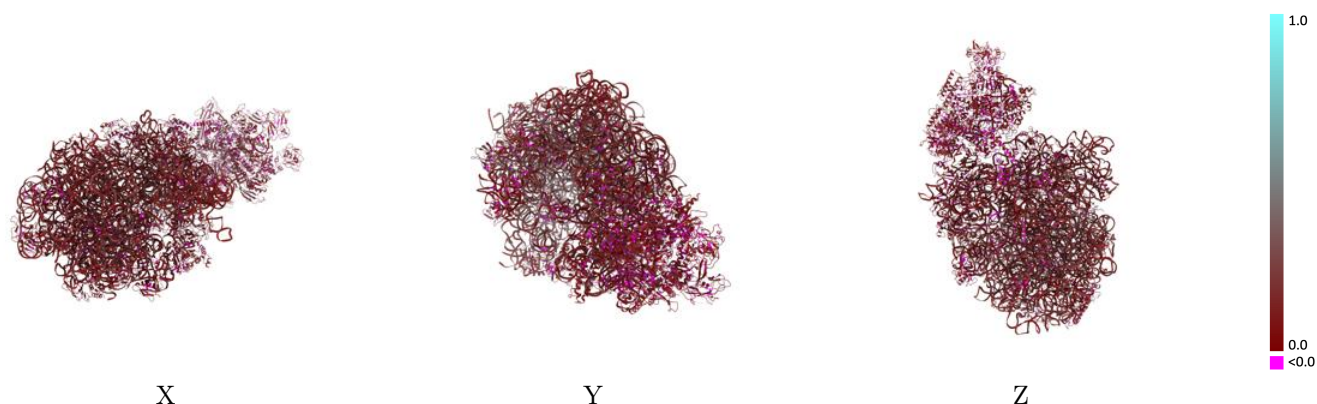
This section contains information regarding the fit between EMDB map EMD-38940 and PDB model 8Y5K. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

9.1 Map-model overlay [i](#)



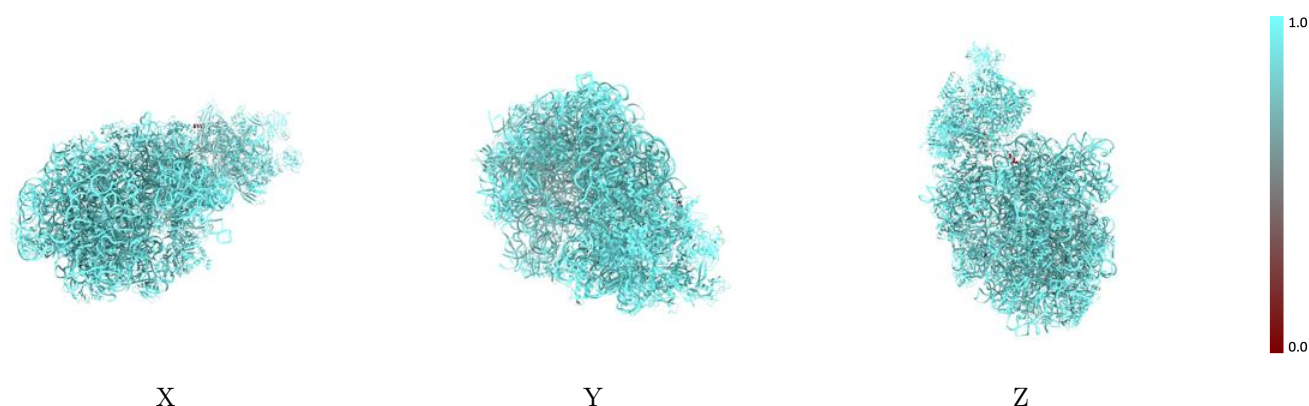
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



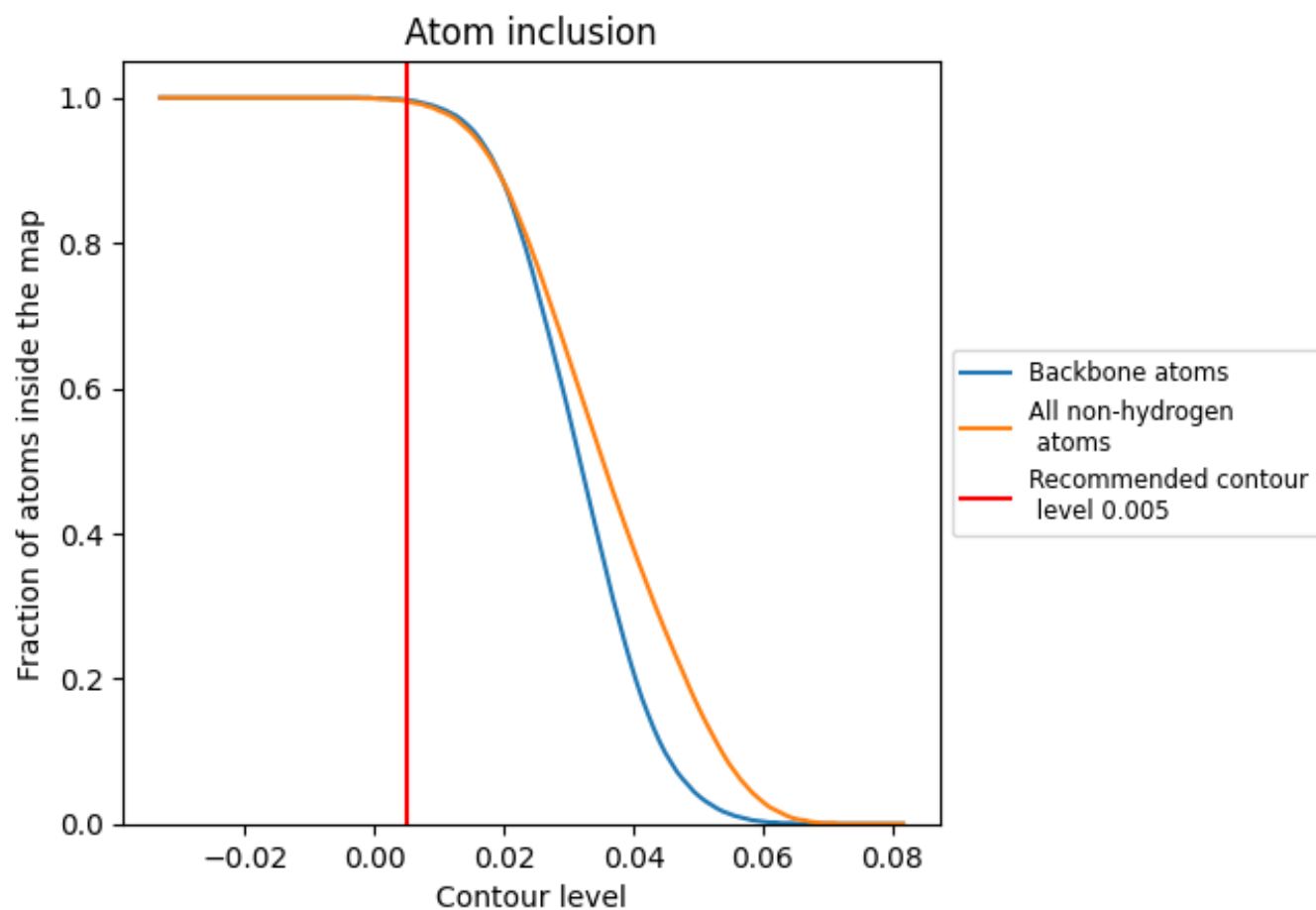
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.005).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9950	 0.1370
0	 0.9740	 0.1210
1	 1.0000	 0.1650
2	 1.0000	 0.1430
3	 1.0000	 0.1560
4	 1.0000	 0.1610
5	 0.9990	 0.1110
6	 0.9970	 0.1430
8	 1.0000	 0.1480
9	 1.0000	 0.1360
A	 0.9710	 0.0770
A1	 0.9900	 0.1070
A2	 0.9970	 0.1060
B	 1.0000	 0.0900
B1	 0.9880	 0.1060
B2	 0.9870	 0.0970
C	 0.9830	 0.0980
D	 0.9920	 0.0780
E	 1.0000	 0.0690
F	 1.0000	 0.0830
G	 0.9990	 0.1160
H	 0.9930	 0.1260
I	 0.9990	 0.1050
J	 0.9980	 0.1210
K	 0.9890	 0.1230
L	 0.9850	 0.1180
M	 0.9950	 0.1150
N	 0.9980	 0.0880
NG	 1.0000	 0.1490
O	 0.9990	 0.1010
P	 0.9990	 0.1250
Q	 0.9630	 0.1070
R	 0.9990	 0.1290
S	 1.0000	 0.0990
T	 0.9990	 0.1140



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Chain	Atom inclusion	Q-score
U	 1.0000	 0.1040
V	 0.9970	 0.1090
W	 1.0000	 0.1070
W0	 0.6910	 0.0270
X	 1.0000	 0.1030
Y	 0.9970	 0.1150
Z	 0.9850	 0.1060
a	 0.9930	 0.0730
b	 0.9940	 0.1240
c	 0.9940	 0.1070
d	 0.9970	 0.1100
e	 0.9790	 0.1070
f	 0.9960	 0.1110
g	 0.9390	 0.1060
h	 1.0000	 0.1450
i	 0.9920	 0.0860
j	 0.9990	 0.1100
k	 0.9890	 0.1430
l	 0.9980	 0.0860
m	 0.9960	 0.1220
n	 0.9990	 0.0980
o	 1.0000	 0.1050
p	 0.9890	 0.1370
q	 1.0000	 0.1070
r	 1.0000	 0.0990
s	 0.9990	 0.1160
t	 0.9960	 0.0920
u	 0.9990	 0.0980
v	 0.9990	 0.1030
w	 1.0000	 0.0880
x	 1.0000	 0.1150
y	 0.9980	 0.1170
z	 1.0000	 0.1140