



wwPDB EM Validation Summary Report ⓘ

Jun 27, 2026 – 01:58 PM EDT

PDB ID : 8UX8 / pdb_00008ux8
EMDB ID : EMD-42714
Title : E. coli 70S ribosome with unmodified Lys-tRNA^{Pro}(GGG) bound to slippery P-site CCC-C codon in the +1 mRNA reading frame
Authors : Kimbrough, E.M.; Dunham, C.M.; Nguyen, H.A.
Deposited on : 2023-11-09
Resolution : 3.60 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:

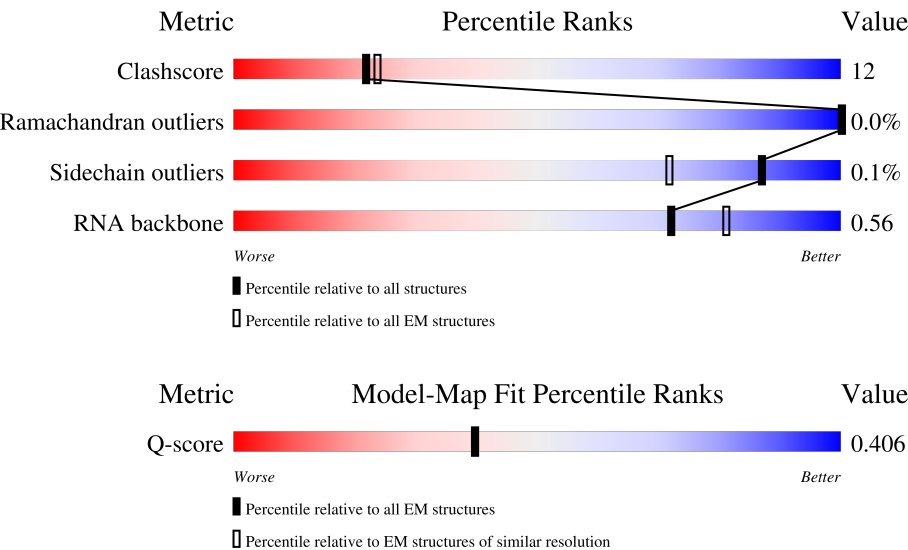
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 3.60 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.



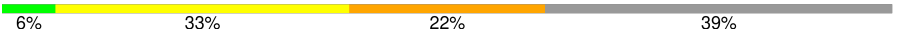
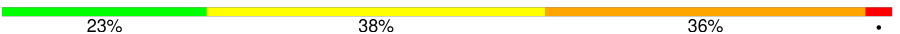
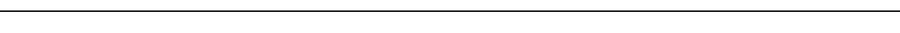
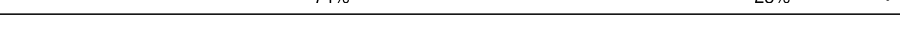
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	1	2904	
2	2	1540	
3	3	120	

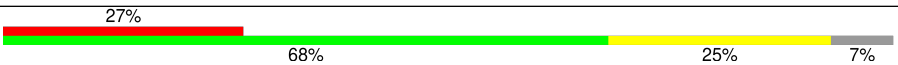
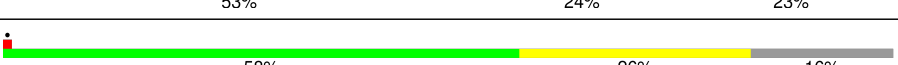
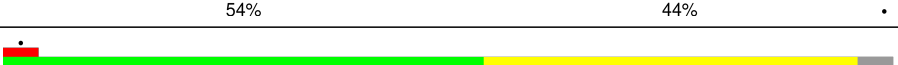
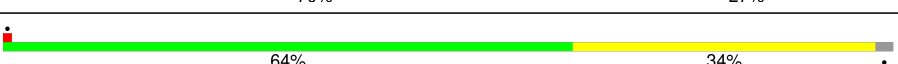
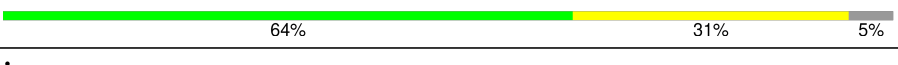
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Mol	Chain	Length	Quality of chain
4	4	18	
5	5	77	
6	A	229	
7	B	273	
8	C	209	
9	D	201	
10	E	179	
11	F	177	
12	G	149	
13	J	142	
14	K	123	
15	L	144	
16	M	136	
17	N	127	
18	O	117	
19	P	115	
20	Q	118	
21	R	103	
22	S	110	
23	T	100	
24	U	104	
25	V	94	
26	W	84	
27	X	78	
28	Y	63	

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Mol	Chain	Length	Quality of chain
29	Z	59	
30	a	70	
31	b	57	
32	c	55	
33	d	46	
34	e	65	
35	f	38	
36	g	241	
37	h	233	
38	i	206	
39	j	167	
40	k	135	
41	l	179	
42	m	130	
43	n	130	
44	o	103	
45	p	129	
46	q	124	
47	r	118	
48	s	101	
49	t	89	
50	u	82	
51	v	84	
52	w	75	
53	x	92	

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Mol	Chain	Length	Quality of chain
54	y	87	75% 24%
55	z	71	20% 87% 11%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 146547 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62334	27814	11470	20147	2903		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	11	Total	C	N	O	P	0	0
			230	103	38	78	11		

- Molecule 5 is a RNA chain called Lys-tRNA^{pro}L.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	77	Total	C	N	O	P	0	0
			1648	733	297	541	77		

- Molecule 6 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	67	Total	C	N	O	S	0	0
			507	321	90	95	1		

- Molecule 7 is a protein called 50S ribosomal protein L2.

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

- Molecule 8 is a protein called 50S ribosomal protein L3.

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

- Molecule 9 is a protein called 50S ribosomal protein L4.

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

- Molecule 10 is a protein called 50S ribosomal protein L5.

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

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 12 is a protein called 50S ribosomal protein L9.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 16 is a protein called 50S ribosomal protein L16.

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

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 18 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 19 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 20 is a protein called 50S ribosomal protein L20.

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

- Molecule 21 is a protein called Ribosomal protein L21.

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

- Molecule 22 is a protein called 50S ribosomal protein L22.

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

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	103	Total	C	N	O		0	0
			788	498	148	142			

- Molecule 25 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 26 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 27 is a protein called 50S ribosomal protein L28.

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

- Molecule 28 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 30 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 31 is a protein called 50S ribosomal protein L32.

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

- Molecule 32 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 33 is a protein called 50S ribosomal protein L34.

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

- Molecule 34 is a protein called 50S ribosomal protein L35.

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

- Molecule 35 is a protein called 50S ribosomal protein L36.

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

- Molecule 36 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 37 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 38 is a protein called 30S ribosomal protein S4.

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

- Molecule 39 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 41 is a protein called 30S ribosomal protein S7.

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

- Molecule 42 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 43 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 44 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 45 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 46 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 47 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 48 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 49 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 50 is a protein called 30S ribosomal protein S16.

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

- Molecule 51 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 53 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

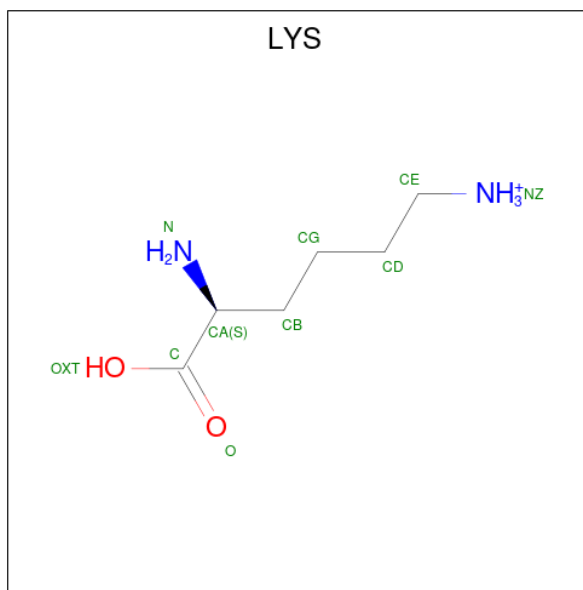
- Molecule 55 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	1	262	Total 262	Mg 262	0
56	2	111	Total 111	Mg 111	0
56	3	10	Total 10	Mg 10	0
56	5	1	Total 1	Mg 1	0
56	B	3	Total 3	Mg 3	0
56	L	2	Total 2	Mg 2	0
56	M	1	Total 1	Mg 1	0
56	Q	1	Total 1	Mg 1	0
56	X	1	Total 1	Mg 1	0
56	b	1	Total 1	Mg 1	0
56	l	1	Total 1	Mg 1	0
56	z	1	Total 1	Mg 1	0

- Molecule 57 is LYSINE (CCD ID: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
57	5	1	Total	C	N	O	0
			9	6	2	1	

- Molecule 58 is water.

Mol	Chain	Residues	Atoms				AltConf
58	1	700	Total	O			0
			700	700			
58	2	341	Total	O			0
			341	341			
58	3	7	Total	O			0
			7	7			
58	4	1	Total	O			0
			1	1			
58	5	10	Total	O			0
			10	10			
58	B	2	Total	O			0
			2	2			
58	C	7	Total	O			0
			7	7			
58	D	10	Total	O			0
			10	10			
58	E	4	Total	O			0
			4	4			
58	F	6	Total	O			0
			6	6			
58	G	12	Total	O			0
			12	12			
58	J	7	Total	O			0
			7	7			
58	K	4	Total	O			0
			4	4			
58	L	3	Total	O			0
			3	3			
58	M	2	Total	O			0
			2	2			
58	N	2	Total	O			0
			2	2			
58	O	6	Total	O			0
			6	6			
58	P	6	Total	O			0
			6	6			
58	Q	7	Total	O			0
			7	7			

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Mol	Chain	Residues	Atoms		AltConf
58	R	7	Total 7	O 7	0
58	S	4	Total 4	O 4	0
58	T	2	Total 2	O 2	0
58	U	6	Total 6	O 6	0
58	V	1	Total 1	O 1	0
58	W	2	Total 2	O 2	0
58	Y	8	Total 8	O 8	0
58	Z	2	Total 2	O 2	0
58	a	2	Total 2	O 2	0
58	b	2	Total 2	O 2	0
58	f	1	Total 1	O 1	0
58	g	20	Total 20	O 20	0
58	h	14	Total 14	O 14	0
58	i	8	Total 8	O 8	0
58	j	3	Total 3	O 3	0
58	k	7	Total 7	O 7	0
58	l	5	Total 5	O 5	0
58	m	3	Total 3	O 3	0
58	n	4	Total 4	O 4	0
58	o	3	Total 3	O 3	0
58	p	5	Total 5	O 5	0

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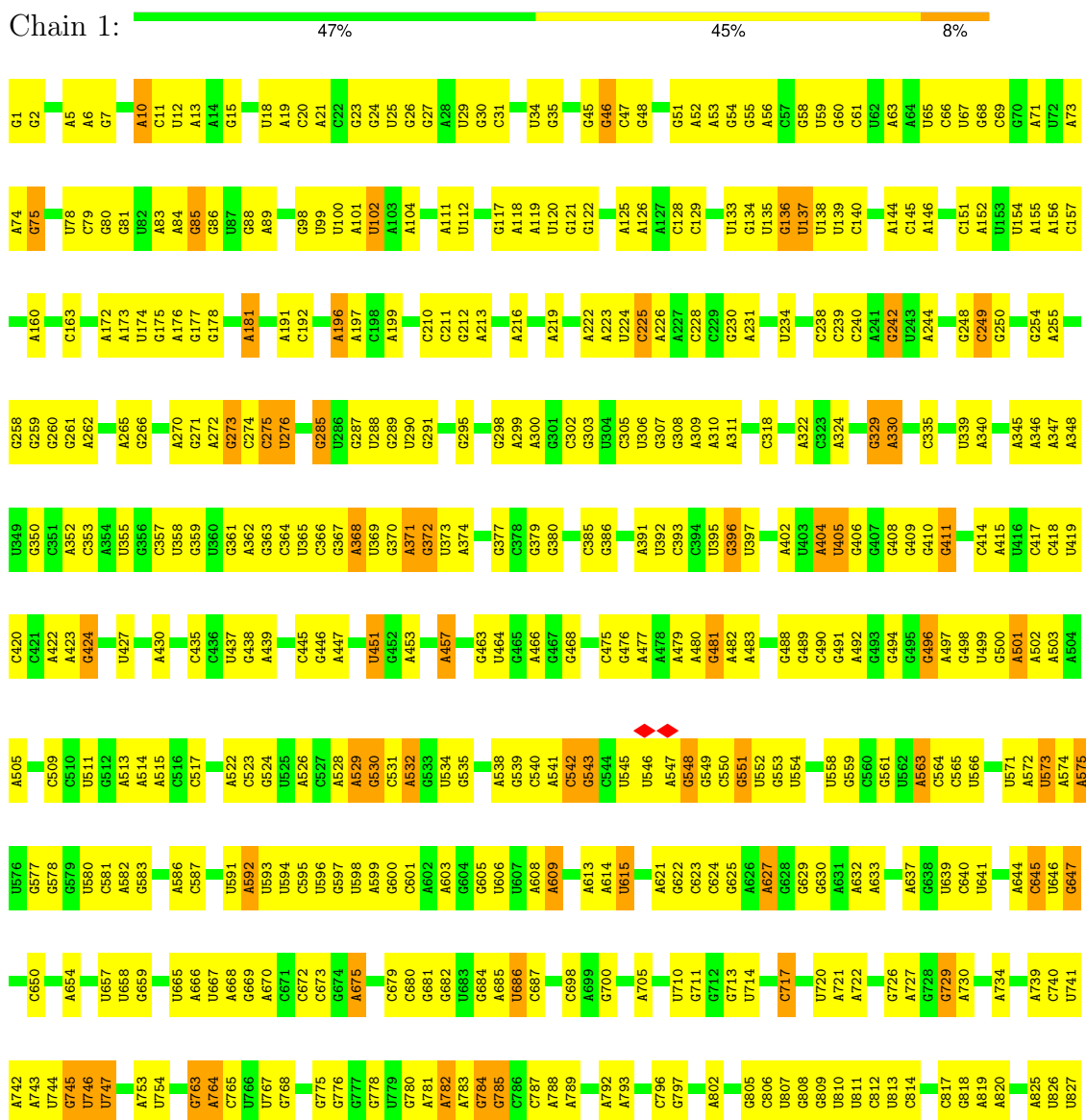
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Mol	Chain	Residues	Atoms		AltConf
58	q	1	Total 1	O 1	0
58	r	4	Total 4	O 4	0
58	t	1	Total 1	O 1	0
58	u	4	Total 4	O 4	0
58	v	3	Total 3	O 3	0
58	w	3	Total 3	O 3	0
58	x	1	Total 1	O 1	0
58	z	4	Total 4	O 4	0

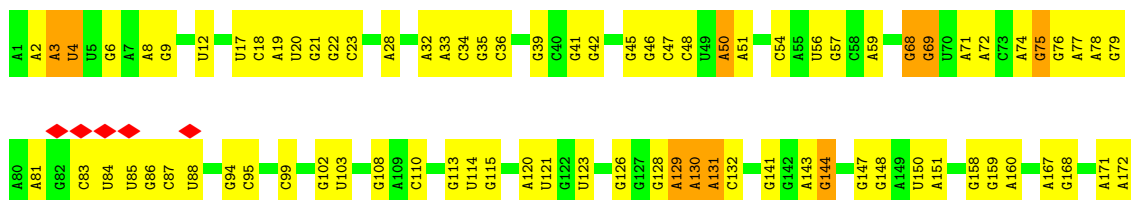
3 Residue-property plots

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.

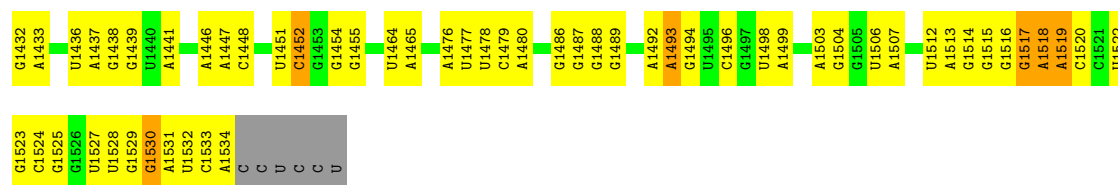
• Molecule 1: 23S rRNA



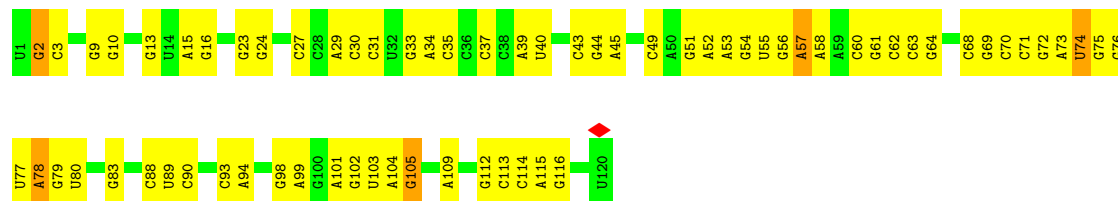
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C1384	U1301	A1197	U1126	C1031	U960	U884	C798	U798	C613	A532	A459	A375	G292	G211
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C1402	G1315	C1226	G1138	G1053	A975	C896	U820	G731	A642	A547	U473	U390	G226	C226
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C1411	G1321	C1230	G1143	U1060	C980	U905	C823	C735	A649	A553	U480	G394	U321	U231
C1412	A1322	G1231	G1144	G1061	U981	A908	G824	C736	G650	A554	G481	A320	A321	G232
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G1419	C1327	U1240	A1150	G1071	U992	A913	G832	G745	U662	C564	C489	U405	A329	C328
U1428	G1241	G1242	A1151	C1072	U993	A914	G832	A746	A663	G567	C490	U407	A329	A246
A1429	G1242	A1250	A1152	U1073	A994	U916	U835	A747	G684	G570	C491	U408	C330	G247
G1334	U1330	G1253	C1157	G1074	A996	G917	U836	G748	A665	G570	C493	U409	G332	G247
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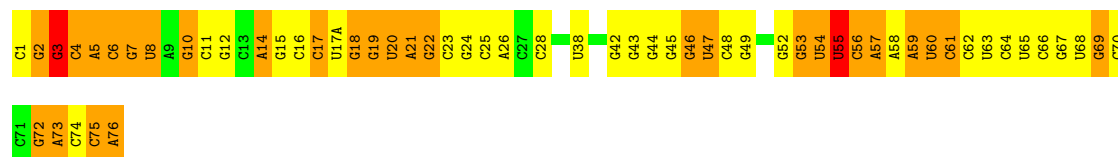
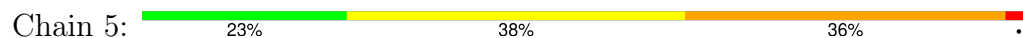
- Molecule 3: 5S ribosomal RNA



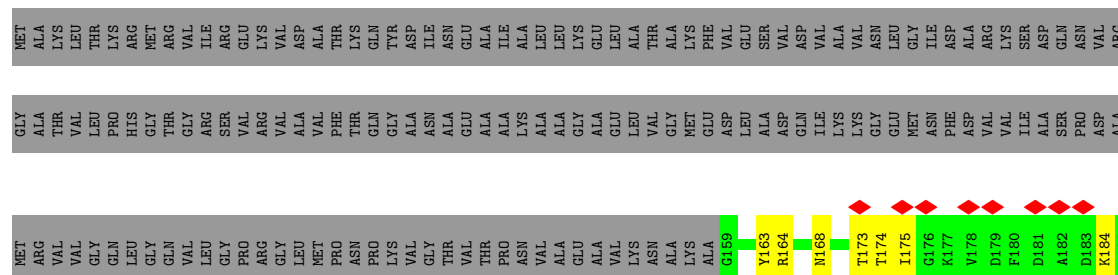
- Molecule 4: mRNA



- Molecule 5: Lys-tRNA^{proL}

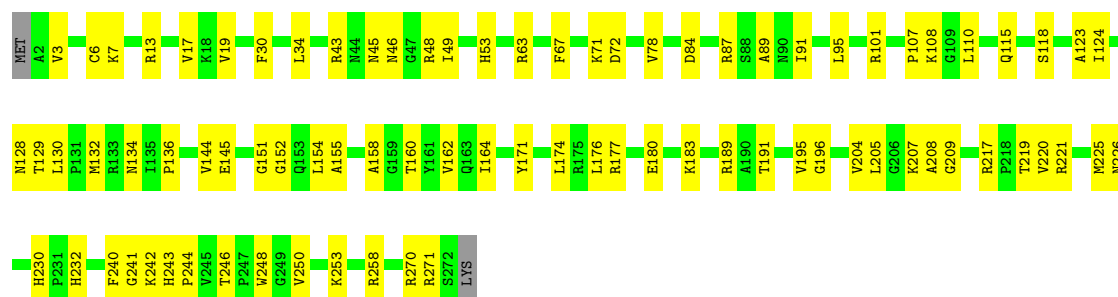


- Molecule 6: Large ribosomal subunit protein uL1



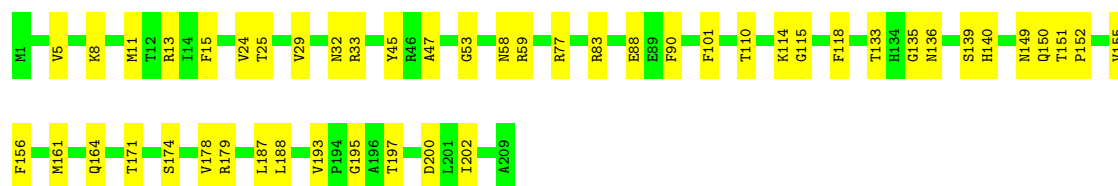
- Molecule 7: 50S ribosomal protein L2

Chain B: 



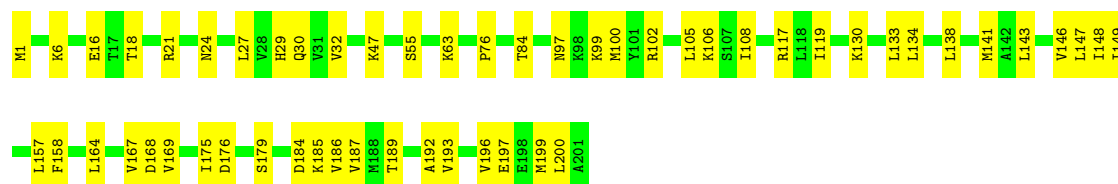
- Molecule 8: 50S ribosomal protein L3

Chain C: 



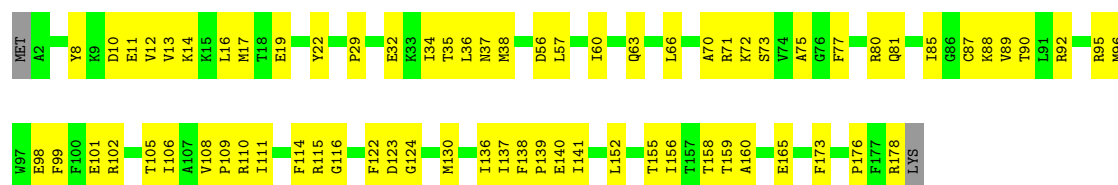
- Molecule 9: 50S ribosomal protein L4

Chain D: 



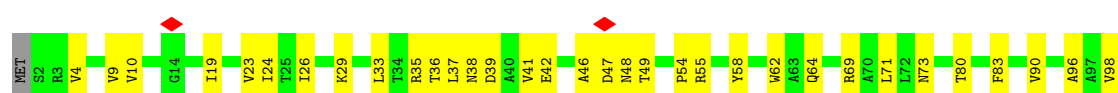
- Molecule 10: 50S ribosomal protein L5

Chain E: 



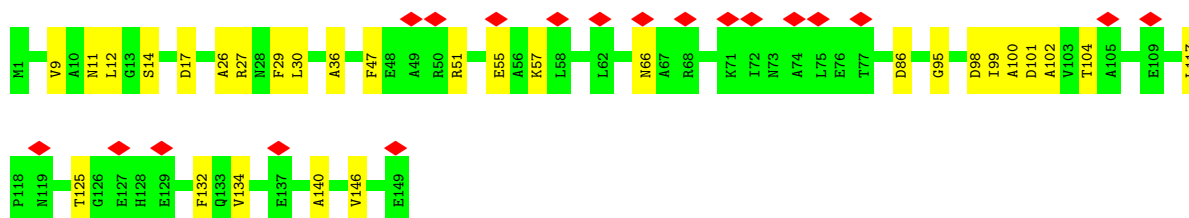
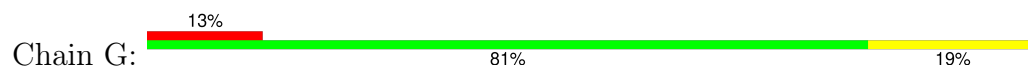
- Molecule 11: 50S ribosomal protein L6

Chain F: 

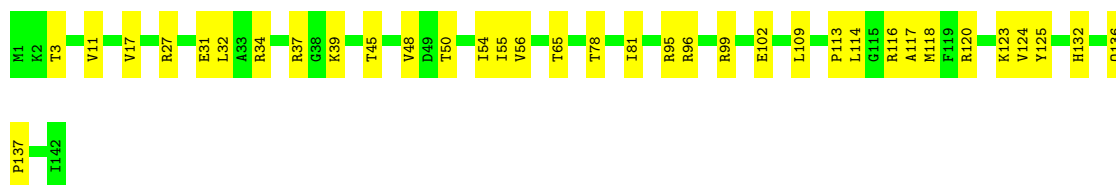




- Molecule 12: 50S ribosomal protein L9



- Molecule 13: Large ribosomal subunit protein uL13



- Molecule 14: 50S ribosomal protein L14



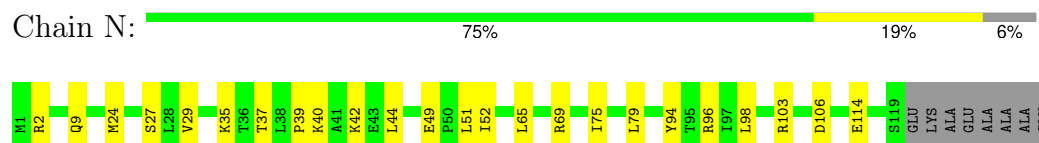
- Molecule 15: 50S ribosomal protein L15



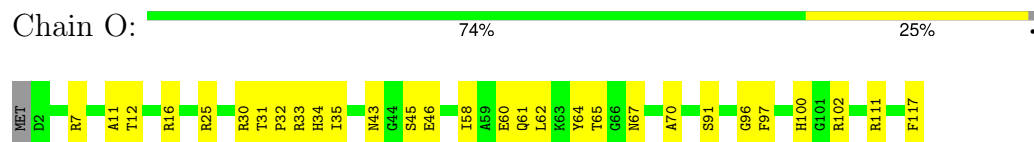
- Molecule 16: 50S ribosomal protein L16



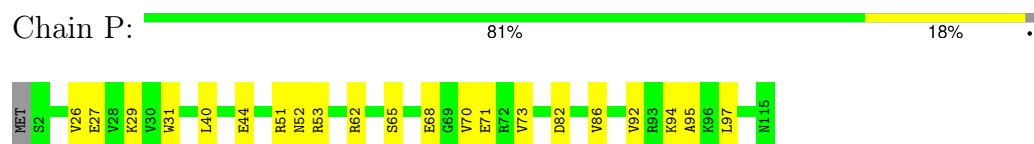
- Molecule 17: 50S ribosomal protein L17



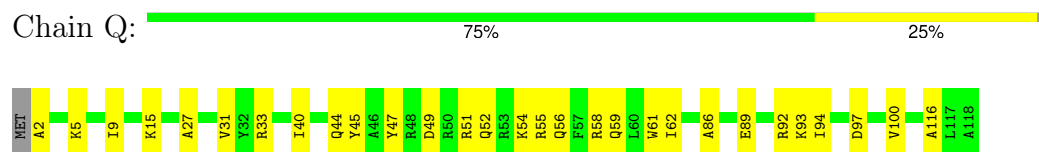
- Molecule 18: Large ribosomal subunit protein uL18



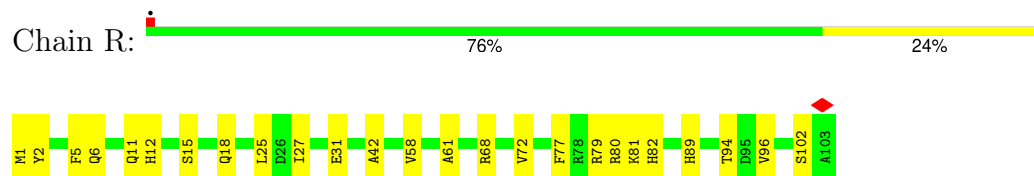
- Molecule 19: Large ribosomal subunit protein bL19



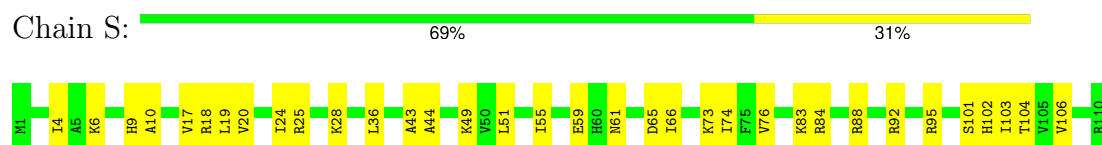
- Molecule 20: 50S ribosomal protein L20



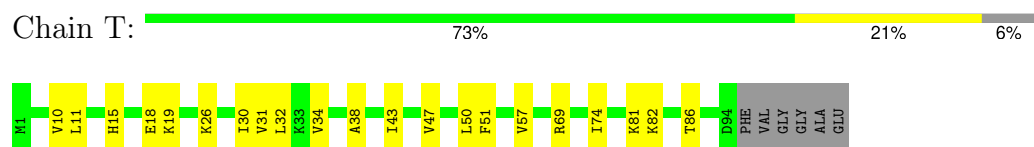
- Molecule 21: Ribosomal protein L21



- Molecule 22: 50S ribosomal protein L22

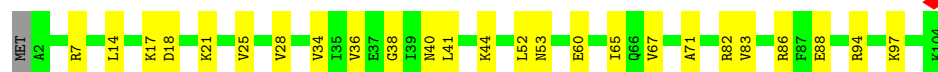


- Molecule 23: 50S ribosomal protein L23



- Molecule 24: 50S ribosomal protein L24

Chain U:  75% 24%



- Molecule 25: Large ribosomal subunit protein bL25

Chain V:  81% 19%



- Molecule 26: Large ribosomal subunit protein bL27

Chain W:  67% 24% 10%



- Molecule 27: 50S ribosomal protein L28

Chain X:  79% 19%



- Molecule 28: Large ribosomal subunit protein uL29

Chain Y:  84% 14%



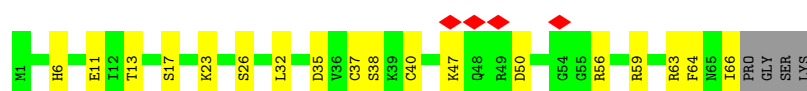
- Molecule 29: 50S ribosomal protein L30

Chain Z:  75% 24%



- Molecule 30: 50S ribosomal protein L31

Chain a:  6% 69% 26% 6%



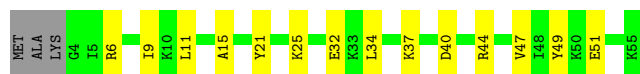
- Molecule 31: 50S ribosomal protein L32

Chain b:  74% 25% .



- Molecule 32: 50S ribosomal protein L33

Chain c:  69% 25% 5%



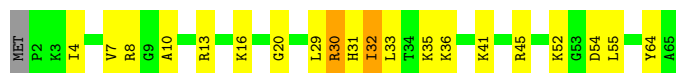
- Molecule 33: 50S ribosomal protein L34

Chain d:  70% 30%



- Molecule 34: 50S ribosomal protein L35

Chain e:  68% 28% . .



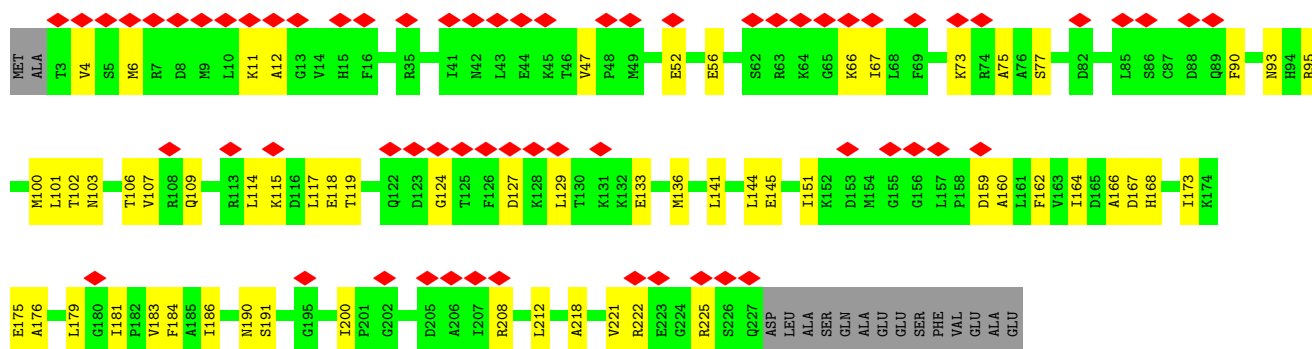
- Molecule 35: 50S ribosomal protein L36

Chain f:  74% 26%



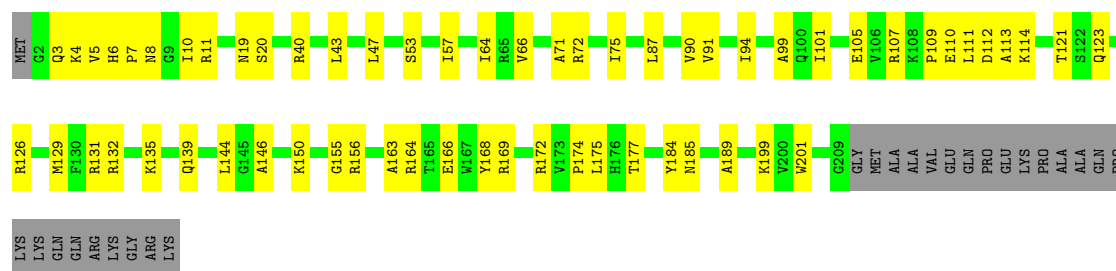
- Molecule 36: 30S ribosomal protein S2

Chain g:  27% 68% 25% 7%



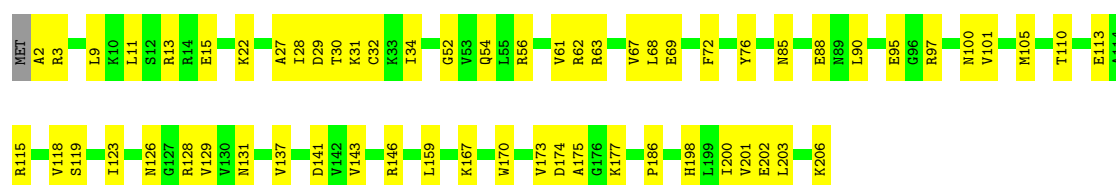
- Molecule 37: 30S ribosomal protein S3

Chain h:  63% 26% 11%



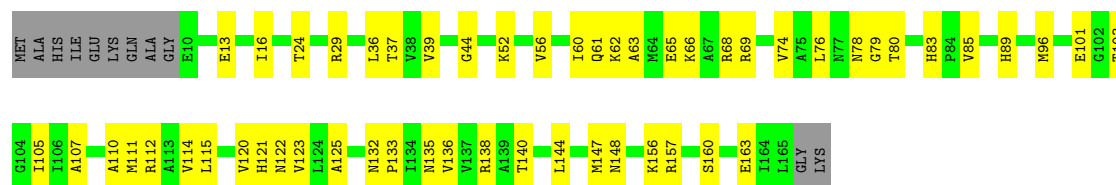
- Molecule 38: 30S ribosomal protein S4

Chain i:  70% 30%



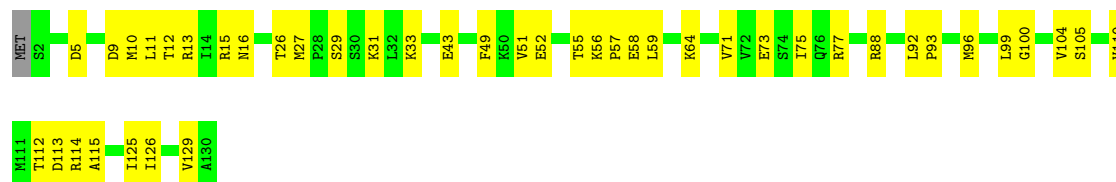
- Molecule 39: 30S ribosomal protein S5

Chain j:  61% 32% 7%

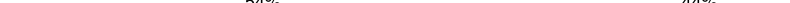


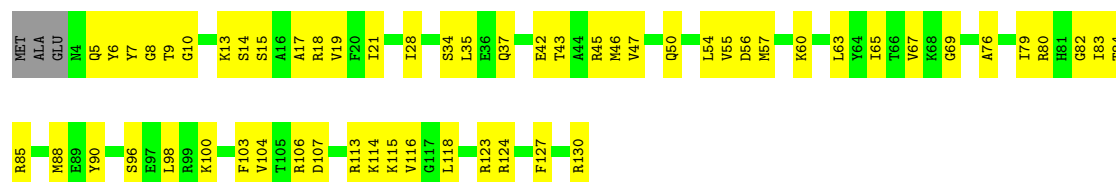
- Molecule 42: Small ribosomal subunit protein uS8

Chain m:

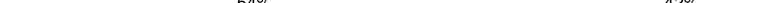


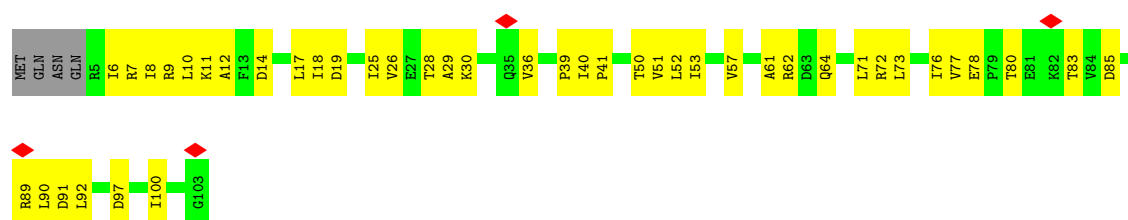
- Molecule 43: Small ribosomal subunit protein uS9

Chain n:  54% 44% .

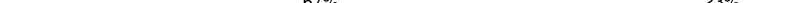


- Molecule 44: Small ribosomal subunit protein uS10

Chain o:  10% 54% 42%



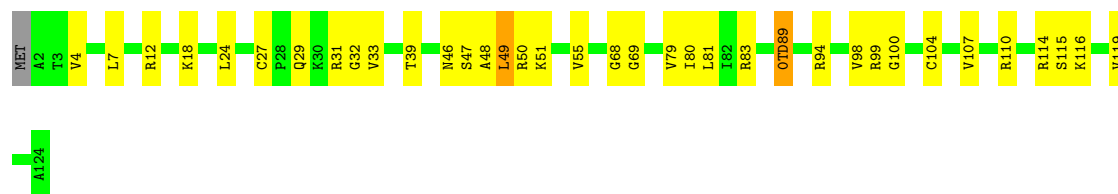
- Molecule 45: 30S ribosomal protein S11

Chain p: 



- Molecule 46: Small ribosomal subunit protein uS12

Chain q:  70% 27% ..



- Molecule 47: 30S ribosomal protein S13



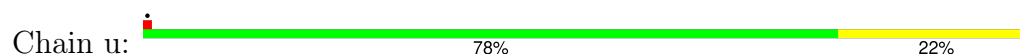
- Molecule 48: Small ribosomal subunit protein uS14



- Molecule 49: Small ribosomal subunit protein uS15



- Molecule 50: 30S ribosomal protein S16

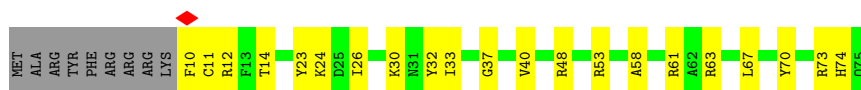


- Molecule 51: Small ribosomal subunit protein uS17



- Molecule 52: 30S ribosomal protein S18





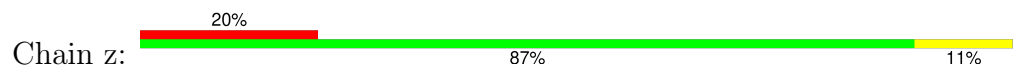
- Molecule 53: Small ribosomal subunit protein uS19



- Molecule 54: 30S ribosomal protein S20



- Molecule 55: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	69316	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	61.23	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.056	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	547.328, 547.328, 547.328	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.069, 1.069, 1.069	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, UR3, 1MG, MG, 0TD, 6MZ, OMU, OMG, 5MU, 7MG, 4OC, MA6, G7M, 5MC, PSU, OMC, 2MG

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	1	0.14	0/69335	0.25	0/108168
2	2	0.13	0/36590	0.23	0/57074
3	3	0.11	0/2872	0.23	0/4478
4	4	0.34	0/255	0.55	0/394
5	5	0.30	0/1841	0.54	2/2870 (0.1%)
6	A	0.10	0/511	0.28	0/685
7	B	0.14	0/2121	0.29	0/2852
8	C	0.14	0/1586	0.32	0/2134
9	D	0.15	0/1571	0.35	0/2113
10	E	0.14	0/1434	0.38	0/1926
11	F	0.12	0/1333	0.28	0/1805
12	G	0.13	0/1122	0.33	0/1515
13	J	0.16	0/1152	0.34	0/1551
14	K	0.12	0/955	0.25	0/1279
15	L	0.14	0/1062	0.28	0/1413
16	M	0.14	0/1093	0.29	0/1460
17	N	0.15	0/964	0.34	0/1289
18	O	0.13	0/902	0.31	0/1209
19	P	0.14	0/929	0.28	0/1242
20	Q	0.17	0/960	0.33	0/1278
21	R	0.14	0/829	0.34	0/1107
22	S	0.16	0/864	0.35	0/1156
23	T	0.13	0/752	0.29	0/1005
24	U	0.14	0/796	0.32	0/1062
25	V	0.15	0/766	0.36	0/1025
26	W	0.13	0/589	0.25	0/779
27	X	0.15	0/635	0.31	0/848
28	Y	0.13	0/502	0.33	0/667
29	Z	0.13	0/452	0.27	0/605
30	a	0.12	0/531	0.30	0/709
31	b	0.13	0/450	0.29	0/599

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	c	0.13	0/433	0.26	0/576
33	d	0.14	0/380	0.26	0/498
34	e	0.39	0/513	0.62	1/676 (0.1%)
35	f	0.13	0/303	0.33	0/397
36	g	0.14	0/1791	0.39	0/2413
37	h	0.14	0/1663	0.36	0/2241
38	i	0.12	0/1665	0.26	0/2227
39	j	0.16	0/1165	0.36	0/1568
40	k	0.15	0/867	0.37	0/1171
41	l	0.14	0/1195	0.37	0/1602
42	m	0.16	0/989	0.39	0/1326
43	n	0.22	0/1034	0.50	0/1375
44	o	0.15	0/800	0.38	0/1082
45	p	0.19	0/893	0.37	0/1205
46	q	0.27	0/960	0.40	0/1286
47	r	0.13	0/909	0.35	0/1215
48	s	0.12	0/817	0.27	0/1088
49	t	0.13	0/722	0.31	0/964
50	u	0.16	0/659	0.33	0/884
51	v	0.12	0/657	0.31	0/881
52	w	0.17	0/553	0.29	0/743
53	x	0.12	0/680	0.28	0/915
54	y	0.16	0/675	0.34	0/895
55	z	0.10	0/597	0.24	0/792
All	All	0.14	0/156674	0.28	3/234317 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	e	30	ARG	N-CA-C	-11.61	92.49	108.86
5	5	55	U	C3'-C2'-O2'	6.24	120.05	110.70
5	5	3	G	C4'-C3'-O3'	5.85	118.18	109.40

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	1	62334	0	31367	1170	0
2	2	32929	0	16587	576	0
3	3	2569	0	1301	46	0
4	4	230	0	119	8	0
5	5	1648	0	833	73	0
6	A	507	0	542	10	0
7	B	2082	0	2154	58	0
8	C	1565	0	1616	40	0
9	D	1552	0	1619	50	0
10	E	1410	0	1444	53	0
11	F	1313	0	1358	32	0
12	G	1111	0	1148	18	0
13	J	1129	0	1162	34	0
14	K	946	0	1023	25	0
15	L	1053	0	1129	30	0
16	M	1074	0	1157	29	0
17	N	951	0	994	17	0
18	O	892	0	923	26	0
19	P	917	0	962	18	0
20	Q	947	0	1019	30	0
21	R	816	0	839	25	0
22	S	857	0	922	26	0
23	T	746	0	811	15	0
24	U	788	0	844	18	0
25	V	753	0	780	17	0
26	W	582	0	599	15	0
27	X	625	0	652	11	0
28	Y	501	0	531	10	0
29	Z	448	0	488	11	0
30	a	522	0	524	19	0
31	b	444	0	458	16	0
32	c	426	0	464	11	0
33	d	377	0	418	16	0
34	e	504	0	572	25	0
35	f	302	0	343	9	0
36	g	1760	0	1787	39	0
37	h	1636	0	1710	42	0
38	i	1643	0	1707	45	0
39	j	1152	0	1196	40	0
40	k	848	0	846	27	0
41	l	1181	0	1238	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	m	979	0	1031	35	0
43	n	1022	0	1070	44	0
44	o	790	0	831	36	0
45	p	877	0	887	28	0
46	q	957	0	1017	34	0
47	r	900	0	965	31	0
48	s	805	0	844	27	0
49	t	714	0	734	23	0
50	u	649	0	666	16	0
51	v	648	0	691	18	0
52	w	544	0	560	15	0
53	x	663	0	688	32	0
54	y	669	0	719	19	0
55	z	589	0	629	6	0
56	1	262	0	0	0	0
56	2	111	0	0	0	0
56	3	10	0	0	0	0
56	5	1	0	0	0	0
56	B	3	0	0	0	0
56	L	2	0	0	0	0
56	M	1	0	0	0	0
56	Q	1	0	0	0	0
56	X	1	0	0	0	0
56	b	1	0	0	0	0
56	l	1	0	0	0	0
56	z	1	0	0	0	0
57	5	9	0	12	0	0
58	1	700	0	0	22	0
58	2	341	0	0	5	0
58	3	7	0	0	0	0
58	4	1	0	0	0	0
58	5	10	0	0	3	0
58	B	2	0	0	0	0
58	C	7	0	0	0	0
58	D	10	0	0	2	0
58	E	4	0	0	1	0
58	F	6	0	0	1	0
58	G	12	0	0	0	0
58	J	7	0	0	3	0
58	K	4	0	0	2	0
58	L	3	0	0	3	0
58	M	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	N	2	0	0	0	0
58	O	6	0	0	1	0
58	P	6	0	0	0	0
58	Q	7	0	0	1	0
58	R	7	0	0	5	0
58	S	4	0	0	1	0
58	T	2	0	0	0	0
58	U	6	0	0	0	0
58	V	1	0	0	0	0
58	W	2	0	0	0	0
58	Y	8	0	0	2	0
58	Z	2	0	0	1	0
58	a	2	0	0	0	0
58	b	2	0	0	0	0
58	f	1	0	0	0	0
58	g	20	0	0	1	0
58	h	14	0	0	2	0
58	i	8	0	0	2	0
58	j	3	0	0	0	0
58	k	7	0	0	1	0
58	l	5	0	0	1	0
58	m	3	0	0	0	0
58	n	4	0	0	0	0
58	o	3	0	0	0	0
58	p	5	0	0	1	0
58	q	1	0	0	0	0
58	r	4	0	0	0	0
58	t	1	0	0	0	0
58	u	4	0	0	0	0
58	v	3	0	0	0	0
58	w	3	0	0	1	0
58	x	1	0	0	0	0
58	z	4	0	0	0	0
All	All	146547	0	97530	2747	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 2747 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)
5:5:67:G:H5'	58:5:206:HOH:O	1.65	0.95
1:1:408:G:H1	1:1:419:U:H3	1.16	0.94
5:5:18:G:H1	5:5:57:A:N6	1.68	0.91
54:y:57:ILE:HG13	54:y:61:GLN:HE22	1.36	0.89
1:1:1270:C:H5''	1:1:1271:G:H5'	1.55	0.88

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	
6	A	65/229 (28%)	63 (97%)	2 (3%)	0	100	100
7	B	269/273 (98%)	257 (96%)	12 (4%)	0	100	100
8	C	207/209 (99%)	196 (95%)	11 (5%)	0	100	100
9	D	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
10	E	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
11	F	173/177 (98%)	168 (97%)	4 (2%)	1 (1%)	21	54
12	G	147/149 (99%)	142 (97%)	5 (3%)	0	100	100
13	J	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
14	K	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
15	L	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
16	M	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
17	N	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
18	O	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
19	P	112/115 (97%)	112 (100%)	0	0	100	100
20	Q	115/118 (98%)	115 (100%)	0	0	100	100
21	R	101/103 (98%)	95 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
23	T	92/100 (92%)	89 (97%)	3 (3%)	0	100	100
24	U	101/104 (97%)	98 (97%)	3 (3%)	0	100	100
25	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
26	W	74/84 (88%)	70 (95%)	4 (5%)	0	100	100
27	X	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
28	Y	60/63 (95%)	56 (93%)	4 (7%)	0	100	100
29	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
30	a	64/70 (91%)	59 (92%)	5 (8%)	0	100	100
31	b	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
32	c	50/55 (91%)	50 (100%)	0	0	100	100
33	d	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
34	e	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
35	f	36/38 (95%)	36 (100%)	0	0	100	100
36	g	223/241 (92%)	214 (96%)	9 (4%)	0	100	100
37	h	206/233 (88%)	196 (95%)	10 (5%)	0	100	100
38	i	203/206 (98%)	196 (97%)	7 (3%)	0	100	100
39	j	154/167 (92%)	145 (94%)	9 (6%)	0	100	100
40	k	102/135 (76%)	100 (98%)	2 (2%)	0	100	100
41	l	149/179 (83%)	142 (95%)	7 (5%)	0	100	100
42	m	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
43	n	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
44	o	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
45	p	115/129 (89%)	114 (99%)	1 (1%)	0	100	100
46	q	120/124 (97%)	108 (90%)	12 (10%)	0	100	100
47	r	114/118 (97%)	107 (94%)	7 (6%)	0	100	100
48	s	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
49	t	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
50	u	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
51	v	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
52	w	64/75 (85%)	62 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	x	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
54	y	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
55	z	68/71 (96%)	68 (100%)	0	0	100	100
All	All	5673/6141 (92%)	5465 (96%)	207 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	F	47	ASP

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	
6	A	54/177 (30%)	54 (100%)	0	100	100
7	B	216/218 (99%)	215 (100%)	1 (0%)	81	80
8	C	164/164 (100%)	164 (100%)	0	100	100
9	D	165/165 (100%)	165 (100%)	0	100	100
10	E	148/150 (99%)	148 (100%)	0	100	100
11	F	136/138 (99%)	136 (100%)	0	100	100
12	G	114/114 (100%)	114 (100%)	0	100	100
13	J	116/116 (100%)	116 (100%)	0	100	100
14	K	104/104 (100%)	104 (100%)	0	100	100
15	L	103/103 (100%)	103 (100%)	0	100	100
16	M	109/109 (100%)	109 (100%)	0	100	100
17	N	99/103 (96%)	99 (100%)	0	100	100
18	O	86/87 (99%)	86 (100%)	0	100	100
19	P	99/100 (99%)	99 (100%)	0	100	100
20	Q	89/90 (99%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	R	84/84 (100%)	84 (100%)	0	100	100
22	S	93/93 (100%)	93 (100%)	0	100	100
23	T	81/84 (96%)	81 (100%)	0	100	100
24	U	84/85 (99%)	84 (100%)	0	100	100
25	V	78/78 (100%)	78 (100%)	0	100	100
26	W	58/62 (94%)	58 (100%)	0	100	100
27	X	67/68 (98%)	67 (100%)	0	100	100
28	Y	54/55 (98%)	54 (100%)	0	100	100
29	Z	48/49 (98%)	48 (100%)	0	100	100
30	a	59/62 (95%)	59 (100%)	0	100	100
31	b	47/48 (98%)	47 (100%)	0	100	100
32	c	47/49 (96%)	47 (100%)	0	100	100
33	d	38/38 (100%)	38 (100%)	0	100	100
34	e	51/52 (98%)	49 (96%)	2 (4%)	28	54
35	f	34/34 (100%)	34 (100%)	0	100	100
36	g	187/199 (94%)	187 (100%)	0	100	100
37	h	171/190 (90%)	171 (100%)	0	100	100
38	i	172/173 (99%)	172 (100%)	0	100	100
39	j	119/126 (94%)	119 (100%)	0	100	100
40	k	91/116 (78%)	91 (100%)	0	100	100
41	l	124/147 (84%)	124 (100%)	0	100	100
42	m	104/105 (99%)	104 (100%)	0	100	100
43	n	105/107 (98%)	103 (98%)	2 (2%)	50	67
44	o	86/90 (96%)	86 (100%)	0	100	100
45	p	90/99 (91%)	90 (100%)	0	100	100
46	q	102/103 (99%)	100 (98%)	2 (2%)	48	66
47	r	94/96 (98%)	94 (100%)	0	100	100
48	s	83/84 (99%)	83 (100%)	0	100	100
49	t	76/77 (99%)	76 (100%)	0	100	100
50	u	65/65 (100%)	65 (100%)	0	100	100
51	v	74/78 (95%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	w	57/65 (88%)	57 (100%)	0	100	100
53	x	72/79 (91%)	72 (100%)	0	100	100
54	y	65/66 (98%)	65 (100%)	0	100	100
55	z	60/61 (98%)	60 (100%)	0	100	100
All	All	4722/5005 (94%)	4715 (100%)	7 (0%)	87	87

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	n	5	GLN
43	n	9	THR
46	q	49	LEU
46	q	47	SER
34	e	32	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
38	i	136	GLN
49	t	80	GLN
40	k	14	GLN
41	l	148	ASN
53	x	52	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2904 (99%)	456 (15%)	10 (0%)
2	2	1532/1540 (99%)	228 (14%)	3 (0%)
3	3	119/120 (99%)	20 (16%)	0
4	4	10/18 (55%)	8 (80%)	0
5	5	76/77 (98%)	34 (44%)	5 (6%)
All	All	4639/4659 (99%)	746 (16%)	18 (0%)

5 of 746 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A

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Mol	Chain	Res	Type
1	1	27	G
1	1	34	U
1	1	35	G
1	1	46	G

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	5	3	G
5	5	72	G
5	5	59	A
1	1	2425	A
5	5	2	G

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

32 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	$\# Z > 2$
1	OMG	1	2251	1,5	23,26,27	0.47	0	32,38,41	0.53	0
2	2MG	2	1207	2	23,26,27	0.46	0	33,38,41	0.48	0
2	PSU	2	516	2	18,21,22	1.08	1 (5%)	21,30,33	1.87	5 (23%)
2	2MG	2	966	2	23,26,27	1.35	4 (17%)	33,38,41	2.28	9 (27%)
2	7MG	2	527	2	23,26,27	1.09	1 (4%)	27,39,42	0.89	2 (7%)
2	5MC	2	967	2	19,22,23	1.53	3 (15%)	26,32,35	1.35	4 (15%)
1	PSU	1	955	1	18,21,22	1.13	1 (5%)	21,30,33	1.85	4 (19%)
2	2MG	2	1516	2	23,26,27	0.48	0	33,38,41	0.57	0
1	5MU	1	1939	56,1	19,22,23	0.42	0	27,32,35	0.49	0
1	2MG	1	2445	1	23,26,27	0.47	0	33,38,41	0.49	0
1	PSU	1	2457	1	18,21,22	1.07	1 (5%)	21,30,33	1.92	6 (28%)
1	G7M	1	2069	1	23,26,27	2.78	9 (39%)	34,39,42	2.22	11 (32%)
1	5MU	1	747	1	19,22,23	0.43	0	27,32,35	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	2MG	1	1835	1	23,26,27	0.45	0	33,38,41	0.48	0
1	PSU	1	2605	1	18,21,22	1.13	1 (5%)	21,30,33	1.96	5 (23%)
1	PSU	1	2504	1	18,21,22	1.57	5 (27%)	21,30,33	2.11	4 (19%)
1	PSU	1	2580	1	18,21,22	1.10	2 (11%)	21,30,33	2.17	6 (28%)
1	1MG	1	745	1	23,26,27	3.10	7 (30%)	33,39,42	1.92	9 (27%)
1	PSU	1	1917	1	18,21,22	1.10	1 (5%)	21,30,33	1.96	5 (23%)
1	6MZ	1	1618	1	22,25,26	3.75	12 (54%)	29,36,39	3.74	12 (41%)
1	PSU	1	746	56,1	18,21,22	1.09	1 (5%)	21,30,33	1.87	5 (23%)
1	OMU	1	2552	1	19,22,23	3.07	8 (42%)	25,31,34	1.82	5 (20%)
2	MA6	2	1519	2	23,26,27	1.53	4 (17%)	33,38,41	3.29	12 (36%)
2	MA6	2	1518	2	23,26,27	1.53	3 (13%)	33,38,41	3.20	11 (33%)
46	0TD	q	89	46	8,9,10	1.78	2 (25%)	6,11,13	1.77	1 (16%)
1	OMC	1	2498	1	19,22,23	0.55	0	25,31,34	0.67	0
2	4OC	2	1402	2	20,23,24	3.20	8 (40%)	25,32,35	0.88	1 (4%)
1	PSU	1	1911	1	18,21,22	1.13	1 (5%)	21,30,33	1.95	5 (23%)
2	5MC	2	1407	2	19,22,23	0.55	0	26,32,35	0.63	0
1	5MC	1	1962	1	19,22,23	0.57	0	26,32,35	0.58	0
2	UR3	2	1498	2	19,22,23	2.80	8 (42%)	26,32,35	1.58	4 (15%)
1	2MA	1	2503	56,1	22,25,26	4.63	14 (63%)	32,37,40	2.98	10 (31%)

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
1	OMG	1	2251	1,5	-	0/9/27/28	0/3/3/3
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
2	7MG	2	527	2	-	3/7/37/38	0/3/3/3
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
1	5MU	1	1939	56,1	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	0/9/27/28	0/3/3/3
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	0/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	1/9/27/28	0/3/3/3
1	PSU	1	746	56,1	-	0/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	0/9/27/28	0/2/2/2
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
46	0TD	q	89	46	-	3/7/12/14	-
1	OMC	1	2498	1	-	0/9/27/28	0/2/2/2
2	4OC	2	1402	2	-	1/9/29/30	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
2	UR3	2	1498	2	-	2/7/25/26	0/2/2/2
1	2MA	1	2503	56,1	-	3/7/25/26	0/3/3/3

The worst 5 of 97 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2503	2MA	C4-N3	10.93	1.48	1.34
1	1	1618	6MZ	C3'-C4'	-9.25	1.29	1.53
1	1	1618	6MZ	C6-N6	9.25	1.44	1.34
1	1	2503	2MA	C3'-C4'	-9.14	1.29	1.53
1	1	745	1MG	C2-N3	8.99	1.47	1.33

The worst 5 of 136 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1519	MA6	N1-C6-N6	-11.98	102.26	116.86
2	2	1518	MA6	N1-C6-N6	-11.59	102.74	116.86
1	1	1618	6MZ	C1'-N9-C8	-11.54	101.47	127.09
1	1	1618	6MZ	C4-N9-C1'	10.19	150.46	126.63
1	1	2503	2MA	C1'-N9-C8	-8.84	107.48	127.09

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
1	1	2504	PSU	O4'-C4'-C5'-O5'
2	2	967	5MC	O4'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'

There are no ring outliers.

15 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	516	PSU	1	0
1	1	955	PSU	1	0
2	2	1516	2MG	2	0
1	1	1939	5MU	1	0
1	1	2069	G7M	1	0
1	1	747	5MU	1	0
1	1	2580	PSU	2	0
1	1	745	1MG	1	0
1	1	1917	PSU	1	0
1	1	746	PSU	1	0
1	1	2552	OMU	2	0
2	2	1518	MA6	1	0
46	q	89	0TD	4	0
2	2	1402	4OC	2	0
1	1	1962	5MC	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 396 ligands modelled in this entry, 395 are monoatomic - leaving 1 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
57	LYS	5	101	5	7,8,9	1.10	1 (14%)	3,8,10	0.54	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
57	LYS	5	101	5	-	3/6/7/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	5	101	LYS	O-C	2.61	1.29	1.20

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	5	101	LYS	CE-CD-CG-CB
57	5	101	LYS	CG-CD-CE-NZ
57	5	101	LYS	CA-CB-CG-CD

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.

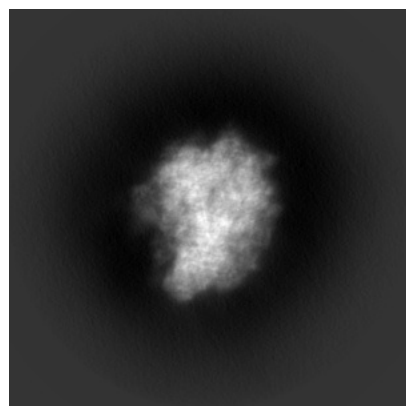
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42714. These allow visual inspection of the internal detail of the map and identification of artifacts.

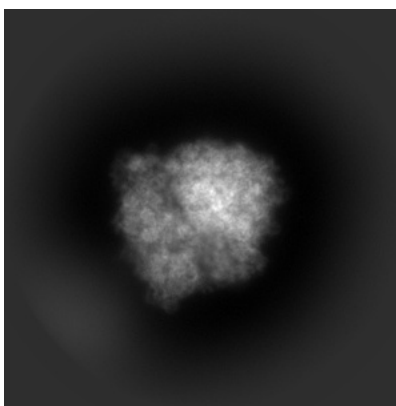
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

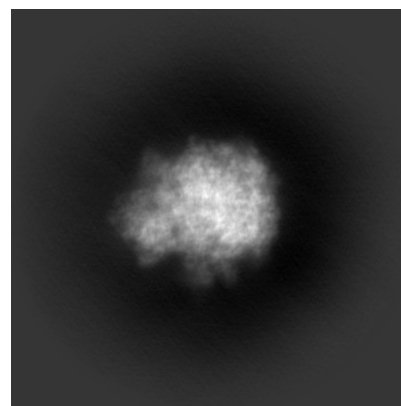
6.1.1 Primary map



X

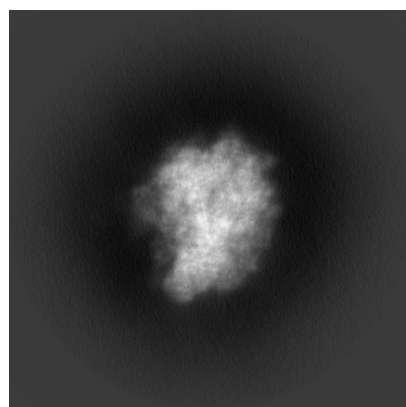


Y

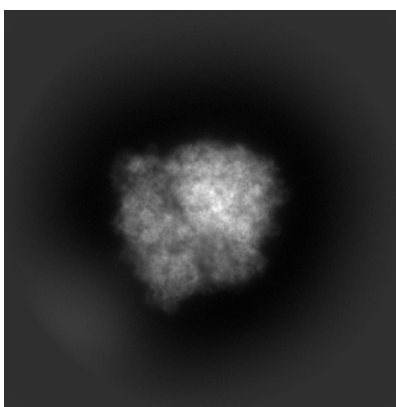


Z

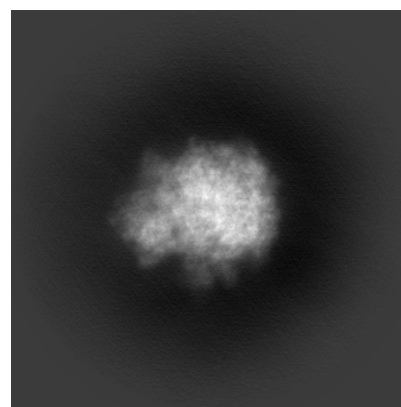
6.1.2 Raw map



X



Y

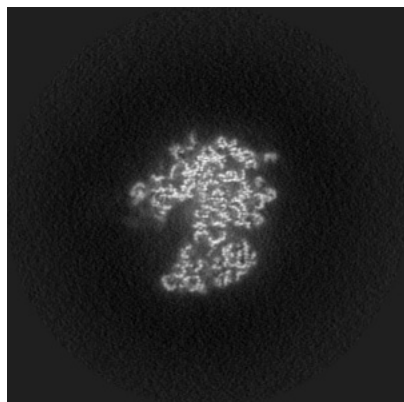


Z

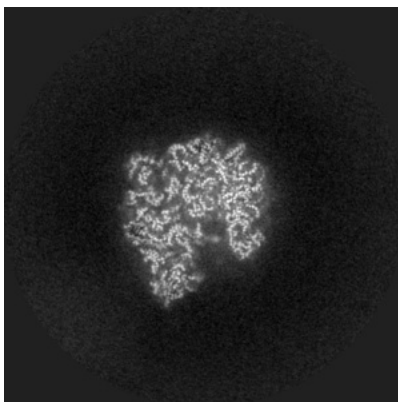
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

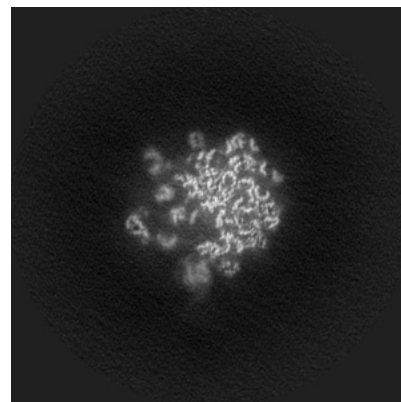
6.2.1 Primary map



X Index: 256

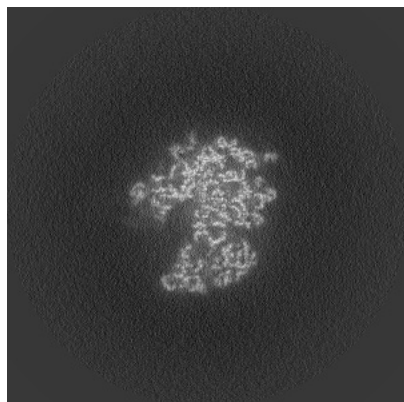


Y Index: 256

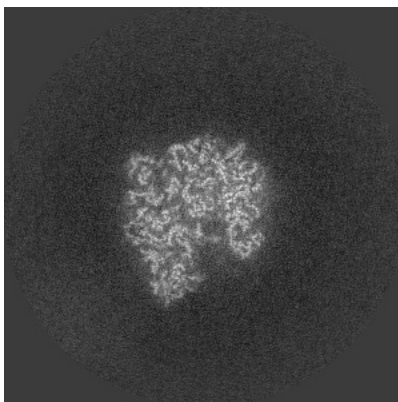


Z Index: 256

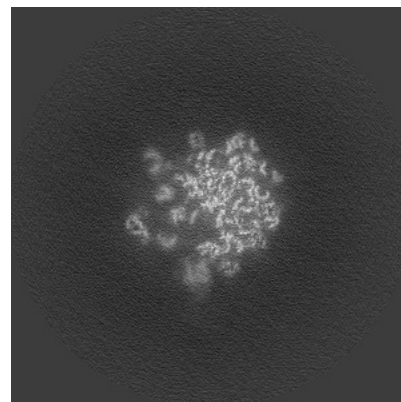
6.2.2 Raw map



X Index: 256



Y Index: 256

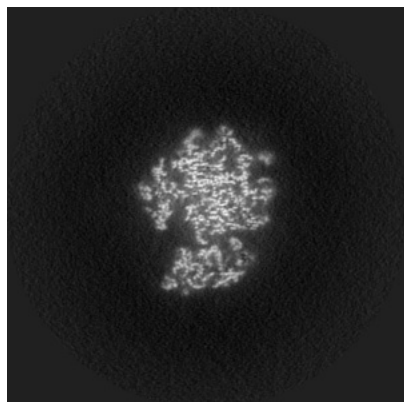


Z Index: 256

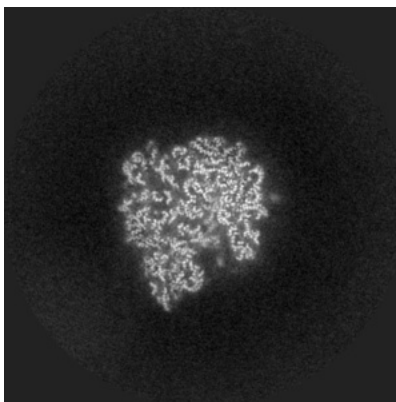
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

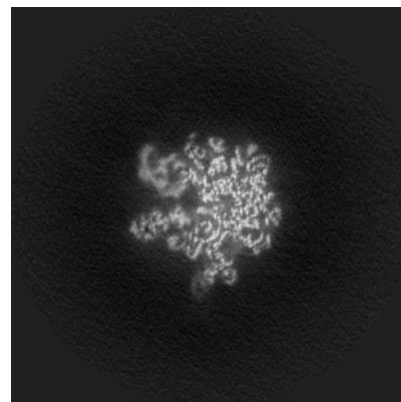
6.3.1 Primary map



X Index: 264

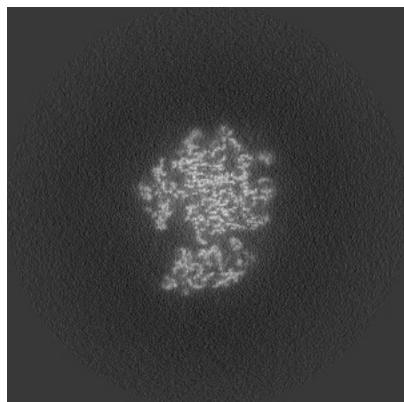


Y Index: 250

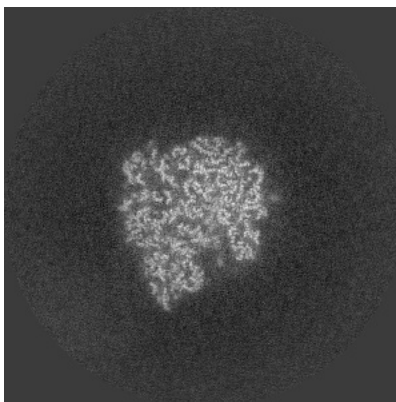


Z Index: 274

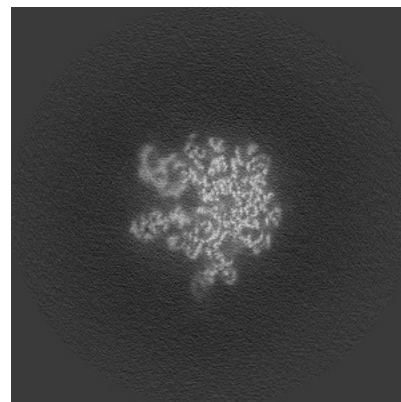
6.3.2 Raw map



X Index: 264



Y Index: 250

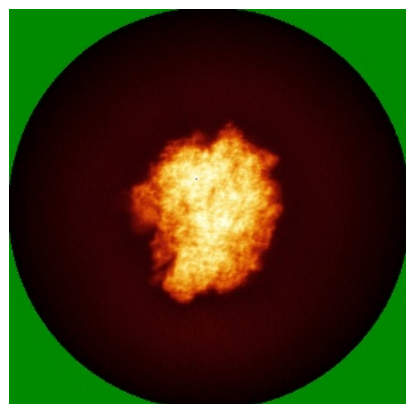


Z Index: 274

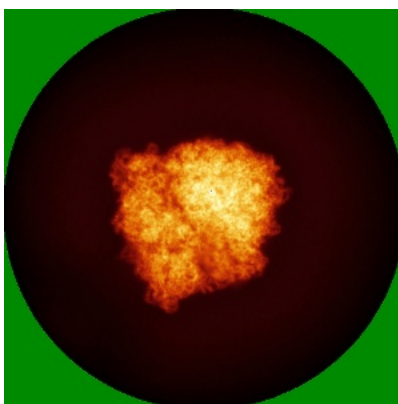
The images above show the largest variance slices of the map in three orthogonal directions.

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

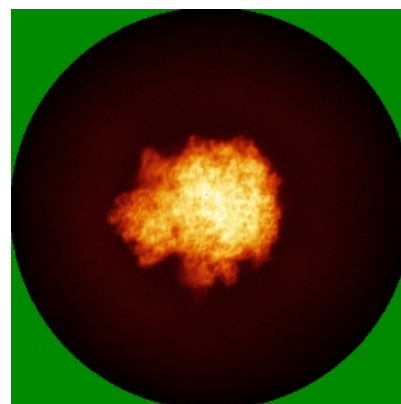
6.4.1 Primary map



X

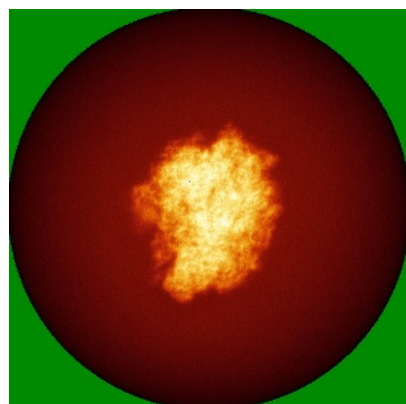


Y

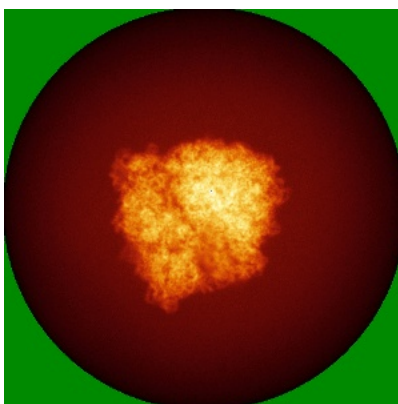


Z

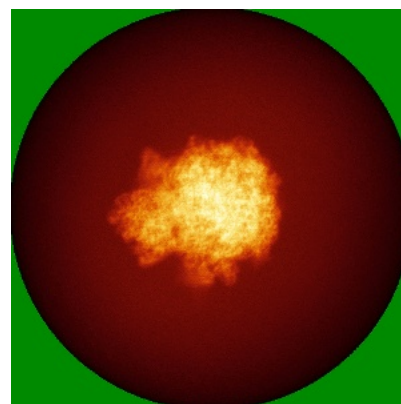
6.4.2 Raw map



X



Y

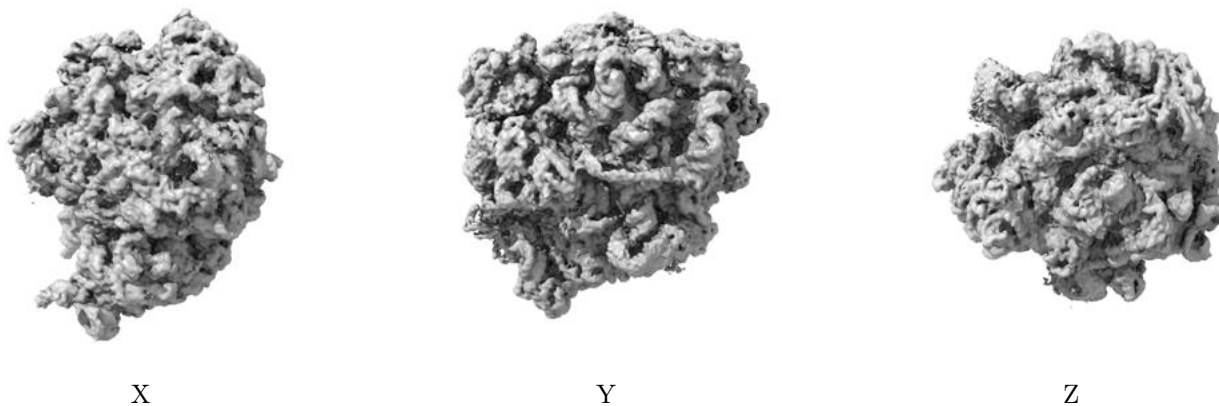


Z

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.

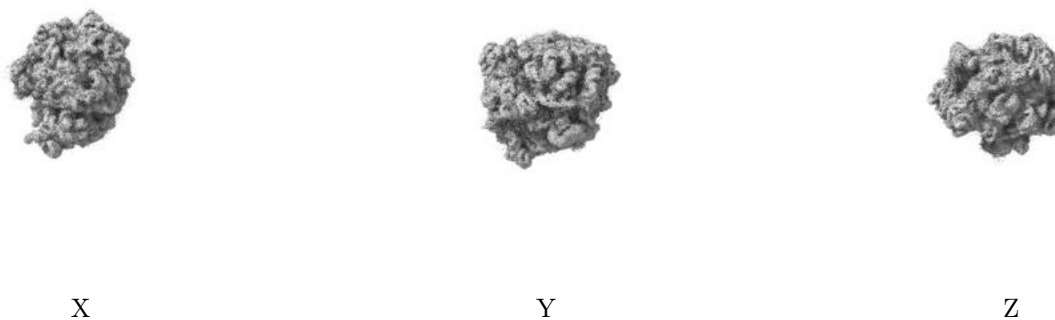
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.012. 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.

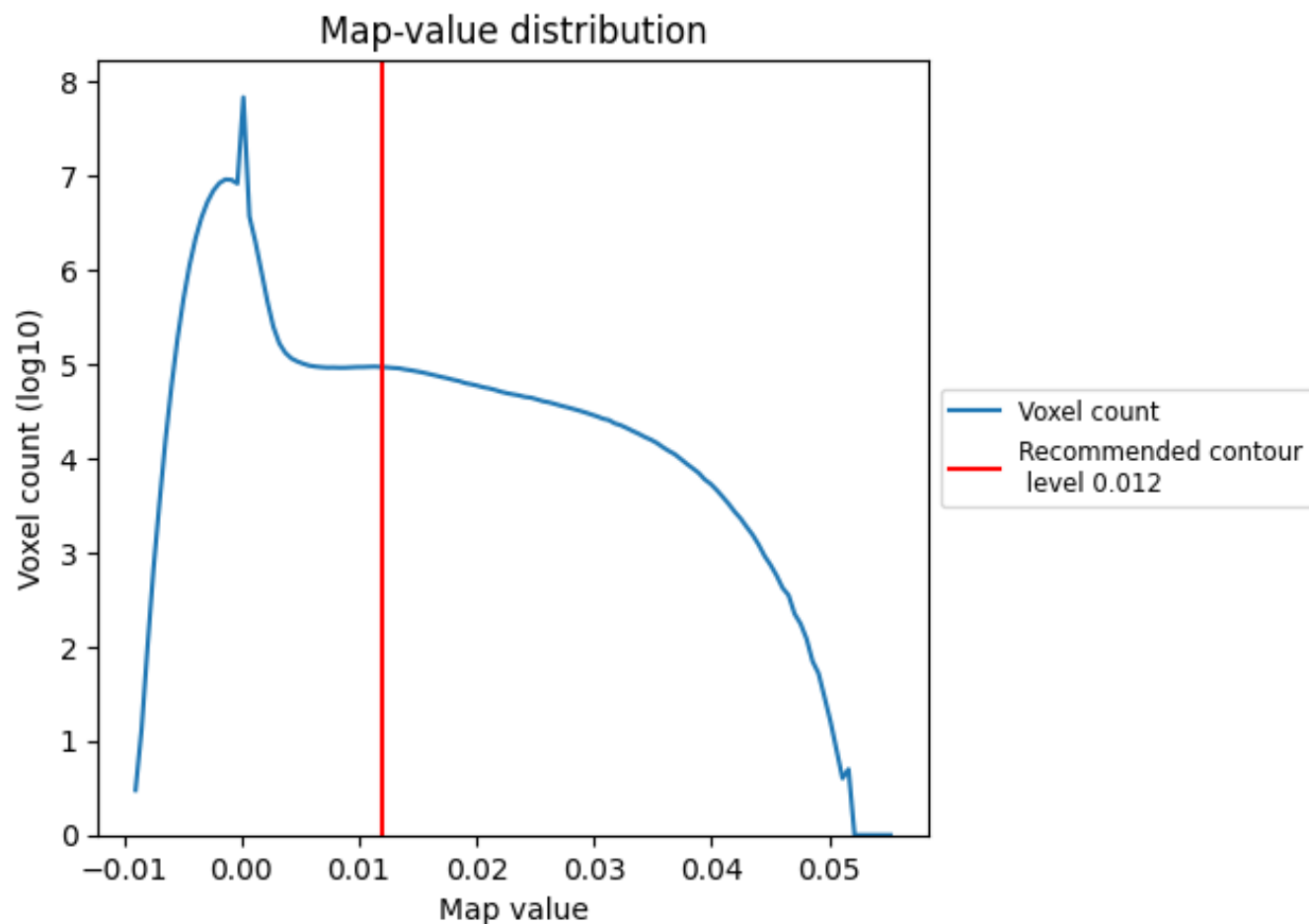
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

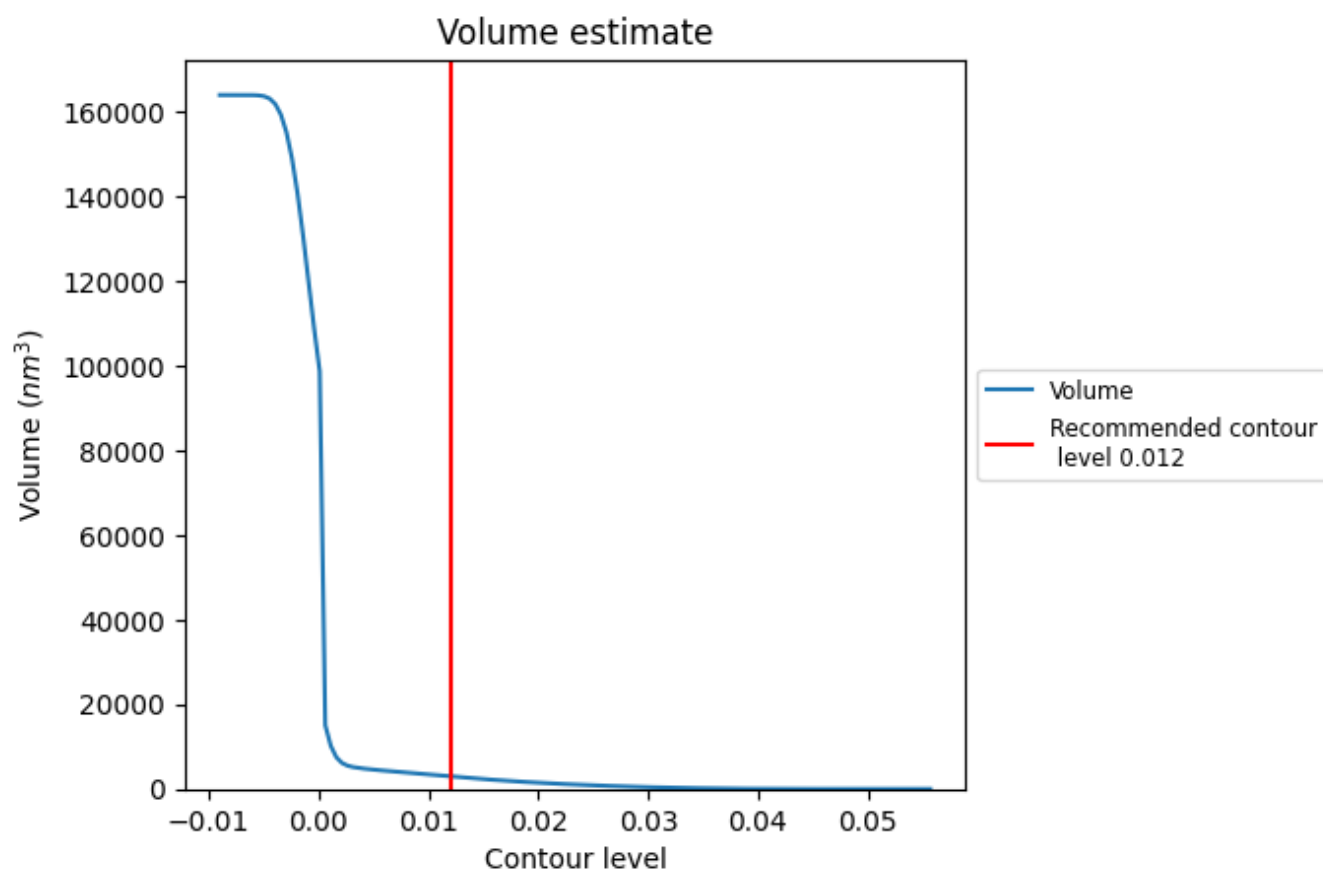
This section contains the results of statistical analysis of the map.

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.

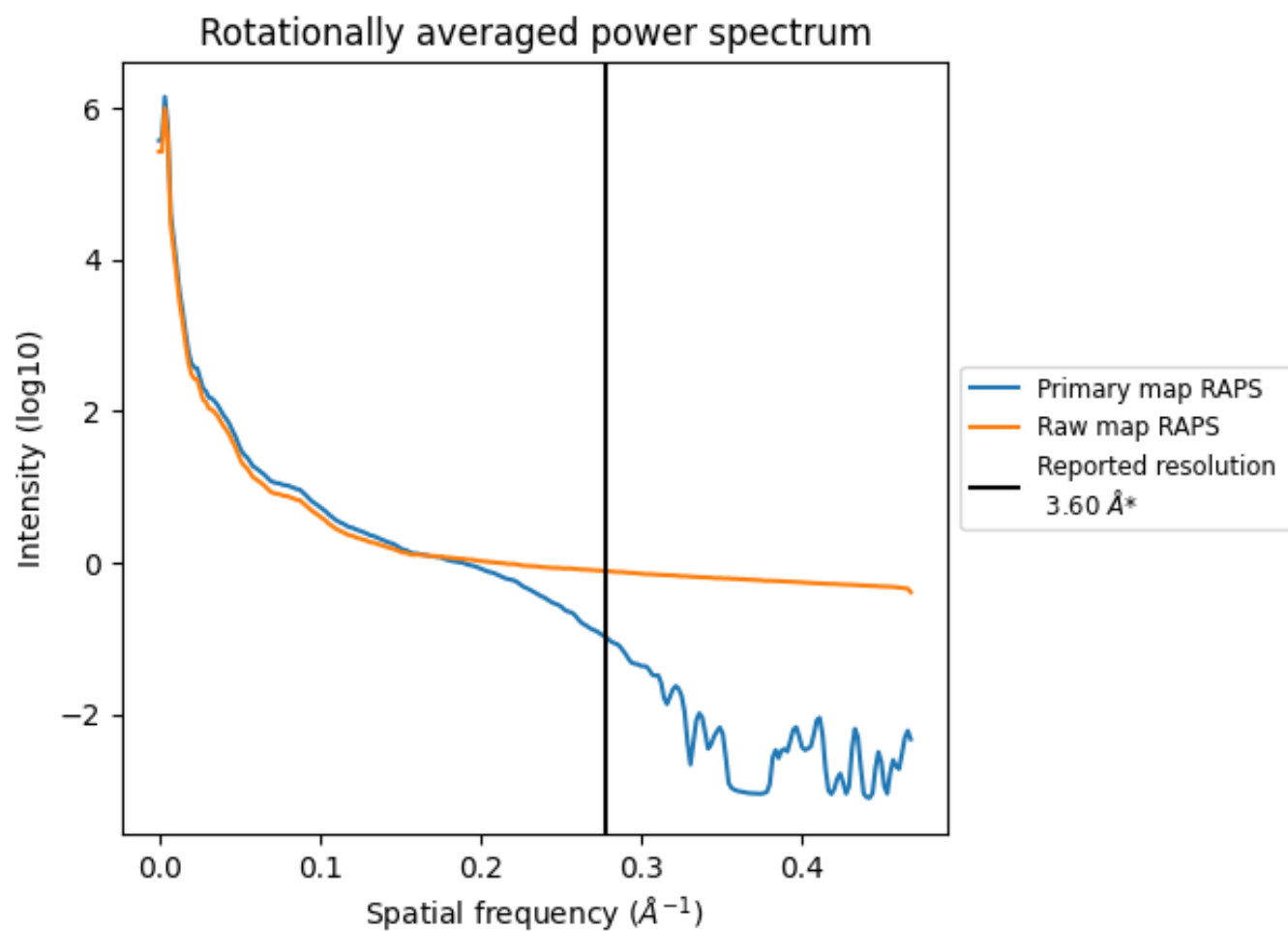
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2984 nm³; this corresponds to an approximate mass of 2696 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 ⓘ

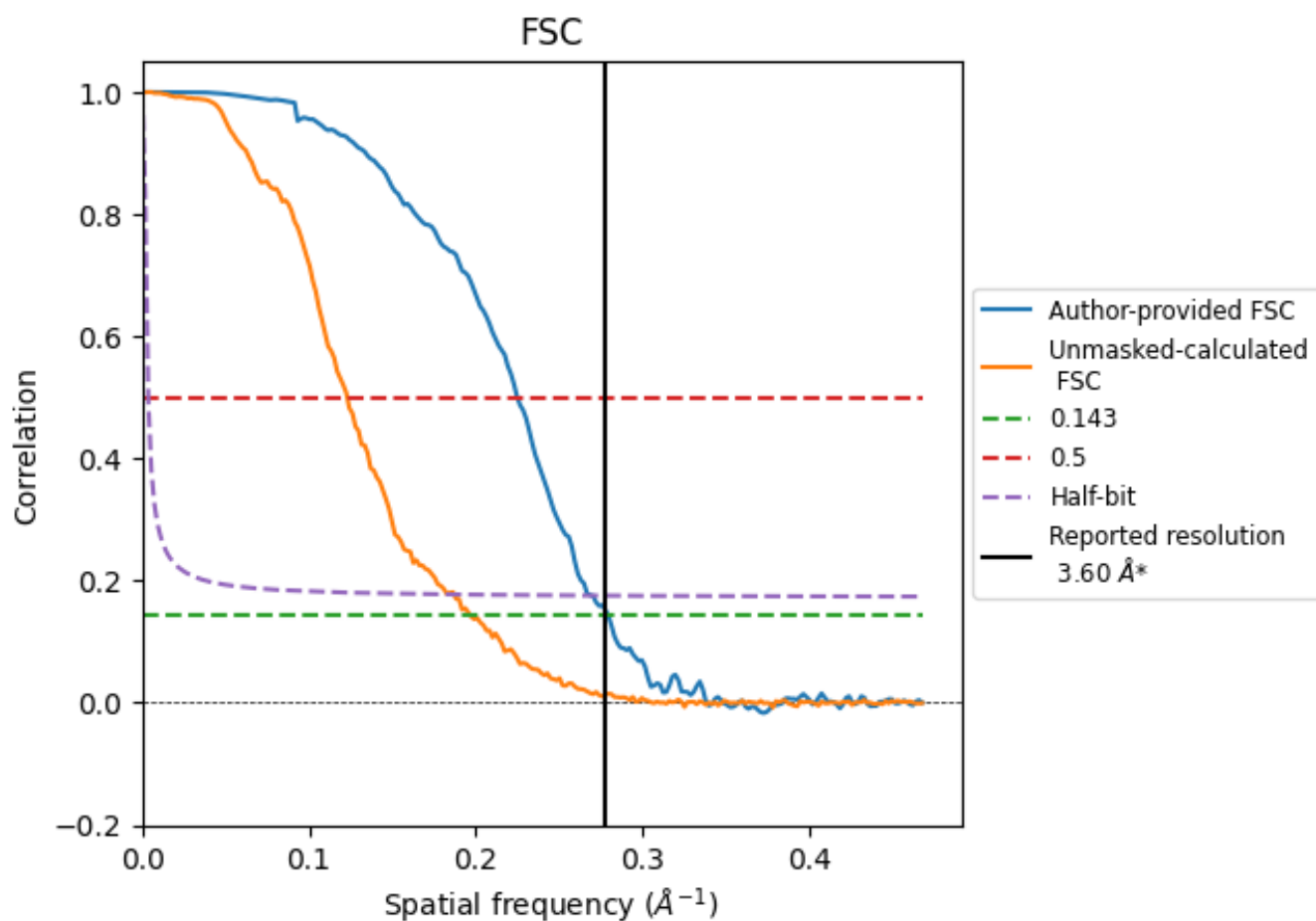


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

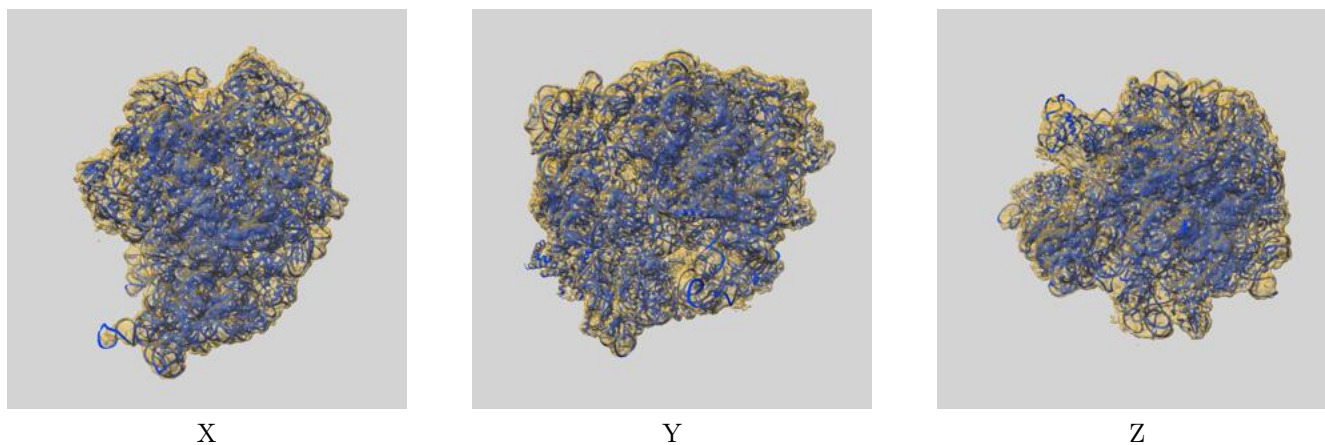
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.58	4.44	3.71
Unmasked-calculated*	5.08	8.13	5.35

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.08 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

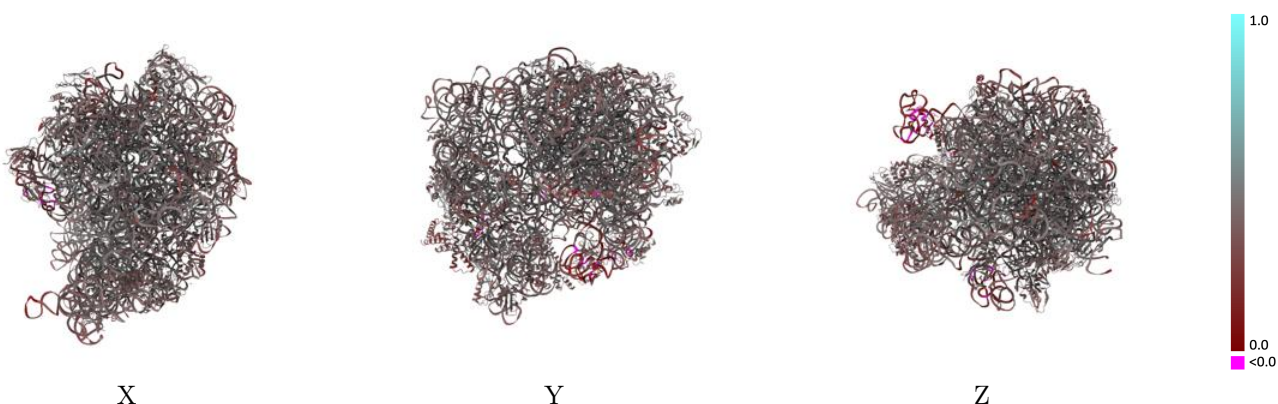
This section contains information regarding the fit between EMDB map EMD-42714 and PDB model 8UX8. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



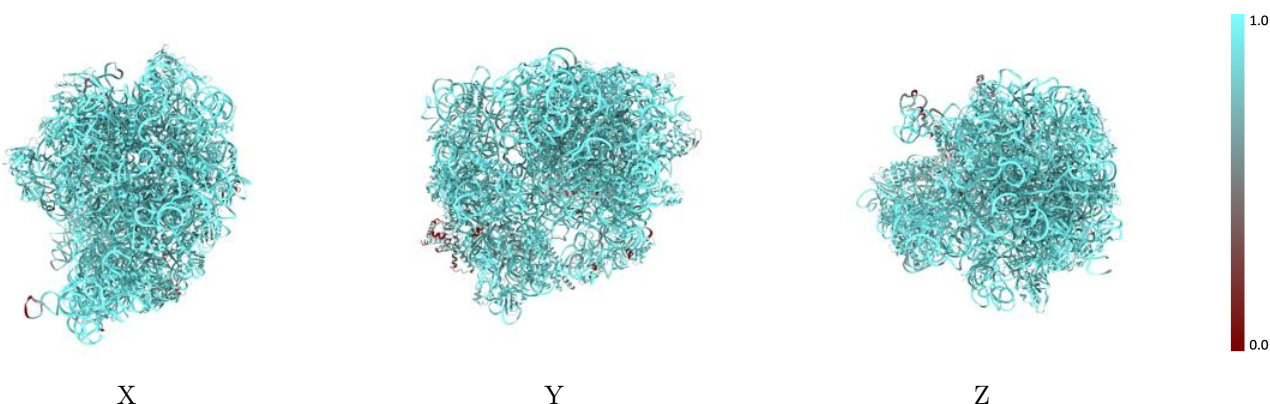
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



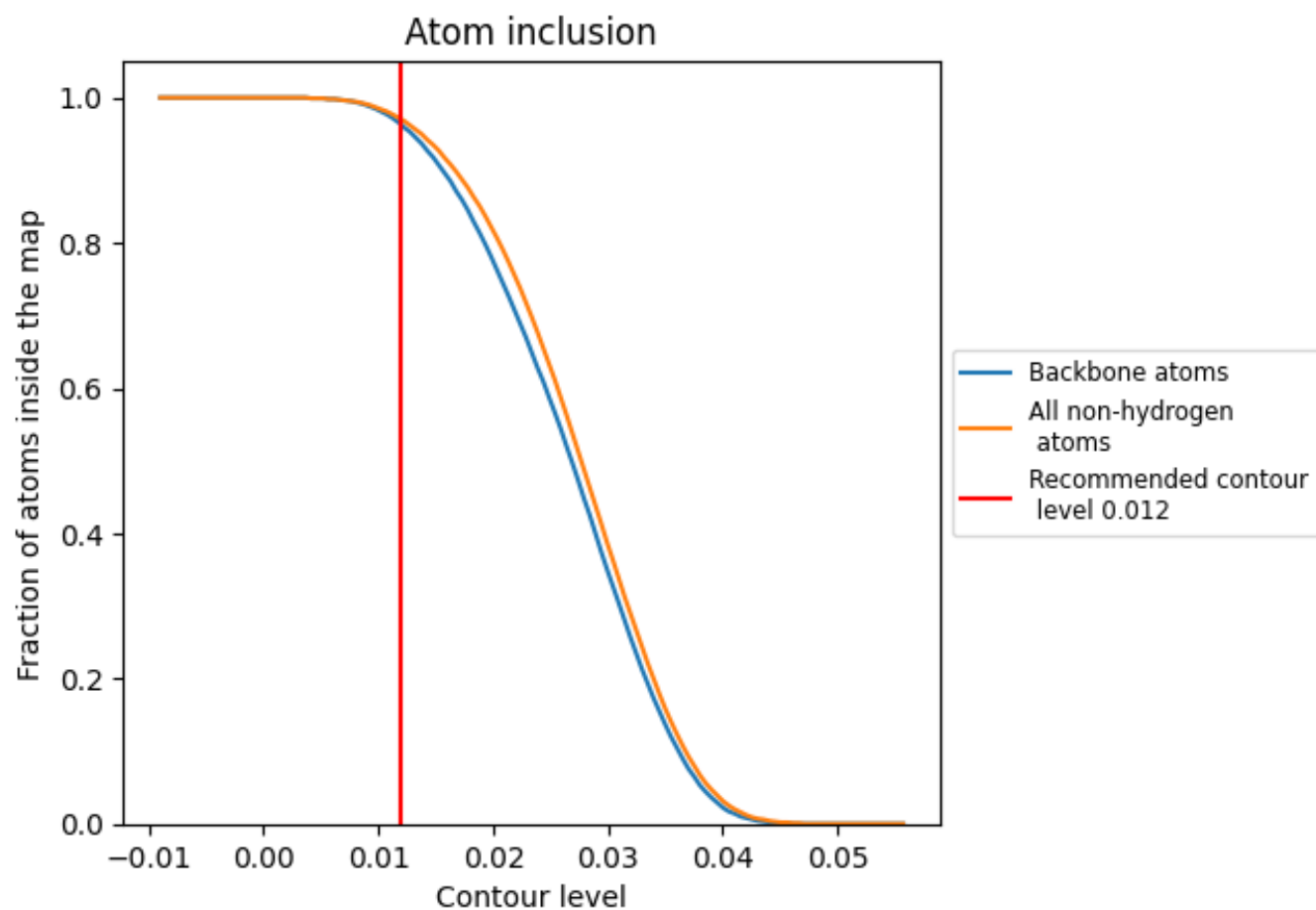
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.012).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.4060
1	 0.9890	 0.4060
2	 0.9870	 0.4080
3	 0.9770	 0.3810
4	 1.0000	 0.3440
5	 1.0000	 0.3840
A	 0.7680	 0.1920
B	 0.9980	 0.4600
C	 0.9680	 0.4520
D	 0.9180	 0.4220
E	 0.9290	 0.3660
F	 0.9180	 0.3970
G	 0.7430	 0.3310
J	 0.9860	 0.4350
K	 0.9970	 0.4530
L	 0.9570	 0.4370
M	 0.9920	 0.4400
N	 0.9950	 0.4330
O	 0.9470	 0.4010
P	 0.9800	 0.4490
Q	 0.9770	 0.4080
R	 0.9320	 0.4390
S	 0.9870	 0.4400
T	 0.9600	 0.4270
U	 0.9250	 0.4120
V	 0.9270	 0.4140
W	 0.9950	 0.4500
X	 0.9870	 0.4330
Y	 0.9280	 0.3600
Z	 0.9470	 0.4310
a	 0.8200	 0.3530
b	 0.9860	 0.4470
c	 0.9950	 0.4220
d	 1.0000	 0.4510
e	 1.0000	 0.4430



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Chain	Atom inclusion	Q-score
f	 1.0000	 0.4460
g	 0.5550	 0.3390
h	 0.9580	 0.4090
i	 0.9280	 0.3870
j	 0.9780	 0.4190
k	 0.9380	 0.4030
l	 0.9550	 0.3640
m	 0.9540	 0.4270
n	 0.9350	 0.4010
o	 0.8710	 0.3690
p	 0.9730	 0.4190
q	 0.9890	 0.4310
r	 0.9230	 0.3740
s	 0.9700	 0.3920
t	 0.9830	 0.3800
u	 0.9390	 0.4220
v	 0.9830	 0.4110
w	 0.9430	 0.3650
x	 0.9400	 0.3940
y	 0.9760	 0.3600
z	 0.7110	 0.3290