



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 03:18 PM UTC

PDB ID : 8Y5L / pdb_00008y5l
EMDB ID : EMD-38941
Title : E.coli transcription translation coupling complex in TTC-B state 1 (subclass1) containing mRNA with 30-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 : 3.70 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

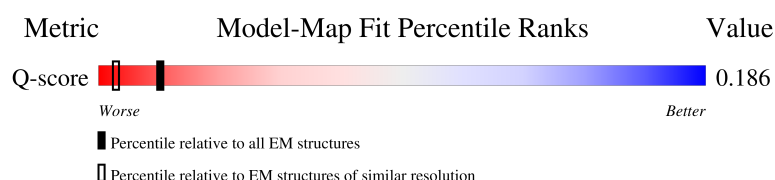
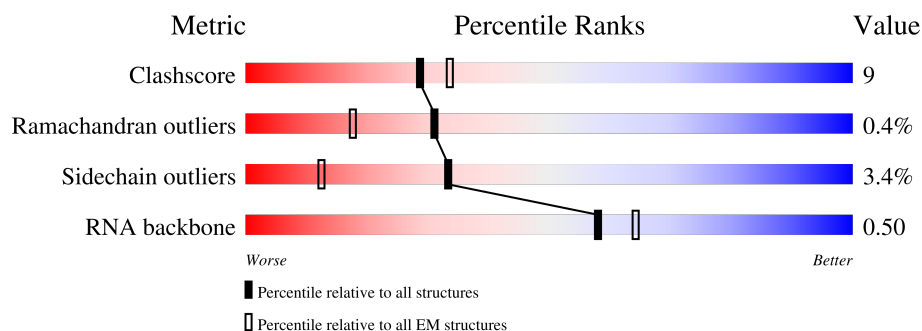
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



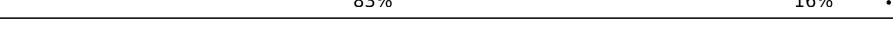
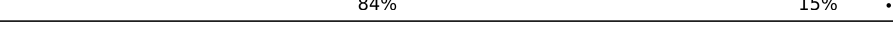
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	A	70	
2	B	57	
3	C	55	

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Mol	Chain	Length	Quality of chain
4	D	46	
5	E	65	
6	F	38	
7	G	241	
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	

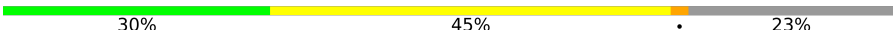
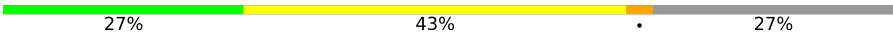
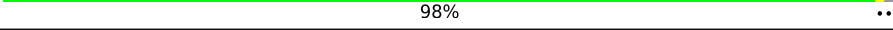
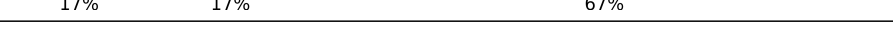
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Mol	Chain	Length	Quality of chain
29	d	201	
30	e	179	
31	f	177	
32	g	149	
33	i	142	
34	j	142	
35	k	123	
36	l	144	
37	m	136	
38	n	127	
39	o	117	
40	p	115	
41	q	118	
42	r	103	
43	s	110	
44	t	100	
45	u	104	
46	v	94	
47	w	85	
48	x	78	
49	y	63	
50	z	59	
51	1	2904	
52	2	120	
53	3	1542	

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Mol	Chain	Length	Quality of chain
54	4	47	
55	8	37	
56	9	37	
57	A1	329	
57	A2	329	
58	B1	1407	
59	B2	1342	
60	W0	91	
61	NA	495	
62	NG	181	
63	5	76	
64	6	77	
64	7	77	
65	h	6	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
65	5OH	h	6	-	-	X	-

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 178150 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
			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
			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
			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	52	Total	C	N	O	S	0	0
			400	256	73	70	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	36	Total	C	N	O	P	0	0
			749	335	107	271	36		

- 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	301	Total	C	N	O	S	0	0
			2088	1293	380	409	6		
57	A2	288	Total	C	N	O	S	0	0
			2029	1257	366	400	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 NusA.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	NA	492	Total	C	N	O	0	0
			2432	1448	492	492		

- Molecule 62 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	NG	154	Total	C	N	O	0	0
			758	450	154	154		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
63	5	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 64 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
64	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
64	7	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 65 is a protein (with D amino acids) called viomycin.

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

- Molecule 66 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

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: 



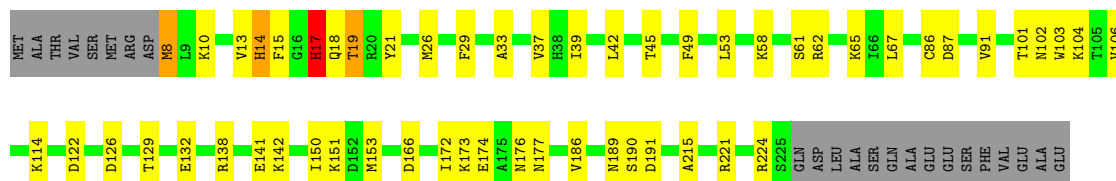
- Molecule 6: 50S ribosomal protein L36

Chain F:  71% 26% .



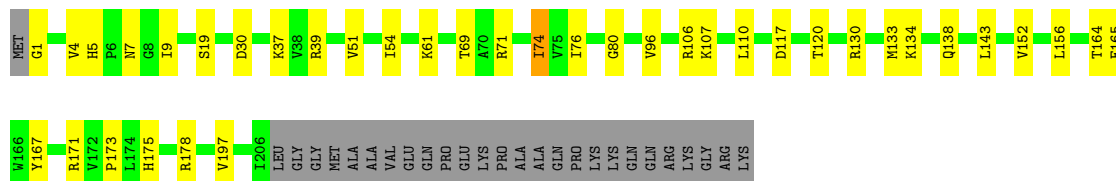
- Molecule 7: 30S ribosomal protein S2

Chain G:  68% 21% . 10%



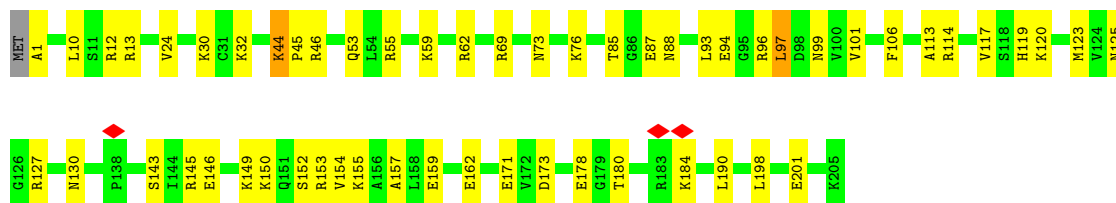
- Molecule 8: 30S ribosomal protein S3

Chain H:  72% 16% 12%



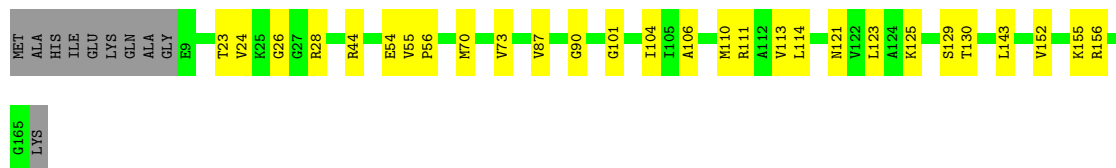
- Molecule 9: 30S ribosomal protein S4

Chain I:  72% 26% .



- Molecule 10: 30S ribosomal protein S5

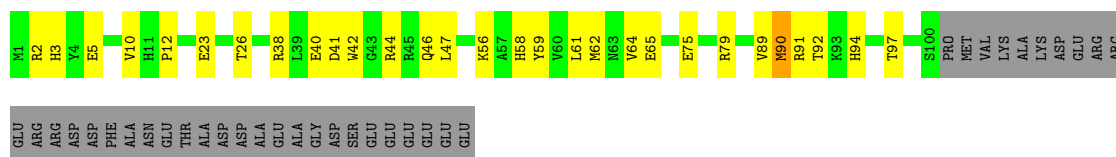
Chain J:  77% 17% 6%



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

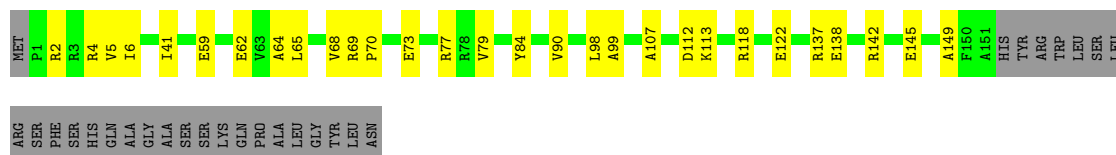
Chain K:  53% 21% . 26%





- Molecule 12: 30S ribosomal protein S7

Chain L: 68% 16% 16%



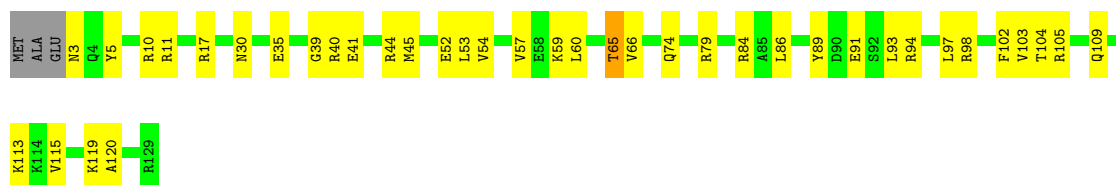
- Molecule 13: 30S ribosomal protein S8

Chain M: 88% 11%



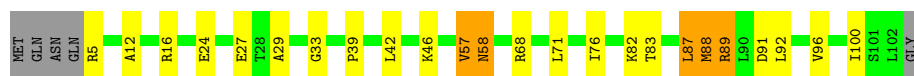
- Molecule 14: 30S ribosomal protein S9

Chain N: 68% 29%



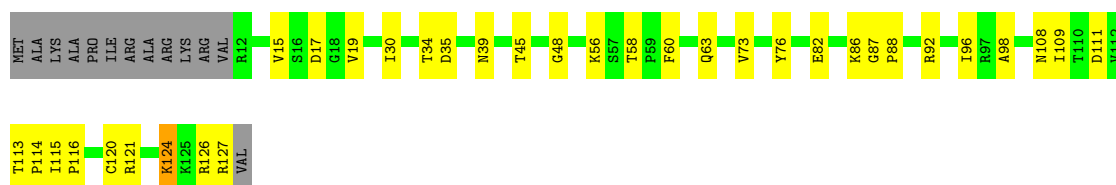
- Molecule 15: 30S ribosomal protein S10

Chain O: 72% 18% 5% 5%

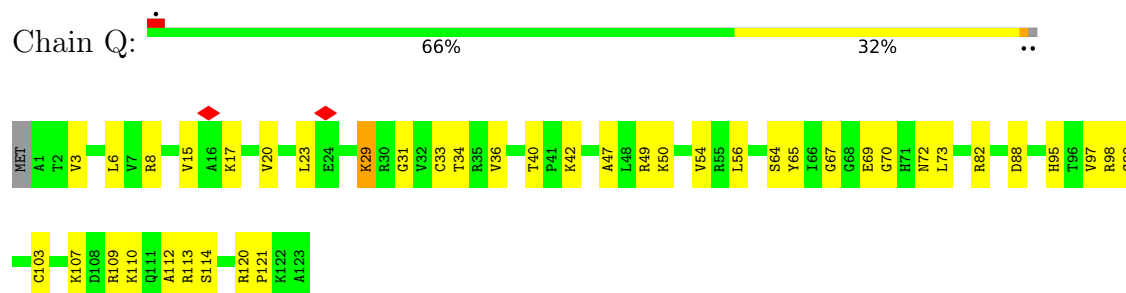


- Molecule 16: 30S ribosomal protein S11

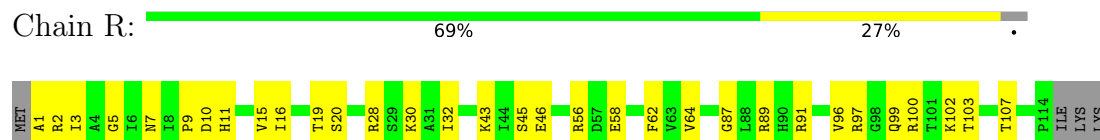
Chain P: 64% 26% 10% 10%



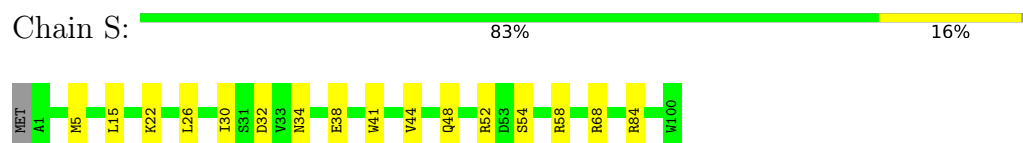
- Molecule 17: 30S ribosomal protein S12



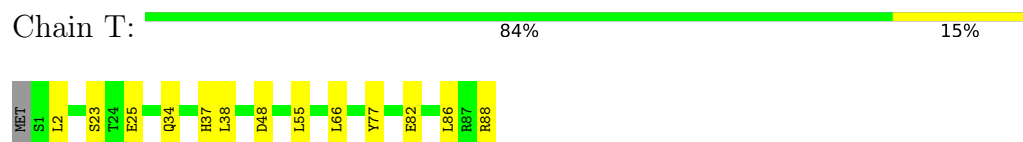
- Molecule 18: 30S ribosomal protein S13



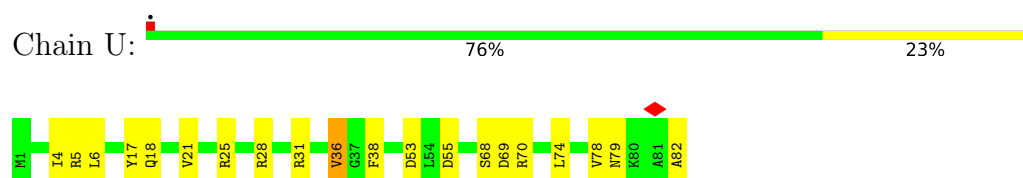
- Molecule 19: 30S ribosomal protein S14



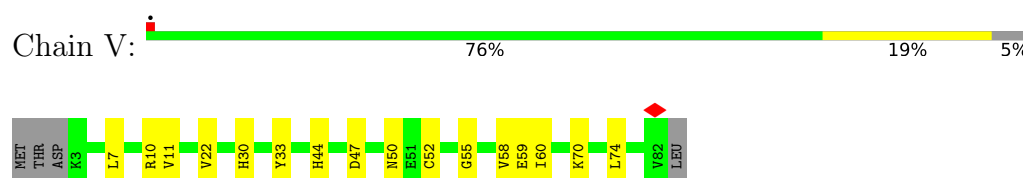
- Molecule 20: 30S ribosomal protein S15



- Molecule 21: 30S ribosomal protein S16

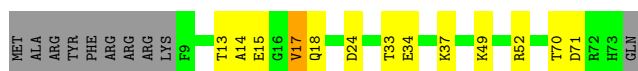


- Molecule 22: 30S ribosomal protein S17



- Molecule 23: 30S ribosomal protein S18

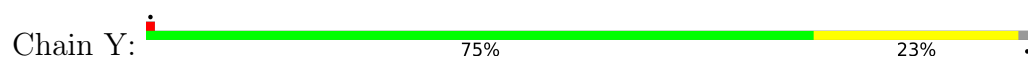




- Molecule 24: 30S ribosomal protein S19



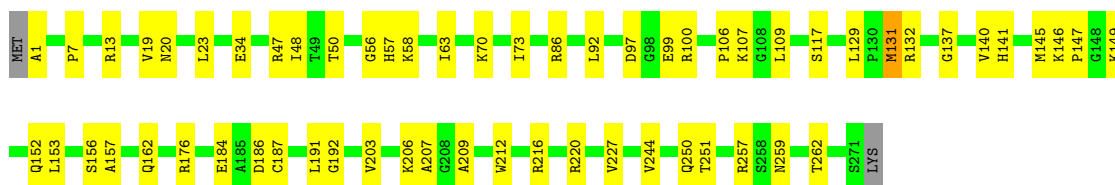
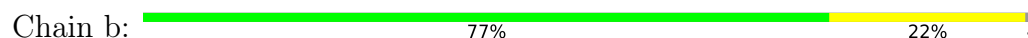
- Molecule 25: 30S ribosomal protein S20



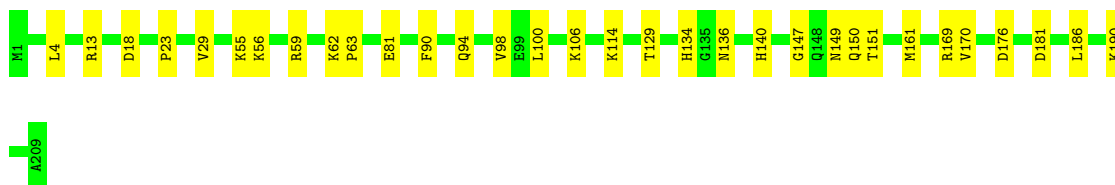
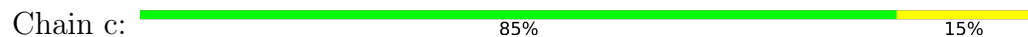
- Molecule 26: 30S ribosomal protein S21



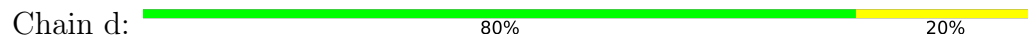
- Molecule 27: 50S ribosomal protein L2



- Molecule 28: 50S ribosomal protein L3

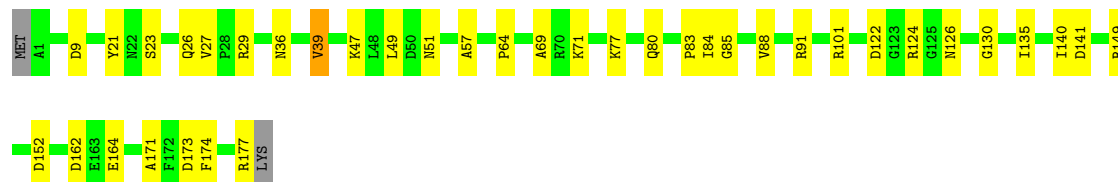


- Molecule 29: 50S ribosomal protein L4



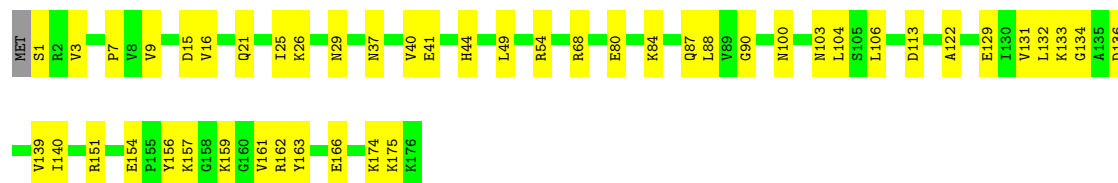
- Molecule 30: 50S ribosomal protein L5

Chain e: 78% 21% ..

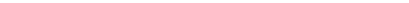


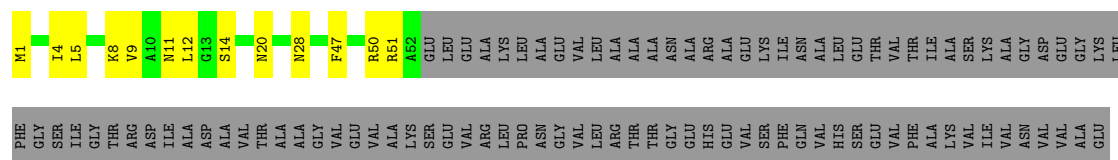
- Molecule 31: 50S ribosomal protein L6

Chain f: 73% 27%

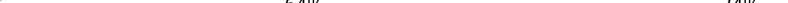


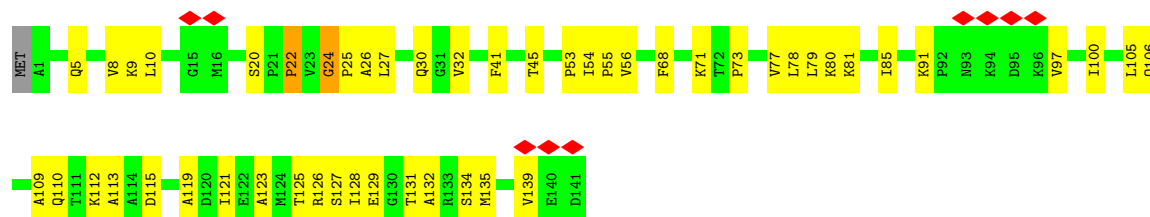
- Molecule 32: 50S ribosomal protein L9

Chain g:  26% 9% 65%



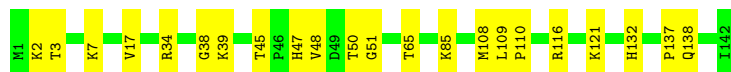
- Molecule 33: 50S ribosomal protein L11

Chain i:  6% 64% 34% ..



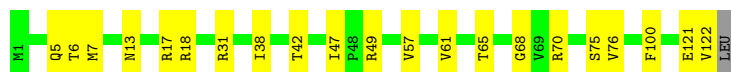
- Molecule 34: 50S ribosomal protein L13

Chain j:  85% 15%



- Molecule 35: 50S ribosomal protein L14

Chain k:  82% 17%



- Molecule 36: 50S ribosomal protein L15

Chain l:  86% 13%



- Molecule 37: 50S ribosomal protein L16

Chain m:  83% 17%



- Molecule 38: 50S ribosomal protein L17

Chain n:  76% 18% 6%



- Molecule 39: 50S ribosomal protein L18

Chain o:  81% 18%



- Molecule 40: 50S ribosomal protein L19

Chain p:  83% 16%



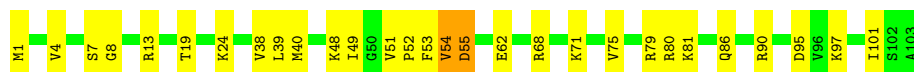
- Molecule 41: 50S ribosomal protein L20

Chain q:  83% 15% ..



- Molecule 42: 50S ribosomal protein L21

Chain r:  72% 26% .



- Molecule 43: 50S ribosomal protein L22

Chain s:  85% 15%



- Molecule 44: 50S ribosomal protein L23

Chain t:  75% 18% 7%



- Molecule 45: 50S ribosomal protein L24

Chain u:  72% 26% .



- Molecule 46: 50S ribosomal protein L25

Chain v:  85% 15%



- Molecule 47: 50S ribosomal protein L27

Chain w:  73% 15% 12%



- Molecule 48: 50S ribosomal protein L28

Chain x:  76% 22% ..



- Molecule 49: 50S ribosomal protein L29

Chain y:  73% 27%

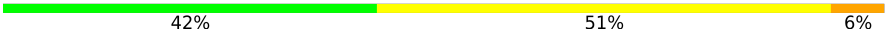


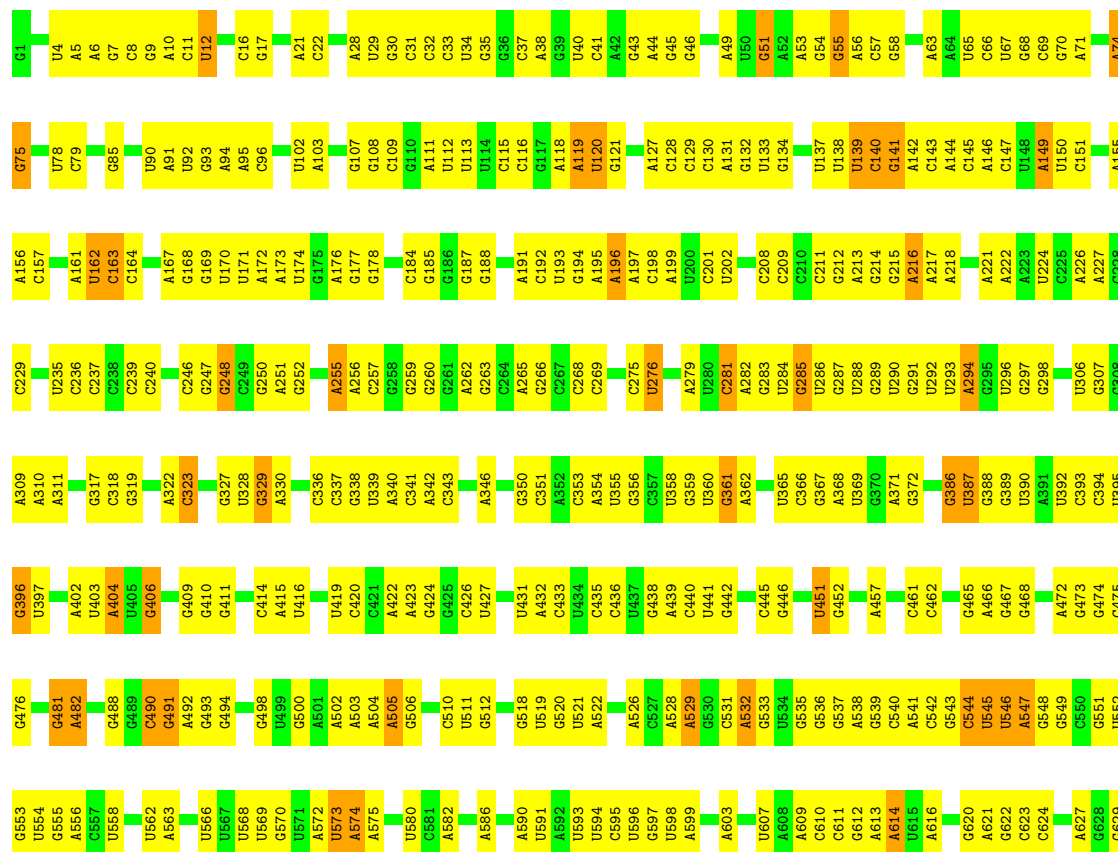
- Molecule 50: 50S ribosomal protein L30

Chain z:  76% 22% .



- Molecule 51: 23S rRNA

Chain 1:  42% 51% 6%

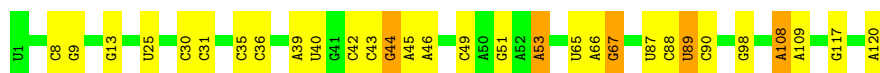




C2888	A2726	G2644	A2566	A2469	A2386	G2304	A2225	A2158	U2092	C1990	G1910	U1827
C2889		G2645	G2567	G2470	U2387	U2305	C2226	G2159	G2093	U1991	U1911	G1828
G2890	G2729	G2646	G2568	A2471	A2388	C2306	A2227	C2160	A2094	A1912	A1912	A1829
A2893	G2730	U2647	G2569		G2389	A2309		C2161	A2095	A1913	A1913	C1832
G2894	G2731	G2648	G2570	A2476	U2390	A2310	G2230	A2162	C2096	C1914	U1915	C1833
G2895	G2732	G2649	A2572	A2482	A2392	A2311	U2233	A2163	A2097	U1916	U1916	U1834
C2896	A2733	U2650	G2573	C2483	U2393	A2312	G2234	C2165	U2098	A1998	A1917	
U2897	G2734	C2652	G2574	G2488	C2394	C2313	G2235	U2166	U2099	C1999	U1918	
U2898	A2735		G2575	G2489	C2395	A2314	U2236	U2167	A2101	G2012	A1919	G1845
A2899	A2736		G2576	U2489	G2396	G2315	G2237	G2238	G2102	A2013	A1920	A1847
C2815	G2737		G2577	G2490	G2396	G2316	G2238	A2170	C2103	A2014	G1921	A1848
A2900		G2658	A2578	U2491	U2402	U2321	G2239	U2171	G2104	A2015	G1922	
C2901	A2741	G2659	G2579	U2492	C2403	U2322	U2240	U2172	U2105	U2016	U1923	U1851
G2902	G2742	G2661	C2580	U2493	U2404	G2325	A2241	U2173	G2106	A2017	U1924	U1852
U2903	U2743	A2662	G2581	C2496	G2405	G2326	G2242	C2174	G2107	A2018	C1924	
U	G2744	G2663	G2582	C2497	A2406	A2327	U2243			C2020		
			G2583	C2498	A2407	U2328			G2110	C2021	A1927	
C2830	G2747		U2584	C2499	A2408	U2329	A2244		U2111	C2022	A1928	U1855
		G2667	U2585		A2411	U2330	C2245		G2112	C2023	G1929	U1856
G2834	A2670		U2586		A2412	G2331	G2250		U2113	G2024	G1930	U1857
A2835	G2671				A2413	G2332			A2114	C2025	U1931	A1858
U2836	U2672				C2420	G2333			G2115	U2026		
A2837		G2676	G2595	G2505	G2421	A2334	U2257			G2027	G1935	G1863
G2838				G2506	G2422	U2335	C2258			A2030	A1936	U1864
C2839				C2507	U2423	A2336	U2259			A2031	A1937	U1865
C2840					G2424	G2337	C2260			G2032	A1938	A1866
G2843	A2679		A2598	C2510	G2425	A2338				A2033	U1939	C1867
U2844	U2680		G2599	U2511	A2426	C2339	U2261			U2034	C1942	C1868
G2845	C2681		A2600		G2427	A2340	A2262			G2035	U1943	C1870
U2846	A2682		G2601	A2516	G2428	A2341	A2263			C2036		A1871
G2847	C2683		A2602	C2517	G2429	U2342				A2037	G1948	A1872
U2848	U2684		U2609	A2518	A2430	A2343	G2271			G2038		A1873
G2849			C2610	G2525	G2431	U2344	C2275			U2039	A1952	C1874
U2850			C2611	G2526	A2432	U2345				C2043	A1953	G1875
G2851	U2687		G2612	C2527	A2433	U2346	A2278				U1955	
U2852	G2688		U2613	U2528	A2434	C2350	G2279			C2047	U1956	G1878
C2853	U2689		U2614	G2529	A2435	G2351	G2280			G2048		C1879
G2854	U2690		U2615	A2530	G2436	A2352	A2281			C2049	U1963	U1882
U2855			G2616	U2533	G2437	G2353	G2282			C2050	G1964	G1883
C2856			U2617	A2534	C2440	G2362	C2283			A2051	C1965	G1884
G2857	A2700		G2618	U2535	U2441	G2363	C2284			G2052	A1966	U1885
U2858	U2701		C2619			G2364	C2285			A2053	C1967	U1886
A2859	G2702		G2625	C2539	G2445	C2365	A2286			A2054	G1968	C1887
U2860			C2626		G2446	G2366	A2287			C2055	G1888	G1889
U2861	U2707		G2627	G2545	G2447	A2367	G2288			G2056	A1969	A1890
G2862	G2708		C2628	U2546	G2448	C2368	G2289				U1970	
C2863	C2710		U2629	A2547	A2448	G2369	G2290			A2060	U1971	
U2864	A2711		G2630			C2370	U2291			G2061	G1972	C1893
G2865	G2712		G2631	G2553	G2455	G2371	U2292					C1894
U2866	U2713		A2632	U2554	C2456	U2372	G2293			G2069	G1975	
C2867	G2714		G2633	U2555	U2457	U2373	G2294				U1976	
G2868			A2634	G2556	G2458	G2374	C2295				A1977	A1901
U2869			G2635	G2557		G2375	G2296				A1978	C1902
A2870	C2717		A2636	G2558	C2462	G2376	U2297					
U2871	G2718		U2637	U2561	G2463	A2381	A2298				G1983	C1905
A2872	G2719		U2638	U2562	G2464	G2382	U2299				G1984	G1906
G2873	U2720			U2563		G2383					G1985	G1907
C2874				A2564		U2384	U2302				C1986	C1908
U2875				G2565	A2468	C2385	G2303					C1909

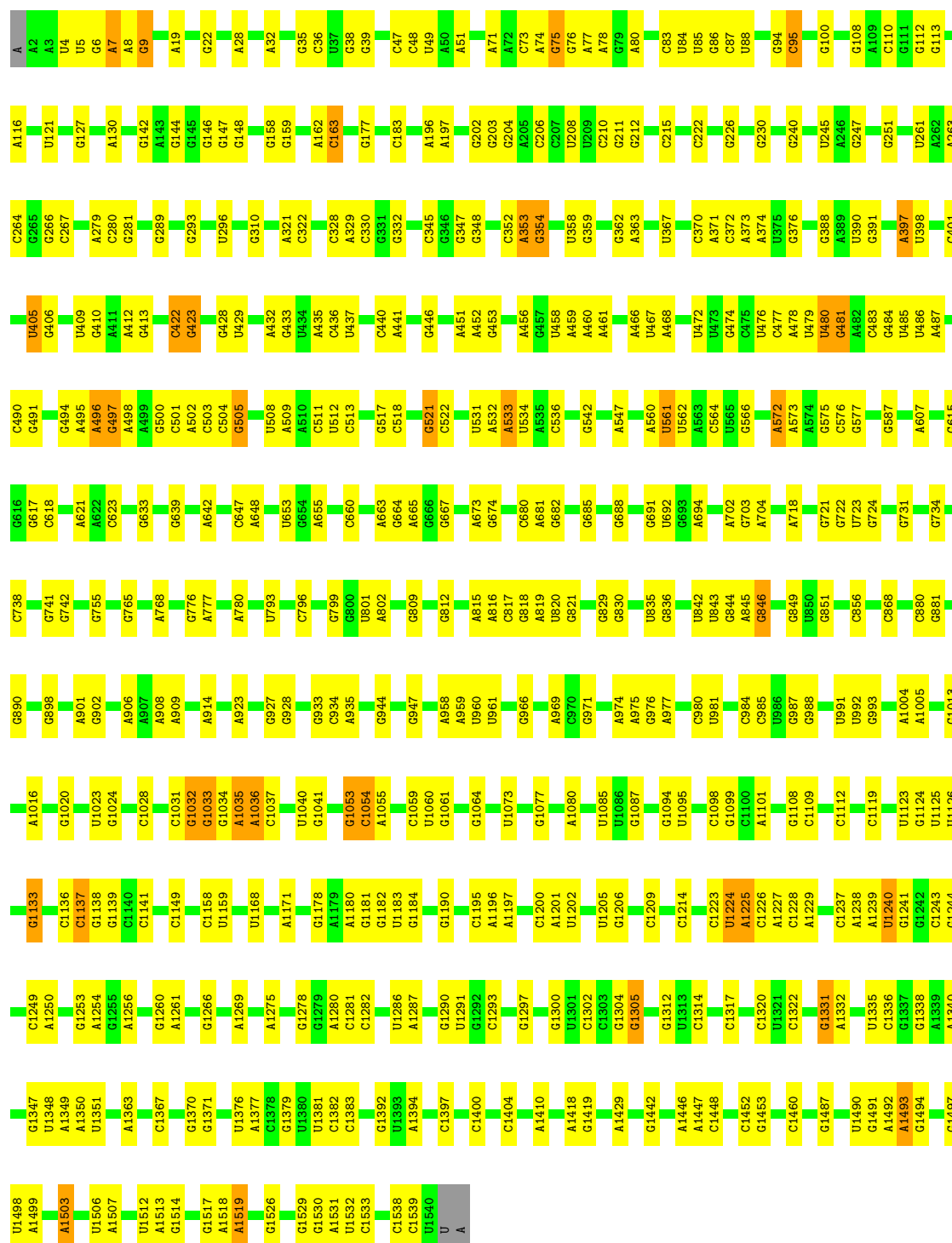
● Molecule 52: 5S rRNA

Chain 2:  75% 21%

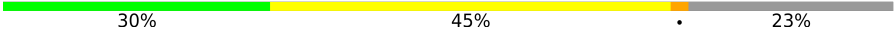


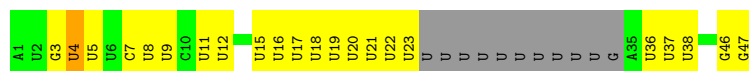
• Molecule 53: 16S rRNA

Chain 3: 68% 29%

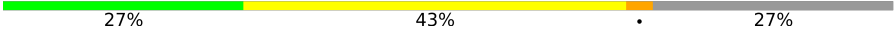


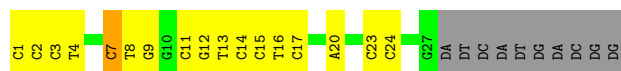
• Molecule 54: mRNA

Chain 4:  30% 45% 23%



- Molecule 55: template DNA strand

Chain 8:  27% 43% 27%



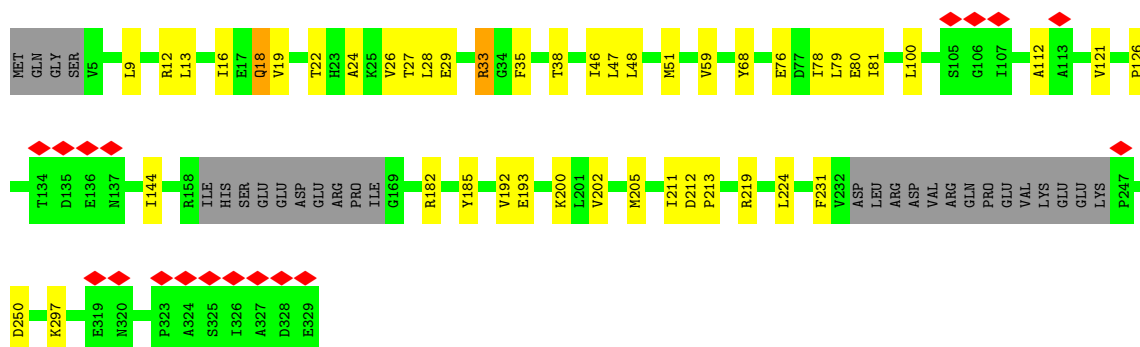
- Molecule 56: non-template DNA strand

Chain 9:  51% 46%



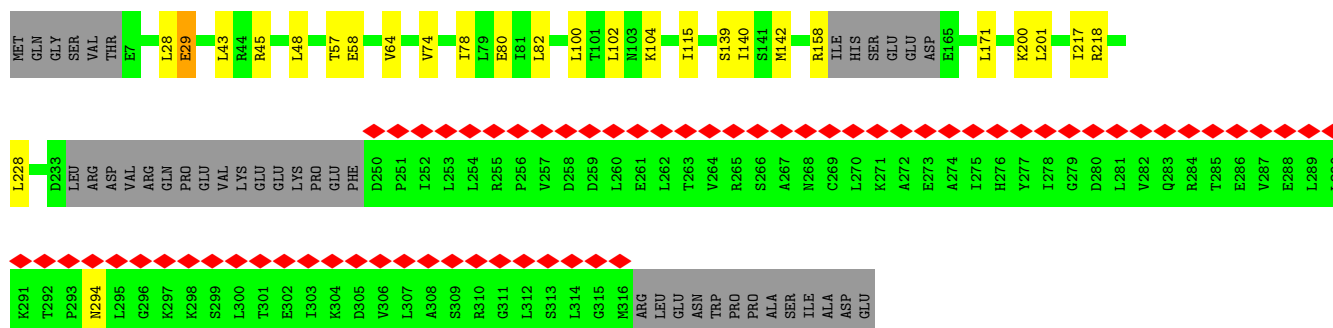
- Molecule 57: DNA-directed RNA polymerase subunit alpha

Chain A1:  5% 78% 13% 9%



- Molecule 57: DNA-directed RNA polymerase subunit alpha

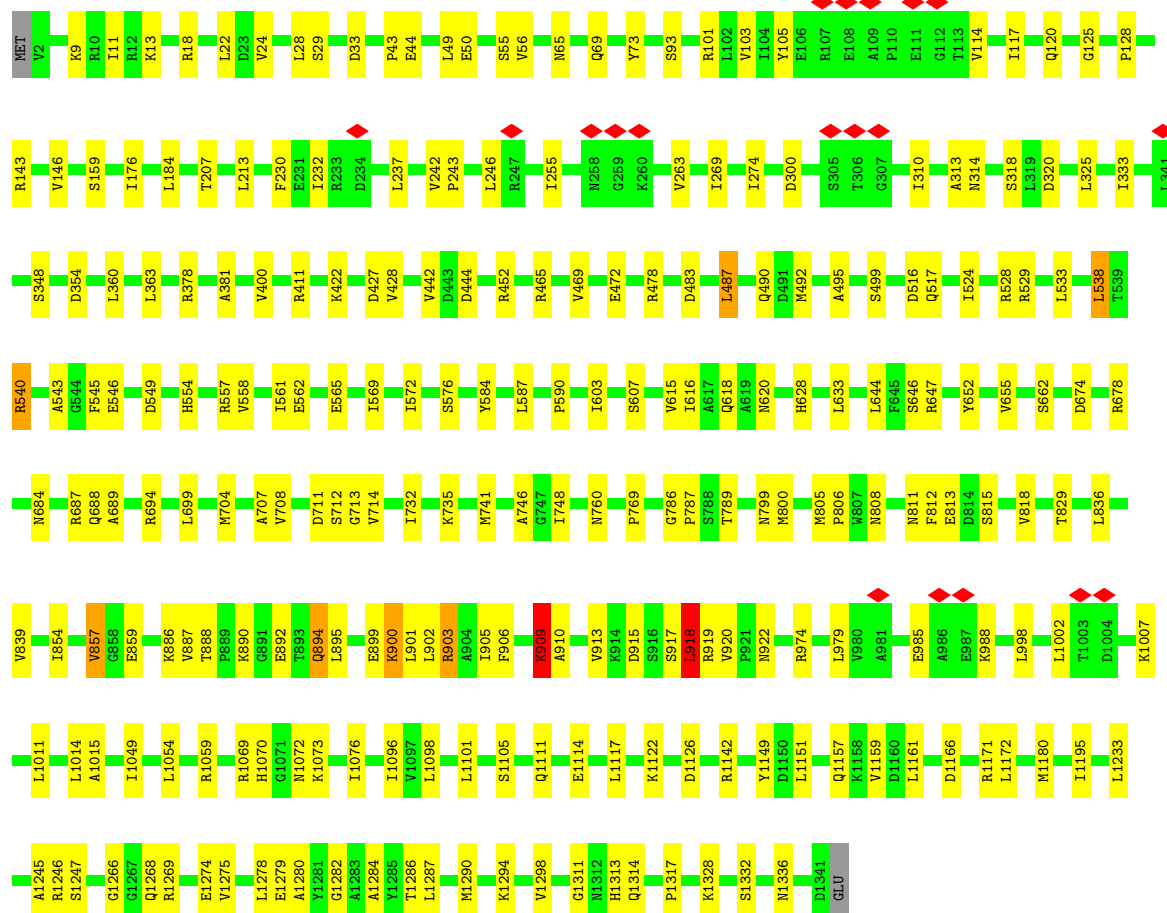
Chain A2:  20% 79% 8% 12%



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

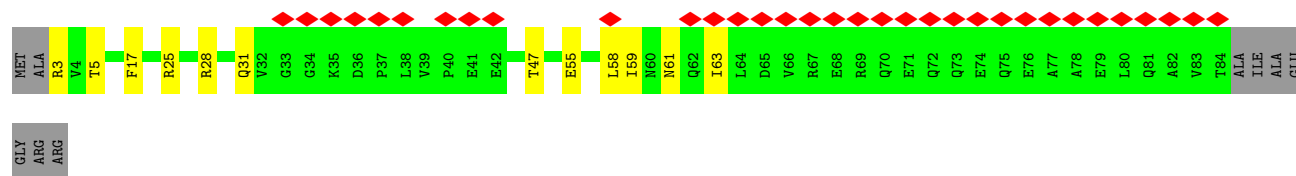


Chain B2:  82% 17%

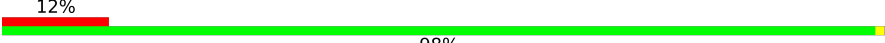


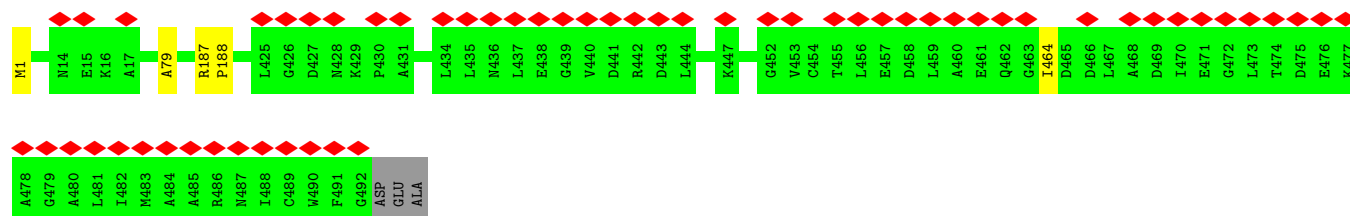
- Molecule 60: DNA-directed RNA polymerase subunit omega

Chain W0:  36% 77% 13% 10%



- Molecule 61: Transcription termination/antitermination protein NusA

Chain NA:  12% 98%



- | | |
|------|--|
| KBE1 | |
| A2 | |
| S3 | |
| S4 | |
| UAL5 | |
| 50H6 | |

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23000	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	0.089	Depositor
Minimum map value	-0.029	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: MG, KBE, 5OH, DPP, UAL

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	0.26	0/531	0.54	0/709
2	B	0.40	0/450	0.60	0/599
3	C	0.27	0/416	0.52	0/554
4	D	0.47	0/380	0.76	2/498 (0.4%)
5	E	0.53	0/513	0.60	0/676
6	F	0.57	0/303	0.65	0/397
7	G	0.37	0/1735	0.64	0/2338
8	H	0.34	0/1651	0.55	0/2225
9	I	0.35	0/1665	0.71	0/2227
10	J	0.38	0/1169	0.68	2/1573 (0.1%)
11	K	0.46	0/835	0.77	0/1128
12	L	0.30	0/1195	0.67	3/1602 (0.2%)
13	M	0.35	0/989	0.52	0/1326
14	N	0.41	0/1034	0.77	0/1375
15	O	0.50	0/796	0.78	2/1077 (0.2%)
16	P	0.45	0/885	0.64	1/1195 (0.1%)
17	Q	0.50	0/969	0.86	2/1300 (0.2%)
18	R	0.33	0/892	0.73	2/1193 (0.2%)
19	S	0.32	0/817	0.61	0/1088
20	T	0.49	0/722	0.64	0/964
21	U	0.30	0/659	0.71	2/884 (0.2%)
22	V	0.44	0/657	0.71	0/881
23	W	0.54	0/544	0.74	1/731 (0.1%)
24	X	0.28	0/652	0.55	0/877
25	Y	0.28	0/671	0.52	0/888
26	Z	0.66	0/550	1.01	2/728 (0.3%)
27	b	0.49	0/2121	0.64	0/2852
28	c	0.42	0/1586	0.59	2/2134 (0.1%)
29	d	0.43	0/1571	0.62	0/2113
30	e	0.37	0/1434	0.60	2/1926 (0.1%)
31	f	0.29	0/1343	0.55	0/1816
32	g	0.32	0/405	0.75	0/544

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.31	0/1046	0.77	3/1410 (0.2%)
34	j	0.41	0/1152	0.55	1/1551 (0.1%)
35	k	0.45	0/947	0.66	0/1268
36	l	0.40	0/1054	0.63	0/1403
37	m	0.56	0/1093	0.74	0/1460
38	n	0.46	0/973	0.72	1/1301 (0.1%)
39	o	0.31	0/902	0.51	0/1209
40	p	0.41	0/929	0.61	0/1242
41	q	0.52	0/960	0.62	1/1278 (0.1%)
42	r	0.43	0/829	0.69	0/1107
43	s	0.43	0/864	0.58	0/1156
44	t	0.33	0/744	0.52	0/994
45	u	0.45	0/787	0.75	0/1051
46	v	0.34	0/766	0.51	0/1025
47	w	0.40	0/582	0.52	0/769
48	x	0.43	0/635	0.63	1/848 (0.1%)
49	y	0.29	0/510	0.64	0/677
50	z	0.41	0/453	0.53	0/605
51	1	0.51	0/69796	0.62	22/108888 (0.0%)
52	2	0.43	0/2872	0.46	0/4479
53	3	0.42	0/36963	0.43	0/57662
54	4	0.52	0/830	0.65	0/1285
55	8	0.56	0/599	0.70	1/919 (0.1%)
56	9	0.47	0/468	0.52	0/719
57	A1	0.55	0/2106	0.81	0/2868
57	A2	0.49	0/2048	0.76	0/2786
58	B1	0.57	6/10510 (0.1%)	0.75	8/14196 (0.1%)
59	B2	0.46	0/10714	0.67	0/14459
60	W0	0.30	0/652	0.61	0/879
61	NA	0.78	0/2431	1.22	0/3385
62	NG	1.13	0/756	1.06	0/1048
63	5	0.57	0/1812	0.86	3/2823 (0.1%)
64	6	0.40	0/1832	0.48	0/2855
64	7	0.39	0/1832	0.57	1/2855 (0.0%)
65	h	3.18	2/11 (18.2%)	0.75	0/13
All	All	0.48	8/191598 (0.0%)	0.62	65/282891 (0.0%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	h	3	SER	CA-C	-6.74	1.38	1.52
65	h	4	SER	CA-C	-6.15	1.40	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	B1	1350	ASN	CG-ND2	-5.28	1.22	1.33
58	B1	424	ASN	CG-ND2	-5.15	1.22	1.33
58	B1	1108	GLN	CD-OE1	5.13	1.33	1.23

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	P	73	VAL	N-CA-C	-9.03	104.53	113.20
41	q	33	VAL	N-CA-C	-8.76	104.76	112.12
12	L	64	ALA	N-CA-C	-7.69	105.06	114.75
51	1	1130	U	C2'-C3'-O3'	7.59	120.89	109.50
64	7	33	U	C2'-C3'-O3'	7.27	120.41	109.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	522	0	524	8	0
2	B	444	0	461	9	0
3	C	409	0	440	3	0
4	D	377	0	418	9	0
5	E	504	0	574	3	0
6	F	302	0	343	5	0
7	G	1704	0	1732	35	0
8	H	1624	0	1699	25	0
9	I	1643	0	1710	37	0
10	J	1156	0	1199	18	0
11	K	817	0	808	15	0
12	L	1181	0	1240	18	0
13	M	979	0	1034	9	0
14	N	1022	0	1070	22	0
15	O	786	0	828	15	0
16	P	869	0	878	23	0
17	Q	955	0	1019	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	R	883	0	944	18	0
19	S	805	0	847	11	0
20	T	714	0	737	6	0
21	U	649	0	666	15	0
22	V	648	0	691	8	0
23	W	535	0	552	7	0
24	X	637	0	665	8	0
25	Y	665	0	714	12	0
26	Z	544	0	579	13	0
27	b	2082	0	2157	49	0
28	c	1565	0	1616	27	0
29	d	1552	0	1619	29	0
30	e	1410	0	1447	24	0
31	f	1323	0	1374	32	0
32	g	400	0	423	7	0
33	i	1032	0	1088	41	0
34	j	1129	0	1162	20	0
35	k	938	0	1012	16	0
36	l	1045	0	1117	16	0
37	m	1074	0	1157	13	0
38	n	960	0	1000	16	0
39	o	892	0	923	15	0
40	p	917	0	965	17	0
41	q	947	0	1022	10	0
42	r	816	0	839	19	0
43	s	857	0	922	11	0
44	t	738	0	807	10	0
45	u	779	0	834	13	0
46	v	753	0	780	9	0
47	w	575	0	592	9	0
48	x	625	0	655	11	0
49	y	509	0	543	13	0
50	z	449	0	491	9	0
51	1	62317	0	31346	1455	0
52	2	2568	0	1303	15	0
53	3	33012	0	16618	189	0
54	4	749	0	374	8	0
55	8	539	0	305	28	0
56	9	417	0	224	1	0
57	A1	2088	0	1895	24	0
57	A2	2029	0	1864	19	0
58	B1	10353	0	10548	325	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	B2	10546	0	10550	163	0
60	W0	650	0	658	10	0
61	NA	2432	0	1171	4	0
62	NG	758	0	334	10	0
63	5	1622	0	821	29	0
64	6	1640	0	837	8	0
64	7	1640	0	837	20	0
65	h	48	0	40	10	0
66	B1	1	0	0	0	0
All	All	178150	0	126642	2806	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 2806 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)
40:p:52:ARG:HH21	51:1:2720:U:H5''	0.95	1.09
51:1:275:C:H2'	51:1:276:U:H4'	1.37	1.06
51:1:2713:U:H3'	51:1:2714:G:H5'	1.41	1.03
51:1:1666:G:H2'	51:1:1667:G:H5'	1.41	1.02
51:1:1672:A:C2	51:1:2582:G:H5'	1.95	1.02

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	64/70 (91%)	59 (92%)	5 (8%)	0	100	100
2	B	54/57 (95%)	48 (89%)	4 (7%)	2 (4%)	2	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
4	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
5	E	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
6	F	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	4	27
7	G	216/241 (90%)	187 (87%)	27 (12%)	2 (1%)	14	45
8	H	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
9	I	203/206 (98%)	172 (85%)	30 (15%)	1 (0%)	24	56
10	J	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
11	K	98/135 (73%)	84 (86%)	14 (14%)	0	100	100
12	L	149/179 (83%)	130 (87%)	19 (13%)	0	100	100
13	M	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
14	N	125/130 (96%)	104 (83%)	21 (17%)	0	100	100
15	O	96/103 (93%)	87 (91%)	8 (8%)	1 (1%)	12	43
16	P	114/129 (88%)	100 (88%)	13 (11%)	1 (1%)	14	45
17	Q	121/124 (98%)	94 (78%)	27 (22%)	0	100	100
18	R	112/118 (95%)	98 (88%)	13 (12%)	1 (1%)	14	45
19	S	98/101 (97%)	83 (85%)	15 (15%)	0	100	100
20	T	86/89 (97%)	75 (87%)	11 (13%)	0	100	100
21	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
22	V	78/84 (93%)	69 (88%)	8 (10%)	1 (1%)	9	38
23	W	63/75 (84%)	56 (89%)	5 (8%)	2 (3%)	3	25
24	X	77/92 (84%)	71 (92%)	6 (8%)	0	100	100
25	Y	83/87 (95%)	78 (94%)	5 (6%)	0	100	100
26	Z	63/71 (89%)	44 (70%)	18 (29%)	1 (2%)	7	35
27	b	269/273 (98%)	244 (91%)	25 (9%)	0	100	100
28	c	207/209 (99%)	189 (91%)	18 (9%)	0	100	100
29	d	199/201 (99%)	186 (94%)	13 (6%)	0	100	100
30	e	175/179 (98%)	157 (90%)	18 (10%)	0	100	100
31	f	174/177 (98%)	159 (91%)	15 (9%)	0	100	100
32	g	50/149 (34%)	44 (88%)	5 (10%)	1 (2%)	6	32
33	i	139/142 (98%)	116 (84%)	23 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	j	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
35	k	120/123 (98%)	106 (88%)	14 (12%)	0	100	100
36	l	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
37	m	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
38	n	118/127 (93%)	103 (87%)	15 (13%)	0	100	100
39	o	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
40	p	112/115 (97%)	103 (92%)	9 (8%)	0	100	100
41	q	115/118 (98%)	110 (96%)	3 (3%)	2 (2%)	7	34
42	r	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	12	43
43	s	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
44	t	91/100 (91%)	82 (90%)	9 (10%)	0	100	100
45	u	100/104 (96%)	84 (84%)	15 (15%)	1 (1%)	12	43
46	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
47	w	73/85 (86%)	67 (92%)	6 (8%)	0	100	100
48	x	75/78 (96%)	72 (96%)	2 (3%)	1 (1%)	9	38
49	y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
50	z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
57	A1	295/329 (90%)	273 (92%)	21 (7%)	1 (0%)	36	65
57	A2	282/329 (86%)	271 (96%)	11 (4%)	0	100	100
58	B1	1329/1407 (94%)	1203 (90%)	122 (9%)	4 (0%)	36	65
59	B2	1338/1342 (100%)	1204 (90%)	129 (10%)	5 (0%)	30	60
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	474 (97%)	14 (3%)	2 (0%)	30	60
62	NG	150/181 (83%)	136 (91%)	10 (7%)	4 (3%)	4	27
65	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	9586/10235 (94%)	8670 (90%)	881 (9%)	35 (0%)	31	60

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	r	54	VAL
48	x	25	LYS
58	B1	121	PRO

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Mol	Chain	Res	Type
61	NA	187	ARG
61	NA	188	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%)	58 (98%)	1 (2%)	53	67
2	B	47/48 (98%)	47 (100%)	0	100	100
3	C	45/49 (92%)	44 (98%)	1 (2%)	45	63
4	D	38/38 (100%)	37 (97%)	1 (3%)	40	60
5	E	51/52 (98%)	49 (96%)	2 (4%)	28	53
6	F	34/34 (100%)	30 (88%)	4 (12%)	5	23
7	G	180/199 (90%)	174 (97%)	6 (3%)	33	55
8	H	170/190 (90%)	167 (98%)	3 (2%)	51	67
9	I	172/173 (99%)	168 (98%)	4 (2%)	44	62
10	J	119/126 (94%)	117 (98%)	2 (2%)	53	67
11	K	87/116 (75%)	82 (94%)	5 (6%)	18	45
12	L	124/147 (84%)	124 (100%)	0	100	100
13	M	104/105 (99%)	103 (99%)	1 (1%)	68	74
14	N	105/107 (98%)	98 (93%)	7 (7%)	15	42
15	O	86/90 (96%)	78 (91%)	8 (9%)	8	32
16	P	89/99 (90%)	86 (97%)	3 (3%)	32	55
17	Q	103/104 (99%)	98 (95%)	5 (5%)	22	48
18	R	92/96 (96%)	91 (99%)	1 (1%)	65	73
19	S	83/84 (99%)	83 (100%)	0	100	100
20	T	76/77 (99%)	73 (96%)	3 (4%)	28	53
21	U	65/65 (100%)	64 (98%)	1 (2%)	57	68
22	V	74/78 (95%)	72 (97%)	2 (3%)	39	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	W	56/65 (86%)	52 (93%)	4 (7%)	13	40
24	X	70/79 (89%)	70 (100%)	0	100	100
25	Y	65/66 (98%)	64 (98%)	1 (2%)	57	68
26	Z	55/61 (90%)	47 (86%)	8 (14%)	3	17
27	b	216/218 (99%)	212 (98%)	4 (2%)	50	65
28	c	164/164 (100%)	164 (100%)	0	100	100
29	d	165/165 (100%)	162 (98%)	3 (2%)	51	67
30	e	148/150 (99%)	145 (98%)	3 (2%)	48	64
31	f	137/138 (99%)	135 (98%)	2 (2%)	57	68
32	g	41/114 (36%)	38 (93%)	3 (7%)	13	40
33	i	109/110 (99%)	108 (99%)	1 (1%)	70	75
34	j	116/116 (100%)	116 (100%)	0	100	100
35	k	103/104 (99%)	103 (100%)	0	100	100
36	l	102/103 (99%)	101 (99%)	1 (1%)	68	74
37	m	109/109 (100%)	103 (94%)	6 (6%)	19	46
38	n	100/103 (97%)	99 (99%)	1 (1%)	68	74
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%)	86 (97%)	3 (3%)	32	55
42	r	84/84 (100%)	82 (98%)	2 (2%)	43	61
43	s	93/93 (100%)	92 (99%)	1 (1%)	65	73
44	t	80/84 (95%)	80 (100%)	0	100	100
45	u	83/85 (98%)	79 (95%)	4 (5%)	23	48
46	v	78/78 (100%)	77 (99%)	1 (1%)	61	71
47	w	57/63 (90%)	57 (100%)	0	100	100
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%)	26	51
57	A1	185/286 (65%)	174 (94%)	11 (6%)	18	44
57	A2	186/286 (65%)	184 (99%)	2 (1%)	65	73
58	B1	1110/1168 (95%)	1016 (92%)	94 (8%)	10	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	B2	1150/1157 (99%)	1118 (97%)	32 (3%)	38	58
60	W0	70/75 (93%)	69 (99%)	1 (1%)	59	70
65	h	2/2 (100%)	2 (100%)	0	100	100
All	All	7381/7914 (93%)	7131 (97%)	250 (3%)	33	55

5 of 250 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	A1	22	THR
59	B2	483	ASP
58	B1	95	THR
59	B2	56	VAL
59	B2	901	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 125 such sidechains are listed below:

Mol	Chain	Res	Type
29	d	90	GLN
58	B1	1259	GLN
36	l	104	GLN
58	B1	1238	GLN
59	B2	688	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	398 (13%)	16 (0%)
52	2	119/120 (99%)	17 (14%)	1 (0%)
53	3	1538/1542 (99%)	255 (16%)	5 (0%)
54	4	34/47 (72%)	17 (50%)	2 (5%)
63	5	75/76 (98%)	43 (57%)	7 (9%)
64	6	76/77 (98%)	10 (13%)	0
64	7	76/77 (98%)	27 (35%)	2 (2%)
All	All	4820/4843 (99%)	767 (15%)	33 (0%)

5 of 767 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	1	10	A

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Mol	Chain	Res	Type
51	1	12	U
51	1	34	U
51	1	35	G
51	1	46	G

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
63	5	48	C
63	5	57	G
64	7	56	C
51	1	1930	G
51	1	1801	A

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	$\# Z > 2$
65	KBE	h	1	65	8,8,9	0.57	0	6,8,10	1.18	0
65	UAL	h	5	65	6,8,9	2.37	2 (33%)	4,9,11	1.87	1 (25%)
65	DPP	h	2	65	4,5,6	0.50	0	1,5,7	0.07	0
65	5OH	h	6	65	7,12,13	0.69	0	4,16,18	1.34	1 (25%)

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
65	KBE	h	1	65	-	0/7/7/8	-
65	UAL	h	5	65	-	0/3/7/9	-
65	DPP	h	2	65	-	0/2/4/6	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
65	5OH	h	6	65	-	0/2/18/20	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	h	5	UAL	C1-N1	-4.98	1.32	1.40
65	h	5	UAL	C-CA	-2.82	1.40	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	h	5	UAL	O-C-CA	-3.28	121.28	125.39
65	h	6	5OH	CR-CB-CA	-2.42	110.04	112.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
65	h	5	UAL	1	0
65	h	2	DPP	3	0
65	h	6	5OH	6	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

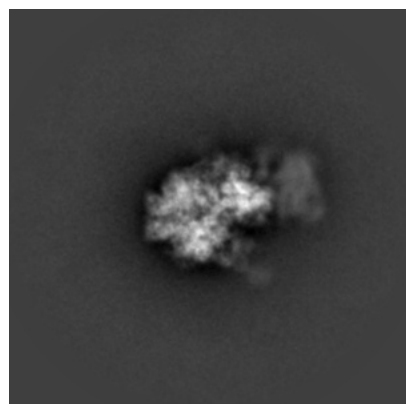
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38941. These allow visual inspection of the internal detail of the map and identification of artifacts.

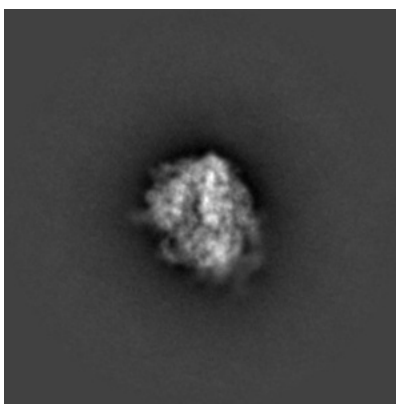
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

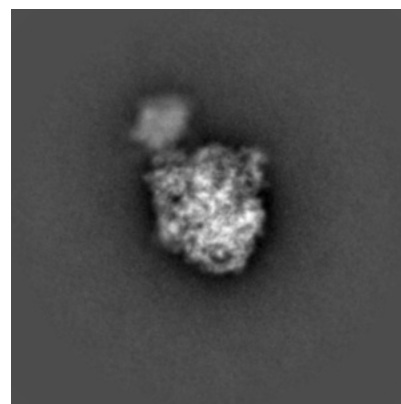
6.1.1 Primary map



X

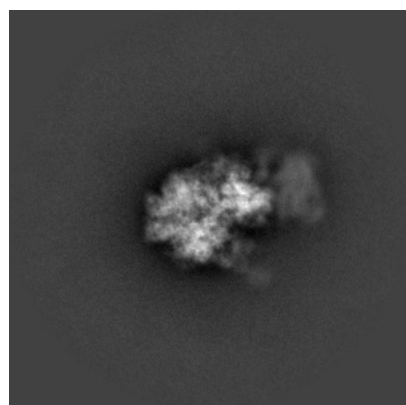


Y

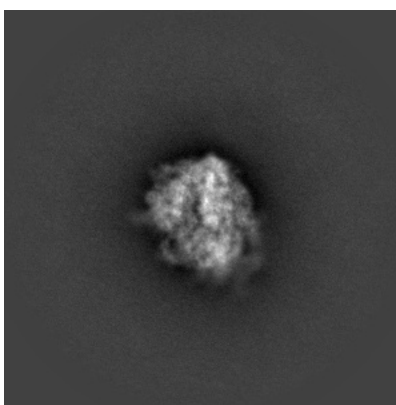


Z

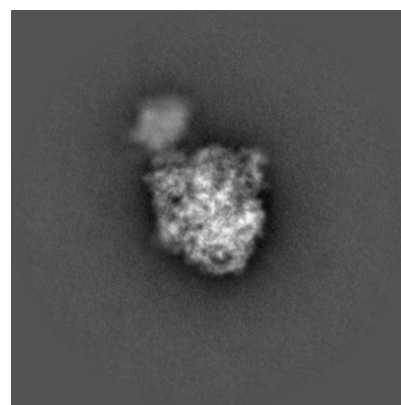
6.1.2 Raw map



X



Y

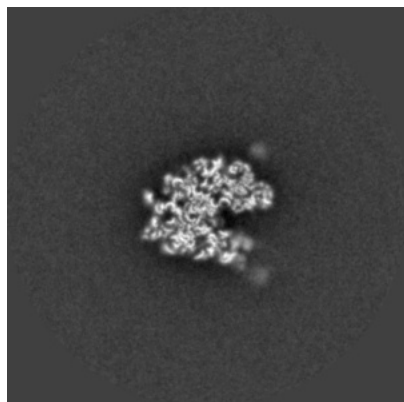


Z

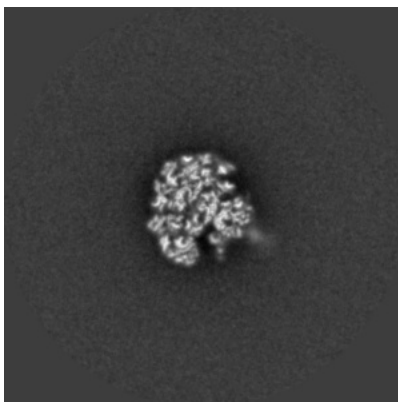
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

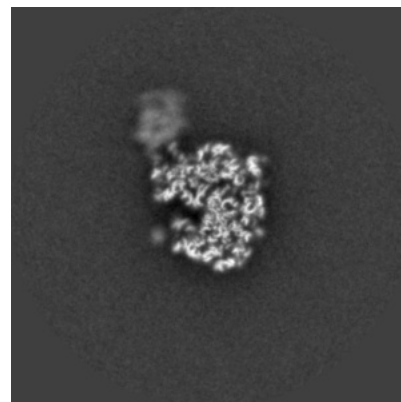
6.2.1 Primary map



X Index: 240

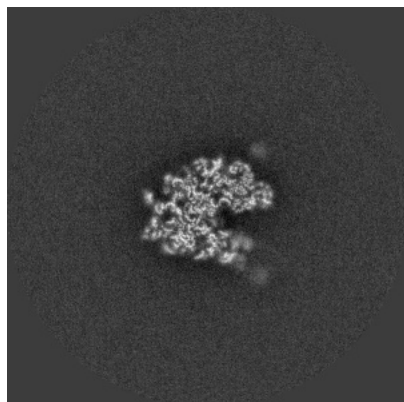


Y Index: 240

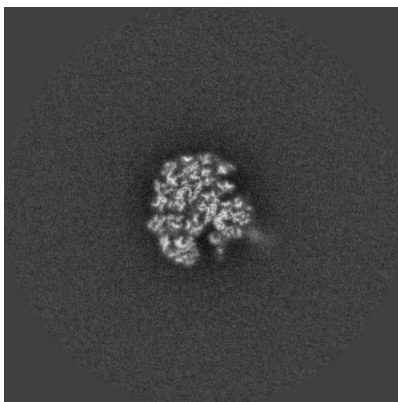


Z Index: 240

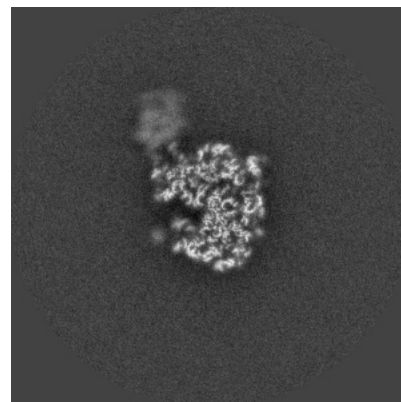
6.2.2 Raw map



X Index: 240



Y Index: 240

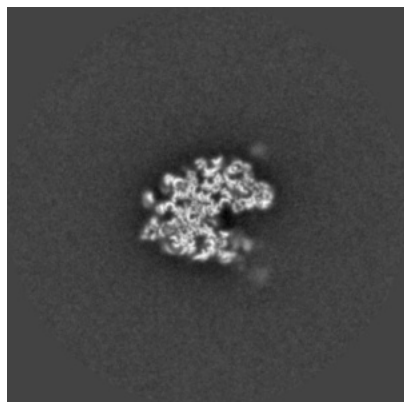


Z Index: 240

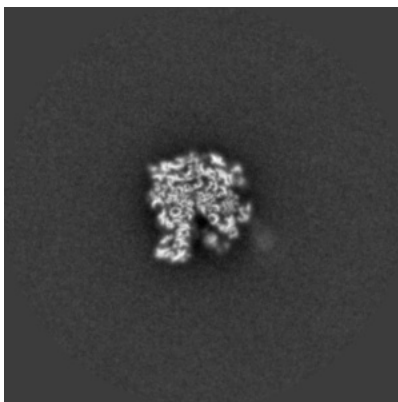
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

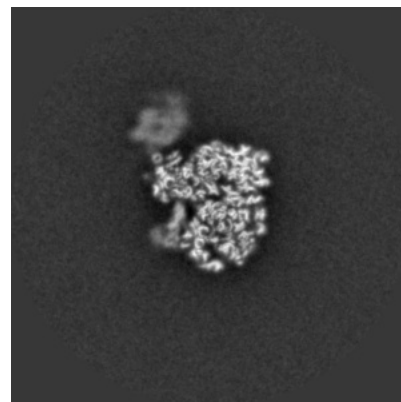
6.3.1 Primary map



X Index: 242

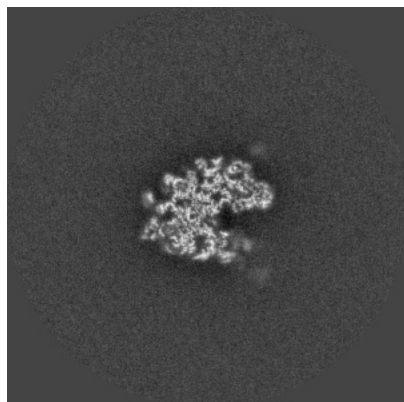


Y Index: 226

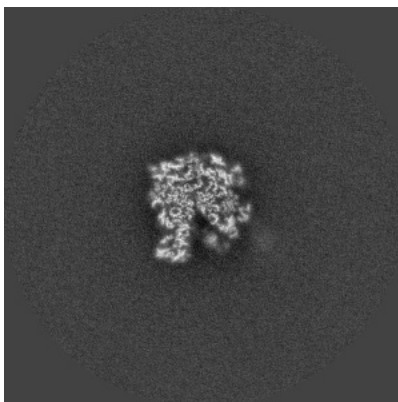


Z Index: 249

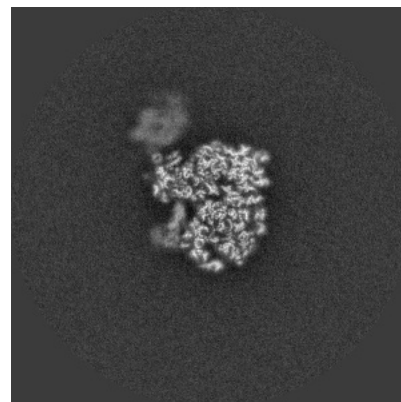
6.3.2 Raw map



X Index: 242



Y Index: 226

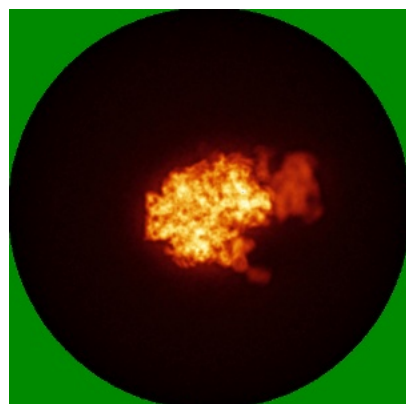


Z Index: 249

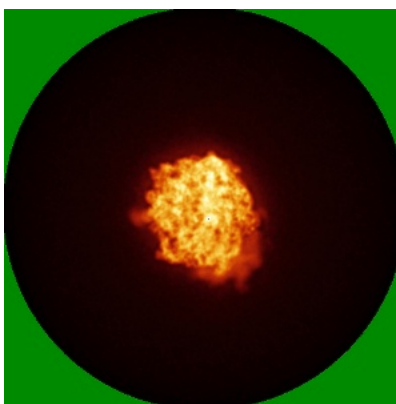
The images above show the largest variance slices of the map in three orthogonal directions.

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

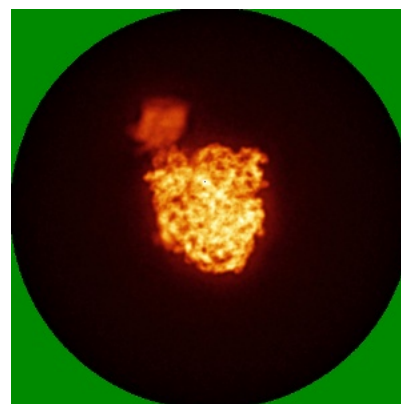
6.4.1 Primary map



X

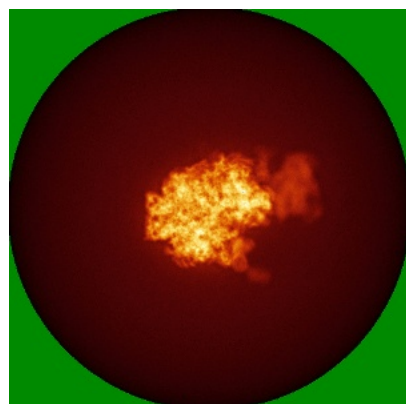


Y

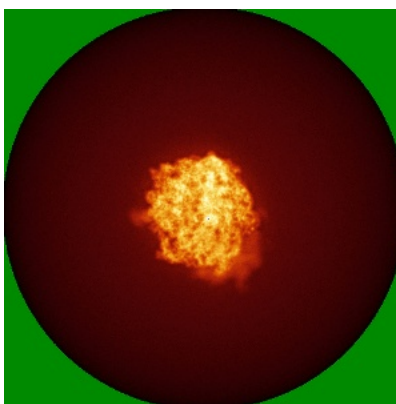


Z

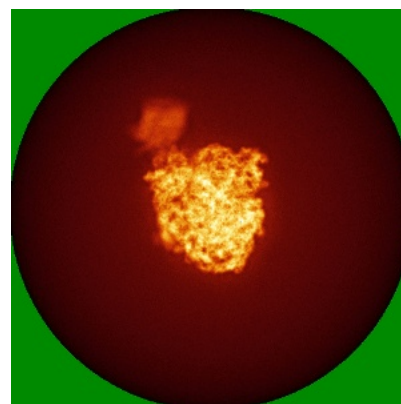
6.4.2 Raw map



X



Y

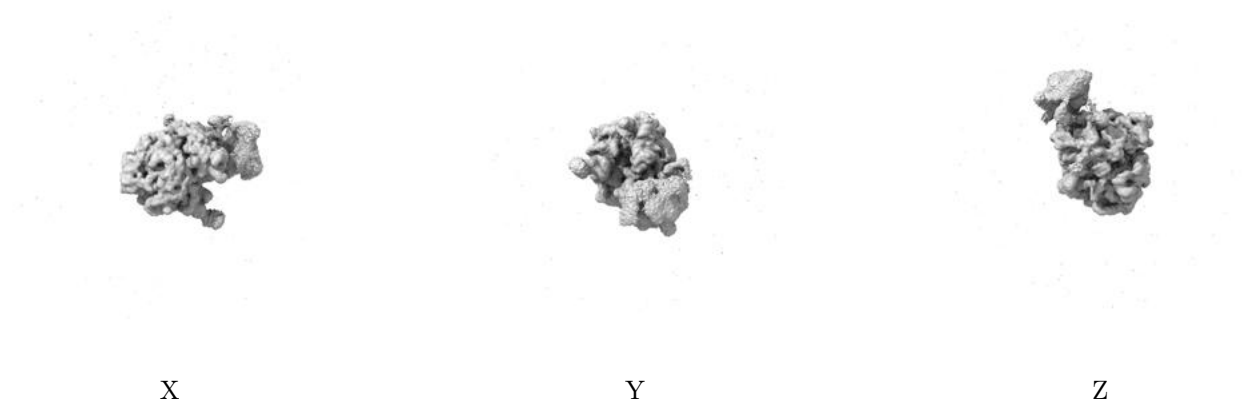


Z

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.

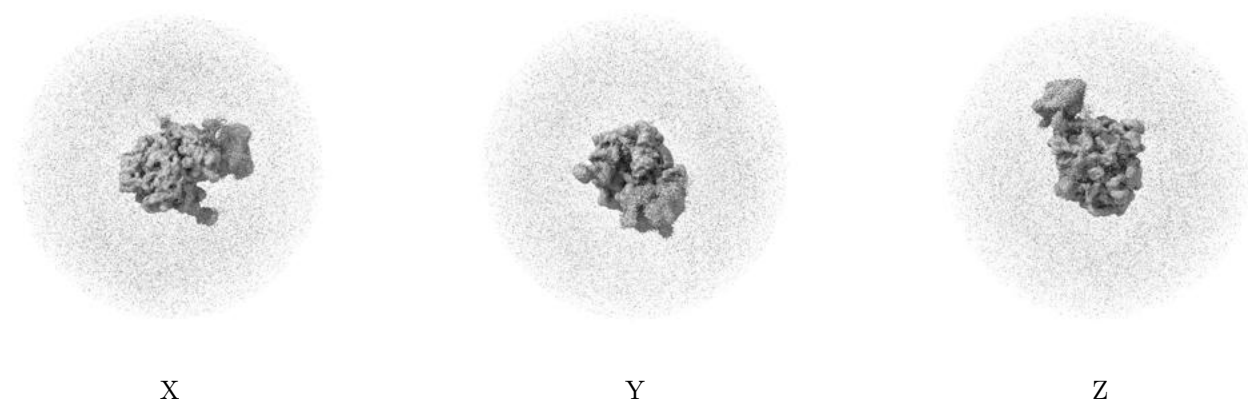
6.5 Orthogonal surface views [i](#)

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.

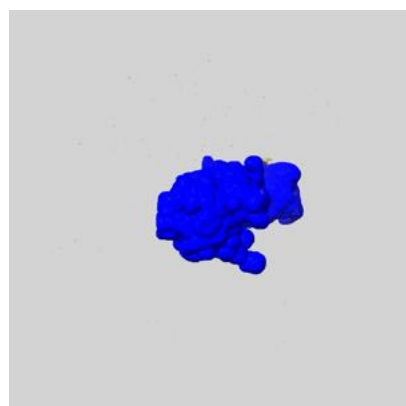
6.6 Mask visualisation [i](#)

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

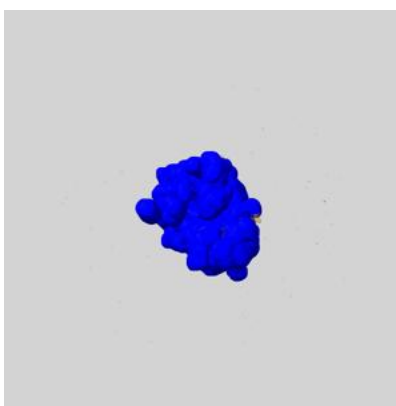
A mask typically either:

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

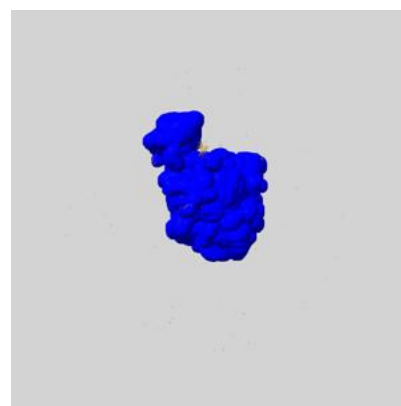
6.6.1 emd_38941_msk_1.map [i](#)



X



Y

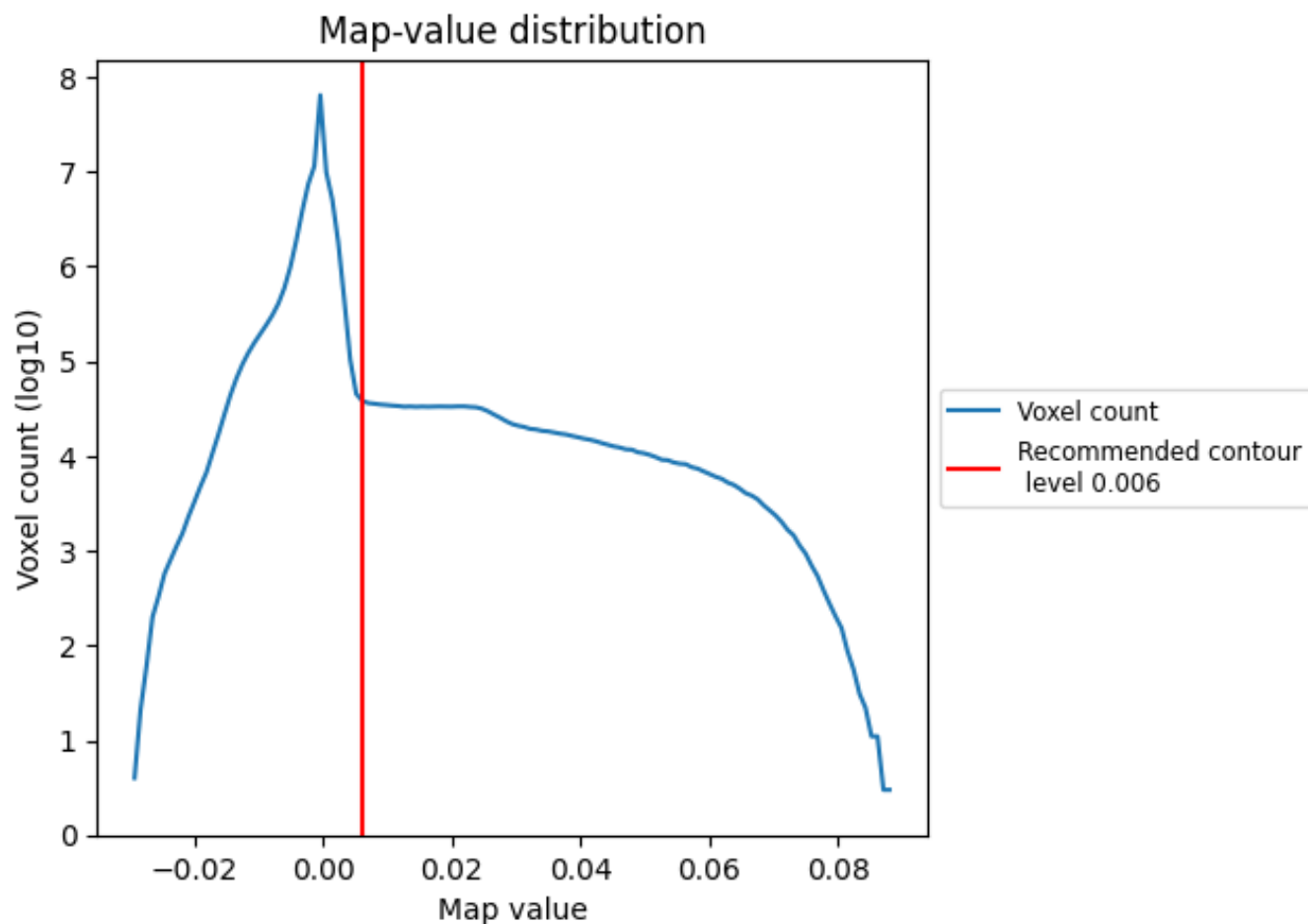


Z

7 Map analysis [i](#)

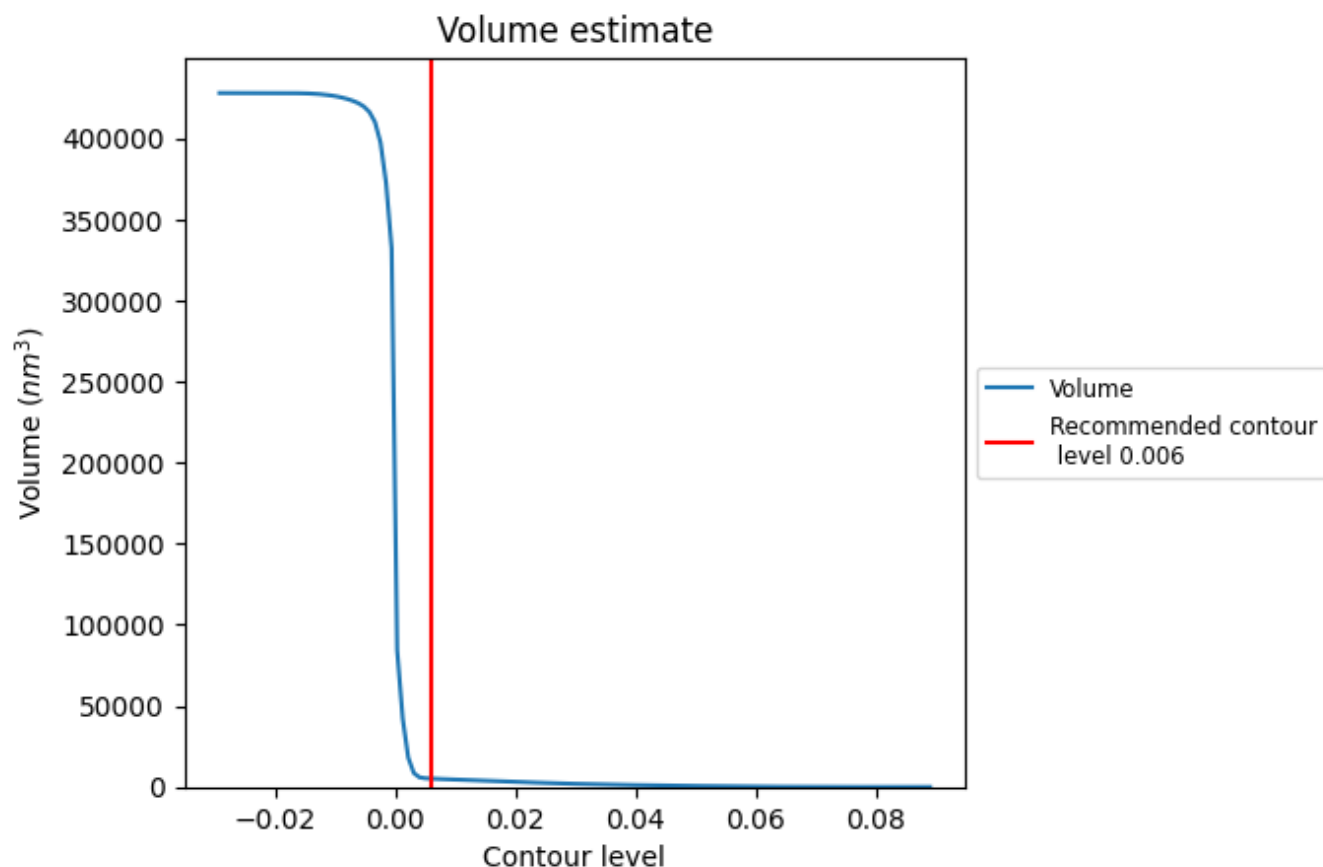
This section contains the results of statistical analysis of the map.

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.

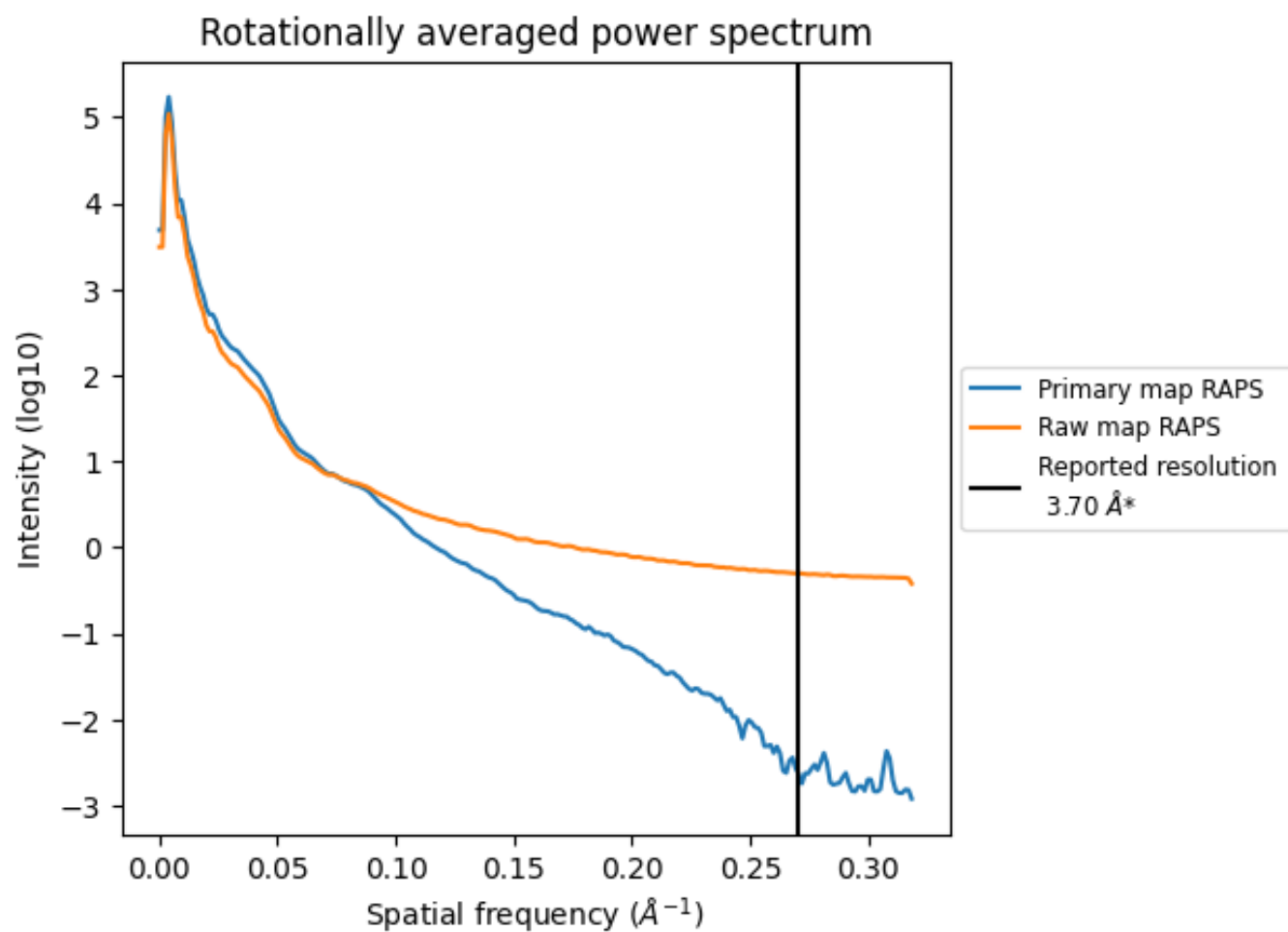
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5140 nm^3 ; this corresponds to an approximate mass of 4643 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

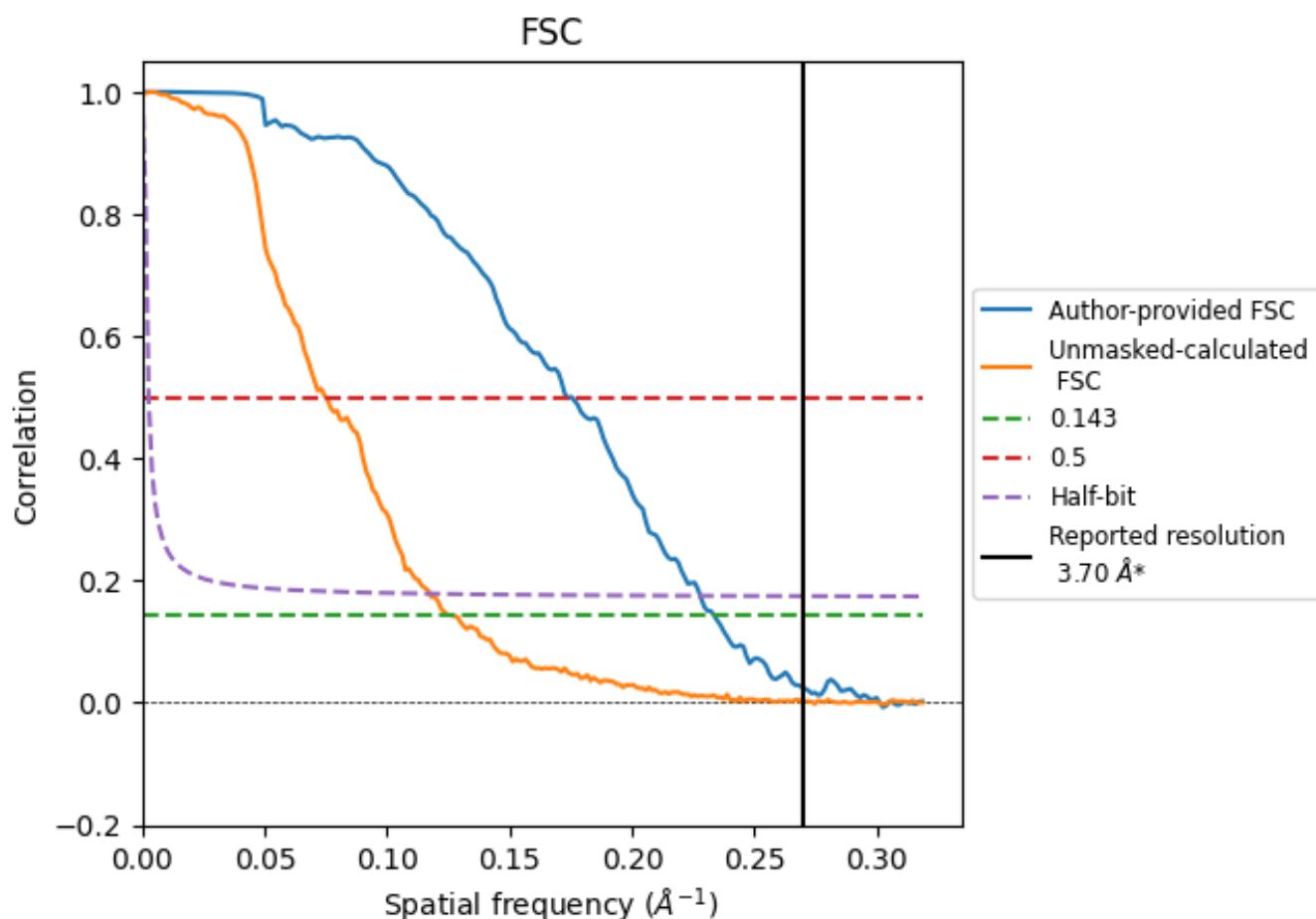


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	4.28	5.76	4.39
Unmasked-calculated*	7.92	13.33	8.52

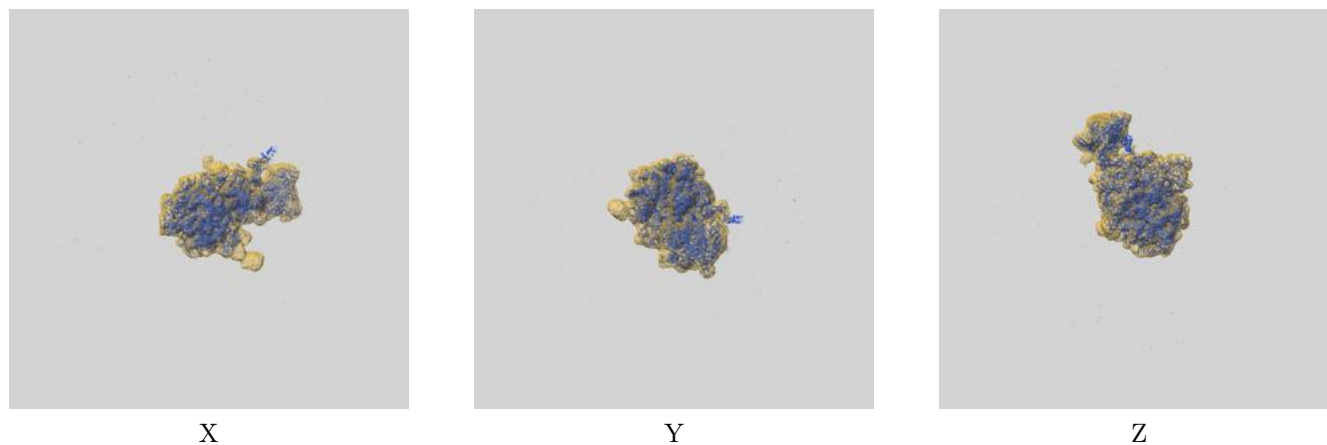
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.28 differs from the reported value 3.7 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.92 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38941 and PDB model 8Y5L. Per-residue inclusion information can be found in section [3](#) on page [16](#).

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](#)

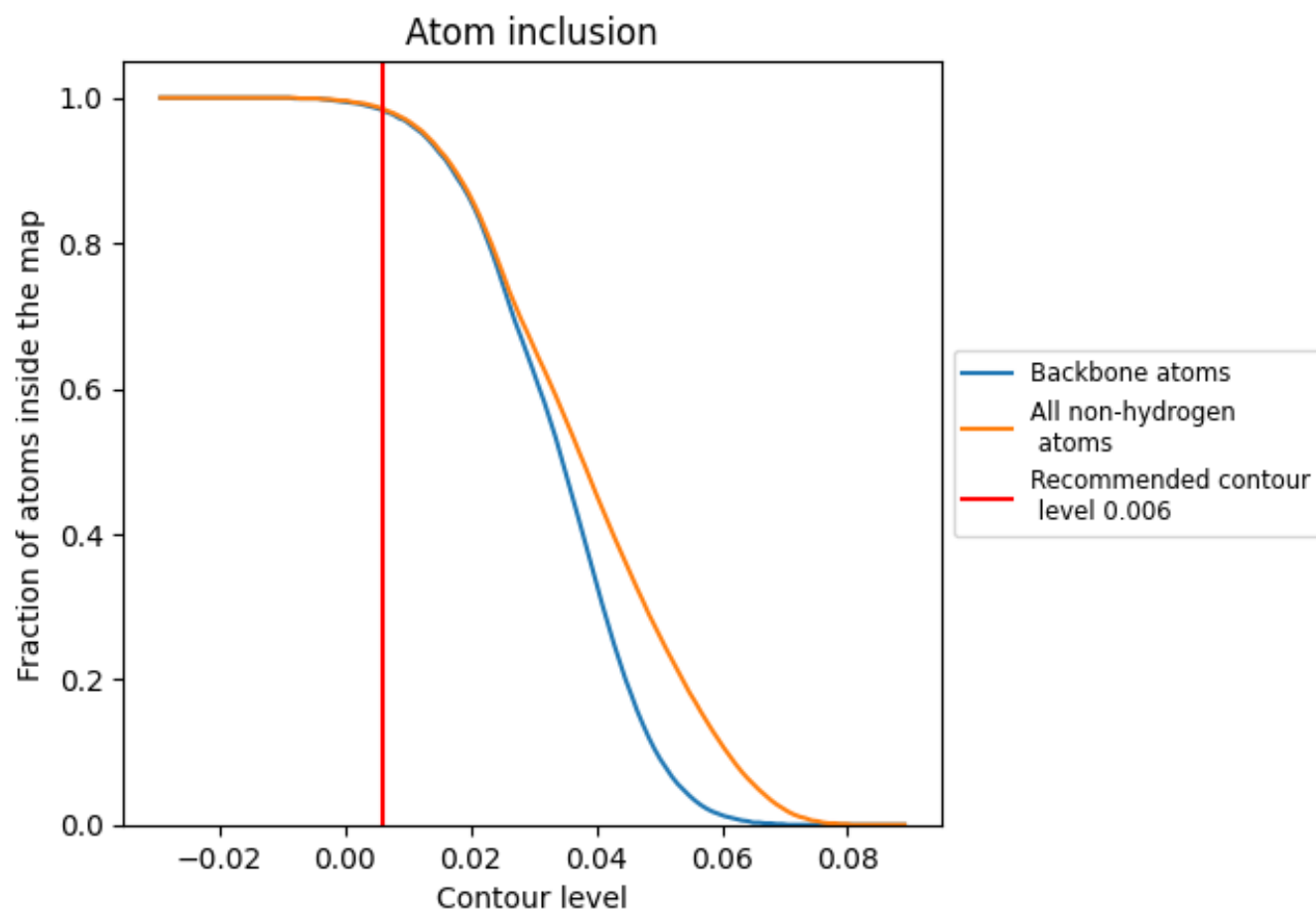


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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	 0.9850	 0.1860
1	 0.9990	 0.2390
2	 1.0000	 0.2210
3	 0.9990	 0.2150
4	 0.9720	 0.0810
5	 0.9750	 0.1340
6	 0.9980	 0.2420
7	 0.8370	 0.0840
8	 1.0000	 0.0720
9	 1.0000	 0.0730
A	 0.9790	 0.1550
A1	 0.9340	 0.0400
A2	 0.8340	 0.0570
B	 0.9980	 0.2030
B1	 0.9650	 0.0450
B2	 0.9780	 0.0560
C	 0.9750	 0.1900
D	 0.9830	 0.1800
E	 0.9980	 0.1920
F	 0.9900	 0.1490
G	 0.9880	 0.1770
H	 0.9790	 0.1970
I	 0.9590	 0.0850
J	 0.9940	 0.2040
K	 0.9940	 0.1880
L	 0.9920	 0.1810
M	 0.9850	 0.1960
N	 0.9990	 0.1550
NA	 0.8780	 0.1540
NG	 0.9510	 0.0880
O	 0.9990	 0.1400
P	 0.9960	 0.1960
Q	 0.9620	 0.1720
R	 0.9970	 0.1680
S	 0.9960	 0.1570



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Chain	Atom inclusion	Q-score
T	 0.9910	 0.1640
U	 0.9570	 0.1090
V	 0.9640	 0.1480
W	 0.9940	 0.1650
W0	 0.5580	 0.0150
X	 0.9920	 0.1550
Y	 0.9770	 0.1560
Z	 0.9520	 0.1400
b	 0.9900	 0.2240
c	 0.9880	 0.1850
d	 0.9950	 0.2110
e	 0.9930	 0.1860
f	 0.9920	 0.1810
g	 0.9980	 0.1850
h	 1.0000	 0.1560
i	 0.9100	 0.0660
j	 0.9960	 0.2020
k	 0.9810	 0.2040
l	 0.9990	 0.1970
m	 0.9860	 0.2070
n	 1.0000	 0.1800
o	 1.0000	 0.1780
p	 0.9820	 0.1940
q	 0.9960	 0.1790
r	 0.9960	 0.2170
s	 0.9900	 0.2040
t	 0.9850	 0.1690
u	 0.9940	 0.1700
v	 0.9990	 0.1790
w	 0.9930	 0.1710
x	 0.9950	 0.1990
y	 1.0000	 0.1610
z	 0.9980	 0.1980