



wwPDB EM Validation Summary Report ⓘ

Jun 23, 2026 – 04:34 PM JST

PDB ID : 8ZTV / pdb_00008ztv
EMDB ID : EMD-60474
Title : 70S ribosome arrested by PepNL with RF2
Authors : Ando, Y.; Kobo, A.; Nureki, O.; Taguchi, H.; Itoh, Y.; Chadani, Y.
Deposited on : 2024-06-07
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

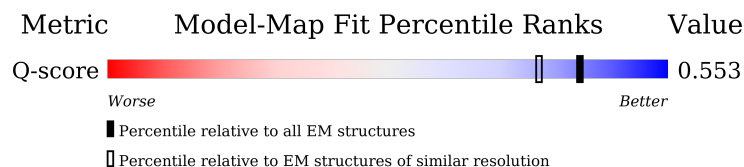
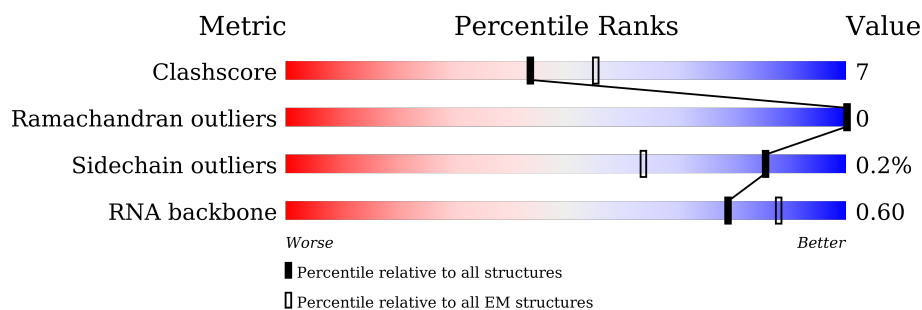
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	13054 (2.40 - 3.40)

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

Mol	Chain	Length	Quality of chain
1	A	1542	
2	B	241	
3	C	233	

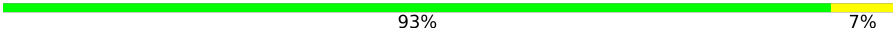
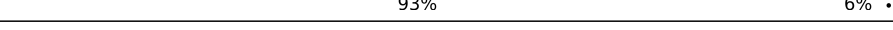
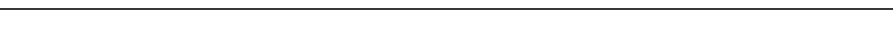
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Mol	Chain	Length	Quality of chain
4	D	206	
5	E	167	
6	F	135	
7	G	179	
8	H	130	
9	I	130	
10	J	103	
11	K	129	
12	L	124	
13	M	118	
14	N	101	
15	O	89	
16	P	82	
17	Q	84	
18	R	75	
19	S	92	
20	T	87	
21	U	71	
22	V	365	
23	W	14	
24	X	9	
25	Y	77	
26	Z	3	
27	a	2904	
28	b	120	

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Mol	Chain	Length	Quality of chain
29	c	273	 86% 13%
30	d	209	 88% 12%
31	e	201	 93% 7%
32	f	179	 78% 21%
33	g	177	 84% 14%
34	h	149	 38% 6% 55%
35	i	142	 85% 15%
36	j	123	 84% 16%
37	k	144	 85% 15%
38	l	136	 79% 21%
39	m	127	 86% 7% 7%
40	n	117	 89% 10%
41	o	115	 90% 8%
42	p	118	 93% 6%
43	q	103	 90% 10%
44	r	110	 89% 11%
45	s	100	 86% 7% 7%
46	t	104	 89% 9%
47	u	94	 77% 23%
48	v	85	 87% 5% 8%
49	w	78	 88% 10%
50	x	63	 90% 8%
51	y	59	 83% 14%
52	z	57	 84% 14%
53	0	55	 75% 18% 7%

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Mol	Chain	Length	Quality of chain
54	1	46	 93%7%
55	2	65	 78%20%
56	3	38	 87%13%
57	4	70	 59%9%33%

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 143031 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1507	Total	C	N	O	P	0	0
			32360	14439	5944	10470	1507		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	225	Total	C	N	O	S	0	0
			1758	1112	316	322	8		

- Molecule 3 is a protein called 30S ribosomal protein S3.

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

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

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

- Molecule 6 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	99	Total	C	N	O	S	0	0
			795	498	152	144	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	conflict	UNP P0A7R9

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

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

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

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

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

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

- Molecule 22 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	357	Total	C	N	O	S	0	0
			2834	1743	498	583	10		

- Molecule 23 is a protein called PepNL.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	14	Total	C	N	O	S	0	0
			108	70	17	20	1		

- Molecule 24 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	9	Total	C	N	O	P	0	0
			194	87	37	61	9		

- Molecule 25 is a RNA chain called RNA (73-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	71	Total	C	N	O	P	0	0
			1517	675	271	500	71		

- Molecule 26 is a RNA chain called RNA (5'-R(P*CP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	2	Total	C	N	O	P	0	0
			42	19	8	13	2		

- Molecule 27 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	2753	Total	C	N	O	P	0	0
			59130	26384	10897	19096	2753		

- Molecule 28 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 29 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 30 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 31 is a protein called 50S ribosomal protein L4.

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

- Molecule 32 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 33 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	174	Total	C	N	O	S	0	0
			1304	820	239	243	2		

- Molecule 34 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	67	Total	C	N	O	S	0	0
			505	322	90	92	1		

- Molecule 35 is a protein called 50S ribosomal protein L13.

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

- Molecule 36 is a protein called 50S ribosomal protein L14.

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

- Molecule 37 is a protein called 50S ribosomal protein L15.

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

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
l	82	MS6	MET	conflict	UNP P0ADY7

- Molecule 39 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 40 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 41 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 42 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 43 is a protein called 50S ribosomal protein L21.

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

- Molecule 44 is a protein called 50S ribosomal protein L22.

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

- Molecule 45 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 46 is a protein called 50S ribosomal protein L24.

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

- Molecule 47 is a protein called 50S ribosomal protein L25.

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

- Molecule 48 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	78	Total	C	N	O	S	0	0
			592	365	119	107	1		

- Molecule 49 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 50 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 51 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 52 is a protein called Large ribosomal subunit protein bL32.

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

- Molecule 53 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 54 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 55 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 56 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 57 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	4	47	Total	C	N	O	S	0	0
			364	227	64	67	6		

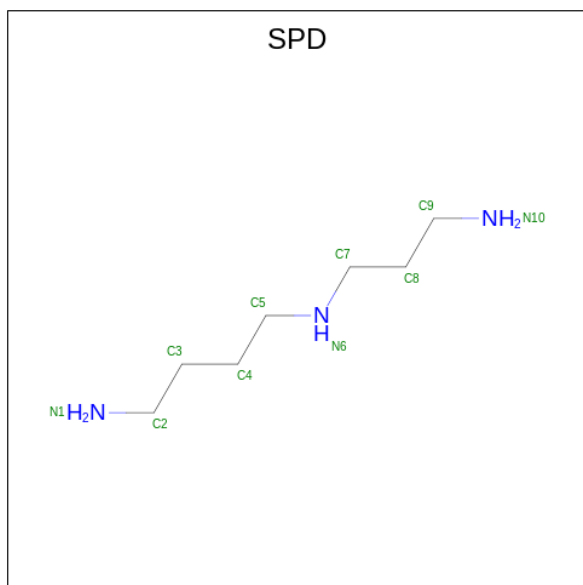
- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	A	83	Total	Mg	0
			83	83	
58	J	1	Total	Mg	0
			1	1	
58	a	209	Total	Mg	0
			209	209	
58	b	5	Total	Mg	0
			5	5	
58	d	1	Total	Mg	0
			1	1	
58	p	1	Total	Mg	0
			1	1	
58	z	1	Total	Mg	0
			1	1	

- Molecule 59 is POTASSIUM ION (CCD ID: K) (formula: K).

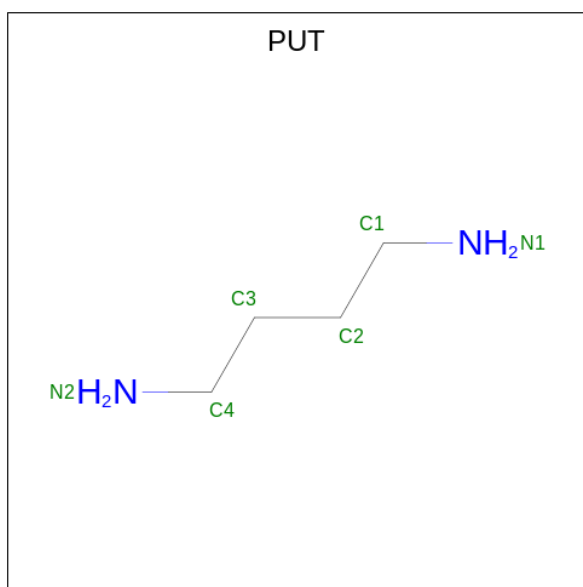
Mol	Chain	Residues	Atoms		AltConf
59	A	4	Total	K	0
			4	4	
59	D	1	Total	K	0
			1	1	
59	a	40	Total	K	0
			40	40	
59	c	2	Total	K	0
			2	2	

- Molecule 60 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			AltConf
60	a	1	Total	C	N	0
			10	7	3	
60	a	1	Total	C	N	0
			10	7	3	
60	a	1	Total	C	N	0
			10	7	3	
60	a	1	Total	C	N	0
			10	7	3	
60	a	1	Total	C	N	0
			10	7	3	
60	a	1	Total	C	N	0
			10	7	3	
60	a	1	Total	C	N	0
			10	7	3	

- Molecule 61 is 1,4-DIAMINOBTUTANE (CCD ID: PUT) (formula: $C_4H_{12}N_2$).



Mol	Chain	Residues	Atoms			AltConf
61	a	1	Total	C	N	0
			6	4	2	

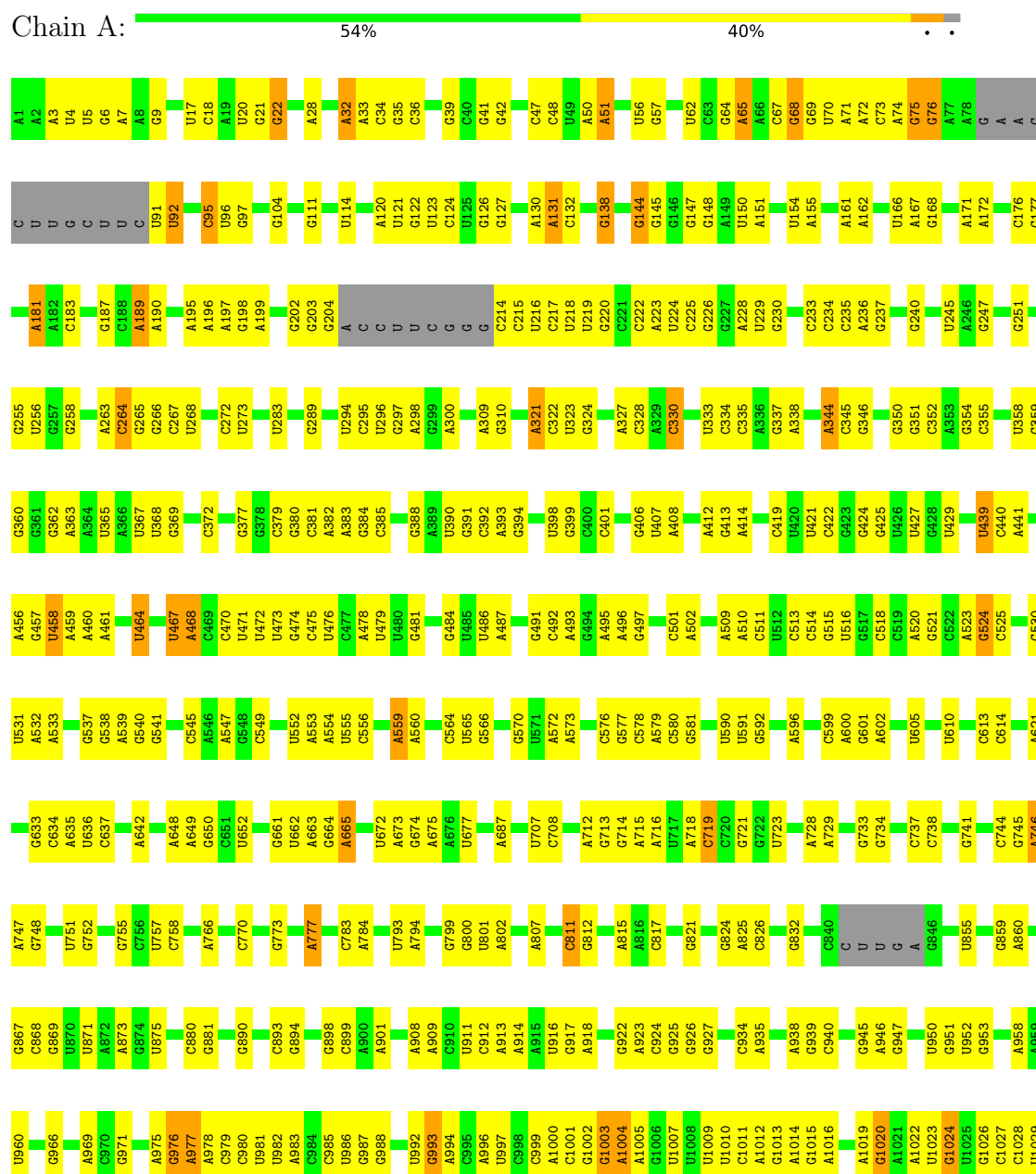
- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
62	3	1	Total	Zn	0
			1	1	
62	4	1	Total	Zn	0
			1	1	

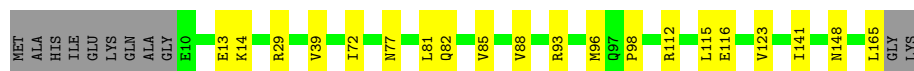
3 Residue-property plots

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: 16S rRNA

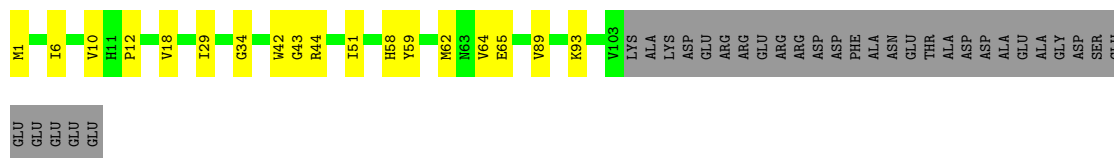


Chain E:  81% 12% 7%



- Molecule 6: 30S ribosomal protein S6, fully modified isoform

Chain F:  63% 13% 24%

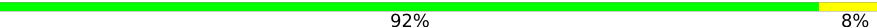


- Molecule 7: 30S ribosomal protein S7

Chain G:  79% 6% 15%



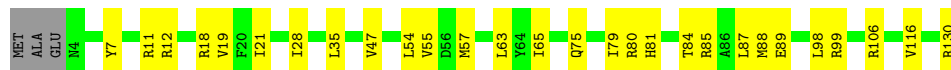
- Molecule 8: 30S ribosomal protein S8

Chain H:  92% 8% .



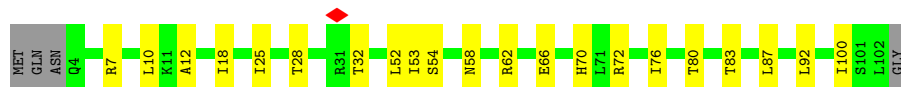
- Molecule 9: 30S ribosomal protein S9

Chain I:  76% 22% .



- Molecule 10: 30S ribosomal protein S10

Chain J:  76% 20% .

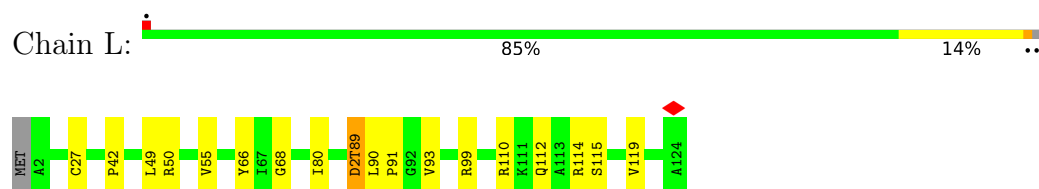


- Molecule 11: 30S ribosomal protein S11

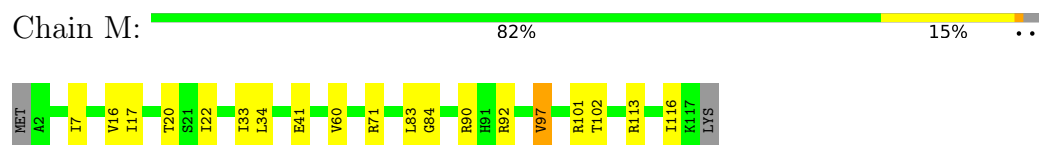
Chain K:  79% 12% 9%



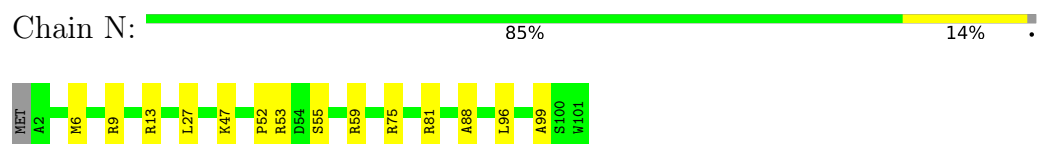
- Molecule 12: 30S ribosomal protein S12



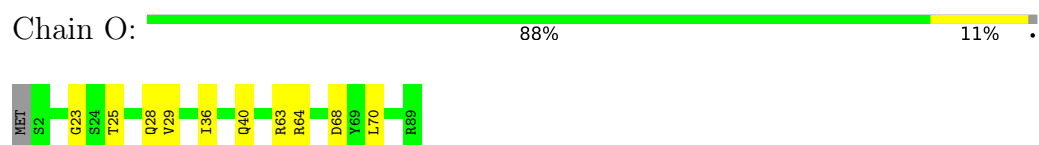
- Molecule 13: 30S ribosomal protein S13



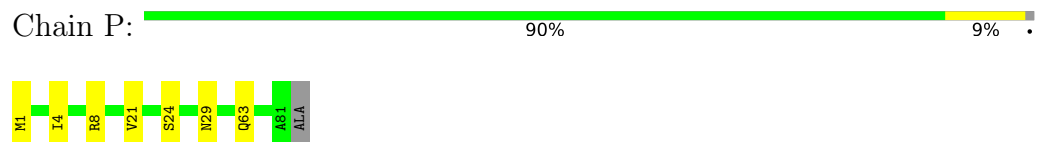
- Molecule 14: 30S ribosomal protein S14



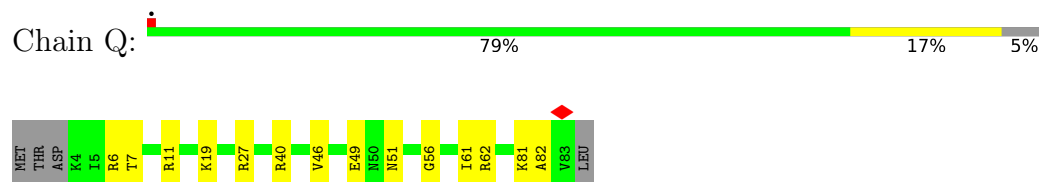
- Molecule 15: 30S ribosomal protein S15



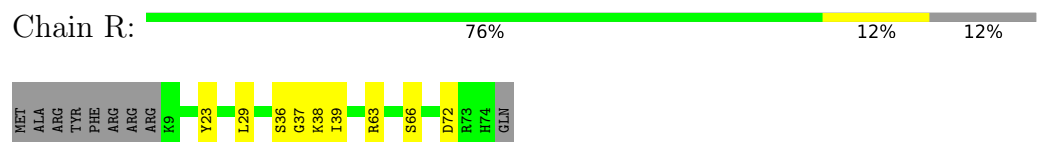
- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17



- Molecule 18: 30S ribosomal protein S18



- Molecule 19: 30S ribosomal protein S19

Chain S:  80% 11% 9%



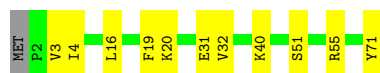
- Molecule 20: 30S ribosomal protein S20

Chain T:  87% 11% .



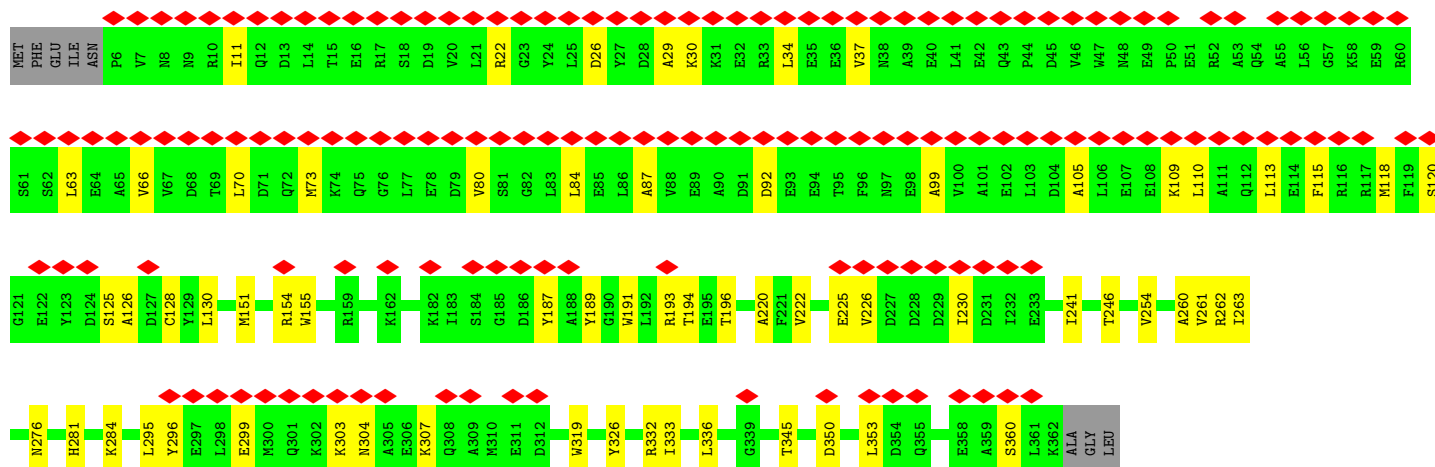
- Molecule 21: 30S ribosomal protein S21

Chain U:  83% 15% .

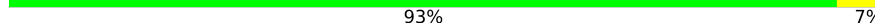


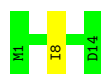
- Molecule 22: Peptide chain release factor 2

Chain V:  43% 80% 18% .



- Molecule 23: PepNL

Chain W:  93% 7%



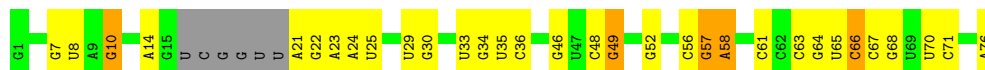
- Molecule 24: mRNA

Chain X:  89% 11%



• Molecule 25: RNA (73-MER)

Chain Y: 51% 35% 6% 8%



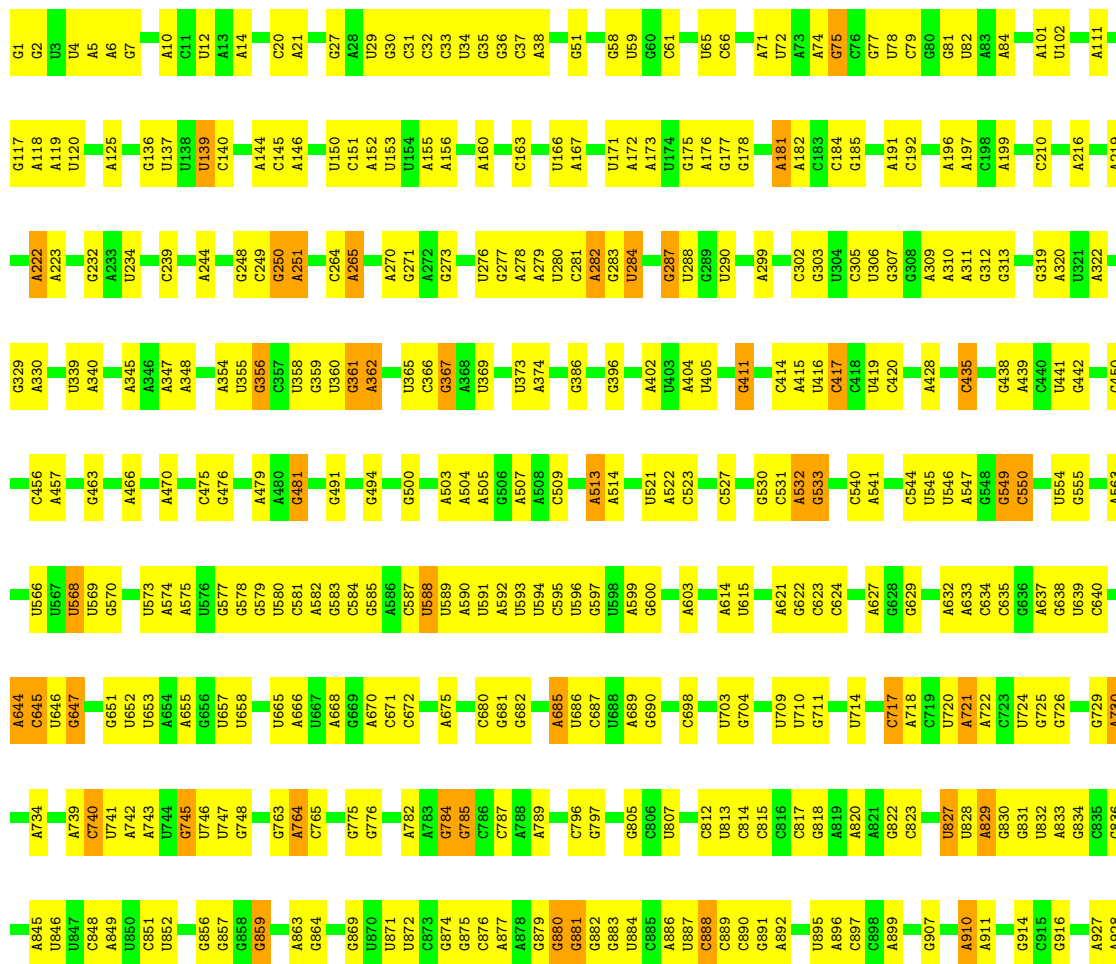
• Molecule 26: RNA (5'-R(P*CP*A)-3')

Chain Z: 67% 33%

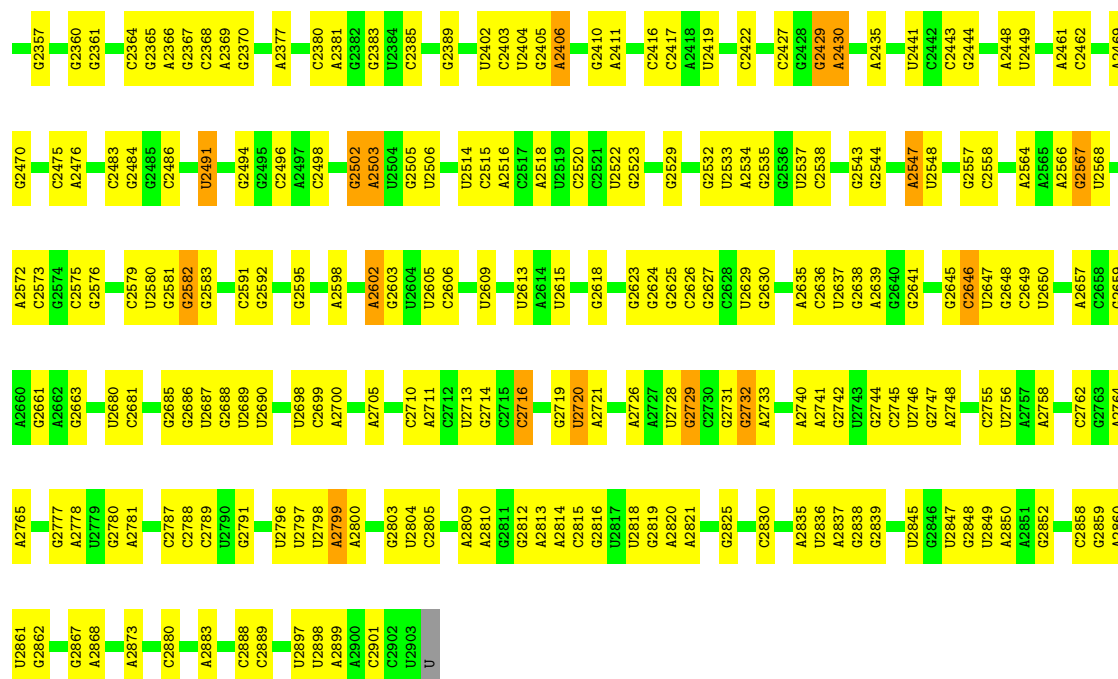


• Molecule 27: 23S rRNA

Chain a: 57% 34% 5%

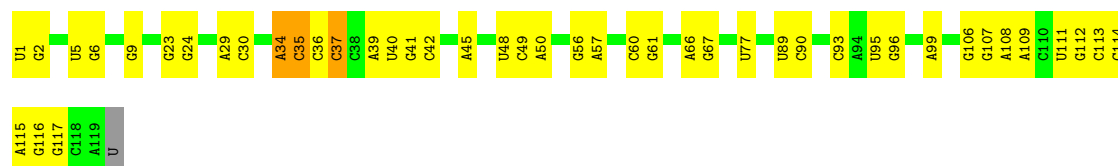


G2250	U	U2039	G1920	G1792	G1478	A1385	C1278	C1172	A	G1026	U928
G2251	A	G2040	U1923	G1793	G1482	C1386	G1279	U	A	A1027	G930
C2258	C	C2043	C1924	C1794	G1490	G1388	G1280	U	G	A1028	U931
A2266	A	C2047	A1927	U1796	A1494	A1392	U1281	A	G	A1032	U934
A2267	C	G2048	A1928	U1797	A1495	A1395	A1286	U	U	U1033	C935
C2271	C	A2051	A1929	U1798	A1496	U1396	A1287	U	A	G1036	A936
U2272	U	G2055	G1930	U1799	U1497	U1397	G1288	U	U	G1037	C937
A2273	U	G2056	A1936	A1801	C1498	C1398	U1289	U	A	G1038	C946
A2274	A	G2057	A1936	U1802	A1509	G1416	G1290	U	G	A1039	A947
U2278	U	A2058	A1952	U1715	A1510	G1417	G1291	U	C	A1040	C948
G2282	G	A2059	A1953	G1716	G1511	G1418	A1301	U	C	G1041	G949
C2283	C	A2060	A1954	U1717	C1512	G1421	G1306	U	A	G1042	A959
A2284	A	G2061	U1955	G1718	A1515	G1425	A1307	U	C	A1045	C961
C2285	C	C2062	U1956	U1719	G1516	G1426	G1308	U	G	G1046	G962
G2286	G	G2063	G1964	U1720	G1517	A1427	G1309	U	C	G1047	U963
A2287	A	C2064	C1965	U1721	C1518	C1428	G1310	U	A	A1048	C964
G2288	G	G2065	A1966	G1722	G1519	G1429	G1311	U	G	A1049	C965
C2289	C	C2066	C1967	U1723	U1520	G1430	G1312	U	A	A1050	G966
G2290	G	U2067	A1968	G1724	G1521	A1431	G1313	U	C	G1051	U967
U2291	U	A2068	A1969	U1725	A1522	G1432	U1325	U	C	C1052	C968
U2292	U	G2069	U1970	U1726	G1523	A1433	U1326	U	A		
C2293	C	C2070	A1971	G1727	G1524	G1435	U1327	U	G		
G2294	G	U2071	U1971	U1728	C1525	C1436	A1328	U	G		
U2305	U	C2072	A1987	U1729	G1526	G1437	U1329	U	A		
G2308	G	G2073	G1988	G1730	A1527	U1438	U1330	U	G		
A2311	A	U2074	U1991	G1731	U1528	A1439	U1340	U	A		
C2314	C	U2075	U1992	G1732	G1529	U1440	G1341	U	G		
G2315	G	C2076	G1993	U1733	A1535	G1441	U1342	U	A		
A2316	A	U2077	U1994	G1734	C1536	U1442	U1343	U	G		
G2317	G	G2078	C1996	A1735	G1537	U1443	U1344	U	A		
U2322	U	A2080	C1997	U1736	U1538	G1444	U1352	U	A		
A2322	A	U2081	U2011	G1737	G1539	C1447	A1353	U	G		
G2323	G	C2082	G2012	U1738	U1542	G1448	A1354	U	A		
U2324	U	U2087	A2013	G1739	U1543	U1449	G1360	U	A		
C2325	C	A2088	A2014	U1740	G1544	G1450	G1361	U	G		
A2326	A	G2093	A2015	U1741	A1548	C1451	C1362	U	C		
C2327	C	C2096	A2020	U1742	A1549	G1452	G1363	U	A		
A2328	A	U2097	C2021	U1743	A1554	U1462	A1365	U	C		
G2329	G	U2098	U2022	U1744	U1554	C1463	G1370	U	A		
U2233	U	U	C2023	C1764	C1557	G1464	G1371	U	U		
G2234	G	C	G2024	U1771	U1558	G1465	A1378	U	U		
U2334	U	A	C2025	G1772	U1559	A1469	U1379	U	A		
A2334	A	G	U2026	A1773	G1674	A1470	A1383	U	A		
G2338	G	C	A2030	U1774	A1678	U1476	U1271	U	G		
U2239	U	A	A2031	U1775	A1679	U1477	U1272	U	A		
G2240	G	C	C2032	U1776	U1679	U1478	U1273	U	A		
A2241	A	U	U2033	U1777	G1682	U1479	U1274	U	A		
U2242	U	U	A2034	A1784	U1683	G1466	U1275	U	A		
C2345	C	U	U2034	U1785	G1684	U1469	U1276	U	A		
A2346	A	G	G2035	A1786	U1689	A1470	A1264	U	A		
C2347	C	A	C2036	U1787	A1689	U1471	G1271	U	A		
U2245	U	U	U2037	A1918	G1703	U1476	U1272	U	A		
C2350	C	U	A2037	A1919	U1791	U1477	U1273	U	A		
G2351	G	U	G2038								



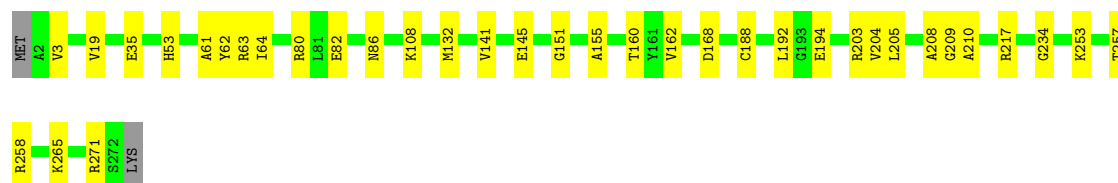
• Molecule 28: 5S rRNA

Chain b: 62% 35%



• Molecule 29: Large ribosomal subunit protein uL2

Chain c: 86% 13%



• Molecule 30: 50S ribosomal protein L3

Chain d: 88% 12%

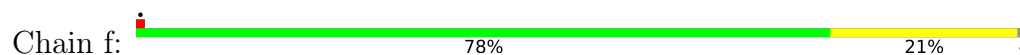


• Molecule 31: 50S ribosomal protein L4

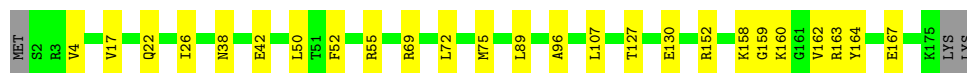
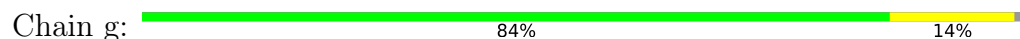
Chain e: 93% 7%



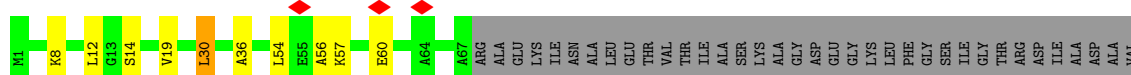
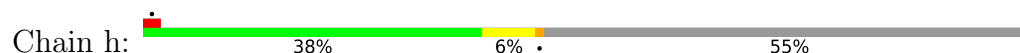
- Molecule 32: Large ribosomal subunit protein uL5



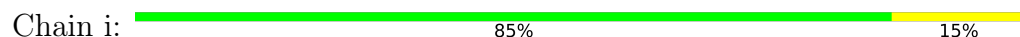
- Molecule 33: Large ribosomal subunit protein uL6



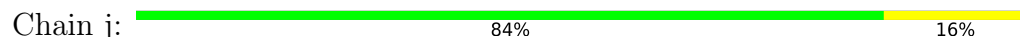
- Molecule 34: 50S ribosomal protein L9



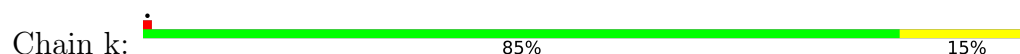
- Molecule 35: 50S ribosomal protein L13

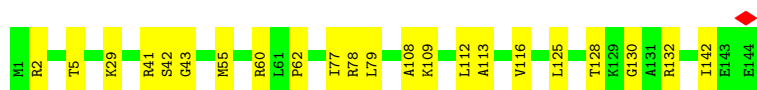


- Molecule 36: 50S ribosomal protein L14

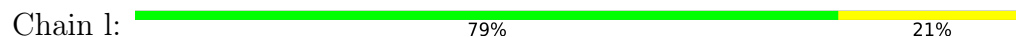


- Molecule 37: 50S ribosomal protein L15

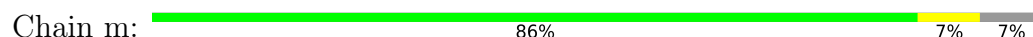




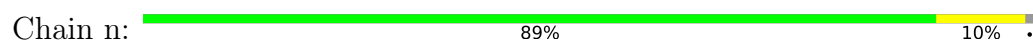
- Molecule 38: 50S ribosomal protein L16



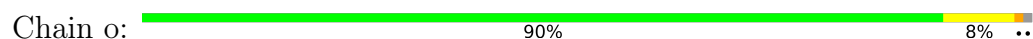
- Molecule 39: Large ribosomal subunit protein bL17



- Molecule 40: Large ribosomal subunit protein uL18



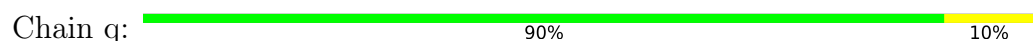
- Molecule 41: Large ribosomal subunit protein bL19



- Molecule 42: Large ribosomal subunit protein bL20



- Molecule 43: 50S ribosomal protein L21



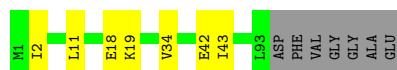
- Molecule 44: 50S ribosomal protein L22





- Molecule 45: Large ribosomal subunit protein uL23

Chain s: 86% 7% 7%



- Molecule 46: 50S ribosomal protein L24

Chain t: 89% 9% .



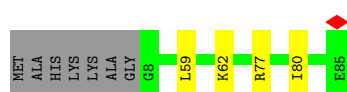
- Molecule 47: 50S ribosomal protein L25

Chain u: 77% 23%



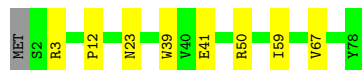
- Molecule 48: Large ribosomal subunit protein bL27

Chain v: 87% 5% 8%



- Molecule 49: Large ribosomal subunit protein bL28

Chain w: 88% 10% .



- Molecule 50: Large ribosomal subunit protein uL29

Chain x: 90% 8% .



- Molecule 51: Large ribosomal subunit protein uL30

Chain y: 83% 14% . .



- Molecule 52: Large ribosomal subunit protein bL32

Chain z: 84% 14% .



- Molecule 53: Large ribosomal subunit protein bL33

Chain 0: 75% 18% 7%



- Molecule 54: 50S ribosomal protein L34

Chain 1: 93% 7%



- Molecule 55: Large ribosomal subunit protein bL35

Chain 2: 78% 20% .



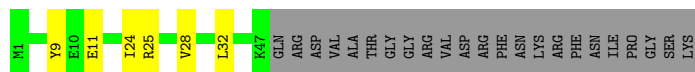
- Molecule 56: 50S ribosomal protein L36

Chain 3: 87% 13%



- Molecule 57: 50S ribosomal protein L31

Chain 4: 59% 9% 33%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	71980	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.916	Depositor
Minimum map value	-0.507	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	358.56, 358.56, 358.56	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SPD, MA6, 4OC, 2MG, D2T, 5MU, MEQ, PSU, G7M, OMG, 5MC, OMU, 4D4, H2U, PUT, MS6, K, 6MZ, 1MG, 2MA, MG, IAS, ZN, FME, UR3, 3TD, OMC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.10	0/35954	0.23	0/56077
2	B	0.08	0/1789	0.22	0/2410
3	C	0.08	0/1651	0.21	0/2225
4	D	0.08	0/1665	0.20	0/2227
5	E	0.09	0/1165	0.22	0/1568
6	F	0.08	0/858	0.20	0/1160
7	G	0.08	0/1219	0.20	0/1635
8	H	0.08	0/989	0.22	0/1326
9	I	0.08	0/1034	0.22	0/1375
10	J	0.10	0/805	0.27	0/1089
11	K	0.10	0/884	0.20	0/1191
12	L	0.08	0/960	0.22	0/1286
13	M	0.08	0/909	0.23	0/1215
14	N	0.07	0/817	0.18	0/1088
15	O	0.08	0/722	0.20	0/964
16	P	0.08	0/653	0.24	0/877
17	Q	0.08	0/657	0.22	0/881
18	R	0.08	0/553	0.20	0/742
19	S	0.07	0/685	0.19	0/922
20	T	0.08	0/676	0.19	0/895
21	U	0.07	0/597	0.19	0/792
22	V	0.08	0/2863	0.24	0/3855
23	W	0.32	0/99	0.42	0/133
24	X	0.08	0/217	0.25	0/336
25	Y	0.12	0/1693	0.30	0/2636
26	Z	0.05	0/46	0.11	0/69
27	a	0.10	0/65651	0.23	0/102413
28	b	0.08	0/2850	0.21	0/4444
29	c	0.09	0/2121	0.24	0/2852
30	d	0.09	0/1576	0.22	0/2119
31	e	0.08	0/1571	0.21	0/2113

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	f	0.09	0/1434	0.23	0/1926
33	g	0.08	0/1324	0.20	0/1794
34	h	0.09	0/510	0.25	0/687
35	i	0.08	0/1152	0.20	0/1551
36	j	0.08	0/955	0.22	0/1279
37	k	0.08	0/1062	0.23	0/1413
38	l	0.08	0/1073	0.22	0/1433
39	m	0.09	0/958	0.26	0/1281
40	n	0.08	0/902	0.21	0/1209
41	o	0.09	0/929	0.20	0/1242
42	p	0.09	0/960	0.20	0/1278
43	q	0.08	0/829	0.20	0/1107
44	r	0.08	0/864	0.20	0/1156
45	s	0.08	0/744	0.21	0/994
46	t	0.07	0/787	0.21	0/1051
47	u	0.08	0/766	0.24	0/1025
48	v	0.08	0/599	0.22	0/792
49	w	0.09	0/635	0.22	0/848
50	x	0.06	0/502	0.15	0/667
51	y	0.08	0/453	0.19	0/605
52	z	0.09	0/450	0.22	0/599
53	0	0.08	0/424	0.21	0/565
54	1	0.08	0/380	0.23	0/498
55	2	0.08	0/513	0.24	0/676
56	3	0.08	0/303	0.22	0/397
57	4	0.07	0/371	0.20	0/496
All	All	0.09	0/153808	0.23	0/229484

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32360	0	16305	417	0
2	B	1758	0	1782	11	0
3	C	1624	0	1696	20	0
4	D	1643	0	1707	23	0
5	E	1152	0	1196	12	0
6	F	839	0	833	11	0
7	G	1203	0	1254	6	0
8	H	979	0	1031	8	0
9	I	1022	0	1070	20	0
10	J	795	0	836	17	0
11	K	877	0	884	10	0
12	L	957	0	1017	16	0
13	M	900	0	965	14	0
14	N	805	0	844	13	0
15	O	714	0	734	5	0
16	P	643	0	661	5	0
17	Q	648	0	691	8	0
18	R	544	0	565	6	0
19	S	668	0	693	6	0
20	T	670	0	719	6	0
21	U	589	0	629	7	0
22	V	2834	0	2731	39	0
23	W	108	0	112	1	0
24	X	194	0	98	0	0
25	Y	1517	0	768	17	0
26	Z	42	0	23	0	0
27	a	59130	0	29761	669	0
28	b	2549	0	1291	34	0
29	c	2082	0	2154	26	0
30	d	1566	0	1617	17	0
31	e	1552	0	1619	9	0
32	f	1410	0	1444	25	0
33	g	1304	0	1345	14	0
34	h	505	0	532	5	0
35	i	1129	0	1162	14	0
36	j	946	0	1023	12	0
37	k	1053	0	1129	14	0
38	l	1075	0	1145	17	0
39	m	945	0	989	4	0
40	n	892	0	923	8	0
41	o	917	0	962	9	0
42	p	947	0	1019	6	0
43	q	816	0	839	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	r	857	0	922	7	0
45	s	738	0	807	5	0
46	t	779	0	831	5	0
47	u	753	0	780	13	0
48	v	592	0	607	3	0
49	w	625	0	652	5	0
50	x	501	0	531	3	0
51	y	449	0	488	5	0
52	z	444	0	458	5	0
53	0	417	0	451	7	0
54	1	377	0	418	3	0
55	2	504	0	572	9	0
56	3	302	0	340	4	0
57	4	364	0	362	4	0
58	A	83	0	0	0	0
58	J	1	0	0	0	0
58	a	209	0	0	0	0
58	b	5	0	0	0	0
58	d	1	0	0	0	0
58	p	1	0	0	0	0
58	z	1	0	0	0	0
59	A	4	0	0	0	0
59	D	1	0	0	0	0
59	a	40	0	0	0	0
59	c	2	0	0	0	0
60	a	70	0	133	3	0
61	a	6	0	12	0	0
62	3	1	0	0	0	0
62	4	1	0	0	0	0
All	All	143031	0	97162	1517	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 7.

The worst 5 of 1517 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)
27:a:881:G:H1	27:a:895:U:H3	1.28	0.82
1:A:111:G:H1	1:A:330:C:H41	1.27	0.80
1:A:1124:G:N2	1:A:1125:U:O4	2.16	0.76
1:A:1149:C:H2'	1:A:1150:A:H8	1.51	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:284:U:H3	27:a:356:G:H1	1.35	0.74

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	B	223/241 (92%)	220 (99%)	3 (1%)	0	100	100
3	C	204/233 (88%)	200 (98%)	4 (2%)	0	100	100
4	D	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
5	E	154/167 (92%)	153 (99%)	1 (1%)	0	100	100
6	F	101/135 (75%)	100 (99%)	1 (1%)	0	100	100
7	G	151/179 (84%)	148 (98%)	3 (2%)	0	100	100
8	H	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
9	I	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
10	J	97/103 (94%)	96 (99%)	1 (1%)	0	100	100
11	K	113/129 (88%)	111 (98%)	2 (2%)	0	100	100
12	L	120/124 (97%)	118 (98%)	2 (2%)	0	100	100
13	M	114/118 (97%)	111 (97%)	3 (3%)	0	100	100
14	N	98/101 (97%)	98 (100%)	0	0	100	100
15	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
16	P	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
17	Q	78/84 (93%)	77 (99%)	1 (1%)	0	100	100
18	R	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	S	82/92 (89%)	82 (100%)	0	0	100	100
20	T	84/87 (97%)	84 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	U	68/71 (96%)	67 (98%)	1 (2%)	0	100	100
22	V	354/365 (97%)	350 (99%)	4 (1%)	0	100	100
23	W	12/14 (86%)	12 (100%)	0	0	100	100
29	c	269/273 (98%)	263 (98%)	6 (2%)	0	100	100
30	d	206/209 (99%)	202 (98%)	4 (2%)	0	100	100
31	e	199/201 (99%)	199 (100%)	0	0	100	100
32	f	175/179 (98%)	173 (99%)	2 (1%)	0	100	100
33	g	172/177 (97%)	169 (98%)	3 (2%)	0	100	100
34	h	65/149 (44%)	64 (98%)	1 (2%)	0	100	100
35	i	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
36	j	121/123 (98%)	120 (99%)	1 (1%)	0	100	100
37	k	142/144 (99%)	140 (99%)	2 (1%)	0	100	100
38	l	132/136 (97%)	132 (100%)	0	0	100	100
39	m	116/127 (91%)	113 (97%)	3 (3%)	0	100	100
40	n	114/117 (97%)	111 (97%)	3 (3%)	0	100	100
41	o	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
42	p	115/118 (98%)	115 (100%)	0	0	100	100
43	q	101/103 (98%)	101 (100%)	0	0	100	100
44	r	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
45	s	91/100 (91%)	91 (100%)	0	0	100	100
46	t	100/104 (96%)	98 (98%)	2 (2%)	0	100	100
47	u	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
48	v	76/85 (89%)	76 (100%)	0	0	100	100
49	w	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
50	x	60/63 (95%)	60 (100%)	0	0	100	100
51	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
52	z	54/57 (95%)	54 (100%)	0	0	100	100
53	0	49/55 (89%)	49 (100%)	0	0	100	100
54	1	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
55	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
56	3	36/38 (95%)	36 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	4	45/70 (64%)	45 (100%)	0	0	100	100
All	All	5864/6292 (93%)	5786 (99%)	78 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	B	186/199 (94%)	186 (100%)	0	100	100
3	C	170/190 (90%)	170 (100%)	0	100	100
4	D	172/173 (99%)	172 (100%)	0	100	100
5	E	119/126 (94%)	119 (100%)	0	100	100
6	F	90/116 (78%)	90 (100%)	0	100	100
7	G	126/147 (86%)	126 (100%)	0	100	100
8	H	104/105 (99%)	104 (100%)	0	100	100
9	I	105/107 (98%)	105 (100%)	0	100	100
10	J	87/90 (97%)	86 (99%)	1 (1%)	65	88
11	K	89/98 (91%)	89 (100%)	0	100	100
12	L	102/103 (99%)	102 (100%)	0	100	100
13	M	94/96 (98%)	93 (99%)	1 (1%)	65	88
14	N	83/84 (99%)	83 (100%)	0	100	100
15	O	76/77 (99%)	76 (100%)	0	100	100
16	P	65/65 (100%)	65 (100%)	0	100	100
17	Q	74/78 (95%)	73 (99%)	1 (1%)	59	85
18	R	57/65 (88%)	57 (100%)	0	100	100
19	S	72/79 (91%)	72 (100%)	0	100	100
20	T	65/66 (98%)	65 (100%)	0	100	100
21	U	60/61 (98%)	59 (98%)	1 (2%)	53	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	V	303/310 (98%)	303 (100%)	0	100	100
23	W	10/10 (100%)	10 (100%)	0	100	100
29	c	216/218 (99%)	216 (100%)	0	100	100
30	d	163/163 (100%)	163 (100%)	0	100	100
31	e	165/165 (100%)	165 (100%)	0	100	100
32	f	148/150 (99%)	148 (100%)	0	100	100
33	g	135/138 (98%)	135 (100%)	0	100	100
34	h	50/114 (44%)	49 (98%)	1 (2%)	48	78
35	i	116/116 (100%)	115 (99%)	1 (1%)	70	90
36	j	104/104 (100%)	104 (100%)	0	100	100
37	k	103/103 (100%)	103 (100%)	0	100	100
38	l	107/107 (100%)	106 (99%)	1 (1%)	70	90
39	m	98/103 (95%)	97 (99%)	1 (1%)	68	89
40	n	86/87 (99%)	86 (100%)	0	100	100
41	o	99/100 (99%)	98 (99%)	1 (1%)	68	89
42	p	89/90 (99%)	89 (100%)	0	100	100
43	q	84/84 (100%)	84 (100%)	0	100	100
44	r	93/93 (100%)	93 (100%)	0	100	100
45	s	80/84 (95%)	80 (100%)	0	100	100
46	t	83/85 (98%)	83 (100%)	0	100	100
47	u	78/78 (100%)	78 (100%)	0	100	100
48	v	59/63 (94%)	59 (100%)	0	100	100
49	w	67/68 (98%)	67 (100%)	0	100	100
50	x	54/55 (98%)	54 (100%)	0	100	100
51	y	48/49 (98%)	47 (98%)	1 (2%)	47	77
52	z	47/48 (98%)	47 (100%)	0	100	100
53	0	46/49 (94%)	46 (100%)	0	100	100
54	1	38/38 (100%)	38 (100%)	0	100	100
55	2	51/52 (98%)	51 (100%)	0	100	100
56	3	34/34 (100%)	34 (100%)	0	100	100
57	4	43/62 (69%)	43 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4893/5145 (95%)	4883 (100%)	10 (0%)	85 96

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	m	98	LEU
41	o	52	ASN
51	y	7	ILE
21	U	40	LYS
34	h	30	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
31	e	115	GLN
39	m	31	HIS
32	f	27	GLN
35	i	80	HIS
42	p	52	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1503/1542 (97%)	197 (13%)	2 (0%)
24	X	8/9 (88%)	1 (12%)	0
25	Y	69/77 (89%)	14 (20%)	1 (1%)
26	Z	1/3 (33%)	0	0
27	a	2749/2904 (94%)	356 (12%)	0
28	b	118/120 (98%)	12 (10%)	0
All	All	4448/4655 (95%)	580 (13%)	3 (0%)

5 of 580 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	A
1	A	9	G
1	A	22	G
1	A	32	A
1	A	39	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	120	A
1	A	264	C
25	Y	57	G

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

42 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	$\# Z > 2$
27	PSU	a	2504	59,27	18,21,22	0.49	0	22,30,33	0.56	0
27	PSU	a	2457	27	18,21,22	0.48	0	22,30,33	0.58	0
1	4OC	A	1402	1	20,23,24	0.32	0	26,32,35	0.46	0
23	FME	W	1	23	8,9,10	0.51	0	7,9,11	0.44	0
27	PSU	a	2580	58,27	18,21,22	0.52	0	22,30,33	0.62	1 (4%)
27	OMG	a	2251	59,25,27	23,26,27	0.28	0	33,38,41	0.38	0
27	OMC	a	2498	58,27	19,22,23	0.28	0	26,31,34	0.41	0
1	2MG	A	1516	1	23,26,27	0.28	0	32,38,41	0.38	0
27	PSU	a	2604	27	18,21,22	0.45	0	22,30,33	0.58	0
27	PSU	a	955	59,27	18,21,22	0.56	0	22,30,33	0.59	0
27	5MU	a	1939	59,27	19,22,23	0.28	0	28,32,35	0.38	0
27	2MG	a	2445	27	23,26,27	0.30	0	32,38,41	0.34	0
1	5MC	A	1407	1	18,22,23	0.30	0	26,32,35	0.46	0
27	PSU	a	2605	27	18,21,22	0.56	0	22,30,33	0.63	0
27	6MZ	a	2030	27	22,25,26	0.29	0	30,36,39	0.41	0
1	G7M	A	527	1	23,26,27	0.34	0	35,39,42	0.47	0
27	6MZ	a	1618	27	22,25,26	0.26	0	30,36,39	0.42	0
11	IAS	K	119	11	6,7,8	0.87	0	6,8,10	0.95	0
27	PSU	a	746	58,27	18,21,22	0.57	1 (5%)	22,30,33	0.67	1 (4%)
27	H2U	a	2449	27	18,21,22	0.45	0	21,30,33	1.02	1 (4%)
12	D2T	L	89	12	7,9,10	0.90	0	6,11,13	1.63	2 (33%)
22	MEQ	V	252	22	8,9,10	0.90	0	5,10,12	0.44	0
30	MEQ	d	150	30	8,9,10	0.88	0	5,10,12	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	5MC	a	1962	59,27	18,22,23	0.28	0	26,32,35	0.46	0
27	2MA	a	2503	58,27	22,25,26	0.95	1 (4%)	33,37,40	1.33	3 (9%)
27	G7M	a	2069	59,27	23,26,27	0.35	0	35,39,42	0.50	0
1	5MC	A	967	1	18,22,23	0.30	0	26,32,35	0.44	0
27	3TD	a	1915	27	18,22,23	0.46	0	22,32,35	0.58	0
38	MS6	l	82	38	5,7,8	0.29	0	2,7,9	0.10	0
27	2MG	a	1835	27	23,26,27	0.27	0	32,38,41	0.33	0
27	OMU	a	2552	27	19,22,23	0.28	0	26,31,34	0.42	0
38	4D4	l	81	38	9,11,12	0.85	0	8,13,15	1.94	3 (37%)
1	UR3	A	1498	1	19,22,23	0.28	0	26,32,35	0.37	0
1	PSU	A	516	1,58	18,21,22	0.52	0	22,30,33	0.65	1 (4%)
1	MA6	A	1519	1	23,26,27	0.32	0	34,38,41	0.63	1 (2%)
27	5MU	a	747	27	19,22,23	0.29	0	28,32,35	0.33	0
27	PSU	a	1917	27	18,21,22	0.51	0	22,30,33	0.55	0
27	PSU	a	1911	27	18,21,22	0.46	0	22,30,33	0.58	0
27	1MG	a	745	27	22,26,27	0.28	0	33,39,42	0.59	1 (3%)
1	2MG	A	966	1	23,26,27	0.29	0	32,38,41	0.35	0
1	MA6	A	1518	1	23,26,27	0.29	0	34,38,41	0.60	1 (2%)
1	2MG	A	1207	1	23,26,27	0.27	0	32,38,41	0.34	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
27	PSU	a	2504	59,27	-	2/7/25/26	0/2/2/2
27	PSU	a	2457	27	-	0/7/25/26	0/2/2/2
1	4OC	A	1402	1	-	0/9/29/30	0/2/2/2
23	FME	W	1	23	-	3/7/9/11	-
27	PSU	a	2580	58,27	-	0/7/25/26	0/2/2/2
27	OMG	a	2251	59,25,27	-	1/9/27/28	0/3/3/3
27	OMC	a	2498	58,27	-	0/9/27/28	0/2/2/2
1	2MG	A	1516	1	-	0/9/27/28	0/3/3/3
27	PSU	a	2604	27	-	0/7/25/26	0/2/2/2
27	PSU	a	955	59,27	-	0/7/25/26	0/2/2/2
27	5MU	a	1939	59,27	-	0/7/25/26	0/2/2/2
27	2MG	a	2445	27	-	0/9/27/28	0/3/3/3
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
27	PSU	a	2605	27	-	0/7/25/26	0/2/2/2
27	6MZ	a	2030	27	-	3/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	G7M	A	527	1	-	2/7/25/26	0/3/3/3
27	6MZ	a	1618	27	-	0/9/27/28	0/3/3/3
11	IAS	K	119	11	-	2/7/7/8	-
27	PSU	a	746	58,27	-	1/7/25/26	0/2/2/2
27	H2U	a	2449	27	-	0/7/38/39	0/2/2/2
12	D2T	L	89	12	-	2/7/12/14	-
22	MEQ	V	252	22	-	4/8/9/11	-
30	MEQ	d	150	30	-	3/8/9/11	-
27	5MC	a	1962	59,27	-	0/7/25/26	0/2/2/2
27	2MA	a	2503	58,27	-	1/7/25/26	0/3/3/3
27	G7M	a	2069	59,27	-	1/7/25/26	0/3/3/3
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
27	3TD	a	1915	27	-	0/7/25/26	0/2/2/2
38	MS6	l	82	38	-	1/4/6/8	-
27	2MG	a	1835	27	-	0/9/27/28	0/3/3/3
27	OMU	a	2552	27	-	0/9/27/28	0/2/2/2
38	4D4	l	81	38	-	5/11/12/14	-
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
1	PSU	A	516	1,58	-	0/7/25/26	0/2/2/2
1	MA6	A	1519	1	-	4/11/29/30	0/3/3/3
27	5MU	a	747	27	-	0/7/25/26	0/2/2/2
27	PSU	a	1917	27	-	0/7/25/26	0/2/2/2
27	PSU	a	1911	27	-	0/7/25/26	0/2/2/2
27	1MG	a	745	27	-	0/7/25/26	0/3/3/3
1	2MG	A	966	1	-	0/9/27/28	0/3/3/3
1	MA6	A	1518	1	-	3/11/29/30	0/3/3/3
1	2MG	A	1207	1	-	0/9/27/28	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	a	2503	2MA	C6-N6	-3.13	1.26	1.34
27	a	746	PSU	O4'-C1'	-2.08	1.41	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	a	2503	2MA	N6-C6-N1	4.50	123.39	117.03
38	l	81	4D4	NE-CZ-NH2	3.95	127.65	120.70
27	a	2503	2MA	C2-N1-C6	3.83	124.05	118.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	a	2503	2MA	C5-C6-N1	-3.54	112.90	119.01
27	a	2449	H2U	C5-C4-N3	-3.12	113.14	116.65

There are no chirality outliers.

5 of 38 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1518	MA6	C5-C6-N6-C9
1	A	1518	MA6	C5-C6-N6-C10
1	A	1519	MA6	C5-C6-N6-C10
38	l	81	4D4	N-CA-CB-CG
38	l	81	4D4	NH2-CZ-NE-CD

There are no ring outliers.

10 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1402	4OC	1	0
27	a	2251	OMG	1	0
1	A	1407	5MC	1	0
27	a	2605	PSU	1	0
27	a	2030	6MZ	2	0
12	L	89	D2T	3	0
27	a	2503	2MA	1	0
27	a	745	1MG	1	0
1	A	966	2MG	1	0
1	A	1518	MA6	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 358 ligands modelled in this entry, 350 are monoatomic - leaving 8 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	SPD	a	6195	-	9,9,9	0.29	0	8,8,8	0.83	0
60	SPD	a	6199	-	9,9,9	0.20	0	8,8,8	0.81	0
60	SPD	a	6198	-	9,9,9	0.23	0	8,8,8	0.88	0
60	SPD	a	6194	-	9,9,9	0.27	0	8,8,8	0.86	0
61	PUT	a	6200	-	5,5,5	0.13	0	4,4,4	0.15	0
60	SPD	a	6193	-	9,9,9	0.27	0	8,8,8	0.86	0
60	SPD	a	6197	-	9,9,9	0.23	0	8,8,8	0.89	0
60	SPD	a	6196	-	9,9,9	0.24	0	8,8,8	0.83	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	SPD	a	6195	-	-	0/7/7/7	-
60	SPD	a	6199	-	-	0/7/7/7	-
60	SPD	a	6198	-	-	0/7/7/7	-
60	SPD	a	6194	-	-	0/7/7/7	-
61	PUT	a	6200	-	-	0/3/3/3	-
60	SPD	a	6193	-	-	0/7/7/7	-
60	SPD	a	6197	-	-	2/7/7/7	-
60	SPD	a	6196	-	-	1/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	a	6196	SPD	N6-C7-C8-C9
60	a	6197	SPD	N6-C7-C8-C9
60	a	6197	SPD	C3-C4-C5-N6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	a	6193	SPD	1	0
60	a	6197	SPD	2	0

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.

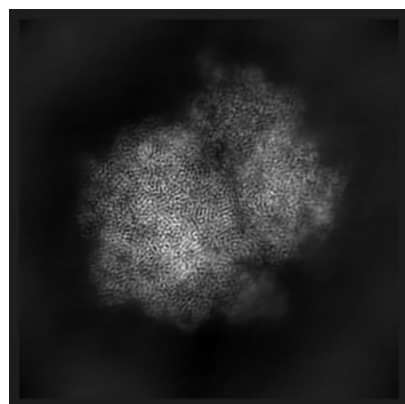
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60474. These allow visual inspection of the internal detail of the map and identification of artifacts.

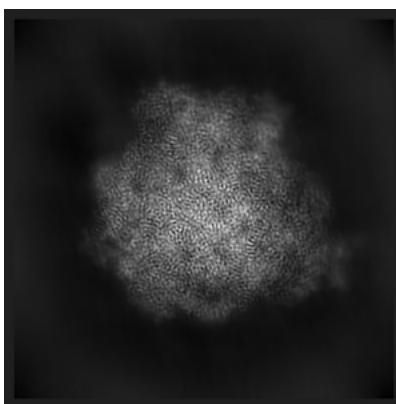
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

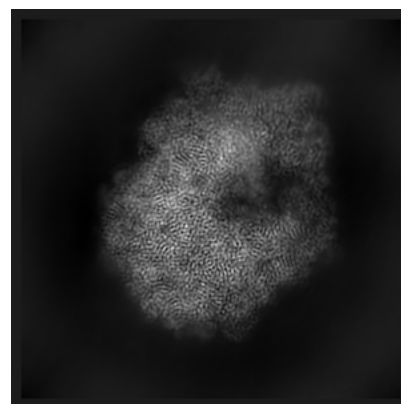
6.1.1 Primary map



X

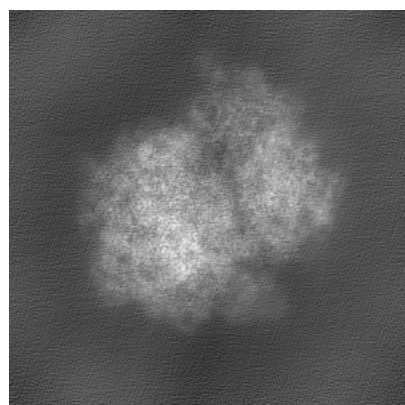


Y

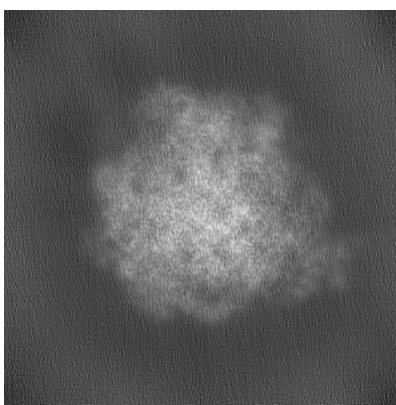


Z

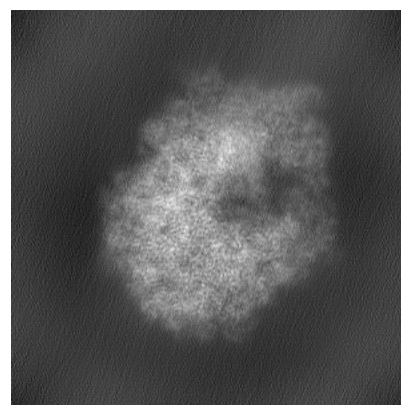
6.1.2 Raw map



X



Y

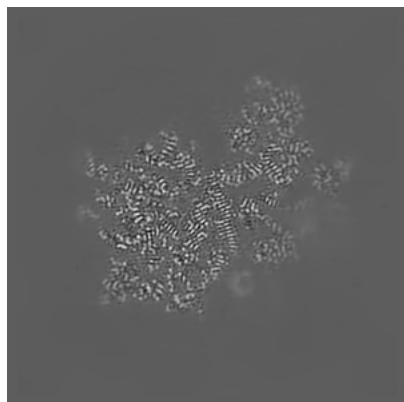


Z

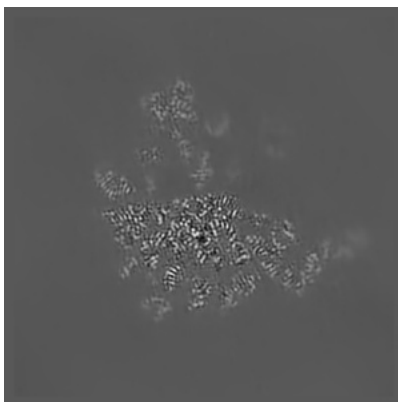
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

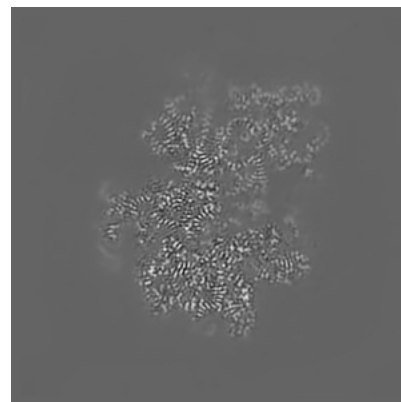
6.2.1 Primary map



X Index: 216

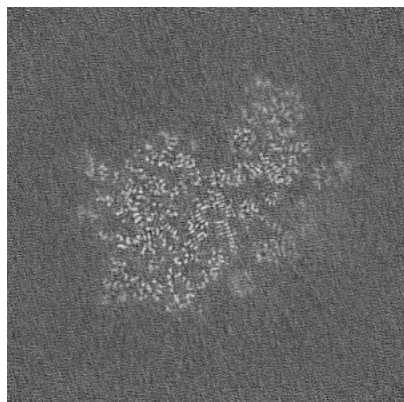


Y Index: 216

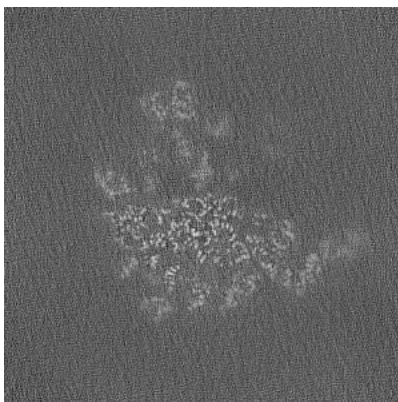


Z Index: 216

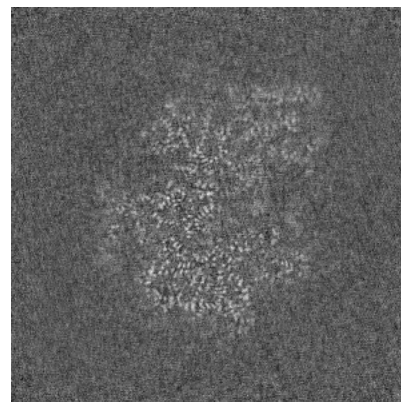
6.2.2 Raw map



X Index: 216



Y Index: 216

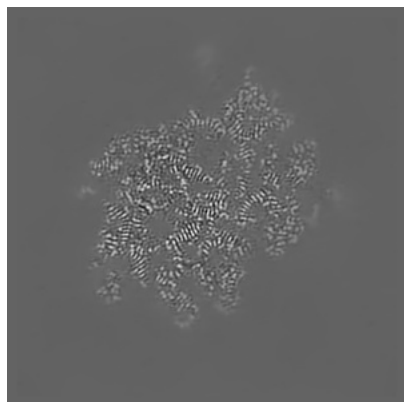


Z Index: 216

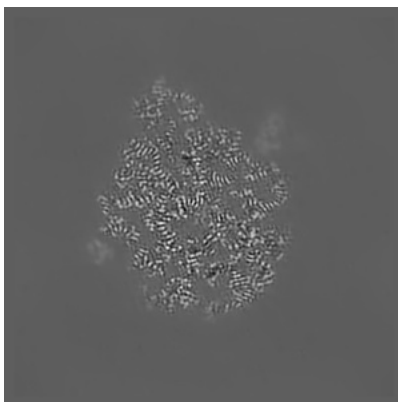
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

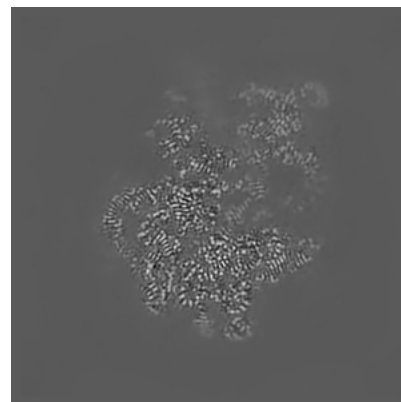
6.3.1 Primary map



X Index: 186

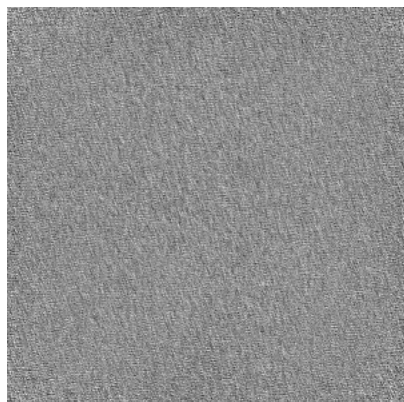


Y Index: 177

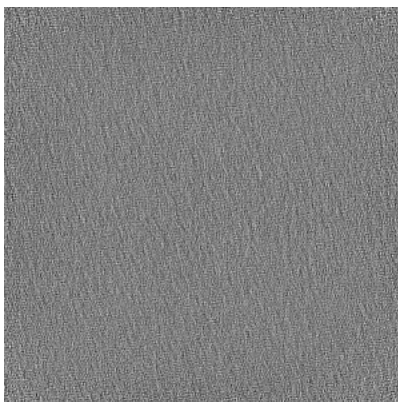


Z Index: 208

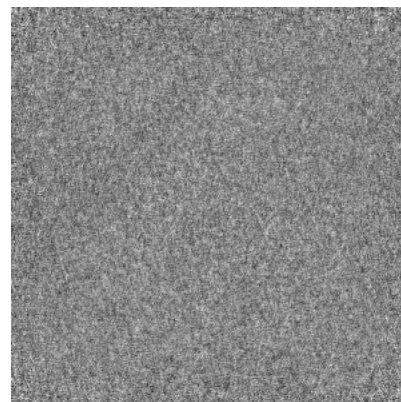
6.3.2 Raw map



X Index: 0



Y Index: 0

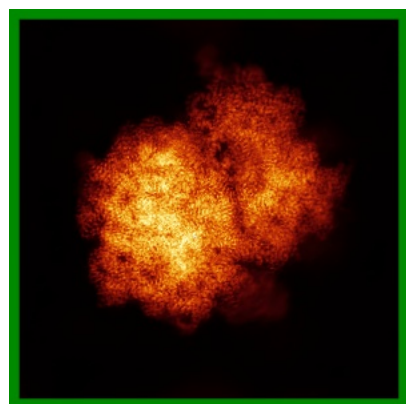


Z Index: 0

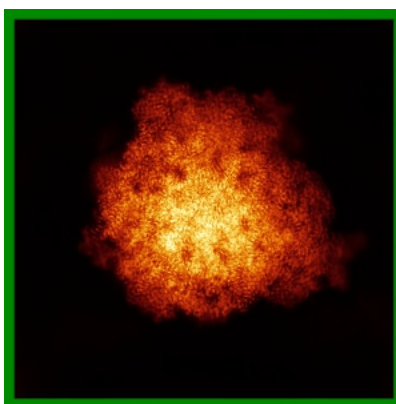
The images above show the largest variance slices of the map in three orthogonal directions.

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

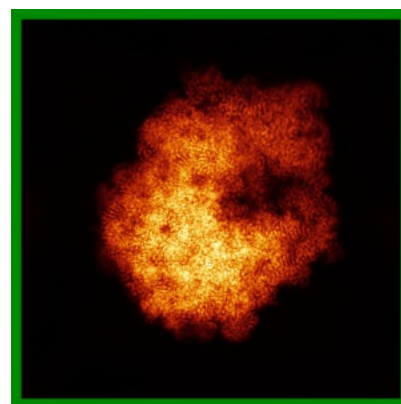
6.4.1 Primary map



X

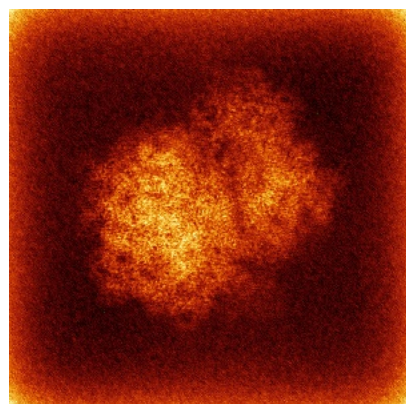


Y

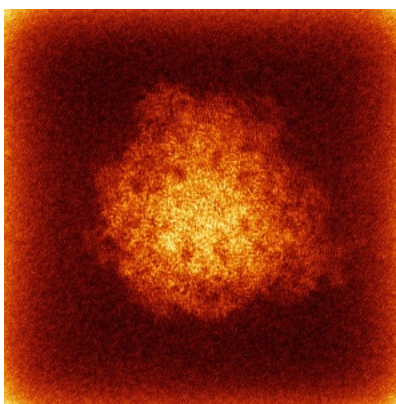


Z

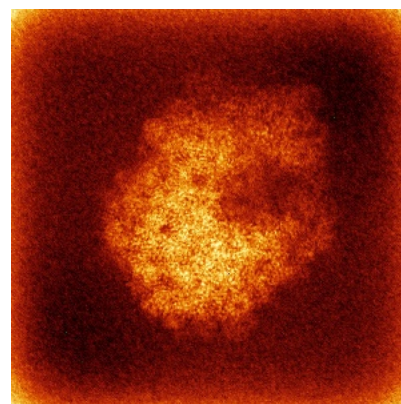
6.4.2 Raw map



X



Y

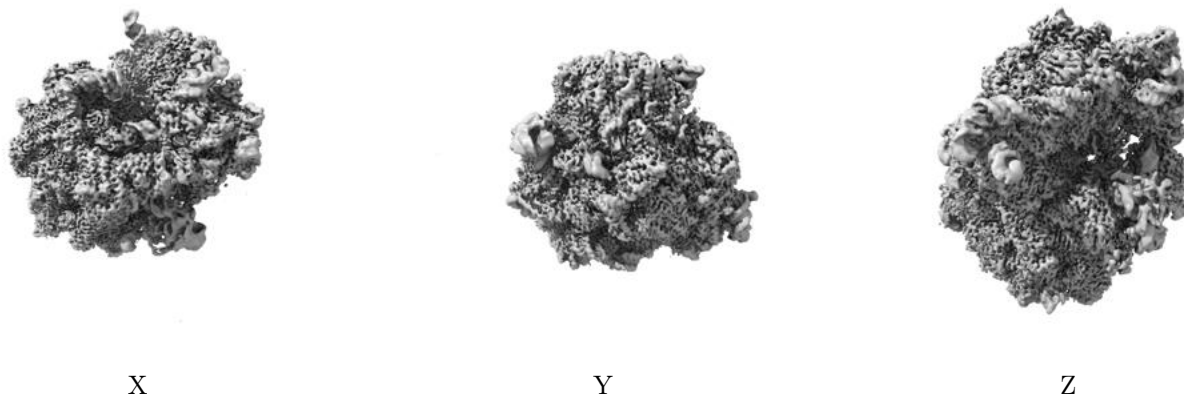


Z

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.

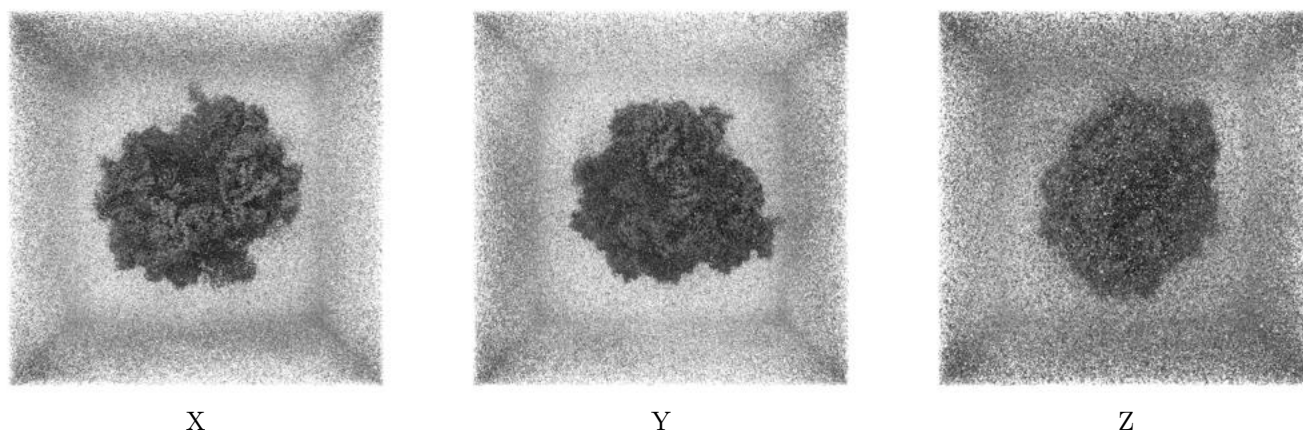
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. 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.

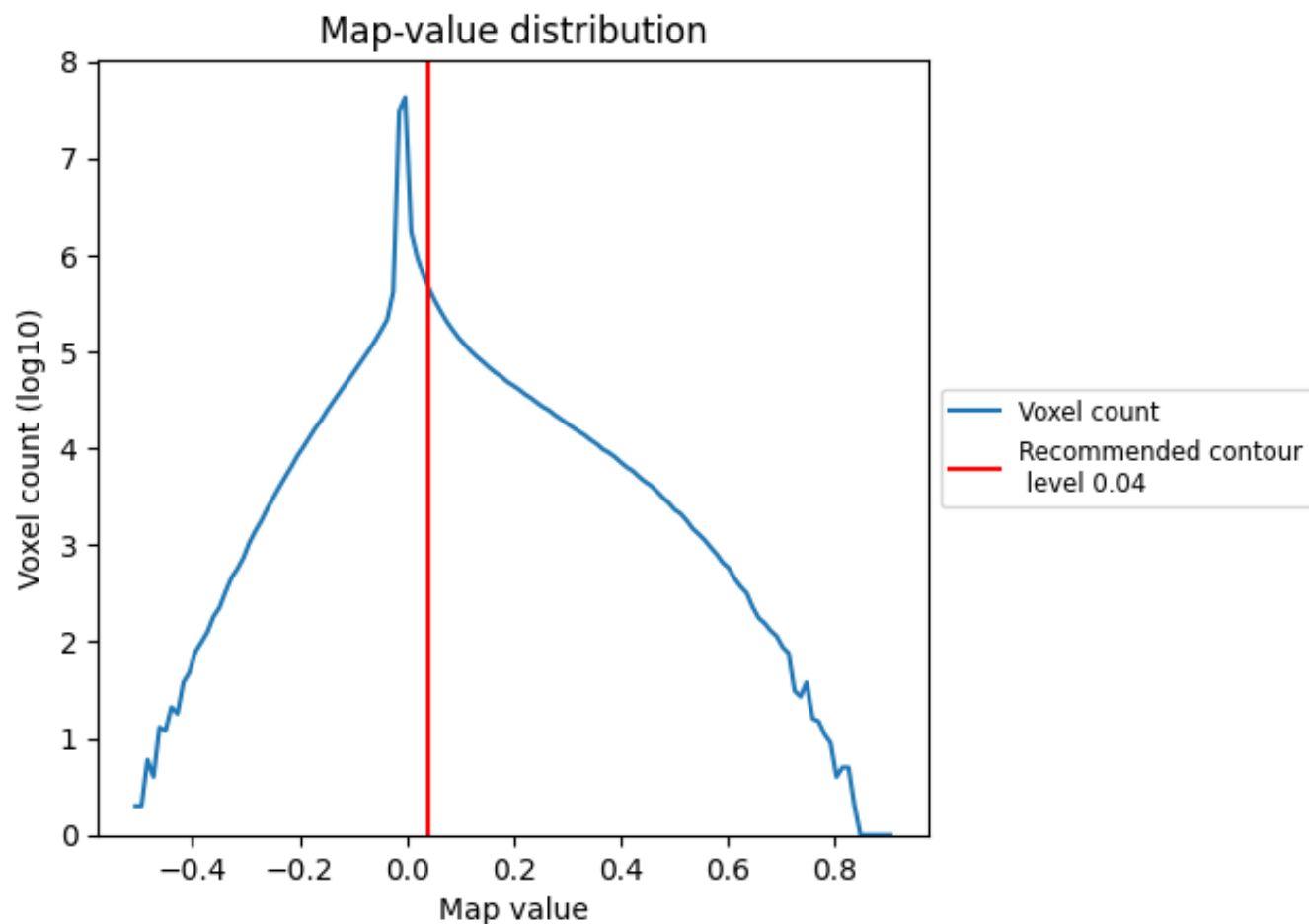
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

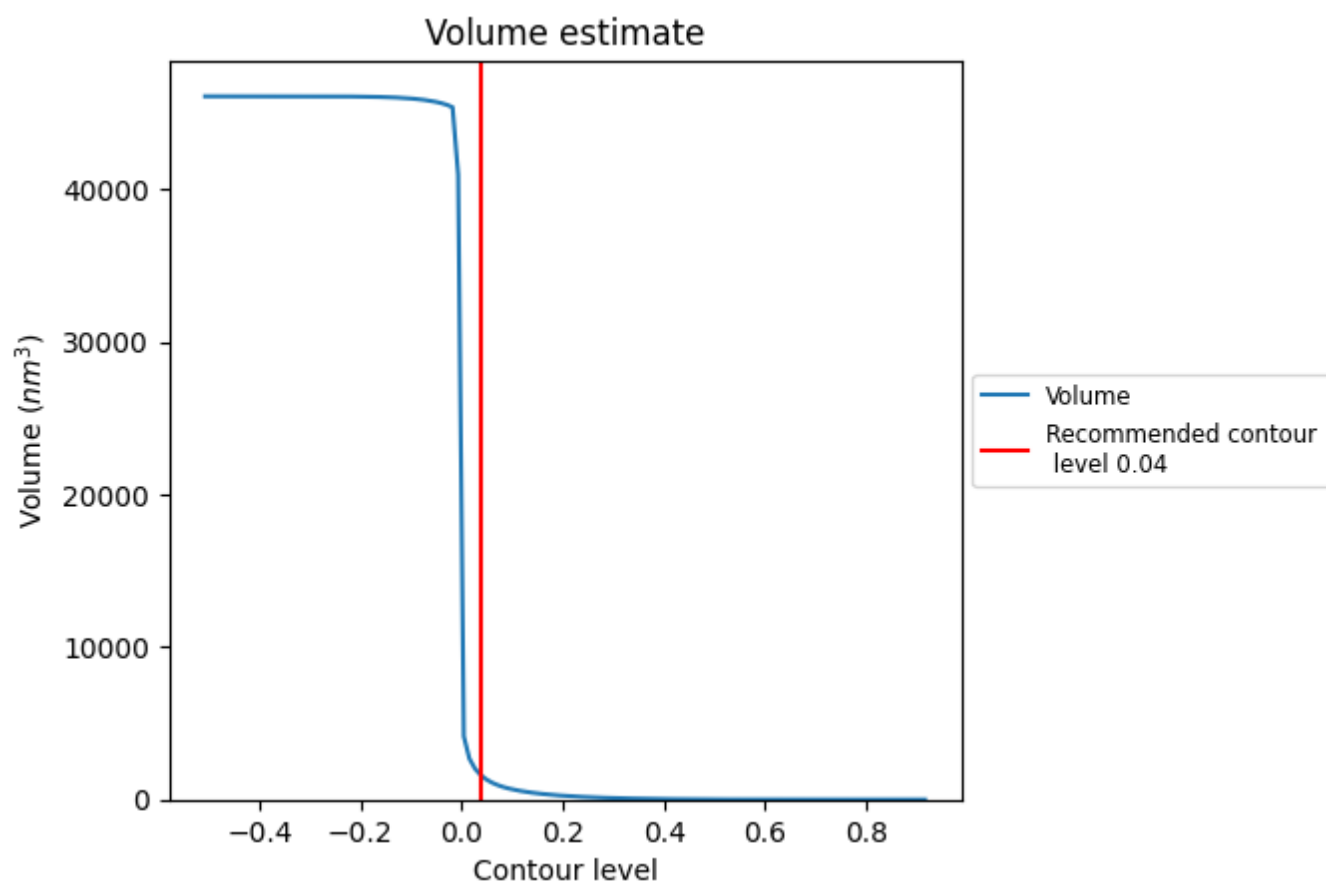
This section contains the results of statistical analysis of the map.

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.

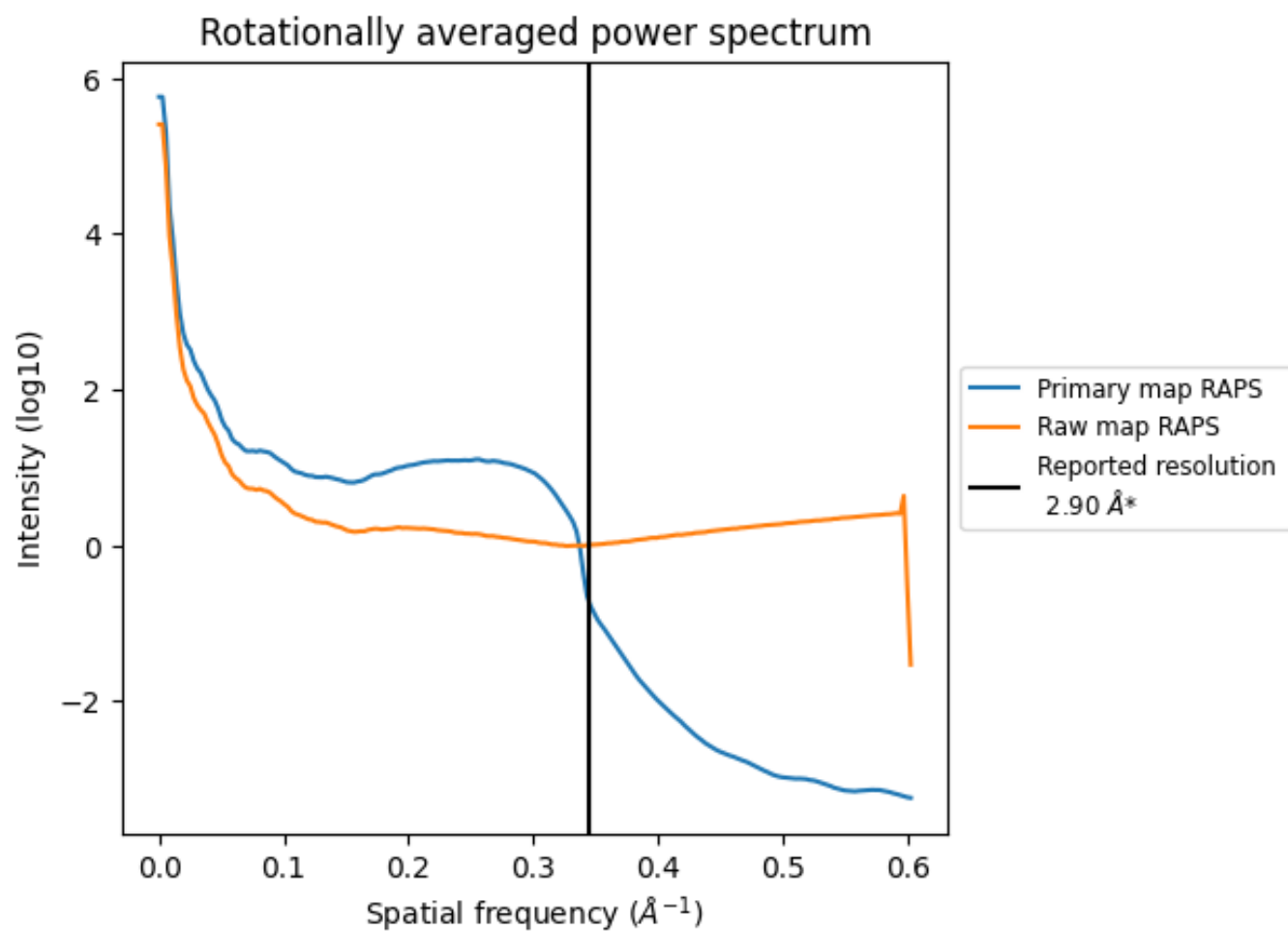
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1554 nm^3 ; this corresponds to an approximate mass of 1403 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 ⓘ

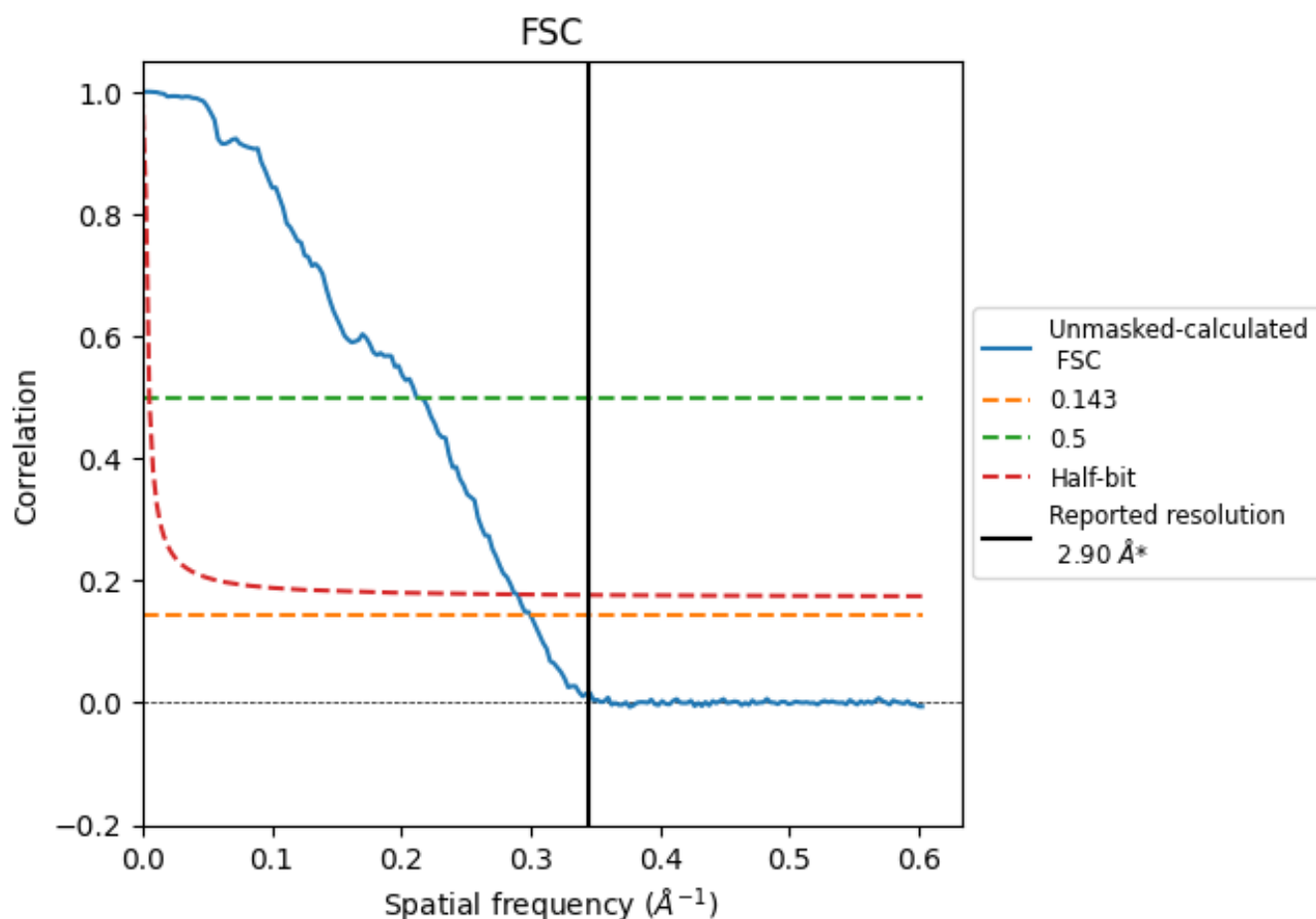


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

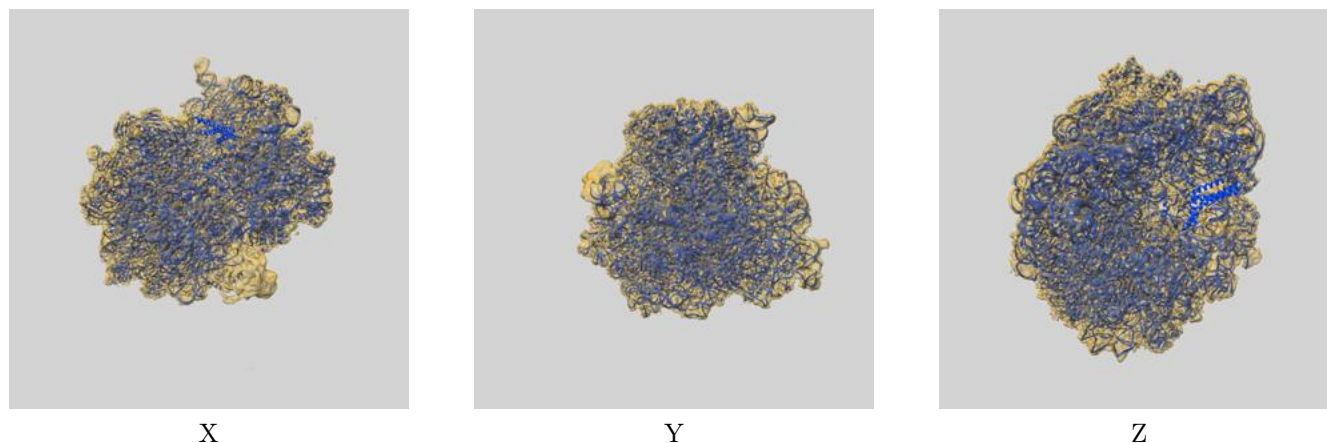
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.34	4.72	3.45

*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 3.34 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

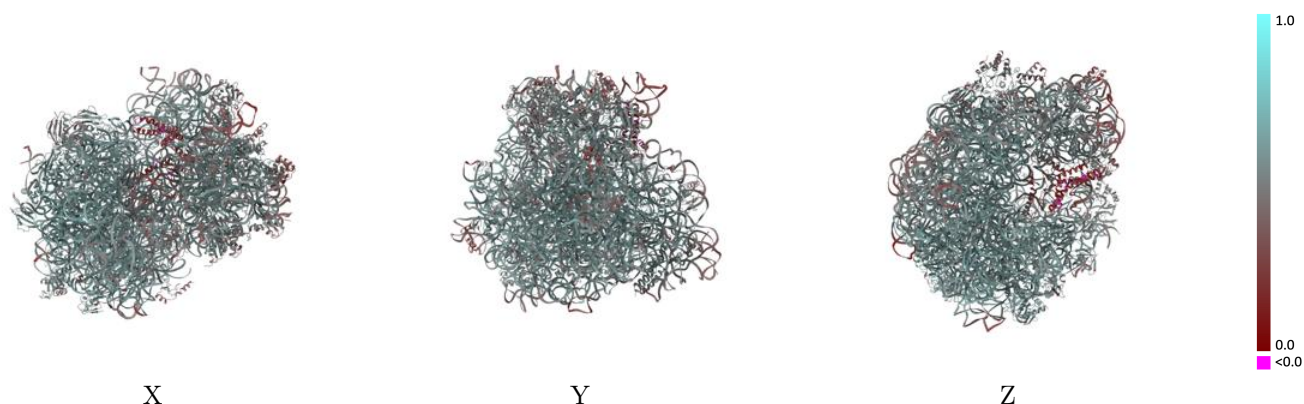
This section contains information regarding the fit between EMDB map EMD-60474 and PDB model 8ZTV. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



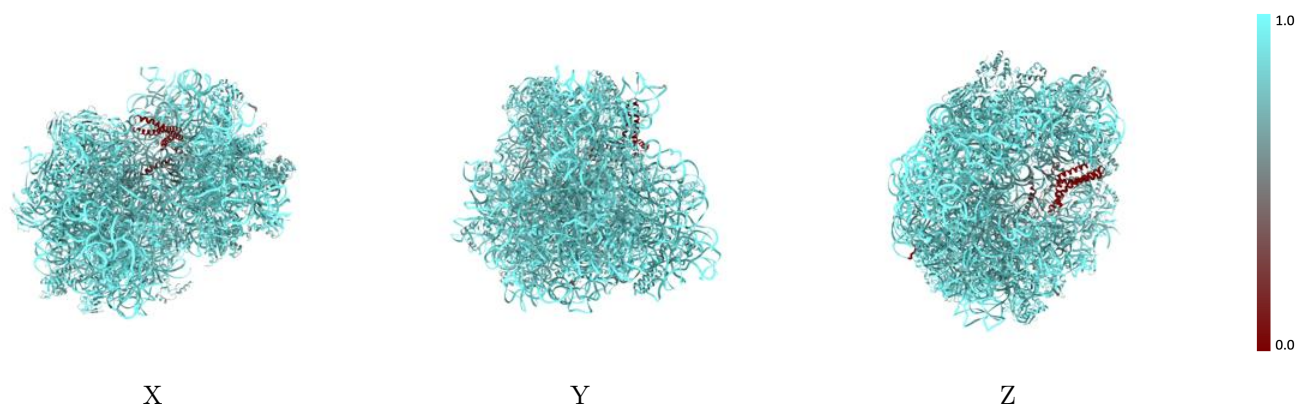
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



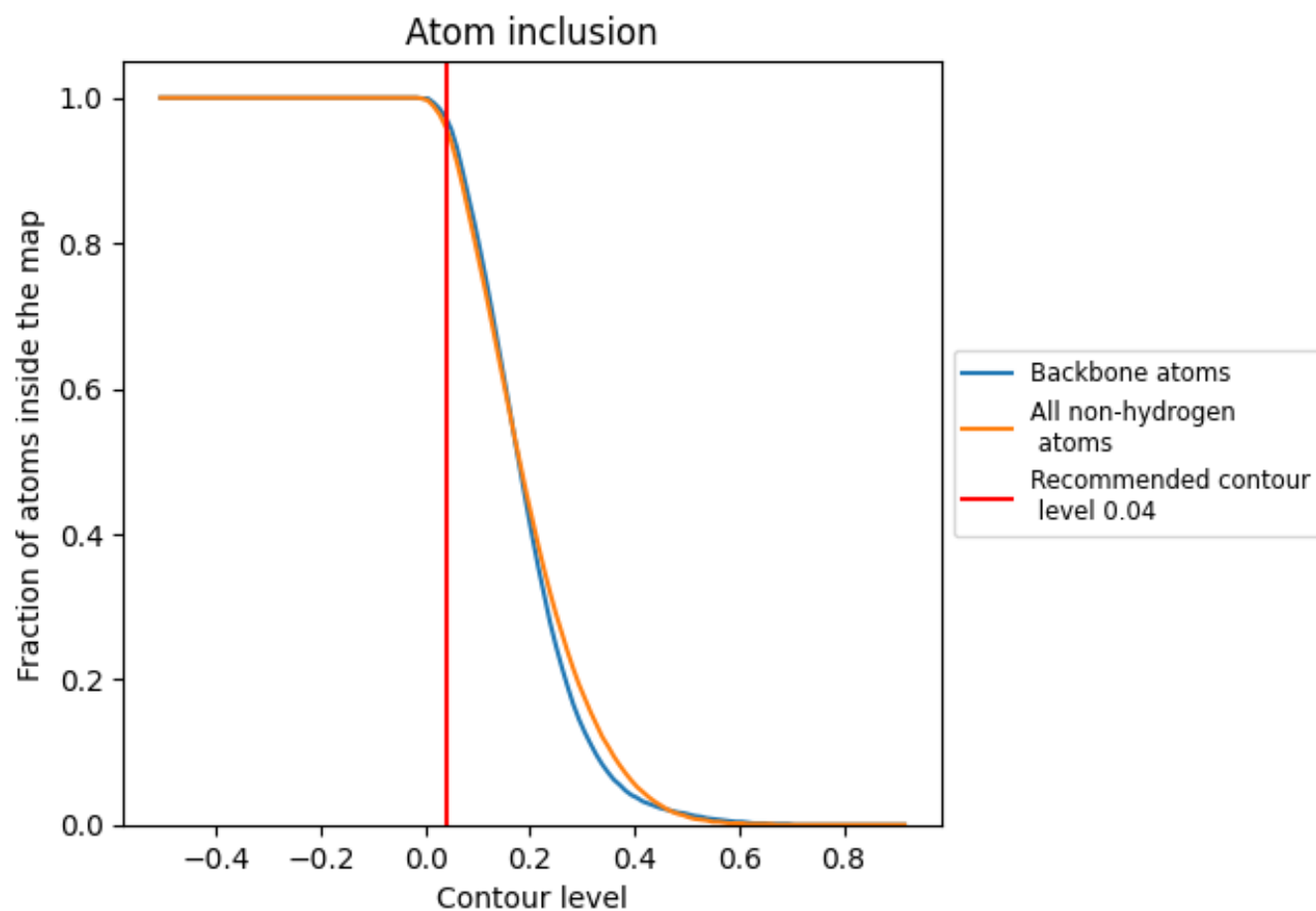
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9580	 0.5530
0	 0.9220	 0.5410
1	 0.9800	 0.6120
2	 0.9860	 0.6100
3	 0.9830	 0.5900
4	 0.8070	 0.4240
A	 0.9860	 0.5430
B	 0.8410	 0.4520
C	 0.9280	 0.5160
D	 0.9030	 0.4920
E	 0.9410	 0.5580
F	 0.8860	 0.5150
G	 0.8820	 0.4790
H	 0.9280	 0.5410
I	 0.8910	 0.4780
J	 0.8500	 0.4320
K	 0.9400	 0.5440
L	 0.9270	 0.5430
M	 0.8820	 0.4750
N	 0.9150	 0.5000
O	 0.9060	 0.5410
P	 0.9210	 0.5140
Q	 0.9020	 0.5180
R	 0.9180	 0.5340
S	 0.8620	 0.4820
T	 0.9240	 0.5100
U	 0.8590	 0.4600
V	 0.4610	 0.3120
W	 0.9440	 0.5140
X	 0.9900	 0.5580
Y	 0.9570	 0.4930
Z	 0.9760	 0.5740
a	 0.9900	 0.5850
b	 0.9800	 0.5400
c	 0.9680	 0.6030



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Chain	Atom inclusion	Q-score
d	 0.9620	 0.5850
e	 0.9260	 0.5480
f	 0.8500	 0.4720
g	 0.8650	 0.4920
h	 0.7810	 0.4120
i	 0.9680	 0.5920
j	 0.9610	 0.5840
k	 0.9470	 0.5760
l	 0.9630	 0.5870
m	 0.9800	 0.5950
n	 0.9140	 0.5260
o	 0.9410	 0.5730
p	 0.9850	 0.6120
q	 0.9500	 0.5730
r	 0.9560	 0.5820
s	 0.9470	 0.5620
t	 0.9350	 0.5430
u	 0.9170	 0.5350
v	 0.9500	 0.5840
w	 0.9630	 0.5790
x	 0.9160	 0.5300
y	 0.9430	 0.5750
z	 0.9560	 0.5740