



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 04:30 PM UTC

PDB ID : 9K0Z / pdb_00009k0z
EMDB ID : EMD-61959
Title : EF-G2 bound 70S ribosome complex of M. smegmatis
Authors : Sengupta, J.; Baid, P.
Deposited on : 2024-10-16
Resolution : 4.70 Å (reported)
Based on initial model : 5O61

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

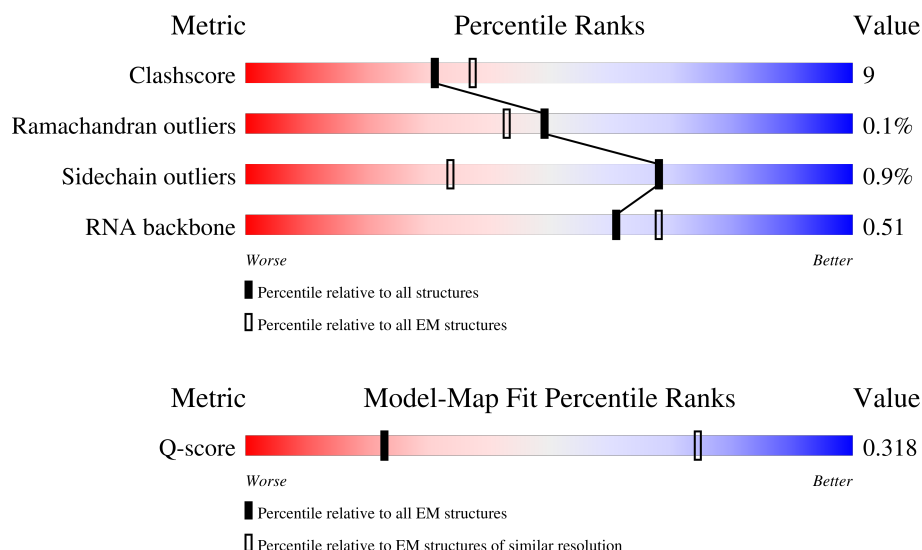
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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	1989 (4.20 - 5.20)

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	2	76	
2	3	23	
3	4	18	

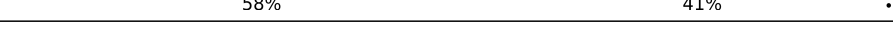
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Mol	Chain	Length	Quality of chain
4	5	69	
5	7	709	
6	A	1511	
7	B	118	
8	C	208	
9	D	200	
10	E	180	
11	F	96	
12	G	155	
13	H	131	
14	I	126	
15	J	99	
16	K	115	
17	L	122	
18	M	116	
19	N	60	
20	O	88	
21	P	113	
22	Q	94	
23	R	65	
24	S	82	
25	T	85	
26	U	97	
27	V	228	
28	W	192	

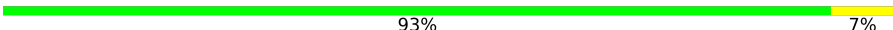
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Mol	Chain	Length	Quality of chain
29	X	79	
30	Y	63	
31	Z	64	
32	a	59	
33	b	54	
34	c	49	
35	d	46	
36	e	63	
37	f	37	
38	g	48	
39	i	275	
40	j	214	
41	k	209	
42	l	182	
43	m	176	
44	n	151	
45	o	126	
46	p	133	
47	q	146	
48	r	122	
49	s	145	
50	t	136	
51	u	118	
52	v	126	
53	w	113	

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Mol	Chain	Length	Quality of chain
54	x	124	 93%7%
55	y	100	 84%16%
56	z	114	 85%15%
57	l	105	 74%18%8%
58	h	3127	 61%31%6% •

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 155552 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 RNA chain called P/P-site Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	76	Total	C	N	O	P	0	0
			1614	721	287	531	75		

- Molecule 2 is a protein called 50S ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 3 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	18	Total	C	N	O	P	0	0
			390	176	80	117	17		

- Molecule 4 is a protein called Large ribosomal subunit protein bL12.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	5	69	Total	C	N	O	0	0
			505	321	83	101		

- Molecule 5 is a protein called Translation elongation factor EF-G.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	709	Total	C	N	O	S	0	0
			5299	3311	931	1039	18		

- Molecule 6 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 7 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 8 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 9 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 10 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 11 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 12 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 13 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 14 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	I	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 15 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 18 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 19 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 20 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	O	88	Total	C	N	O	0	0
			720	449	147	124		

- Molecule 21 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	P	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 22 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 23 is a protein called Small ribosomal subunit protein bS18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 24 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 25 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	T	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 27 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 28 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 29 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 30 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 31 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 32 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 33 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 34 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 35 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 36 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	63	Total	C	N	O	S	0	0
			502	302	115	85			

- Molecule 37 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 38 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 39 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 40 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 41 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 42 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 43 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 44 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 45 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 46 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 47 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 48 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 49 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 50 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 51 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 52 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	126	Total	C	N	O	S	0	0
			956	586	199	171			

- Molecule 53 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 54 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	124	Total	C	N	O	S	0	0
			988	613	203	172			

- Molecule 55 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	100	Total	C	N	O	S	0	0
			754	478	137	139			

- Molecule 56 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	z	114	Total	C	N	O	0	0
			873	543	171	159		

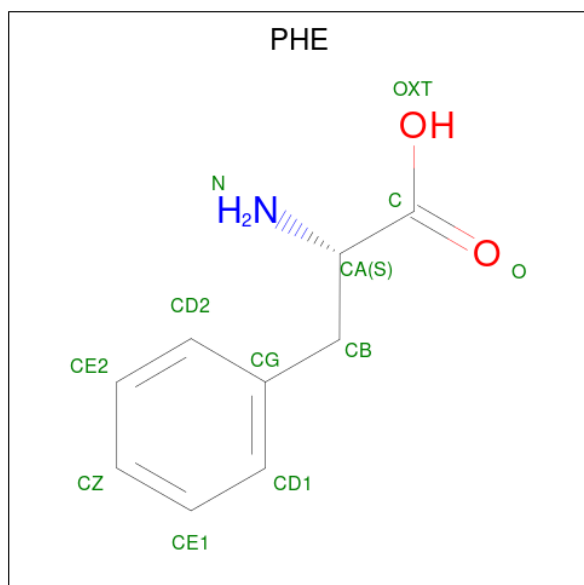
- Molecule 57 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	1	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 58 is a RNA chain called 23S ribosomal RNA.

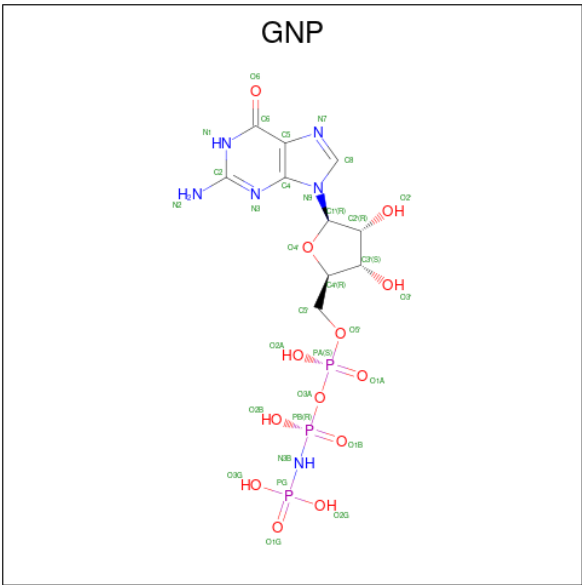
Mol	Chain	Residues	Atoms					AltConf	Trace
58	h	3071	Total	C	N	O	P	0	0
			65953	29397	12129	21356	3071		

- Molecule 59 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms				AltConf
59	2	1	Total	C	N	O	0
			11	9	1	1	

- Molecule 60 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
60	7	1	Total	C	N	O	P	0
			32	10	6	13	3	

- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
61	F	1	Total	Mg	0
			1	1	
61	R	1	Total	Mg	0
			1	1	
61	X	1	Total	Mg	0
			1	1	
61	i	3	Total	Mg	0
			3	3	
61	l	1	Total	Mg	0
			1	1	
61	t	1	Total	Mg	0
			1	1	
61	z	1	Total	Mg	0
			1	1	
61	h	3	Total	Mg	0
			3	3	

- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
62	N	1	Total 1	Zn 1	0
62	R	1	Total 1	Zn 1	0
62	Y	1	Total 1	Zn 1	0
62	c	1	Total 1	Zn 1	0
62	f	1	Total 1	Zn 1	0
62	g	1	Total 1	Zn 1	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: P/P-site Phe-tRNA(Phe)

Chain 2: 



- Molecule 2: 50S ribosomal protein bL37

Chain 3: 



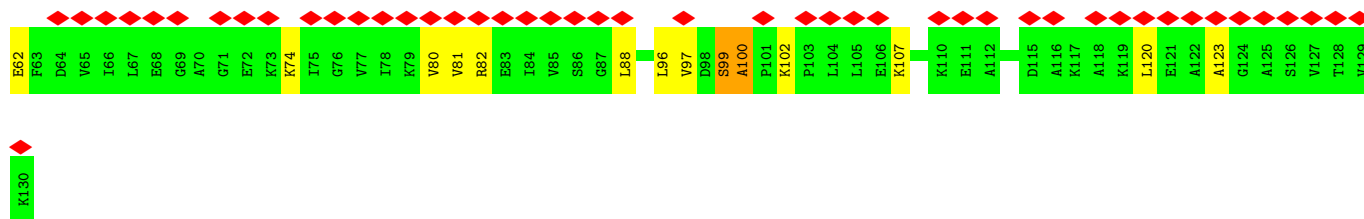
- Molecule 3: mRNA fragment

Chain 4: 



- Molecule 4: Large ribosomal subunit protein bL12

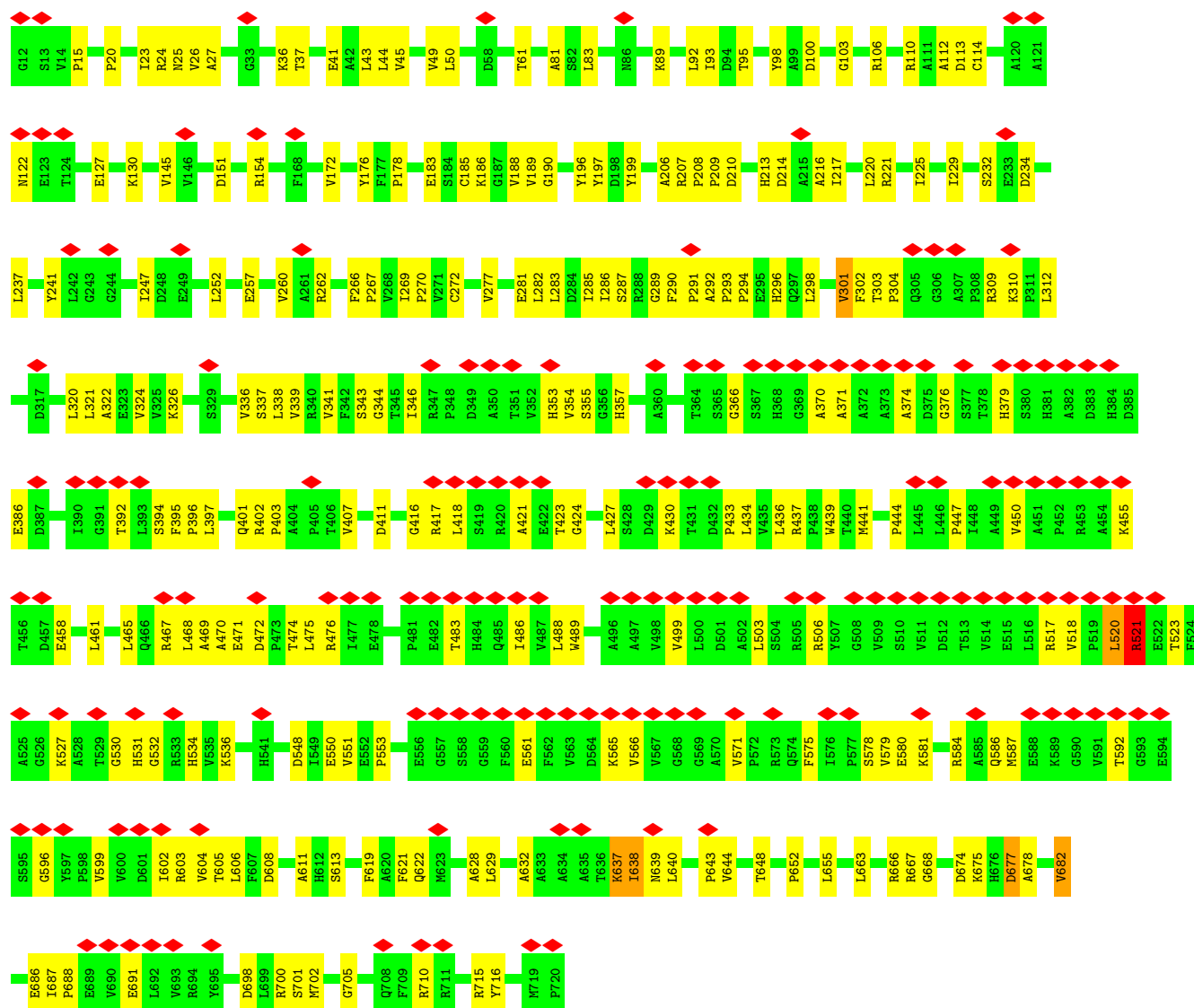
Chain 5: 



- Molecule 5: Translation elongation factor EF-G

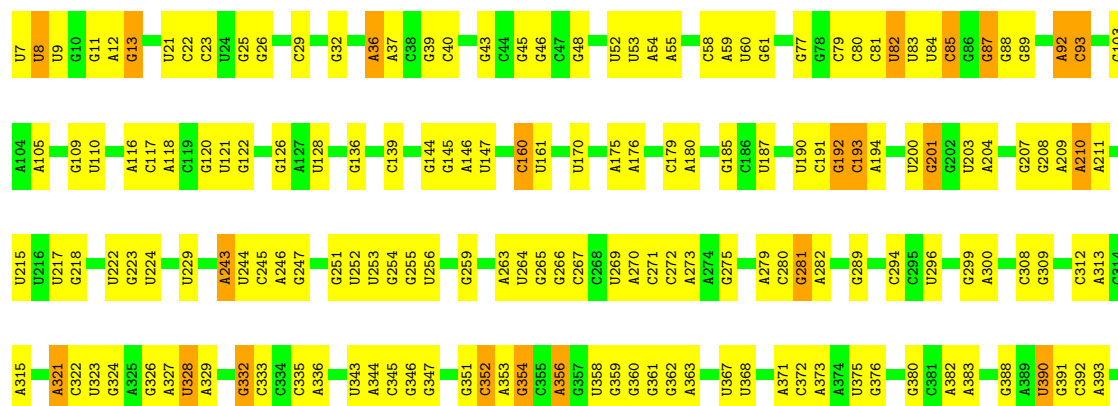
Chain 7: 

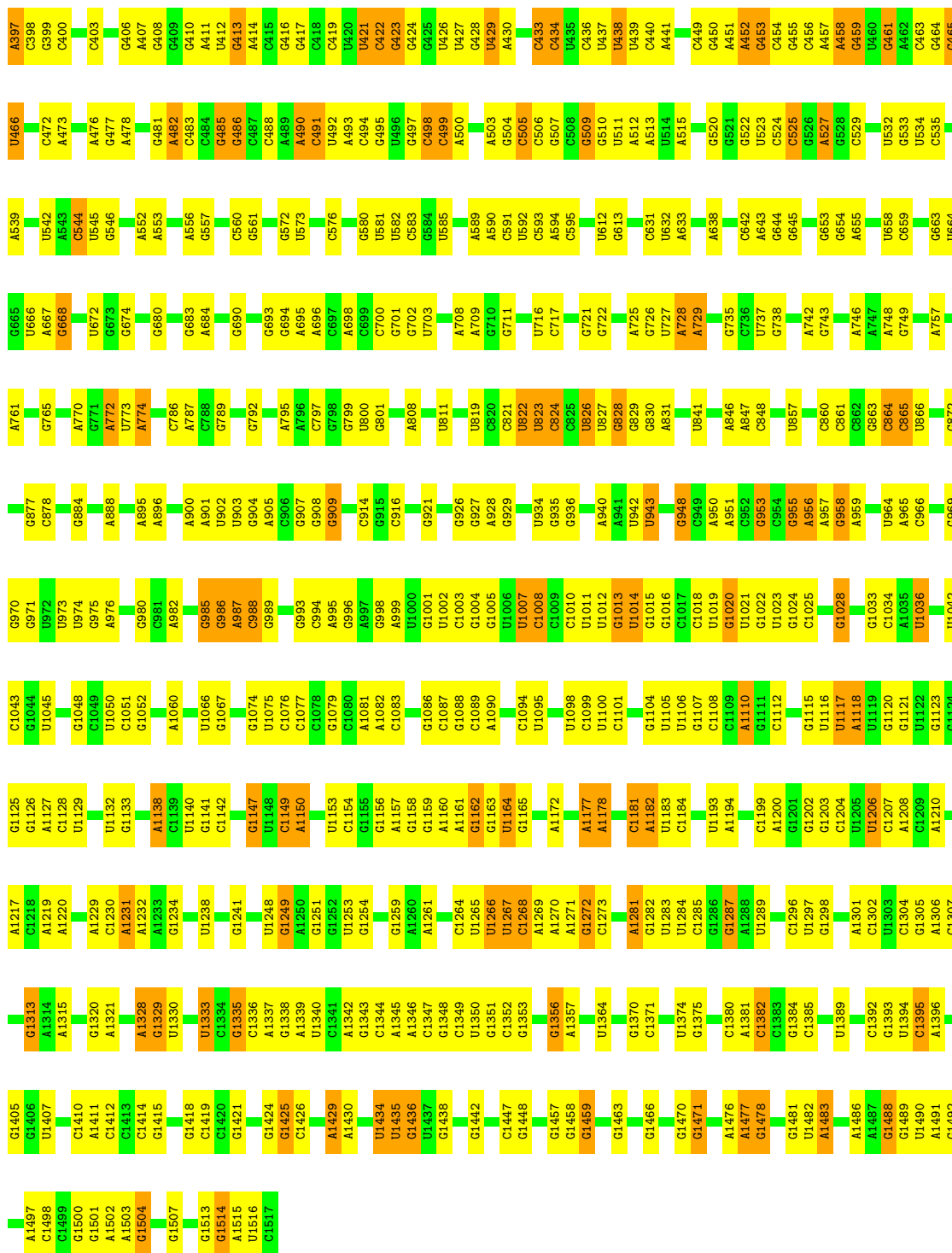




• Molecule 6: 16S ribosomal RNA

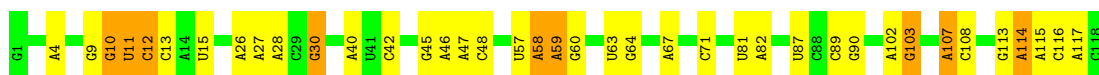
Chain A: 54% 38% 8%





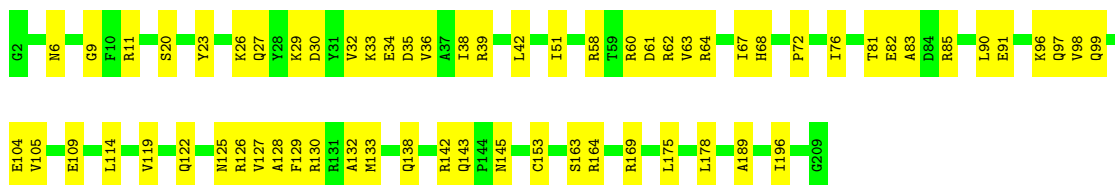
• Molecule 7: 5S ribosomal RNA

Chain B: 67% 25% 8%



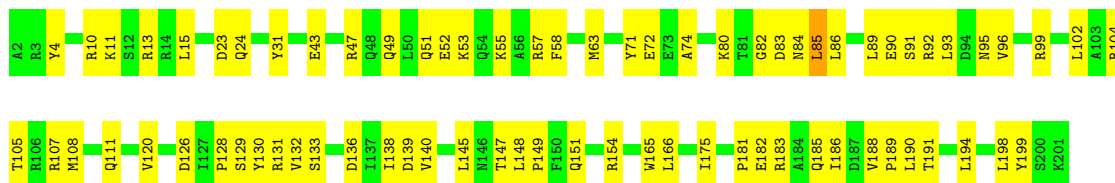
• Molecule 8: Small ribosomal subunit protein uS3

Chain C:  69% 31%



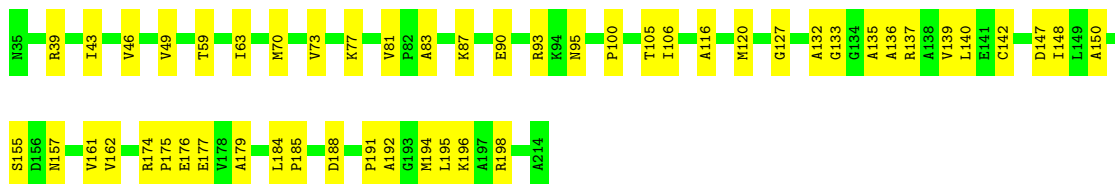
- Molecule 9: Small ribosomal subunit protein uS4

Chain D:  63% 36%



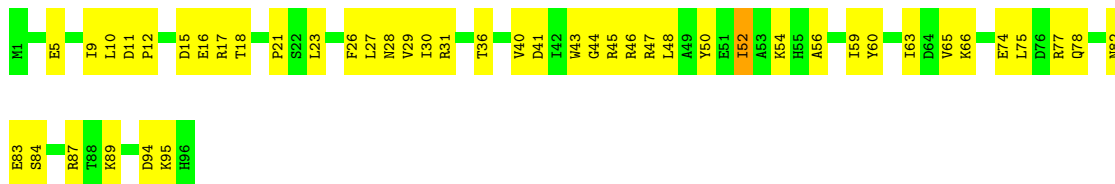
- Molecule 10: Small ribosomal subunit protein uS5

Chain E:  72% 28%



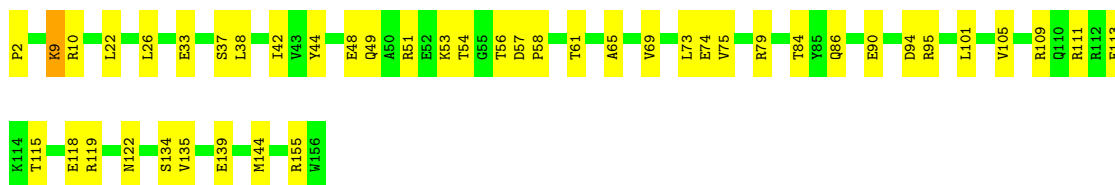
- Molecule 11: Small ribosomal subunit protein bS6

Chain F:  52% 47%



- Molecule 12: Small ribosomal subunit protein uS7

Chain G:  72% 28%



- Molecule 13: Small ribosomal subunit protein uS8

Chain H:  74% 26%



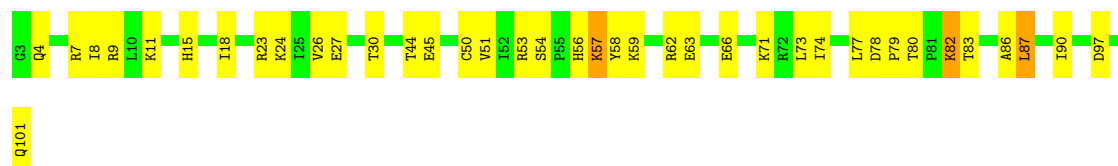
- Molecule 14: Small ribosomal subunit protein uS9

Chain I:  65% 34%



- Molecule 15: Small ribosomal subunit protein uS10

Chain J:  61% 36%



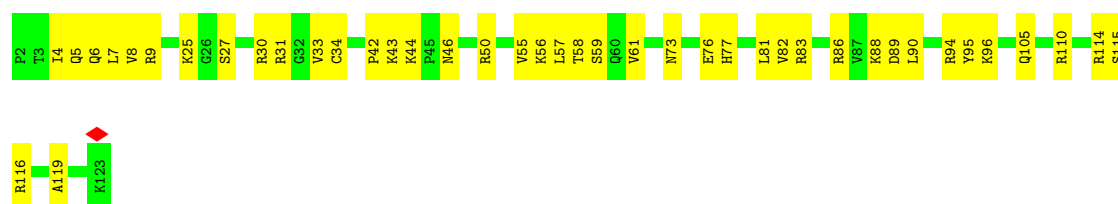
- Molecule 16: Small ribosomal subunit protein uS11

Chain K:  71% 28%



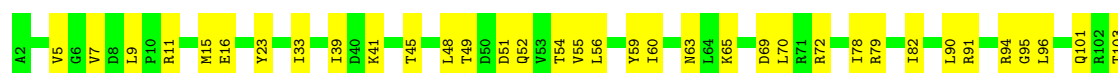
- Molecule 17: Small ribosomal subunit protein uS12

Chain L:  66% 34%



- Molecule 18: Small ribosomal subunit protein uS13

Chain M:  67% 33%





- Molecule 19: Small ribosomal subunit protein uS14B

Chain N: 73% 27%



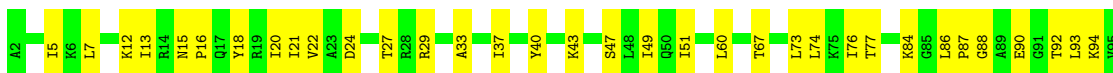
- Molecule 20: Small ribosomal subunit protein uS15

Chain O: 73% 27%



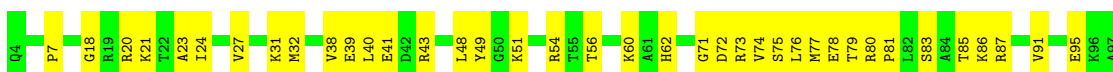
- Molecule 21: Small ribosomal subunit protein bS16

Chain P: 66% 34%



- Molecule 22: Small ribosomal subunit protein uS17

Chain Q: 60% 40%



- Molecule 23: Small ribosomal subunit protein bS18B

Chain R: 85% 15%



- Molecule 24: Small ribosomal subunit protein uS19

Chain S: 76% 23%



- Molecule 25: Small ribosomal subunit protein bS20

Chain T:  61% 38%



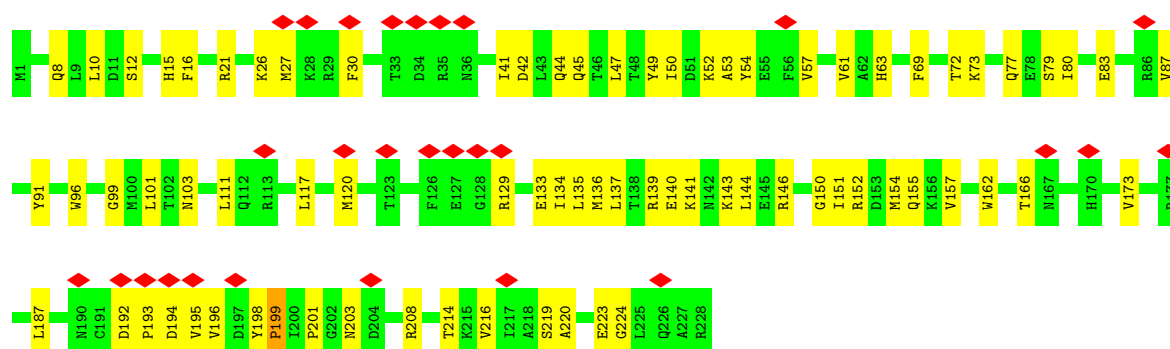
- Molecule 26: Large ribosomal subunit protein uL23

Chain U:  80% 20%



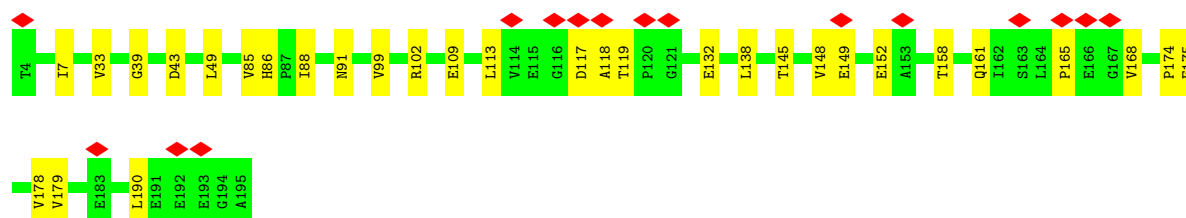
- Molecule 27: Small ribosomal subunit protein uS2

Chain V:  12% 67% 33%



- Molecule 28: Large ribosomal subunit protein bL25

Chain W:  8% 84% 16%



- Molecule 29: Large ribosomal subunit protein bL27

Chain X:  82% 18%



- Molecule 30: Large ribosomal subunit protein bL28

Chain Y:  81% 19%



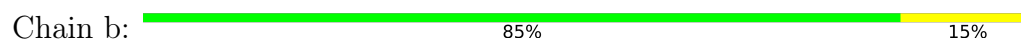
- Molecule 31: Large ribosomal subunit protein uL29



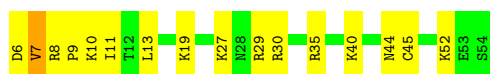
- Molecule 32: Large ribosomal subunit protein uL30



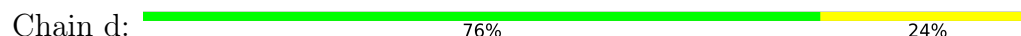
- Molecule 33: Large ribosomal subunit protein bL32



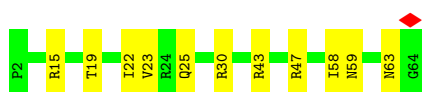
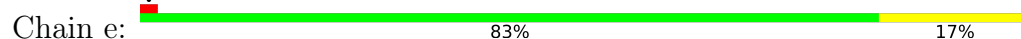
- Molecule 34: Large ribosomal subunit protein bL33A



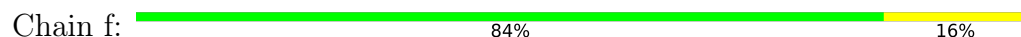
- Molecule 35: Large ribosomal subunit protein bL34



- Molecule 36: Large ribosomal subunit protein bL35

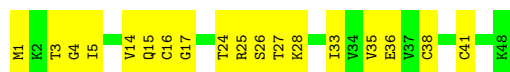


- Molecule 37: 50S ribosomal protein L36

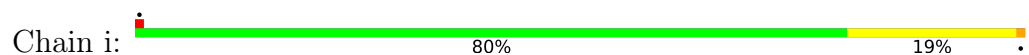




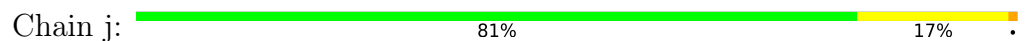
- Molecule 38: Large ribosomal subunit protein bL31



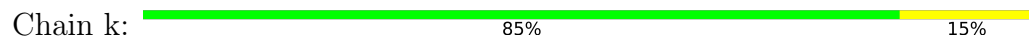
- Molecule 39: Large ribosomal subunit protein uL2



- Molecule 40: Large ribosomal subunit protein uL3

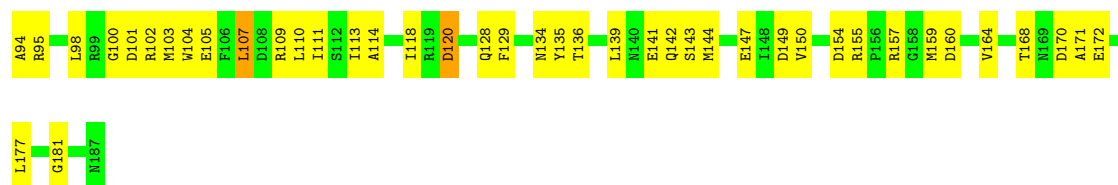


- Molecule 41: Large ribosomal subunit protein uL4



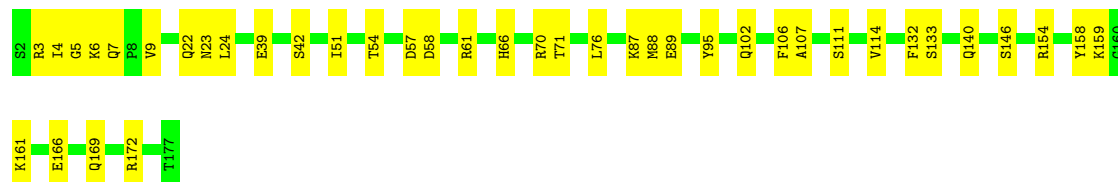
- Molecule 42: Large ribosomal subunit protein uL5





- Molecule 43: Large ribosomal subunit protein uL6

Chain m: 77% 23%



- Molecule 44: 50S ribosomal protein L9

Chain n: 79% 21%



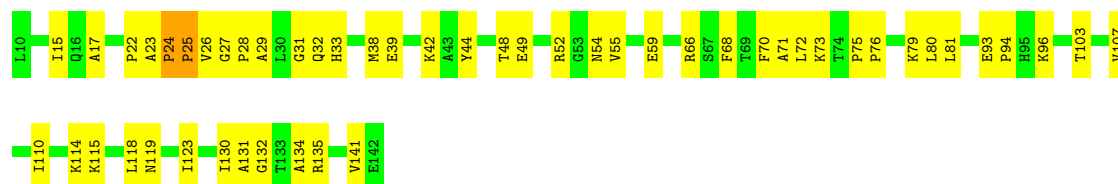
- Molecule 45: Large ribosomal subunit protein uL10

Chain o: 65% 35%



- Molecule 46: Large ribosomal subunit protein uL11

Chain p: 62% 37%



- Molecule 47: Large ribosomal subunit protein uL13

Chain q: 81% 18%



- Molecule 48: 50S ribosomal protein L14

Chain r: 77% 22%



- Molecule 49: Large ribosomal subunit protein uL15

Chain s: 82% 18%



- Molecule 50: Large ribosomal subunit protein uL16

Chain t: 79% 21%



- Molecule 51: Large ribosomal subunit protein bL17

Chain u: 79% 21%



- Molecule 52: Large ribosomal subunit protein uL18

Chain v: 76% 23%



- Molecule 53: 50S ribosomal protein L19

Chain w: 79% 21%

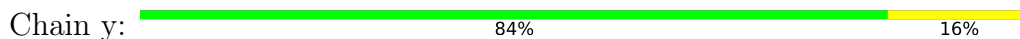


- Molecule 54: Large ribosomal subunit protein bL20

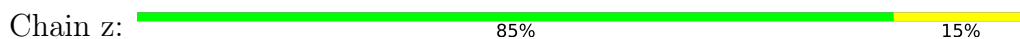
Chain x: 93% 7%



- Molecule 55: Large ribosomal subunit protein bL21



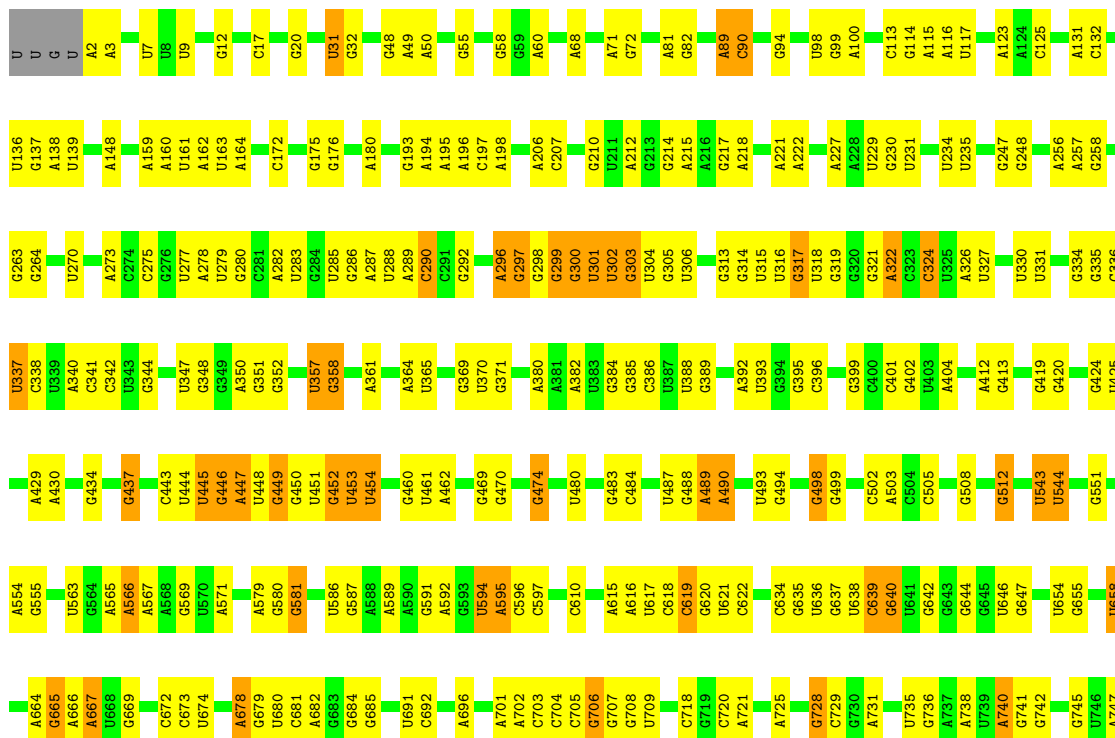
- Molecule 56: Large ribosomal subunit protein uL22



- Molecule 57: Large ribosomal subunit protein uL24



- Molecule 58: 23S ribosomal RNA



A2212	U2091	G1963	A1803	G1703	G	C1545	G1454	A1288	A1195	C1086	A976	U748
U2215	U2092	U1964	G1804	G1703	C	A1546	U1455	U1485	C1198	G1087	G977	C749
G2016	G2093	G1965	G1805	C1705	U	G1547	G1456	G1293	U1199	U1088	A978	C750
U2217	G2094	C1973	U1809	U1706	G	C1548	G1457	G1292	U1200	G1092	A979	A751
A2221	G2095	A1974	A1810	G1707	C1610	G1549	C1466	C1298	G1201	A1101	U981	A756
	G2096	A1975	G1815	U1708	A1611	U1551	U1467	G1326	A1202	G1102	G875	G757
	G2097		G1815	U1709	U1612	A1552	A1468	G1326	A1203	C1103	A758	A758
	A2106	U1981	C1825	U1710	G1613	U1553	A1469	G1334	A1204	G1112	G890	U760
	G2107	A1990	A1826	G1711	G1614	U1554	A1472	G1335	A1205	G1113	G891	G759
				G1712	G1615	U1555	G1473	G1335	A1206	G1114	G891	U760
	U2110	U1996	G1840	U1713	A1616	U1556	G1473	G1343	G1207	G1115	G895	U764
	U2111			U1714		C1557	G1476	A1344	U1208	G1116	G896	G765
	U2112			A1715		C1558	C1477	A1344	G1209	G1117	A896	G766
	A2113			U1716			C1478	G1345	G1210	A1118	A897	
	A2114			U1717			C1479	G1345	G1211	A1119	A898	G767
	A2115			C1718			G1479	A1352	U1212	C1125	G899	G768
	A2125							G1353	A1213	C1002	U772	U772
	C2126							A1362	A1214	A1003	G773	G773
								G1365	U1215	C1004	G774	G774
	C2129							G1369	C1220	A1005	C781	C781
	G2130							U1370	C1221	G1006	U782	U782
								G1371	C1222	G1007	G783	G783
	A2136							U1371	C1223	G1008	G784	G784
	A2137							G1379	U1219	A1011	A785	A785
	U2139							G1386	C1220	A1012	G789	G789
	A2140							G1387	C1221	U1013	A790	A790
	U2141							G1388	C1222	G1014	G921	G921
	A2142							U1389	C1223	A1015	U922	G794
	A2143							G1400	C1224	G1016	G923	G795
	C2144							C1404	U1225	A1020	G924	A796
	C2145							A1415	C1226	G1021	U801	U801
	A2146							A1416	C1227	A1022	U818	U818
	C2147							C1430	U1228	G1023	G819	G819
	C2148							C1430	C1229	G1024	U829	U829
								C1431	C1230	U1044	A830	A830
	G2153							C1432	C1231	A1025	A831	A831
	G2154							C1433	C1232	G1046	G843	G843
	A2160							C1434	C1233	A1047	G844	G844
	A2161							C1435	C1234	G1048	C845	C845
	A2162							C1436	C1235	A1050	C855	C855
	U2163							C1437	C1236	G1051	U857	U857
								C1438	C1237	A1052	A858	A858
	G2178							C1439	C1238	G1053	G859	G859
	U2179							C1440	C1239	U1075	U861	U861
	U2180							C1441	C1240	A1077	U862	U862
	A2184							C1442	C1241	G1078	G863	G863
								C1443	C1242	C1081	A864	A864
	C2189							C1444	C1243	C1082	A865	A865
	A2190							C1445	C1244	C1083	C868	C868
	C2191							C1446	C1245	G1084		
								C1447	C1246	G1085		
	C2194							C1448	C1247	G1086		
	A2195							C1449	C1248	G1087		
	G2196							C1450	C1249	G1088		
								C1451	C1250	G1089		
	C2201							C1452	C1251	G1090		
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								C1455	C1254	G1093		
								C1456	C1255	G1094		
								C1457	C1256	G1095		
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								C1459	C1258	G1097		
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								C1461	C1260	G1099		
								C1462	C1261	G1100		
								C1463	C1262	G1101		
								C1464	C1263	G1102		
								C1465	C1264	G1103		
								C1466	C1265	G1104		
								C1467	C1266	G1105		
								C1468	C1267	G1106		
								C1469	C1268	G1107		
								C1470	C1269	G1108		
								C1471	C1270	G1109		
								C1472	C1271	G1110		
								C1473	C1272	G1111		
								C1474	C1273	G1112		
								C1475	C1274	G1113		
								C1476	C1275	G1114		
								C1477	C1276	G1115		
								C1478	C1277	G1116		
								C1479	C1278	G1117		
								C1480	C1279	G1118		
								C1481	C1280	G1119		
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								C1487	C1286	G1125		
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								C1525	C1324	G1163		
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								C1528	C1327	G1166		
								C1529	C1328	G1167		
								C1530	C1329	G1168		
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								C1532	C1331	G1170		
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								C1535	C1334	G1173		
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								C1537	C1336	G1175		
								C1538	C1337	G1176		
								C1539	C1338	G1177		
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								C1541	C1340	G1179		
								C1542	C1341	G1180		
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								C1553	C1352	G1191		

C3041	C2923	A2814	G2710	A2609	A2497	C2384	U2321
A3042	A2926	C2815	G2715	C2610	G2503	G2385	C2322
C3045	C2936	G2816	U2716	G2613	G2504	U2386	G2323
C3046	C2937	A2826	U2717	U2614	C2505	U2387	A2324
G3055	G2938	G2827	U2718	G2615	G2506	G2388	U2325
A3056	C2939	U2833	G2719	C2616	C2507	A2326	U2326
U3057	U2940	U2837	C2722	C2618	C2508	U2327	G2327
A3058	C2948	A2838	C2723	C2622	A2510	G2328	C2329
A3071	A2949	U2839	G2726	A2623	A2511	U2330	U2331
G3078	C2950	U2842	A2727	C2624	A2512	U2332	G2332
A3081	A2957	G2842	U2728	C2627	U2515	G2333	G2333
U3082	G2961	G2851	G2729	A2630	U2516	U2334	U2334
C3088	A2962	U2852	U2735	G2631	G2528	G2335	G2335
A3089	C2967	C2853	C2736	G2640	A2529	U2336	U2336
A3093	G2968	A2854	G2737	C2644	C2530	A2337	A2337
U3096	C2969	G2862	U2738	C2647	G2531	G2338	G2338
A3100	U2970	G2865	C2739	U2648	G2532	G2339	G2339
C3101	A2971	U2870	A2742	C2649	C2533	A2340	A2340
A3103	G2975	U2871	U2743	A2649	U2536	U2341	U2341
A3104	U2980	C2872	C2744	C2650	C2537	A2342	A2342
C3105	A2981	U2873	C2745	A2651	A2538	G2343	G2343
C3106	A2982	C2874	G2749	G2652	G2539	U2344	G2344
A3113	G2985	C2875	G2750	C2653	U2548	U2345	U2345
A3114	G3001	U2876	G2753	A2654	G2549	G2346	G2346
A3115	A3002	A2877	C2754	U2655	U2552	G2347	G2347
C3116	C3003	A2878	C2757	A2659	G2553	G2348	G2348
U3117	C3004	C2882	U2758	C2665	U2554	A2349	A2349
U3118	C3007	A2883	C2761	C2667	A2557	G2350	G2350
A3119	U3008	A2884	C2762	A2672	C2558	A2351	A2351
C3120	U3009	G2888	G2777	A2677	G2569	C2352	C2352
A	A	A2889	U2778	G2678	A2570	G2353	G2353
A	A	C2890	U2779	U2679	C2571	G2354	G2354
C	C	C2891	C2780	C2680	C2574	U2355	U2355
A	A	G2781	G2781	C2688	G2575	U2356	U2356
		C2782	C2782	C2689	G2581	U2357	U2357
		U2786	U2786	C2690	U2587	A2358	A2358
		U2787	U2787	C2691	C2588	G2359	G2359
		A2788	A2788	A2692	G2589	U2370	U2370
		C2789	C2789	G2694	A2601	G2373	G2373
		G2791	G2791	C2698	A2602	U2374	U2374
		A2912	A2912	C2699	G2603	G2375	G2375
		U2913	U2913	A2700	U2604	G2376	G2376
		A2914	A2914	U2701	C2605	U2471	U2471
		C2915	C2915	A2702	G2606	G2482	G2482
		U2922	U2922	G2705	G2607	G2483	G2483
						A2493	A2493

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	19431	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.090	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.00715	Depositor
Map size (Å)	483.0, 483.0, 483.0	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GNP, MG, ZN

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	2	0.15	0/1802	0.29	0/2807
2	3	0.25	0/191	0.33	0/247
3	4	0.13	0/439	0.27	0/684
4	5	0.17	0/507	0.41	0/678
5	7	0.15	0/5405	0.36	1/7360 (0.0%)
6	A	0.24	0/36309	0.31	0/56657
7	B	0.25	0/2821	0.27	0/4396
8	C	0.20	0/1684	0.48	1/2261 (0.0%)
9	D	0.25	0/1672	0.55	0/2251
10	E	0.26	0/1312	0.45	0/1772
11	F	0.24	0/782	0.45	0/1059
12	G	0.32	1/1252 (0.1%)	0.63	4/1690 (0.2%)
13	H	0.25	0/1025	0.42	0/1385
14	I	0.25	0/1012	0.51	2/1362 (0.1%)
15	J	0.24	0/802	0.49	0/1086
16	K	0.24	0/873	0.49	0/1180
17	L	0.27	0/969	0.50	0/1294
18	M	0.25	0/942	0.51	0/1260
19	N	0.25	0/488	0.42	0/650
20	O	0.24	0/729	0.36	0/977
21	P	0.25	0/908	0.48	0/1226
22	Q	0.26	0/759	0.57	0/1016
23	R	0.24	0/518	0.42	0/693
24	S	0.20	0/680	0.41	0/915
25	T	0.24	0/663	0.48	0/882
26	U	0.28	0/766	0.42	0/1030
27	V	0.21	0/1822	0.53	3/2457 (0.1%)
28	W	0.21	0/1443	0.37	0/1970
29	X	0.28	0/595	0.34	0/798
30	Y	0.33	0/478	0.36	0/641
31	Z	0.24	0/534	0.38	0/713
32	a	0.28	0/477	0.36	0/640

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.30	0/427	0.41	0/572
34	c	0.22	0/413	0.39	0/553
35	d	0.30	0/380	0.32	0/500
36	e	0.26	0/507	0.37	0/672
37	f	0.25	0/303	0.30	0/401
38	g	0.21	0/372	0.44	0/503
39	i	0.32	0/2153	0.42	0/2895
40	j	0.30	0/1609	0.40	0/2165
41	k	0.28	0/1592	0.40	0/2153
42	l	0.25	0/1467	0.51	0/1973
43	m	0.21	0/1369	0.37	0/1848
44	n	0.19	0/1027	0.43	0/1398
45	o	0.13	0/925	0.33	0/1246
46	p	0.17	0/1006	0.42	0/1364
47	q	0.29	0/1157	0.37	0/1567
48	r	0.28	0/946	0.42	0/1268
49	s	0.29	0/1091	0.45	0/1457
50	t	0.28	0/1118	0.42	0/1506
51	u	0.28	0/945	0.37	0/1267
52	v	0.25	0/966	0.41	1/1298 (0.1%)
53	w	0.28	0/921	0.42	0/1236
54	x	0.30	0/1000	0.34	0/1341
55	y	0.27	0/764	0.32	0/1030
56	z	0.28	0/887	0.37	0/1204
57	1	0.24	0/738	0.41	0/987
58	h	0.31	1/73851 (0.0%)	0.32	3/115230 (0.0%)
All	All	0.27	2/168593 (0.0%)	0.35	15/251671 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	h	2894	G	O3'-P	-12.13	1.43	1.61
12	G	2	PRO	N-CD	5.76	1.55	1.47

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	G	2	PRO	CA-N-CD	-13.91	92.53	112.00
58	h	2895	A	O3'-P-O5'	10.16	119.24	104.00
27	V	199	PRO	N-CD-CG	-9.20	89.41	103.20
12	G	2	PRO	N-CD-CG	-8.55	90.37	103.20
14	I	43	PRO	CA-N-CD	-7.98	100.83	112.00

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	2	1614	0	823	19	0
2	3	189	0	205	5	0
3	4	390	0	198	6	0
4	5	505	0	545	10	0
5	7	5299	0	5230	181	0
6	A	32439	0	16321	470	0
7	B	2522	0	1285	19	0
8	C	1660	0	1707	47	0
9	D	1641	0	1668	66	0
10	E	1296	0	1360	36	0
11	F	771	0	797	31	0
12	G	1232	0	1282	31	0
13	H	1010	0	1046	23	0
14	I	994	0	1050	35	0
15	J	788	0	819	33	0
16	K	855	0	863	24	0
17	L	958	0	1045	42	0
18	M	935	0	986	31	0
19	N	477	0	499	15	0
20	O	720	0	760	18	0
21	P	891	0	935	31	0
22	Q	748	0	795	31	0
23	R	513	0	537	8	0
24	S	662	0	677	13	0
25	T	660	0	712	27	0
26	U	756	0	802	12	0
27	V	1793	0	1839	54	0
28	W	1428	0	1443	18	0
29	X	586	0	601	11	0
30	Y	470	0	480	8	0
31	Z	531	0	541	12	0
32	a	474	0	500	8	0
33	b	423	0	463	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	c	405	0	407	13	0
35	d	377	0	411	7	0
36	e	502	0	541	11	0
37	f	299	0	321	6	0
38	g	364	0	348	14	0
39	i	2110	0	2165	38	0
40	j	1587	0	1630	32	0
41	k	1569	0	1607	24	0
42	l	1445	0	1476	54	0
43	m	1348	0	1399	31	0
44	n	1018	0	988	25	0
45	o	918	0	959	31	0
46	p	990	0	1021	38	0
47	q	1130	0	1167	23	0
48	r	938	0	1000	20	0
49	s	1078	0	1151	20	0
50	t	1092	0	1128	18	0
51	u	928	0	972	15	0
52	v	956	0	991	21	0
53	w	907	0	938	17	0
54	x	988	0	1038	6	0
55	y	754	0	802	8	0
56	z	873	0	909	12	0
57	1	732	0	782	13	0
58	h	65953	0	33183	675	0
59	2	11	0	8	0	0
60	7	32	0	13	2	0
61	F	1	0	0	0	0
61	R	1	0	0	0	0
61	X	1	0	0	0	0
61	h	3	0	0	0	0
61	i	3	0	0	0	0
61	l	1	0	0	0	0
61	t	1	0	0	0	0
61	z	1	0	0	0	0
62	N	1	0	0	0	0
62	R	1	0	0	0	0
62	Y	1	0	0	0	0
62	c	1	0	0	0	0
62	f	1	0	0	0	0
62	g	1	0	0	0	0
All	All	155552	0	106169	2267	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 2267 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)
7:B:60:G:H4'	52:v:12:GLU:HG3	1.42	0.98
58:h:3013:C:H5'	58:h:3014:A:H5'	1.49	0.92
6:A:993:G:H1	6:A:1002:U:H3	1.14	0.89
58:h:1211:G:H21	58:h:1216:A:H62	1.19	0.86
58:h:2528:G:H22	58:h:2536:U:H3	1.20	0.85

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	
2	3	21/23 (91%)	20 (95%)	1 (5%)	0	100	100
4	5	67/69 (97%)	61 (91%)	4 (6%)	2 (3%)	3	22
5	7	707/709 (100%)	673 (95%)	33 (5%)	1 (0%)	48	83
8	C	206/208 (99%)	192 (93%)	14 (7%)	0	100	100
9	D	198/200 (99%)	186 (94%)	12 (6%)	0	100	100
10	E	178/180 (99%)	168 (94%)	10 (6%)	0	100	100
11	F	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
12	G	153/155 (99%)	149 (97%)	4 (3%)	0	100	100
13	H	129/131 (98%)	127 (98%)	2 (2%)	0	100	100
14	I	124/126 (98%)	116 (94%)	8 (6%)	0	100	100
15	J	97/99 (98%)	92 (95%)	4 (4%)	1 (1%)	12	47
16	K	113/115 (98%)	110 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	L	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
18	M	114/116 (98%)	107 (94%)	7 (6%)	0	100	100
19	N	58/60 (97%)	50 (86%)	8 (14%)	0	100	100
20	O	86/88 (98%)	85 (99%)	1 (1%)	0	100	100
21	P	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
22	Q	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
23	R	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
24	S	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
25	T	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
26	U	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
27	V	226/228 (99%)	215 (95%)	10 (4%)	1 (0%)	30	67
28	W	190/192 (99%)	183 (96%)	7 (4%)	0	100	100
29	X	77/79 (98%)	71 (92%)	6 (8%)	0	100	100
30	Y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
31	Z	62/64 (97%)	61 (98%)	1 (2%)	0	100	100
32	a	57/59 (97%)	56 (98%)	1 (2%)	0	100	100
33	b	52/54 (96%)	50 (96%)	2 (4%)	0	100	100
34	c	47/49 (96%)	45 (96%)	1 (2%)	1 (2%)	5	29
35	d	44/46 (96%)	44 (100%)	0	0	100	100
36	e	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
37	f	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
38	g	46/48 (96%)	43 (94%)	3 (6%)	0	100	100
39	i	273/275 (99%)	261 (96%)	12 (4%)	0	100	100
40	j	212/214 (99%)	200 (94%)	12 (6%)	0	100	100
41	k	207/209 (99%)	201 (97%)	6 (3%)	0	100	100
42	l	180/182 (99%)	170 (94%)	10 (6%)	0	100	100
43	m	174/176 (99%)	169 (97%)	5 (3%)	0	100	100
44	n	149/151 (99%)	138 (93%)	11 (7%)	0	100	100
45	o	124/126 (98%)	118 (95%)	6 (5%)	0	100	100
46	p	131/133 (98%)	123 (94%)	6 (5%)	2 (2%)	8	38
47	q	144/146 (99%)	141 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	r	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
49	s	143/145 (99%)	126 (88%)	17 (12%)	0	100	100
50	t	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
51	u	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
52	v	124/126 (98%)	123 (99%)	1 (1%)	0	100	100
53	w	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
54	x	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
55	y	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
56	z	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
57	1	93/105 (89%)	92 (99%)	1 (1%)	0	100	100
All	All	6714/6830 (98%)	6408 (95%)	298 (4%)	8 (0%)	49	83

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	5	99	SER
34	c	7	VAL
27	V	155	GLN
5	7	677	ASP
15	J	57	LYS

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	
2	3	18/18 (100%)	18 (100%)	0	100	100
4	5	53/53 (100%)	53 (100%)	0	100	100
5	7	564/564 (100%)	557 (99%)	7 (1%)	63	74
8	C	170/170 (100%)	169 (99%)	1 (1%)	78	81
9	D	175/175 (100%)	174 (99%)	1 (1%)	78	81
10	E	127/127 (100%)	125 (98%)	2 (2%)	55	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	F	85/85 (100%)	82 (96%)	3 (4%)	32	54
12	G	131/131 (100%)	130 (99%)	1 (1%)	73	78
13	H	107/107 (100%)	107 (100%)	0	100	100
14	I	102/102 (100%)	100 (98%)	2 (2%)	48	66
15	J	89/89 (100%)	87 (98%)	2 (2%)	45	64
16	K	89/89 (100%)	87 (98%)	2 (2%)	45	64
17	L	103/103 (100%)	103 (100%)	0	100	100
18	M	99/99 (100%)	99 (100%)	0	100	100
19	N	49/49 (100%)	49 (100%)	0	100	100
20	O	76/76 (100%)	76 (100%)	0	100	100
21	P	92/92 (100%)	92 (100%)	0	100	100
22	Q	80/80 (100%)	80 (100%)	0	100	100
23	R	55/55 (100%)	54 (98%)	1 (2%)	51	67
24	S	73/73 (100%)	70 (96%)	3 (4%)	27	49
25	T	69/69 (100%)	67 (97%)	2 (3%)	37	58
26	U	83/83 (100%)	82 (99%)	1 (1%)	63	74
27	V	191/191 (100%)	190 (100%)	1 (0%)	81	82
28	W	155/155 (100%)	155 (100%)	0	100	100
29	X	58/58 (100%)	58 (100%)	0	100	100
30	Y	50/50 (100%)	50 (100%)	0	100	100
31	Z	58/58 (100%)	58 (100%)	0	100	100
32	a	52/52 (100%)	51 (98%)	1 (2%)	50	66
33	b	43/43 (100%)	43 (100%)	0	100	100
34	c	47/47 (100%)	47 (100%)	0	100	100
35	d	35/35 (100%)	35 (100%)	0	100	100
36	e	53/53 (100%)	53 (100%)	0	100	100
37	f	35/35 (100%)	35 (100%)	0	100	100
38	g	43/43 (100%)	43 (100%)	0	100	100
39	i	215/215 (100%)	213 (99%)	2 (1%)	70	77
40	j	160/160 (100%)	156 (98%)	4 (2%)	42	62
41	k	169/169 (100%)	168 (99%)	1 (1%)	78	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	l	151/151 (100%)	148 (98%)	3 (2%)	48	66
43	m	148/148 (100%)	148 (100%)	0	100	100
44	n	90/116 (78%)	90 (100%)	0	100	100
45	o	89/89 (100%)	89 (100%)	0	100	100
46	p	102/102 (100%)	102 (100%)	0	100	100
47	q	119/119 (100%)	116 (98%)	3 (2%)	42	62
48	r	100/100 (100%)	99 (99%)	1 (1%)	68	76
49	s	112/112 (100%)	112 (100%)	0	100	100
50	t	114/114 (100%)	112 (98%)	2 (2%)	51	67
51	u	97/97 (100%)	97 (100%)	0	100	100
52	v	93/93 (100%)	92 (99%)	1 (1%)	65	74
53	w	100/100 (100%)	100 (100%)	0	100	100
54	x	97/97 (100%)	97 (100%)	0	100	100
55	y	81/81 (100%)	79 (98%)	2 (2%)	42	62
56	z	90/90 (100%)	90 (100%)	0	100	100
57	1	81/86 (94%)	81 (100%)	0	100	100
All	All	5517/5548 (99%)	5468 (99%)	49 (1%)	68	77

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	V	41	ILE
40	j	205	LEU
32	a	58	GLU
40	j	104	GLU
42	l	107	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
47	q	58	ASN
49	s	69	ASN
52	v	16	ASN
27	V	45	GLN
24	S	29	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	75/76 (98%)	16 (21%)	0
3	4	17/18 (94%)	4 (23%)	1 (5%)
58	h	3069/3127 (98%)	563 (18%)	0
6	A	1510/1511 (99%)	299 (19%)	11 (0%)
7	B	117/118 (99%)	17 (14%)	1 (0%)
All	All	4788/4850 (98%)	899 (18%)	13 (0%)

5 of 899 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	16	U
1	2	17	C
1	2	19	G
1	2	20	U
1	2	21	A

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	A	1007	U
6	A	1117	U
7	B	10	G
6	A	1477	A
6	A	1482	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 18 are 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
60	GNP	7	801	-	34,34,34	1.29	5 (14%)	47,54,54	0.64	0
59	PHE	2	101	-	10,11,12	0.39	0	8,13,15	0.17	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	GNP	7	801	-	-	5/18/38/38	0/3/3/3
59	PHE	2	101	-	-	1/5/6/8	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	7	801	GNP	PB-O3A	4.37	1.64	1.59
60	7	801	GNP	PB-O1B	3.12	1.50	1.46
60	7	801	GNP	PG-N3B	3.02	1.71	1.63
60	7	801	GNP	PG-O1G	2.86	1.50	1.46
60	7	801	GNP	PB-O2B	-2.28	1.50	1.56

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

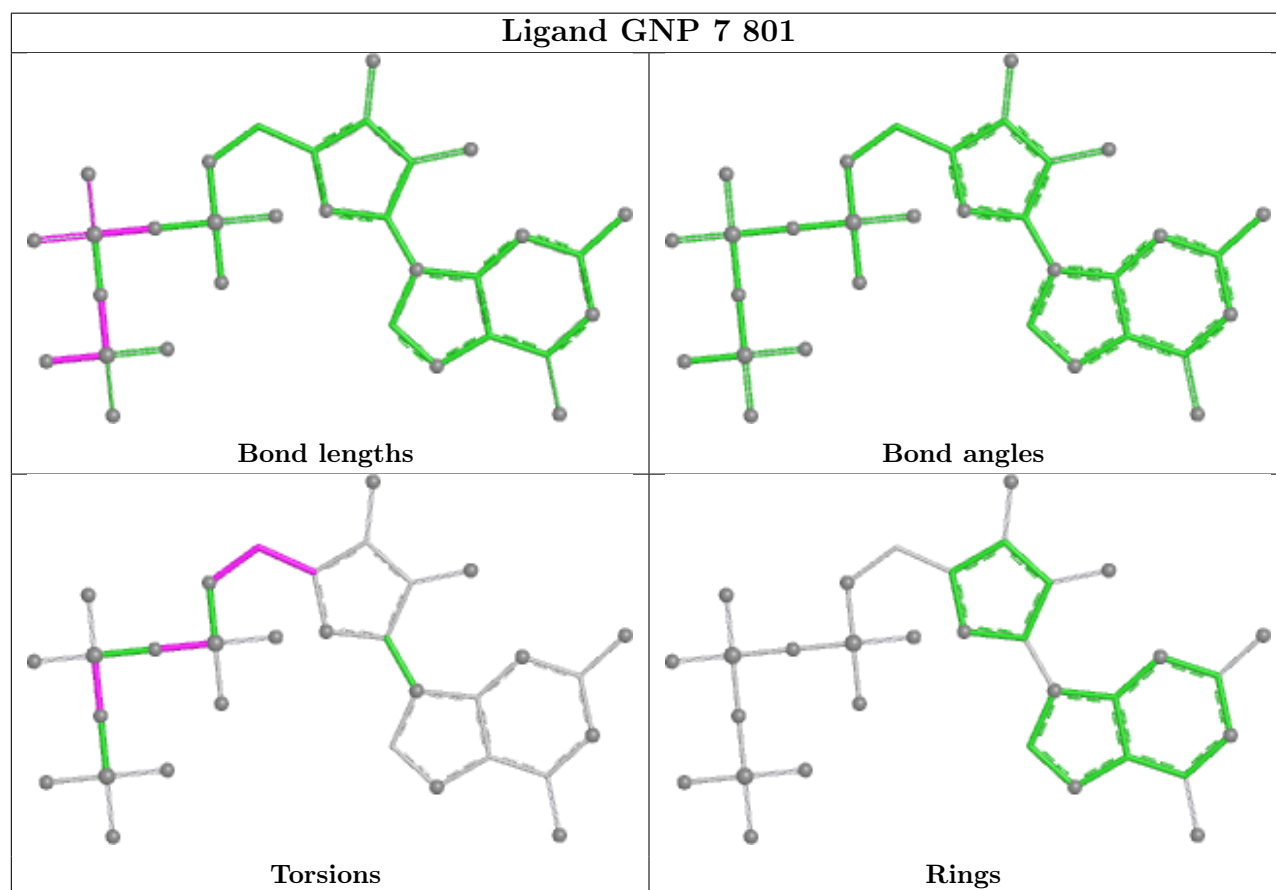
Mol	Chain	Res	Type	Atoms
59	2	101	PHE	O-C-CA-CB
60	7	801	GNP	PG-N3B-PB-O1B
60	7	801	GNP	O4'-C4'-C5'-O5'
60	7	801	GNP	C3'-C4'-C5'-O5'
60	7	801	GNP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	7	801	GNP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

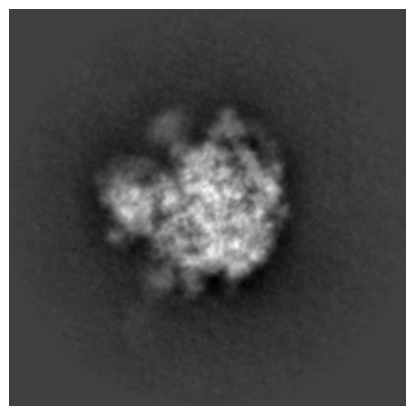
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61959. These allow visual inspection of the internal detail of the map and identification of artifacts.

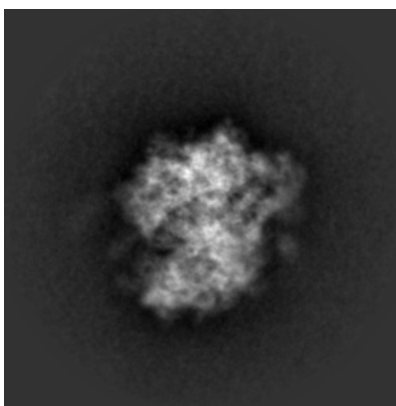
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

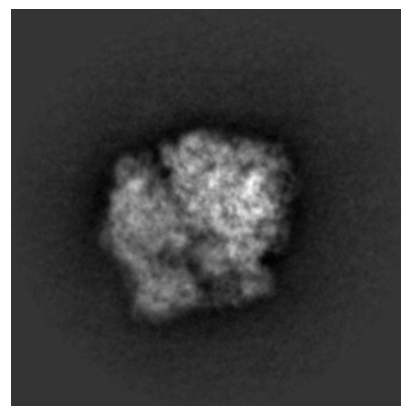
6.1.1 Primary map



X

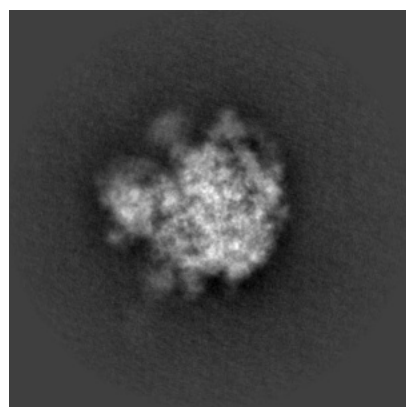


Y

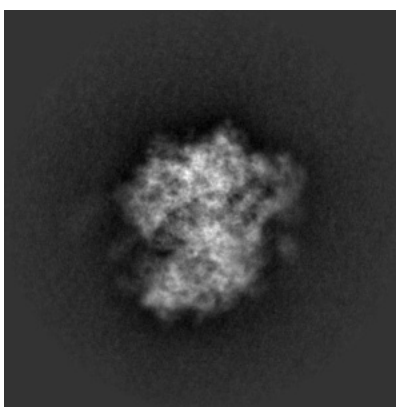


Z

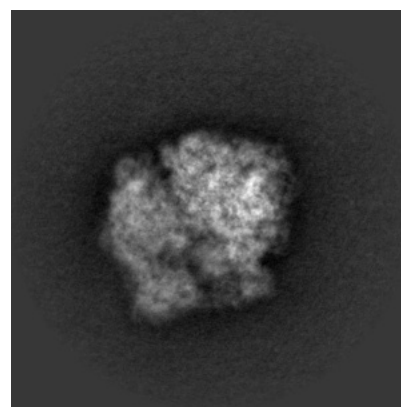
6.1.2 Raw map



X



Y

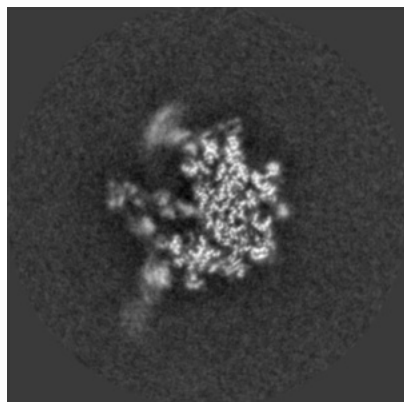


Z

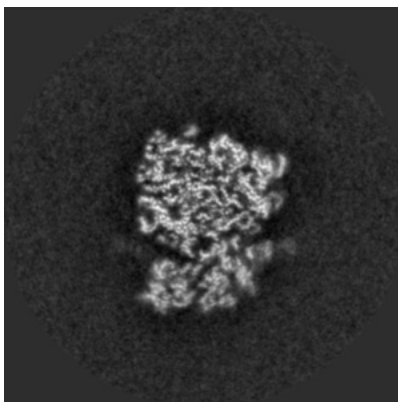
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

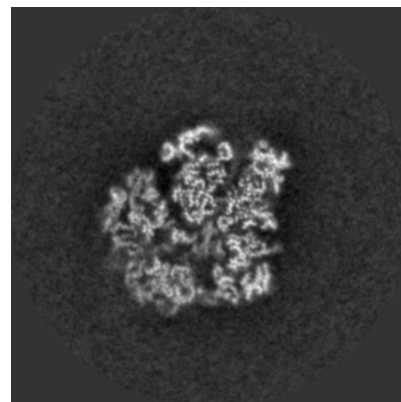
6.2.1 Primary map



X Index: 175

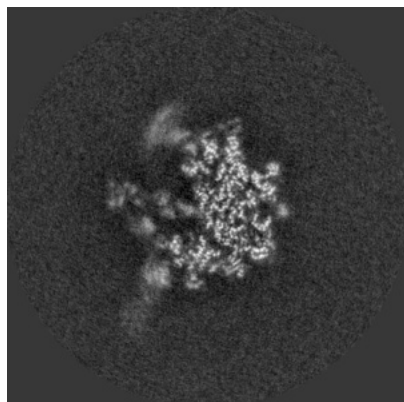


Y Index: 175

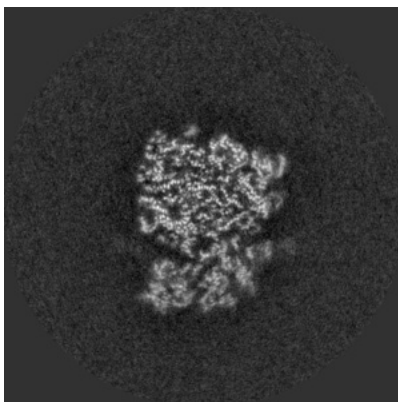


Z Index: 175

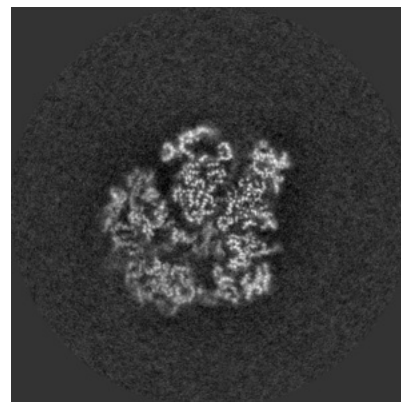
6.2.2 Raw map



X Index: 175



Y Index: 175

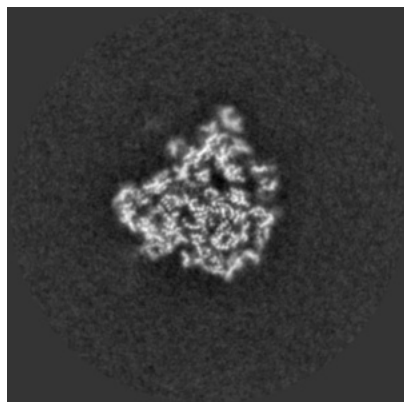


Z Index: 175

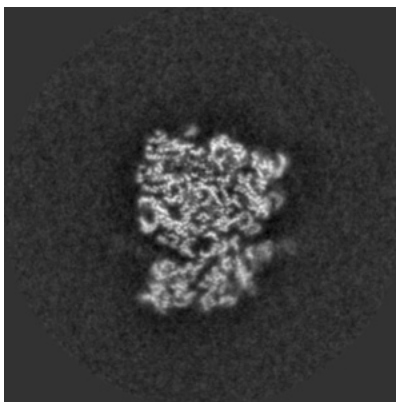
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

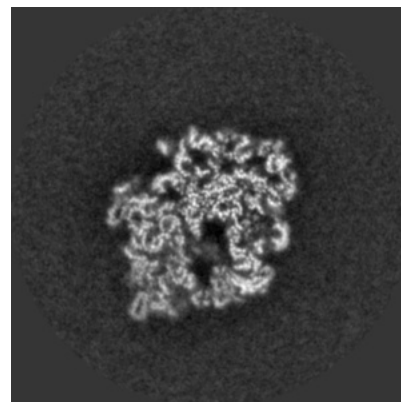
6.3.1 Primary map



X Index: 210

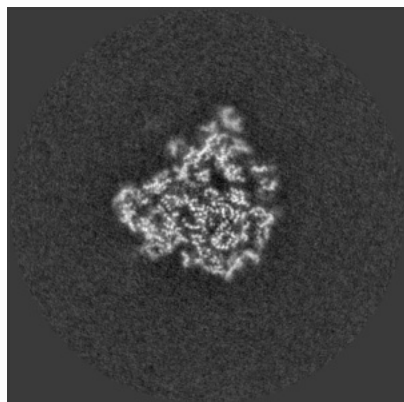


Y Index: 176

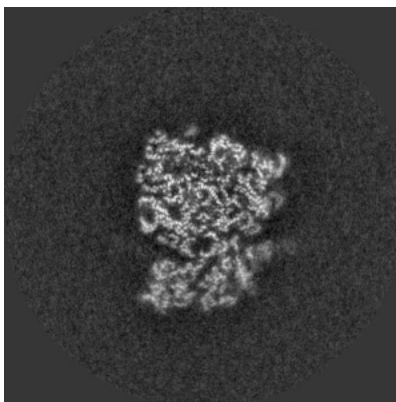


Z Index: 188

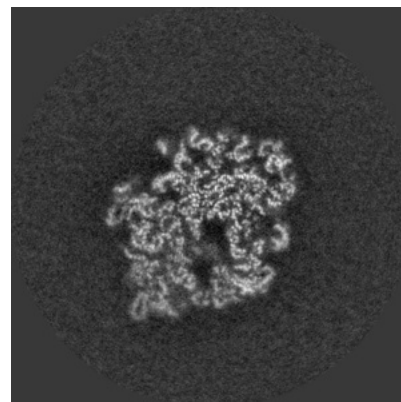
6.3.2 Raw map



X Index: 210



Y Index: 176

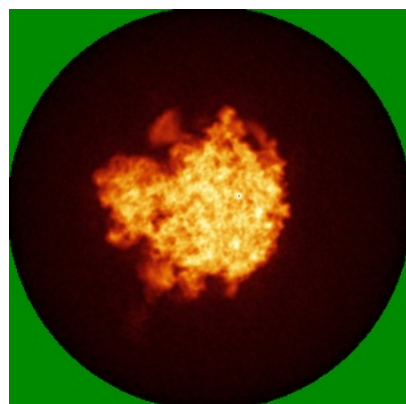


Z Index: 187

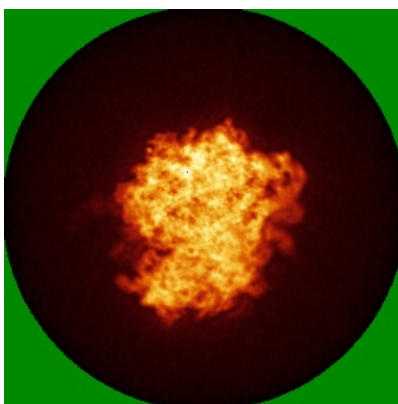
The images above show the largest variance slices of the map in three orthogonal directions.

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

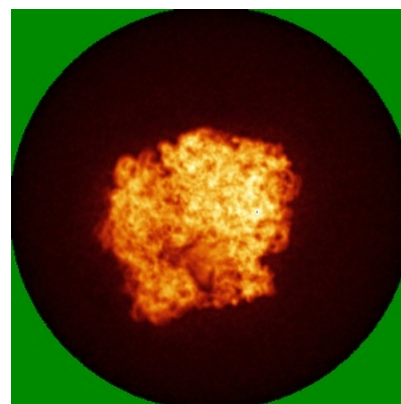
6.4.1 Primary map



X

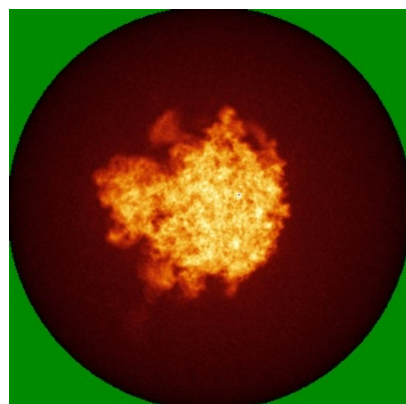


Y

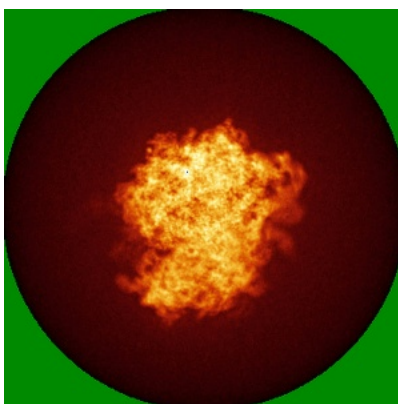


Z

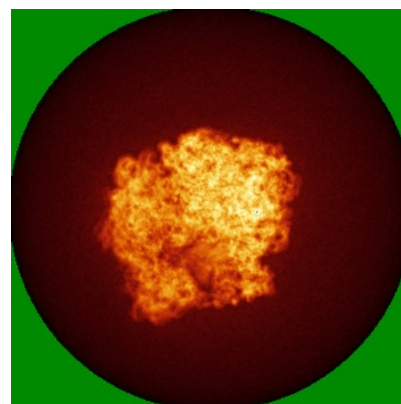
6.4.2 Raw map



X



Y

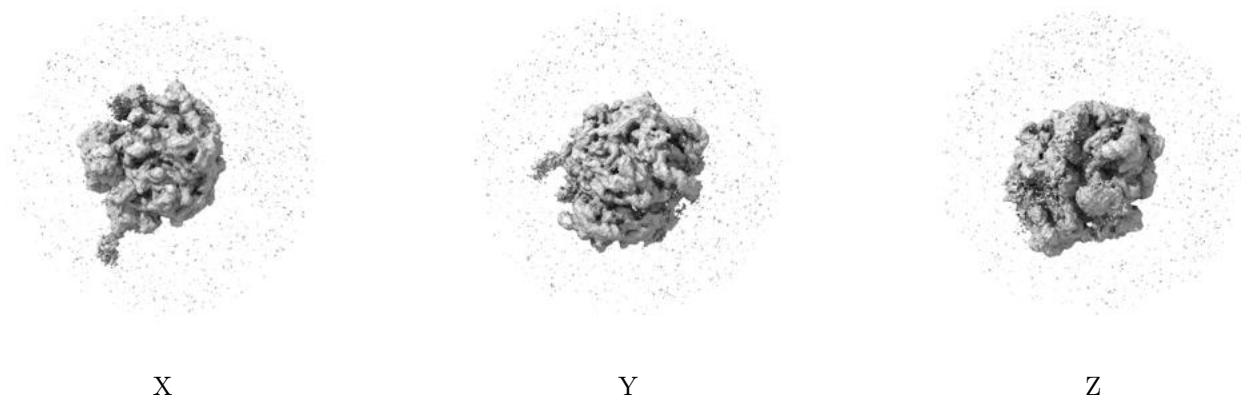


Z

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.

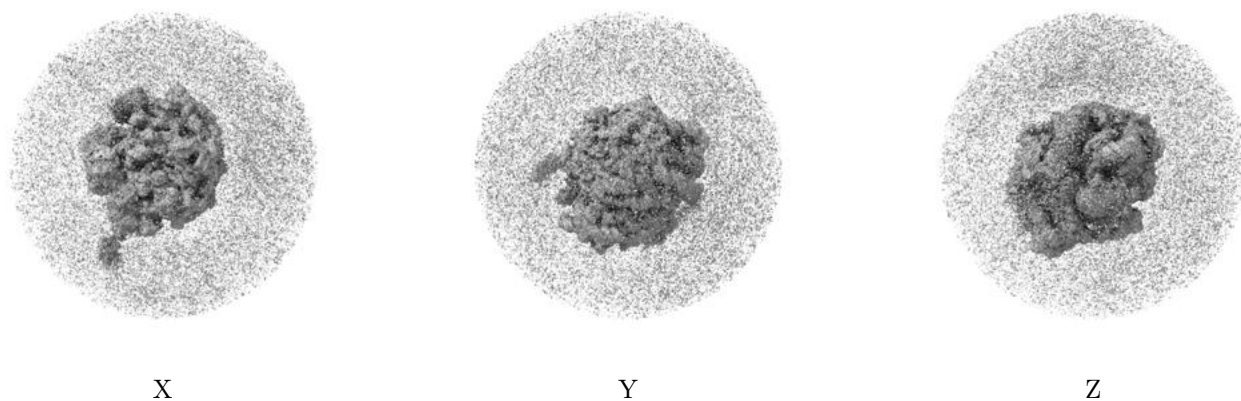
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00715. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

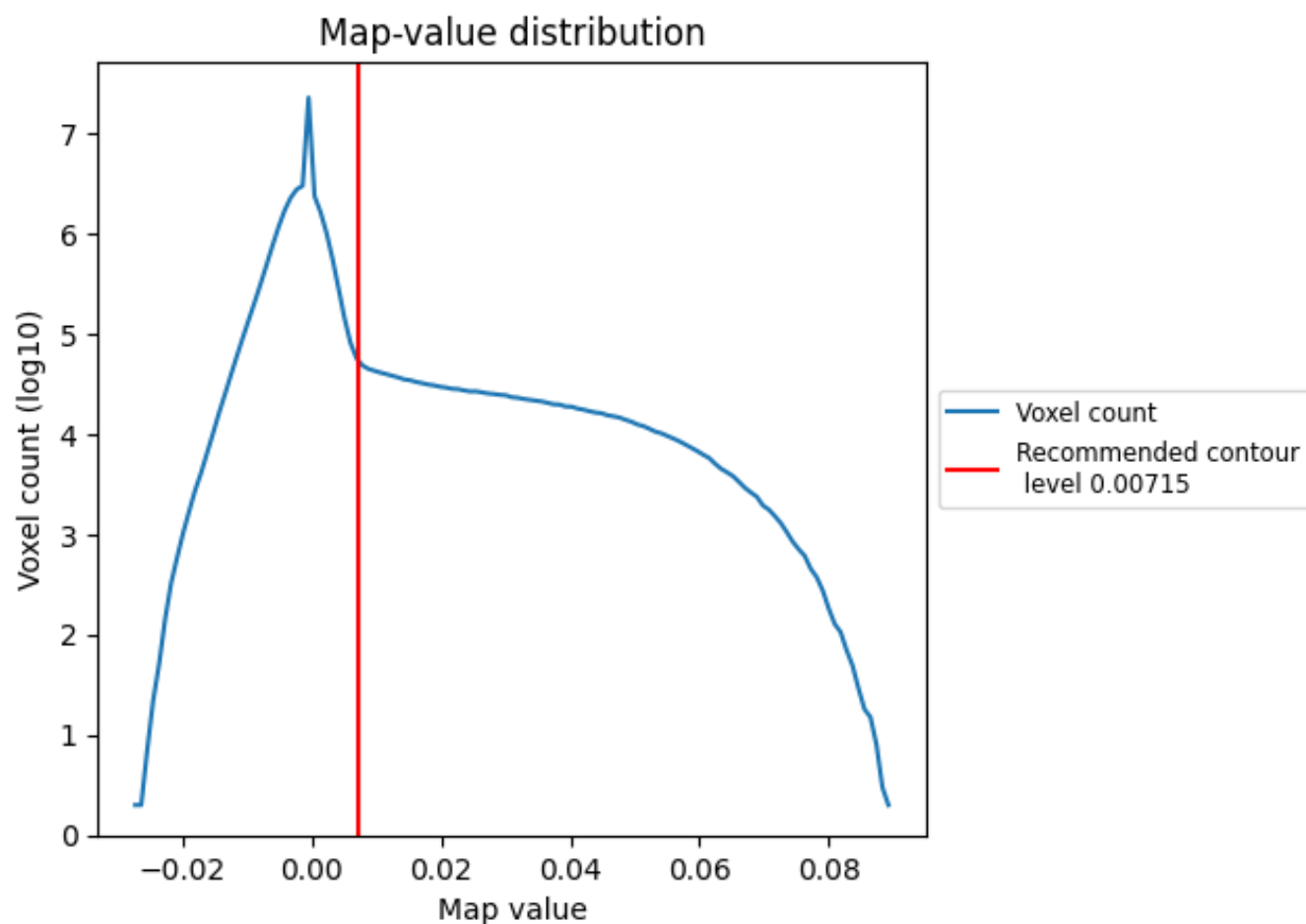
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

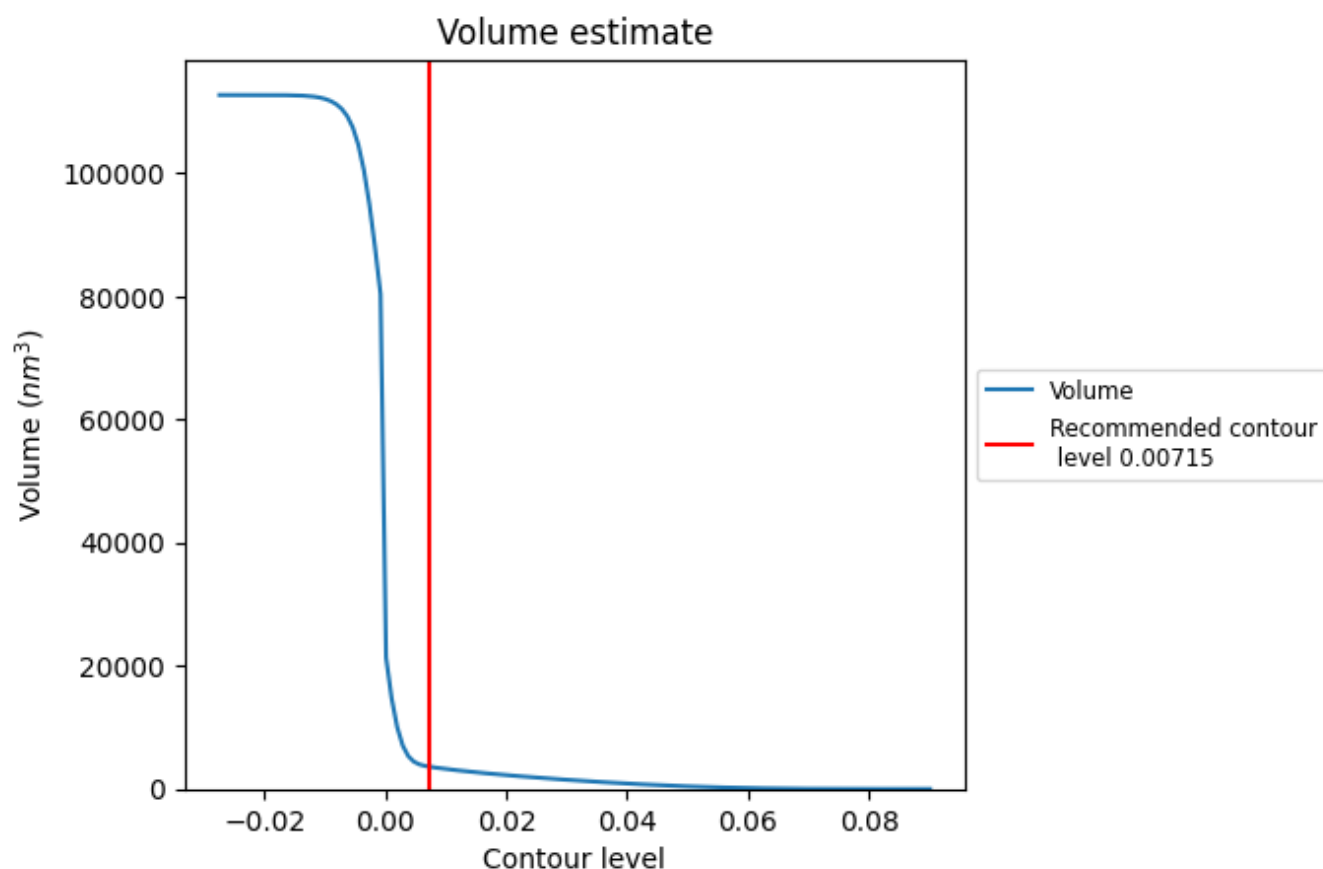
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

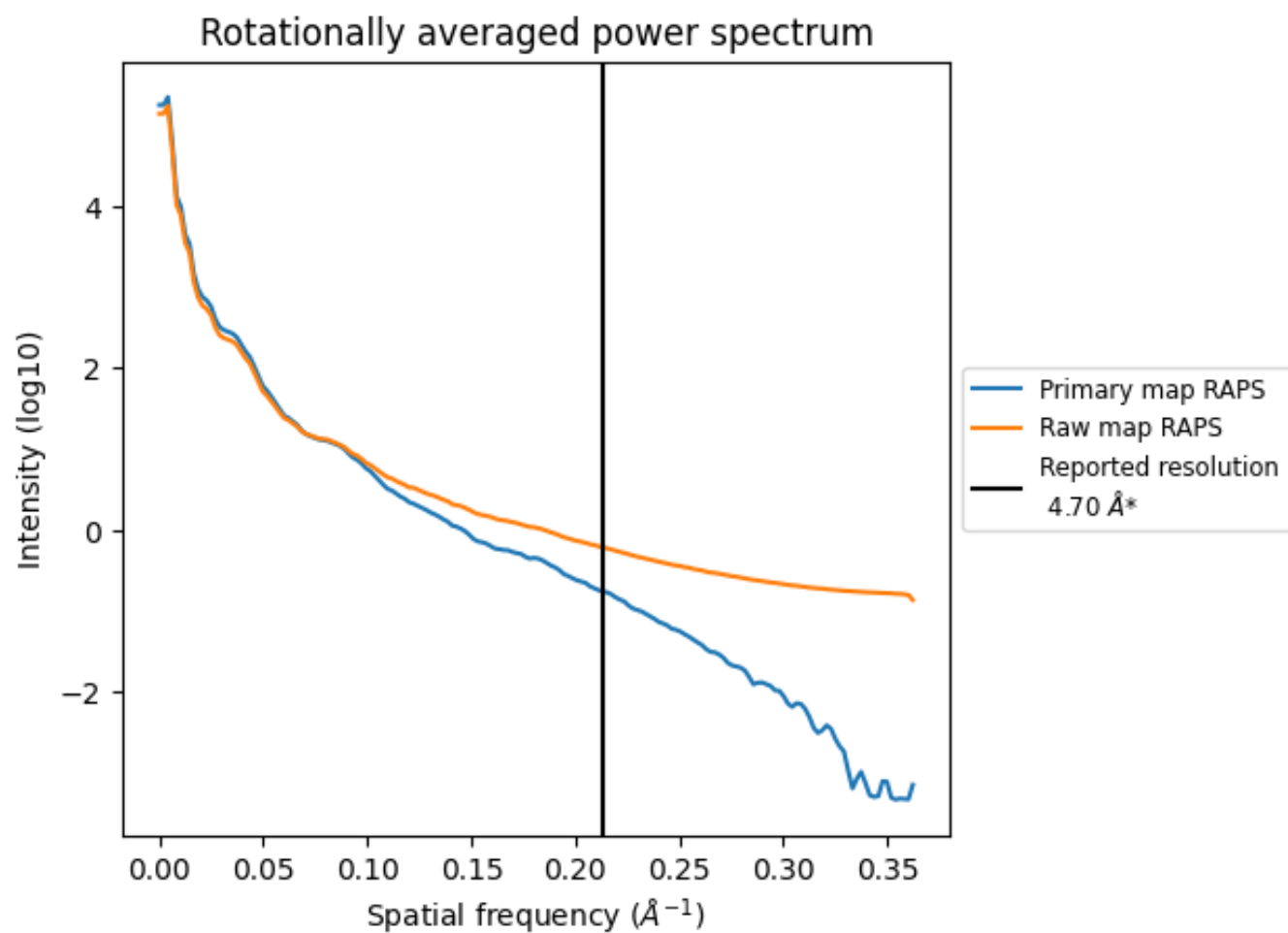
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3647 nm^3 ; this corresponds to an approximate mass of 3295 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 ⓘ

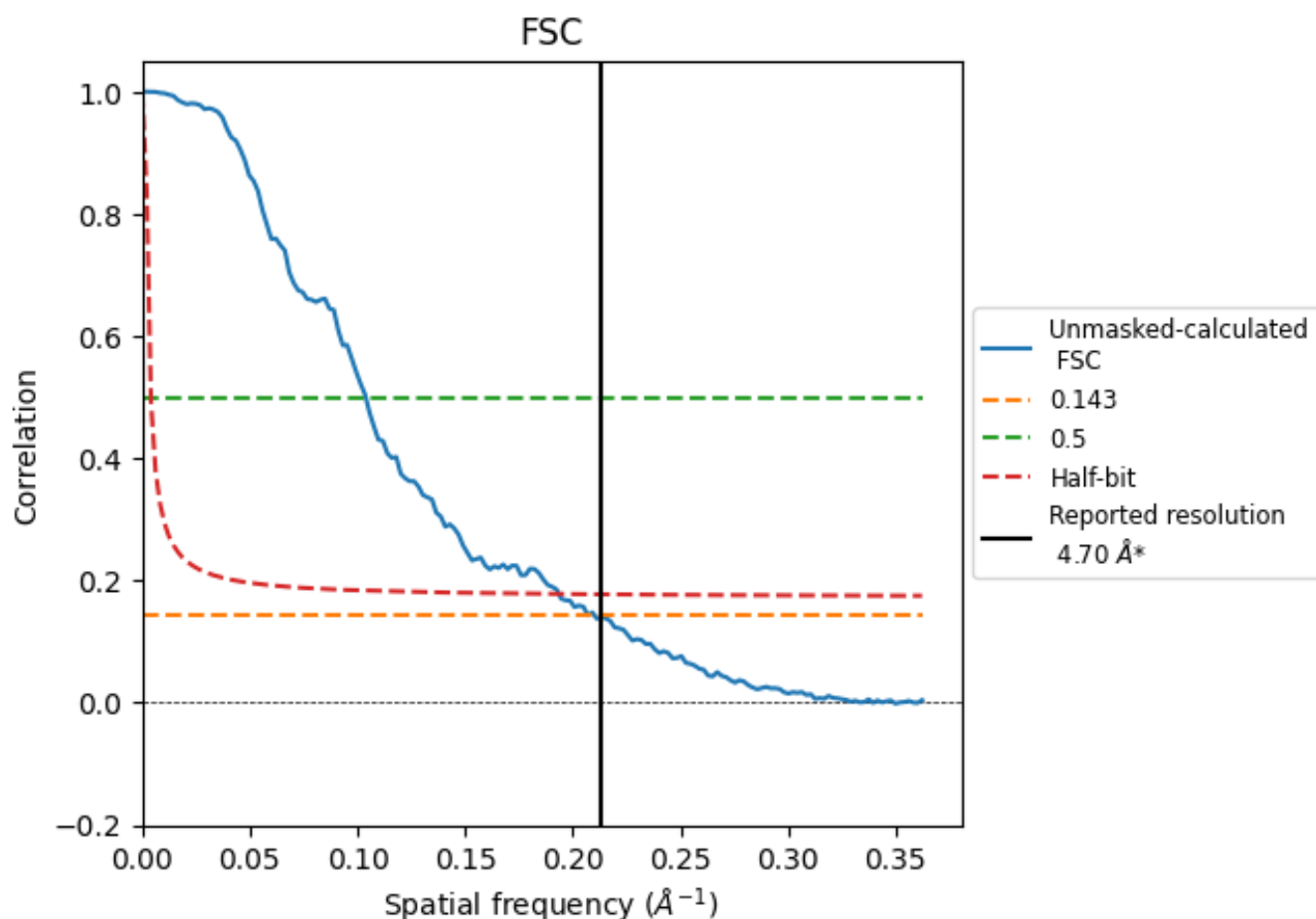


*Reported resolution corresponds to spatial frequency of $0.213 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

8.2 Resolution estimates [i](#)

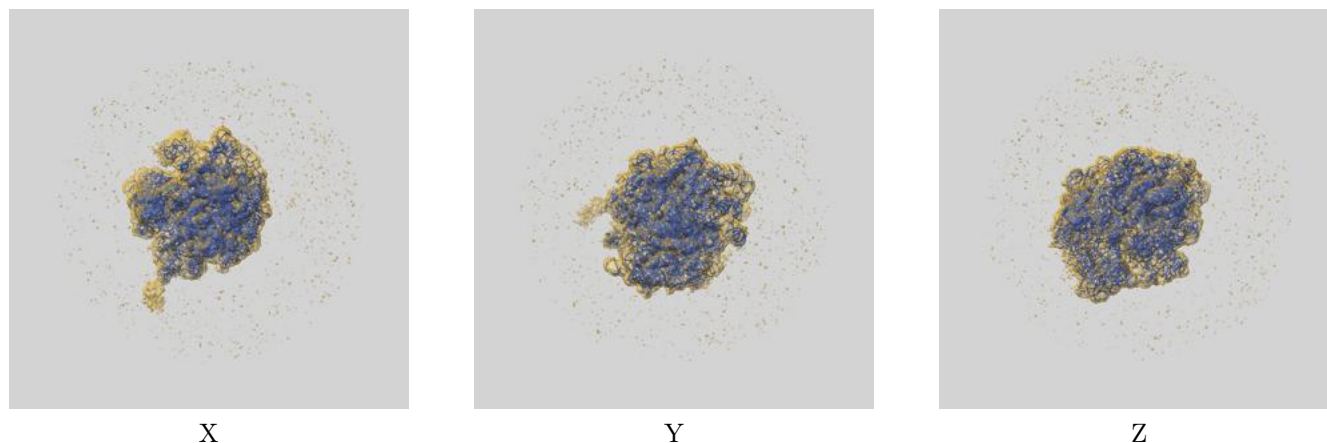
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.83	9.63	5.17

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

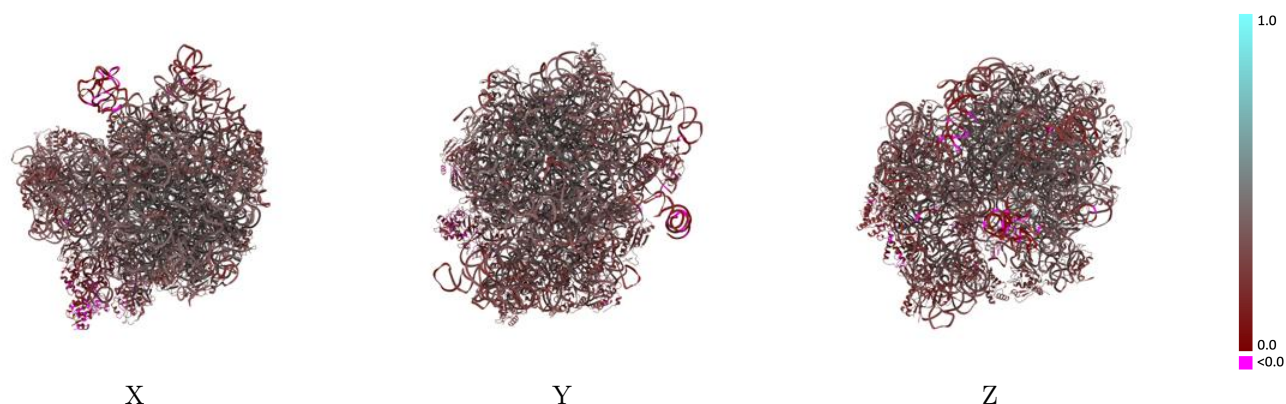
This section contains information regarding the fit between EMDB map EMD-61959 and PDB model 9K0Z. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



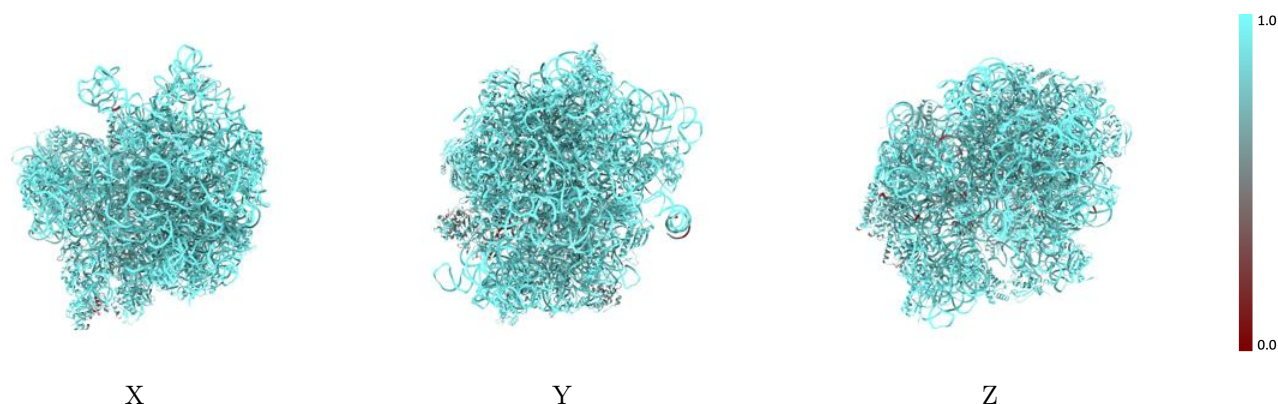
The images above show the 3D surface view of the map at the recommended contour level 0.00715 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



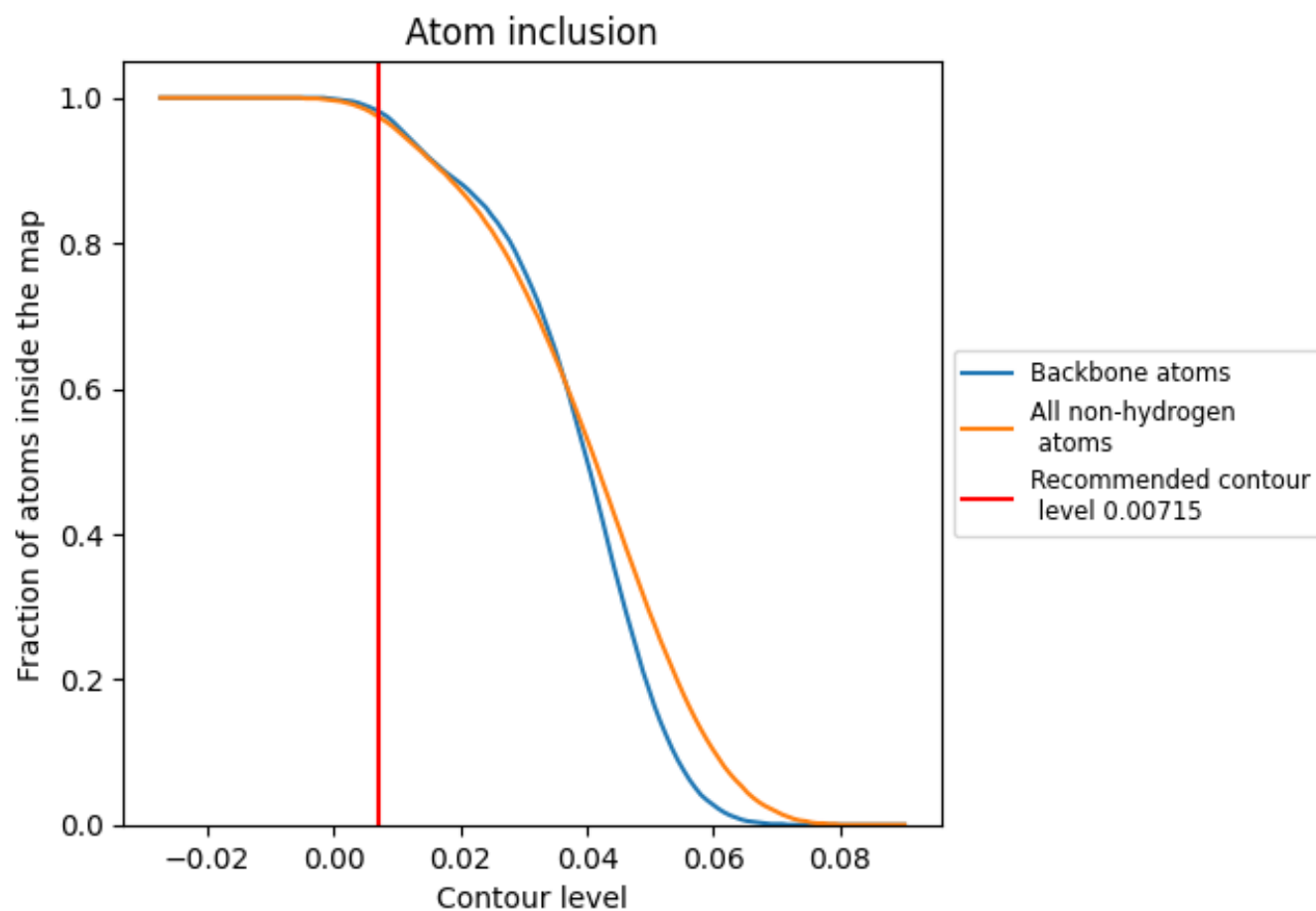
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00715).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (0.00715) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9730	 0.3180
1	 0.9880	 0.2940
2	 0.9910	 0.3160
3	 0.9940	 0.3320
4	 0.9180	 0.1900
5	 0.3080	 0.0730
7	 0.6530	 0.1680
A	 0.9990	 0.3140
B	 0.9990	 0.3430
C	 0.9790	 0.2540
D	 0.9850	 0.2430
E	 0.9570	 0.2700
F	 0.9550	 0.2750
G	 0.9780	 0.2500
H	 0.9920	 0.2790
I	 0.9970	 0.2400
J	 0.9920	 0.2580
K	 0.9920	 0.2920
L	 0.9580	 0.2980
M	 0.9930	 0.2600
N	 0.9890	 0.2880
O	 0.9630	 0.2720
P	 0.9700	 0.2650
Q	 0.9630	 0.2720
R	 0.9960	 0.2770
S	 0.9880	 0.2570
T	 0.9560	 0.2300
U	 0.9850	 0.3260
V	 0.7190	 0.1700
W	 0.8560	 0.2780
X	 0.9980	 0.3770
Y	 0.9910	 0.3660
Z	 0.9960	 0.2740
a	 0.9870	 0.3390
b	 0.9880	 0.3750



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Chain	Atom inclusion	Q-score
c	 0.9620	 0.3280
d	 0.9860	 0.3590
e	 0.8790	 0.2660
f	 0.9970	 0.3430
g	 0.9970	 0.2760
h	 0.9960	 0.3540
i	 0.9760	 0.3580
j	 0.9940	 0.3700
k	 0.9860	 0.3490
l	 0.9890	 0.2730
m	 0.9860	 0.2940
n	 0.9410	 0.2660
o	 0.9000	 0.0890
p	 0.9690	 0.1050
q	 0.9870	 0.3570
r	 0.9770	 0.3520
s	 0.9950	 0.3370
t	 0.9860	 0.3660
u	 0.9890	 0.3480
v	 0.9960	 0.3020
w	 0.9770	 0.3520
x	 0.9920	 0.3360
y	 0.9950	 0.3840
z	 0.9880	 0.3700