



# wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 10:14 am BST

PDB ID : 28UK / pdb\_000028uk  
EMDB ID : EMD-56830  
Title : E. coli 70S ribosome, conformational ground state mutation in SSU-h41, with A- and P-site tRNA  
Authors : Steinmetzger, C.; Riad, M.; Petzold, K.  
Deposited on : 2026-02-20  
Resolution : 2.24 Å(reported)  
Based on initial model : 7K00

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

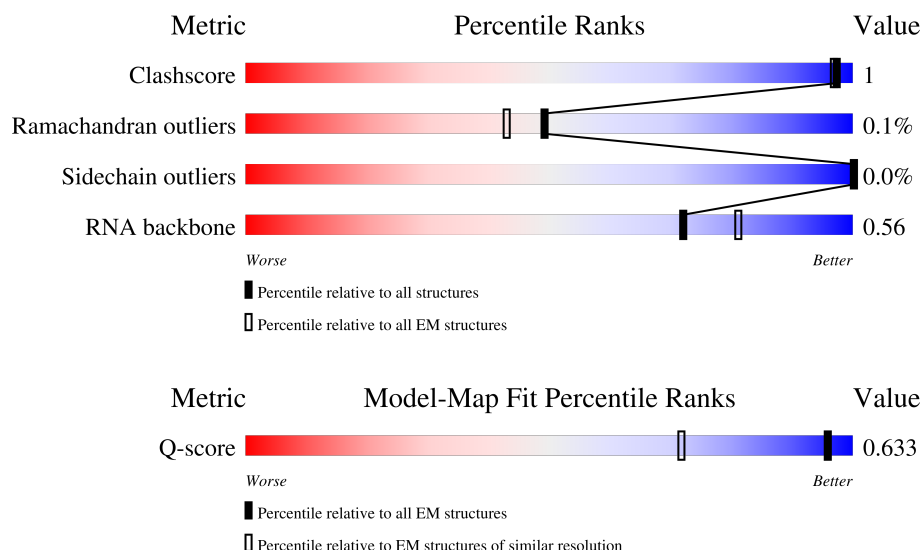
EMDB validation analysis : 0.0.1.dev132  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 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*

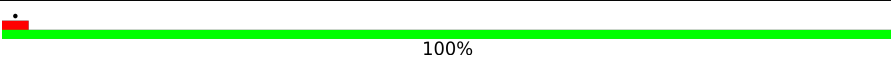
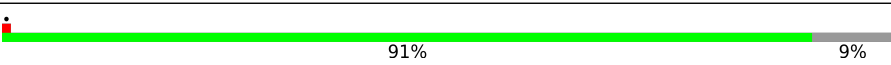
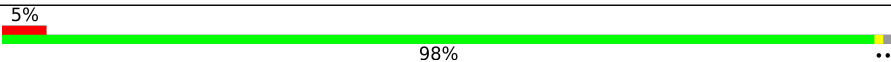
The reported resolution of this entry is 2.24 Å.

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.



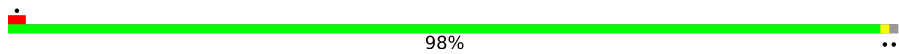
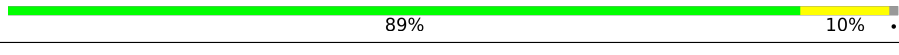
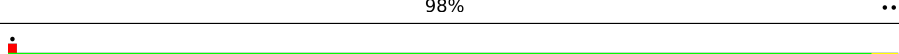
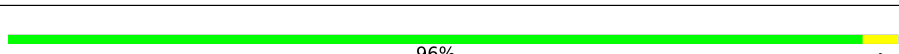
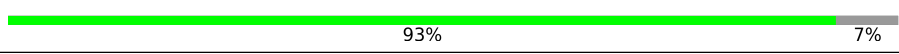
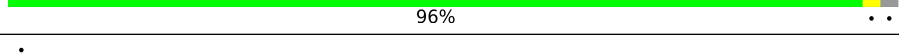


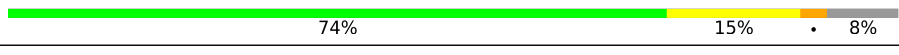
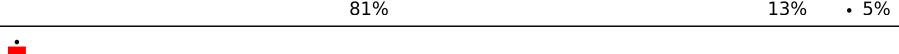
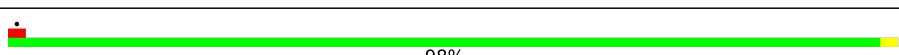
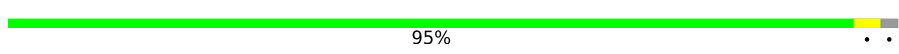
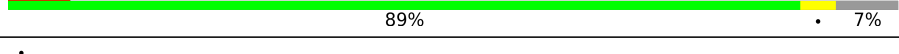
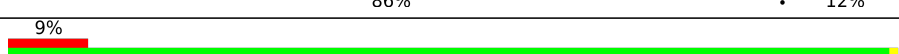
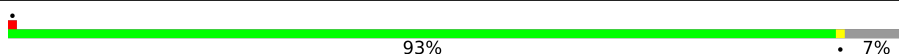

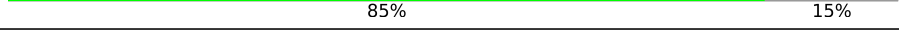
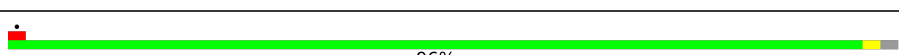
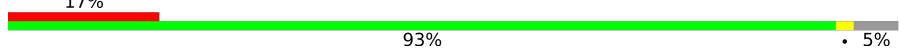
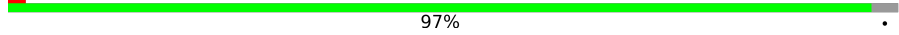



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3381 ( 1.75 - 2.74 )

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  $\geq 3$ , 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	3	38	 100%
2	K	129	 91% 9%
3	L	124	 98% ..

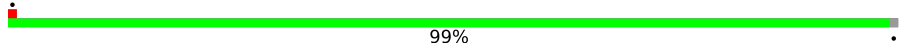
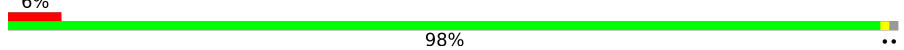
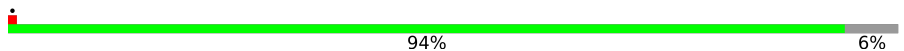

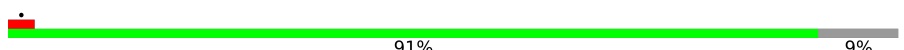
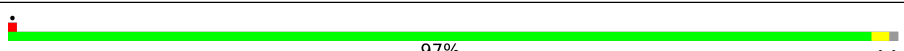
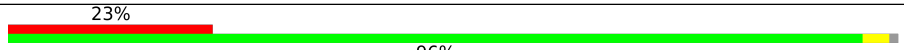

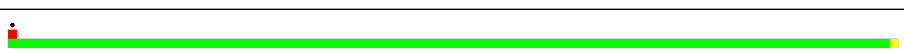
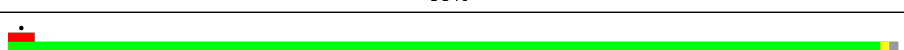
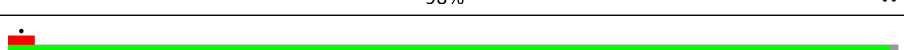
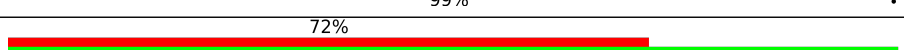
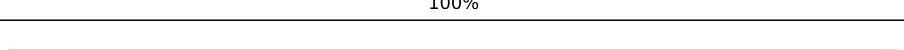
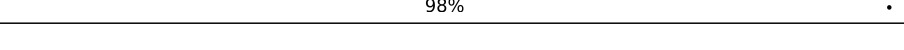
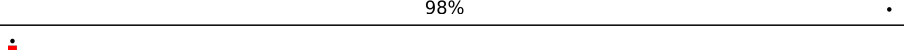
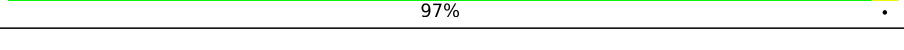
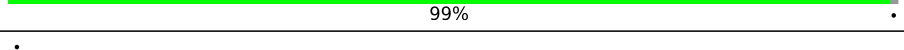
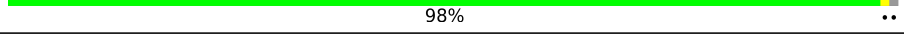
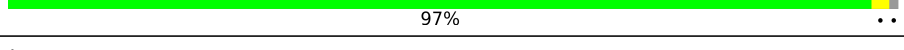
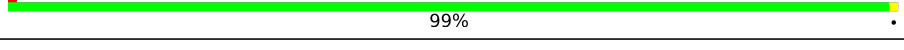
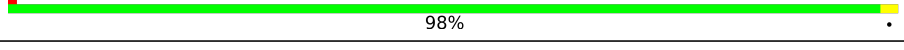
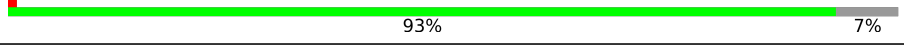
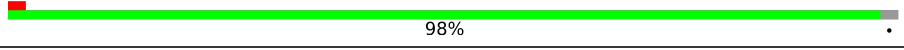
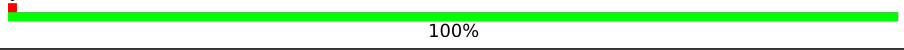
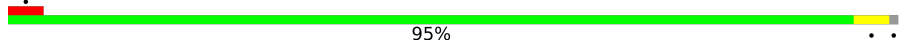
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Mol	Chain	Length	Quality of chain
4	N	101	
5	b	120	
6	c	273	
7	d	209	
8	l	136	
9	m	127	
10	z	57	
11	4	70	
12	A	1542	
13	Y	76	
14	Z	78	
15	a	2904	
16	0	55	
17	1	46	
18	2	65	
19	B	241	
20	C	233	
21	D	206	
22	E	167	
23	F	135	
24	G	179	
25	H	130	
26	I	130	
27	J	103	
28	M	118	

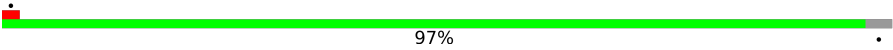
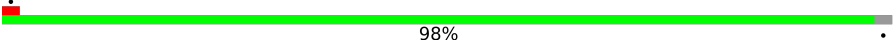
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Mol	Chain	Length	Quality of chain
29	O	89	 99%
30	P	82	 98%
31	Q	84	 94% 6%
32	R	75	 87% 12%
33	S	92	 91% 9%
34	T	87	 97% ..
35	U	71	 96% ..
36	X	10	 80% 20%
37	e	201	 99% .
38	f	179	 98% ..
39	g	177	 99% .
40	h	149	 72% 100%
41	i	142	 98% .
42	j	123	 98% .
43	k	144	 97% .
44	n	117	 99% .
45	o	115	 98% ..
46	p	118	 97% ..
47	q	103	 99% .
48	r	110	 98% .
49	s	100	 93% 7%
50	t	104	 98% .
51	u	94	 100%
52	v	85	 95% ..
53	w	78	 99% .

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Mol	Chain	Length	Quality of chain
54	x	63	 97%
55	y	59	 98%

## 2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 148443 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 2 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	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	modified residue	UNP P0A7R9

- Molecule 3 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 4 is a protein called Small ribosomal subunit protein uS14.

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

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

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

- Molecule 6 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 7 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 8 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 9 is a protein called Large ribosomal subunit protein bL17.

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

- Molecule 10 is a protein called Large ribosomal subunit protein bL32.

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

- Molecule 11 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 12 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A	1519	Total	C	N	O	P	0	0
			32609	14551	5983	10556	1519		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1260	U	G	engineered mutation	GB 2971070070

- Molecule 13 is a RNA chain called A-site Val-tRNA<sup>Val</sup>.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	Y	72	Total	C	N	O	P	S	0	0
			1539	689	280	498	71	1		

- Molecule 14 is a RNA chain called P-site tRNA<sup>fMet</sup>.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	Z	72	Total	C	N	O	P	S	0	0
			1546	690	285	498	72	1		

- Molecule 15 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	a	2757	Total	C	N	O	P		0	0
			59216	26422	10911	19126	2757			

- Molecule 16 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 17 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 18 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 19 is a protein called Small ribosomal subunit protein uS2.



Mol	Chain	Residues	Atoms					AltConf	Trace
19	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 20 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 21 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 22 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 23 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

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

- Molecule 24 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 25 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 26 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 27 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 28 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 29 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 30 is a protein called Small ribosomal subunit protein bS16.

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

- Molecule 31 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 32 is a protein called Small ribosomal subunit protein bS18.

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

- Molecule 33 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 34 is a protein called Small ribosomal subunit protein bS20.

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

- Molecule 35 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	U	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 36 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	X	10	Total	C	N	O	P	0	0
			216	97	41	68	10		

- Molecule 37 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 38 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 39 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 40 is a protein called Large ribosomal subunit protein bL9.

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

- Molecule 41 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 42 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 43 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 44 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 45 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 46 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 47 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 48 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 49 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 50 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 51 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 52 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 53 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 54 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 55 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	3	1	Total	Zn	0
			1	1	
56	4	1	Total	Zn	0
			1	1	

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	N	1	Total	Mg	0
			1	1	
57	b	4	Total	Mg	0
			4	4	
57	c	1	Total	Mg	0
			1	1	
57	d	1	Total	Mg	0
			1	1	
57	z	1	Total	Mg	0
			1	1	
57	A	50	Total	Mg	0
			50	50	
57	Z	1	Total	Mg	0
			1	1	
57	a	168	Total	Mg	0
			168	168	

- Molecule 58 is POTASSIUM ION (CCD ID: K) (formula: K).

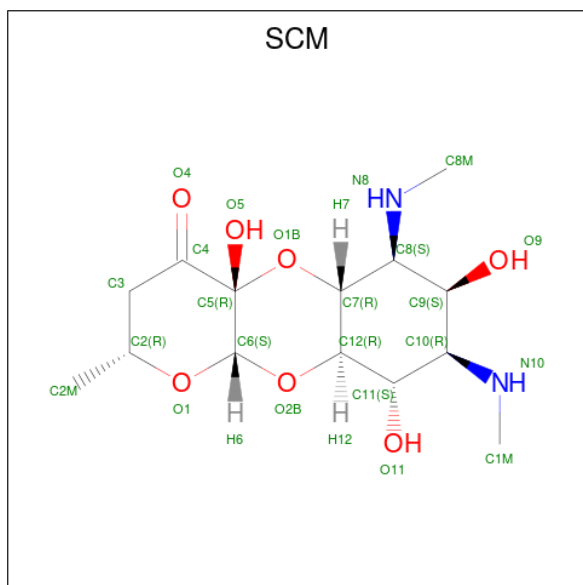
Mol	Chain	Residues	Atoms		AltConf
58	c	3	Total	K	0
			3	3	

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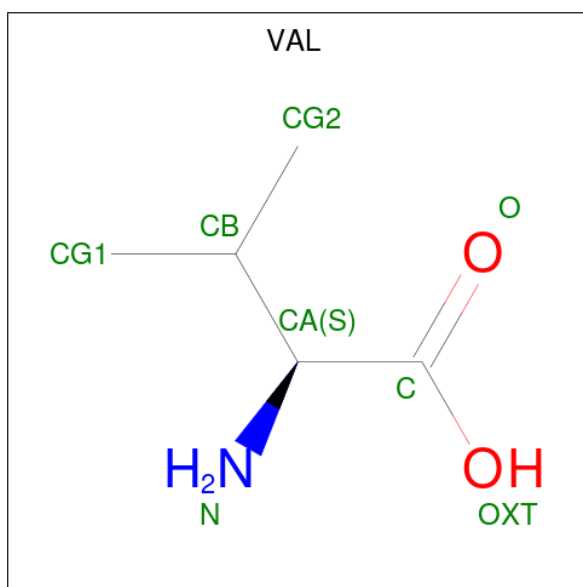
Mol	Chain	Residues	Atoms		AltConf
58	A	10	Total	K	0
			10	10	
58	a	60	Total	K	0
			60	60	
58	t	1	Total	K	0
			1	1	

- Molecule 59 is SPECTINOMYCIN (CCD ID: SCM) (formula:  $C_{14}H_{24}N_2O_7$ ).



Mol	Chain	Residues	Atoms				AltConf
59	A	1	Total	C	N	O	0
			23	14	2	7	

- Molecule 60 is VALINE (CCD ID: VAL) (formula:  $C_5H_{11}NO_2$ ).



Mol	Chain	Residues	Atoms				AltConf
60	Y	1	Total	C	N	O	0
			7	5	1	1	

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		AltConf
61	3	8	Total	O	0
			8	8	
61	K	13	Total	O	0
			13	13	
61	L	12	Total	O	0
			12	12	
61	N	13	Total	O	0
			13	13	
61	b	82	Total	O	0
			82	82	
61	c	83	Total	O	0
			83	83	
61	d	58	Total	O	0
			58	58	
61	l	35	Total	O	0
			35	35	
61	m	13	Total	O	0
			13	13	
61	z	23	Total	O	0
			23	23	
61	A	1183	Total	O	0
			1183	1183	

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Mol	Chain	Residues	Atoms		AltConf
61	Y	13	Total 13	O 13	0
61	Z	20	Total 20	O 20	0
61	a	3717	Total 3717	O 3717	0
61	0	5	Total 5	O 5	0
61	1	10	Total 10	O 10	0
61	2	23	Total 23	O 23	0
61	B	15	Total 15	O 15	0
61	C	10	Total 10	O 10	0
61	D	19	Total 19	O 19	0
61	E	9	Total 9	O 9	0
61	F	4	Total 4	O 4	0
61	G	6	Total 6	O 6	0
61	H	8	Total 8	O 8	0
61	I	9	Total 9	O 9	0
61	J	12	Total 12	O 12	0
61	M	4	Total 4	O 4	0
61	O	10	Total 10	O 10	0
61	P	7	Total 7	O 7	0
61	Q	4	Total 4	O 4	0
61	R	5	Total 5	O 5	0
61	S	7	Total 7	O 7	0

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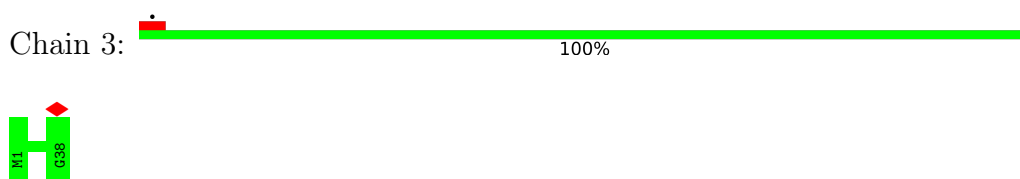
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Mol	Chain	Residues	Atoms		AltConf
61	U	4	Total 4	O 4	0
61	X	6	Total 6	O 6	0
61	e	53	Total 53	O 53	0
61	f	4	Total 4	O 4	0
61	g	5	Total 5	O 5	0
61	h	10	Total 10	O 10	0
61	i	24	Total 24	O 24	0
61	j	28	Total 28	O 28	0
61	k	46	Total 46	O 46	0
61	n	6	Total 6	O 6	0
61	o	23	Total 23	O 23	0
61	p	30	Total 30	O 30	0
61	q	24	Total 24	O 24	0
61	r	33	Total 33	O 33	0
61	s	17	Total 17	O 17	0
61	t	10	Total 10	O 10	0
61	u	11	Total 11	O 11	0
61	v	21	Total 21	O 21	0
61	w	19	Total 19	O 19	0
61	x	4	Total 4	O 4	0
61	y	7	Total 7	O 7	0

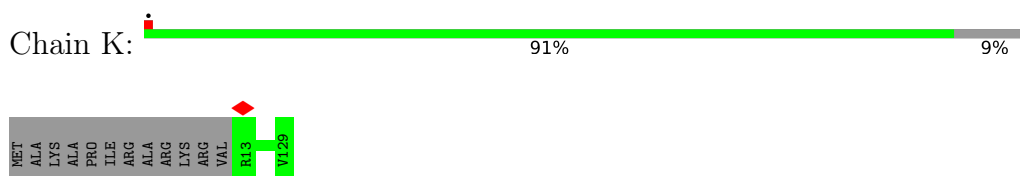
### 3 Residue-property plots [i](#)

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

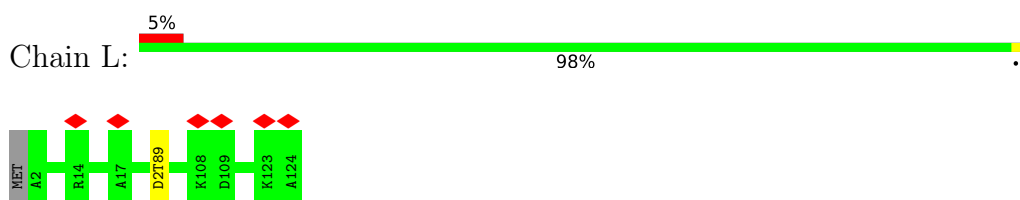
- Molecule 1: Large ribosomal subunit protein bL36A



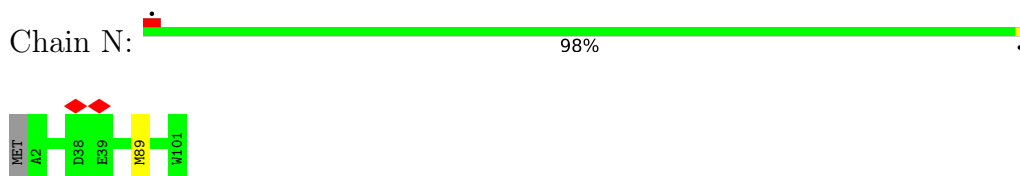
- Molecule 2: Small ribosomal subunit protein uS11



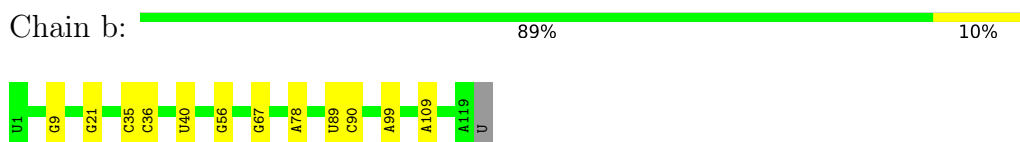
- Molecule 3: Small ribosomal subunit protein uS12



- Molecule 4: Small ribosomal subunit protein uS14



- Molecule 5: 5S rRNA



- Molecule 6: Large ribosomal subunit protein uL2

Chain c:  98% ..



- Molecule 7: Large ribosomal subunit protein uL3

Chain d:  97% .



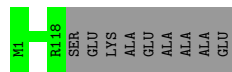
- Molecule 8: Large ribosomal subunit protein uL16

Chain l:  96% .



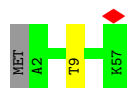
- Molecule 9: Large ribosomal subunit protein bL17

Chain m:  93% 7%




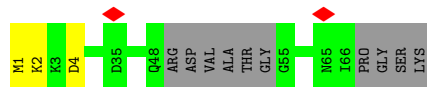
- Molecule 10: Large ribosomal subunit protein bL32

Chain z:  96% ..




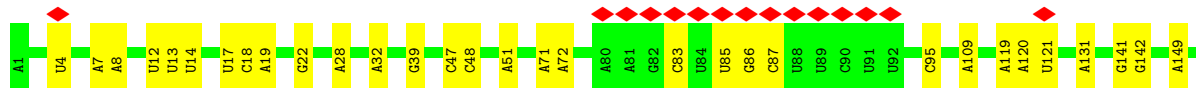
- Molecule 11: Large ribosomal subunit protein bL31

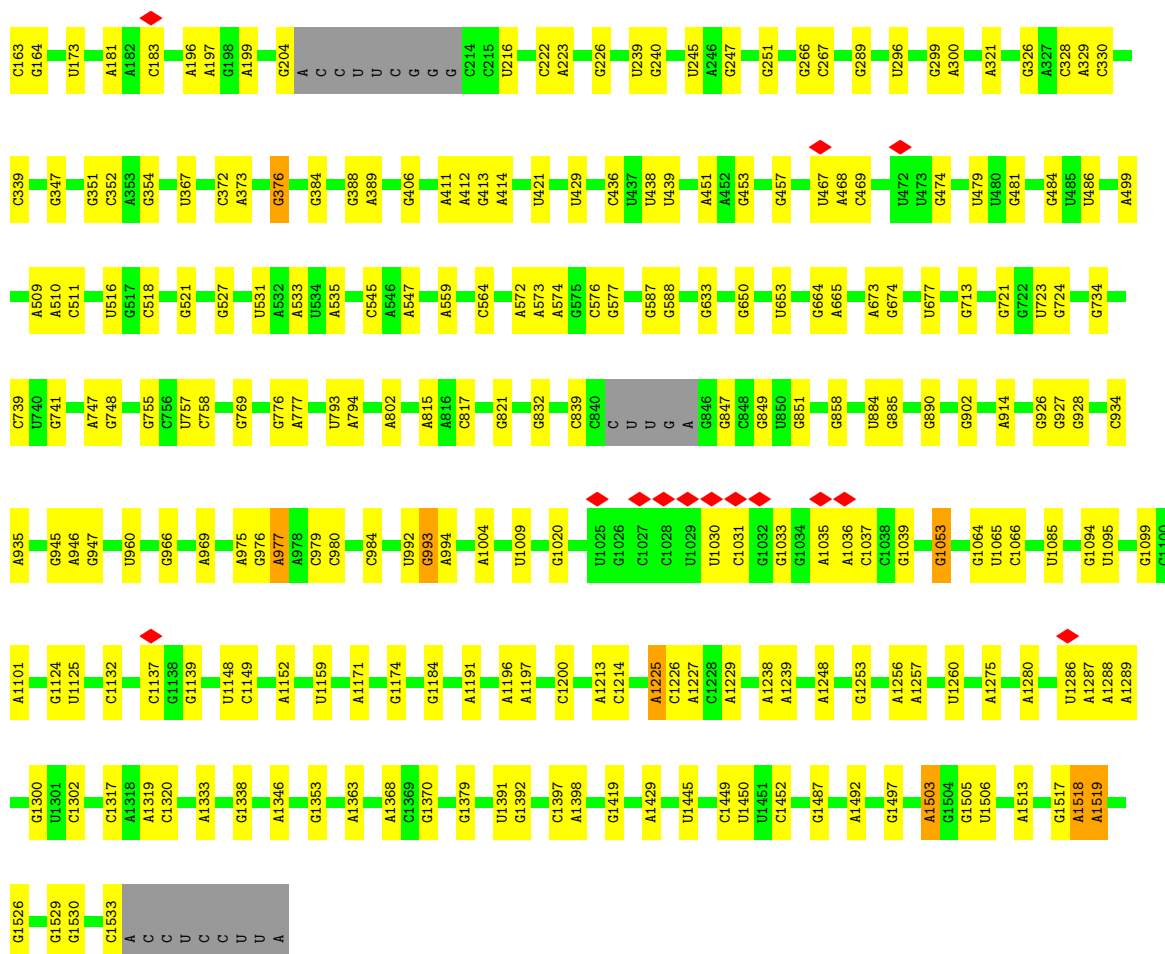
Chain 4:  81% 14%



- Molecule 12: 16S rRNA

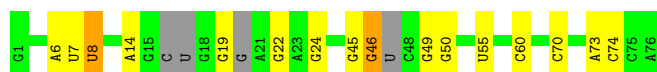
Chain A:  81% 17% ..





• Molecule 13: A-site Val-tRNA<sup>Val</sup>

Chain Y: 74% 18% 5%



• Molecule 14: P-site tRNA<sup>fMet</sup>

Chain Z: 74% 15% 8%

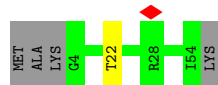


• Molecule 15: 23S rRNA

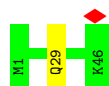
Chain a: 81% 13% 5%







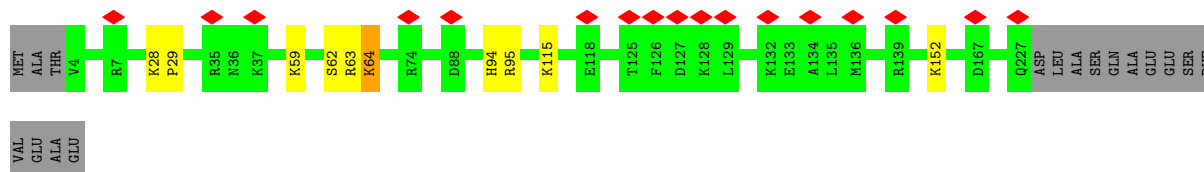
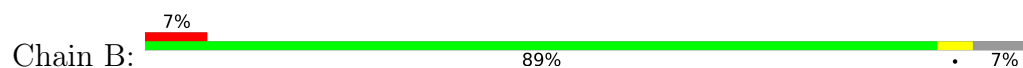
- Molecule 17: Large ribosomal subunit protein bL34



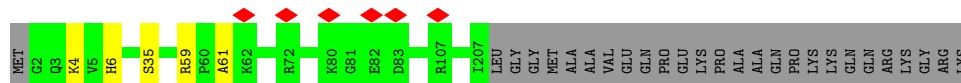
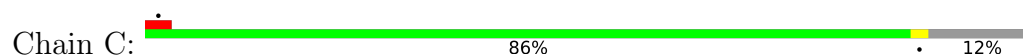
- Molecule 18: Large ribosomal subunit protein bL35



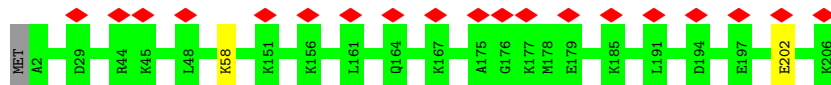
- Molecule 19: Small ribosomal subunit protein uS2



- Molecule 20: Small ribosomal subunit protein uS3

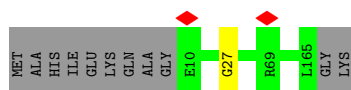


- Molecule 21: Small ribosomal subunit protein uS4

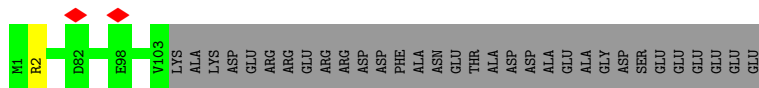
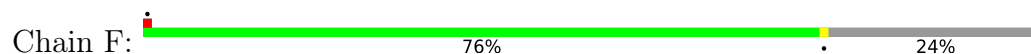


- Molecule 22: Small ribosomal subunit protein uS5

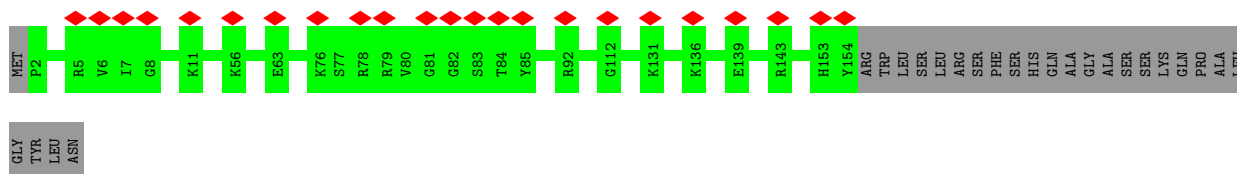
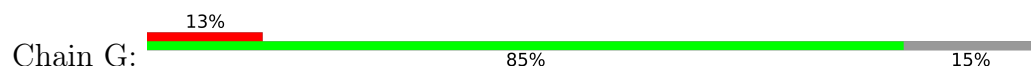




- Molecule 23: Small ribosomal subunit protein bS6, fully modified isoform



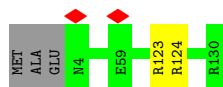
- Molecule 24: Small ribosomal subunit protein uS7



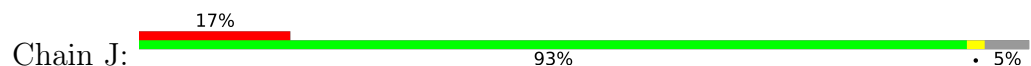
- Molecule 25: Small ribosomal subunit protein uS8



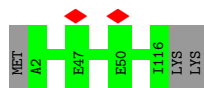
- Molecule 26: Small ribosomal subunit protein uS9



- Molecule 27: Small ribosomal subunit protein uS10



- Molecule 28: Small ribosomal subunit protein uS13





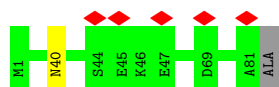
- Molecule 29: Small ribosomal subunit protein uS15

Chain O:  99%



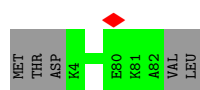
- Molecule 30: Small ribosomal subunit protein bS16

Chain P:  98%




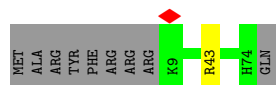
- Molecule 31: Small ribosomal subunit protein uS17

Chain Q:  94%

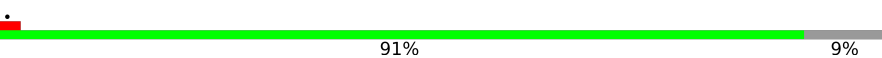


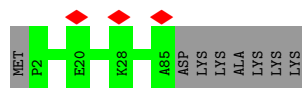
- Molecule 32: Small ribosomal subunit protein bS18

Chain R:  87%



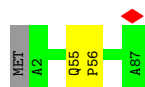
- Molecule 33: Small ribosomal subunit protein uS19

Chain S:  91%



- Molecule 34: Small ribosomal subunit protein bS20

Chain T:  97%



- Molecule 35: Small ribosomal subunit protein bS21

Chain U:  96%



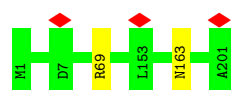
- Molecule 36: mRNA

Chain X: 80% 20%



- Molecule 37: Large ribosomal subunit protein uL4

Chain e: 99%



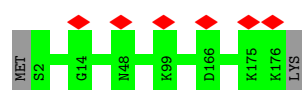
- Molecule 38: Large ribosomal subunit protein uL5

Chain f: 98%



- Molecule 39: Large ribosomal subunit protein uL6

Chain g: 99%



- Molecule 40: Large ribosomal subunit protein bL9

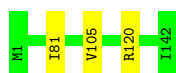
Chain h: 72% 100%



- Molecule 41: Large ribosomal subunit protein uL13

Chain i: 98%





- Molecule 42: Large ribosomal subunit protein uL14

Chain j: 98%



- Molecule 43: Large ribosomal subunit protein uL15

Chain k: 97%



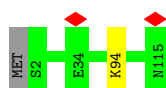
- Molecule 44: Large ribosomal subunit protein uL18

Chain n: 99%



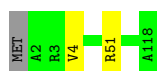
- Molecule 45: Large ribosomal subunit protein bL19

Chain o: 98%



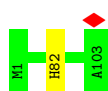
- Molecule 46: Large ribosomal subunit protein bL20

Chain p: 97%

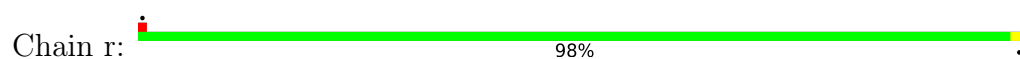


- Molecule 47: Large ribosomal subunit protein bL21

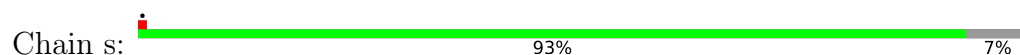
Chain q: 99%



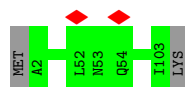
- Molecule 48: Large ribosomal subunit protein uL22



- Molecule 49: Large ribosomal subunit protein uL23



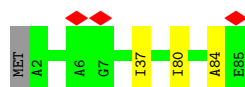
- Molecule 50: Large ribosomal subunit protein uL24



- Molecule 51: Large ribosomal subunit protein bL25



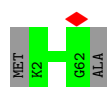
- Molecule 52: Large ribosomal subunit protein bL27



- Molecule 53: Large ribosomal subunit protein bL28



- Molecule 54: Large ribosomal subunit protein uL29



- Molecule 55: Large ribosomal subunit protein uL30

Chain y:  98%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23232	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 ( $e^-/\text{\AA}^2$ )	49.88	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	165000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.556	Depositor
Minimum map value	-0.173	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.0495	Depositor
Map size (Å)	436.32, 436.32, 436.32	wwPDB
Map dimensions	576, 576, 576	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.7575, 0.7575, 0.7575	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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	3	0.49	0/303	0.83	0/397
2	K	0.51	0/884	0.85	0/1191
3	L	0.46	0/960	0.83	0/1286
4	N	0.46	0/817	0.91	0/1088
5	b	0.52	0/2850	0.79	0/4444
6	c	0.48	0/2121	0.84	0/2852
7	d	0.46	0/1576	0.79	0/2119
8	l	0.45	0/1073	0.85	0/1433
9	m	0.45	0/958	0.90	0/1281
10	z	0.47	0/450	0.86	0/599
11	4	0.46	0/488	0.86	0/649
12	A	0.52	0/36232	0.79	1/56513 (0.0%)
13	Y	0.56	0/1596	0.79	0/2478
14	Z	0.56	1/1608 (0.1%)	0.78	0/2500
15	a	0.50	0/65747	0.82	12/102563 (0.0%)
16	0	0.46	0/424	0.79	0/565
17	1	0.47	0/380	0.92	0/498
18	2	0.49	0/513	0.88	0/676
19	B	0.46	0/1784	0.90	0/2403
20	C	0.46	0/1651	0.86	0/2225
21	D	0.44	0/1665	0.91	0/2227
22	E	0.47	0/1165	0.83	0/1568
23	F	0.46	0/858	0.84	0/1160
24	G	0.46	0/1219	0.93	0/1635
25	H	0.46	0/989	0.86	0/1326
26	I	0.45	0/1034	0.90	0/1375
27	J	0.45	0/796	0.85	0/1077
28	M	0.47	0/900	0.93	0/1204
29	O	0.43	0/722	0.96	0/964
30	P	0.46	0/653	0.83	0/877
31	Q	0.45	0/650	0.79	0/871

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	R	0.45	0/553	0.93	0/742
33	S	0.49	0/685	0.84	0/922
34	T	0.46	0/676	0.99	0/895
35	U	0.46	0/598	0.97	0/792
36	X	0.55	0/242	0.78	0/375
37	e	0.45	0/1571	0.86	0/2113
38	f	0.45	0/1434	0.91	0/1926
39	g	0.46	0/1333	0.84	0/1805
40	h	0.46	0/1122	0.82	0/1515
41	i	0.45	0/1152	0.84	0/1551
42	j	0.46	0/956	0.84	0/1279
43	k	0.47	0/1062	0.84	0/1413
44	n	0.46	0/902	0.89	0/1209
45	o	0.46	0/929	0.78	0/1242
46	p	0.44	0/960	0.92	0/1278
47	q	0.44	0/829	0.74	0/1107
48	r	0.46	0/864	0.85	0/1156
49	s	0.44	0/744	0.81	0/994
50	t	0.47	0/787	0.78	0/1051
51	u	0.45	0/766	0.80	0/1025
52	v	0.47	0/642	0.80	0/848
53	w	0.46	0/635	0.84	0/848
54	x	0.41	0/496	0.94	0/660
55	y	0.45	0/453	0.86	0/605
All	All	0.50	1/153457 (0.0%)	0.82	13/229395 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
32	R	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	Z	8	4SU	O3'-P	5.02	1.61	1.56

The worst 5 of 13 bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	a	2546	U	O3'-P-O5'	-7.98	92.03	104.00
15	a	1905	C	O3'-P-O5'	-7.23	93.16	104.00
15	a	781	A	O3'-P-O5'	-6.06	94.91	104.00
15	a	2601	C	O3'-P-O5'	-5.79	95.32	104.00
15	a	73	A	O3'-P-O5'	-5.69	95.47	104.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
32	R	43	ARG	Sidechain

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3	302	0	340	0	0
2	K	877	0	884	0	0
3	L	957	0	1017	0	0
4	N	805	0	844	1	0
5	b	2549	0	1291	2	0
6	c	2082	0	2153	2	0
7	d	1566	0	1618	4	0
8	l	1075	0	1145	3	0
9	m	945	0	989	0	0
10	z	444	0	458	1	0
11	4	480	0	478	1	0
12	A	32609	0	16428	36	0
13	Y	1539	0	791	0	0
14	Z	1546	0	794	2	0
15	a	59216	0	29791	71	0
16	0	417	0	451	1	0
17	1	377	0	418	1	0
18	2	504	0	572	2	0
19	B	1753	0	1780	5	0
20	C	1624	0	1696	3	0
21	D	1643	0	1707	2	0
22	E	1152	0	1196	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	F	839	0	833	1	0
24	G	1203	0	1254	0	0
25	H	979	0	1031	0	0
26	I	1022	0	1070	1	0
27	J	786	0	828	1	0
28	M	891	0	952	0	0
29	O	714	0	734	0	0
30	P	643	0	661	2	0
31	Q	641	0	682	0	0
32	R	544	0	565	0	0
33	S	668	0	693	0	0
34	T	670	0	719	1	0
35	U	590	0	629	1	0
36	X	216	0	108	0	0
37	e	1552	0	1619	2	0
38	f	1410	0	1444	1	0
39	g	1313	0	1358	0	0
40	h	1111	0	1148	0	0
41	i	1129	0	1162	3	0
42	j	947	0	1023	1	0
43	k	1053	0	1129	4	0
44	n	892	0	923	0	0
45	o	917	0	962	2	0
46	p	947	0	1019	2	0
47	q	816	0	839	1	0
48	r	857	0	922	1	0
49	s	738	0	807	0	0
50	t	779	0	830	0	0
51	u	753	0	780	0	0
52	v	634	0	653	1	0
53	w	625	0	652	0	0
54	x	495	0	526	0	0
55	y	449	0	488	0	0
56	3	1	0	0	0	0
56	4	1	0	0	0	0
57	A	50	0	0	0	0
57	N	1	0	0	0	0
57	Z	1	0	0	0	0
57	a	168	0	0	0	0
57	b	4	0	0	0	0
57	c	1	0	0	0	0
57	d	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	z	1	0	0	0	0
58	A	10	0	0	0	0
58	a	60	0	0	0	0
58	c	3	0	0	0	0
58	t	1	0	0	0	0
59	A	23	0	24	2	0
60	Y	7	0	8	1	0
61	0	5	0	0	0	0
61	1	10	0	0	0	0
61	2	23	0	0	0	0
61	3	8	0	0	0	0
61	A	1183	0	0	0	0
61	B	15	0	0	0	0
61	C	10	0	0	0	0
61	D	19	0	0	0	0
61	E	9	0	0	0	0
61	F	4	0	0	0	0
61	G	6	0	0	0	0
61	H	8	0	0	0	0
61	I	9	0	0	0	0
61	J	12	0	0	0	0
61	K	13	0	0	0	0
61	L	12	0	0	0	0
61	M	4	0	0	0	0
61	N	13	0	0	0	0
61	O	10	0	0	0	0
61	P	7	0	0	2	0
61	Q	4	0	0	0	0
61	R	5	0	0	0	0
61	S	7	0	0	0	0
61	U	4	0	0	0	0
61	X	6	0	0	0	0
61	Y	13	0	0	0	0
61	Z	20	0	0	0	0
61	a	3717	0	0	1	0
61	b	82	0	0	0	0
61	c	83	0	0	0	0
61	d	58	0	0	0	0
61	e	53	0	0	0	0
61	f	4	0	0	0	0
61	g	5	0	0	0	0
61	h	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	i	24	0	0	1	0
61	j	28	0	0	0	0
61	k	46	0	0	0	0
61	l	35	0	0	0	0
61	m	13	0	0	0	0
61	n	6	0	0	0	0
61	o	23	0	0	0	0
61	p	30	0	0	0	0
61	q	24	0	0	0	0
61	r	33	0	0	0	0
61	s	17	0	0	0	0
61	t	10	0	0	0	0
61	u	11	0	0	0	0
61	v	21	0	0	0	0
61	w	19	0	0	0	0
61	x	4	0	0	0	0
61	y	7	0	0	0	0
61	z	23	0	0	0	0
All	All	148443	0	95916	137	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 1.

The worst 5 of 137 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)
15:a:568:U:H1'	15:a:2030:6MZ:H9C1	1.69	0.72
15:a:12:U:H2'	15:a:12:U:O2	1.90	0.70
5:b:40:U:H2'	11:4:2:LYS:HE3	1.84	0.60
12:A:1191:A:OP1	20:C:4:LYS:NZ	2.36	0.59
12:A:664:G:H22	12:A:741:G:H1	1.51	0.58

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
2	K	113/129 (88%)	109 (96%)	4 (4%)	0	100	100
3	L	120/124 (97%)	115 (96%)	5 (4%)	0	100	100
4	N	98/101 (97%)	98 (100%)	0	0	100	100
6	c	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
7	d	206/209 (99%)	200 (97%)	6 (3%)	0	100	100
8	l	132/136 (97%)	127 (96%)	5 (4%)	0	100	100
9	m	116/127 (91%)	110 (95%)	6 (5%)	0	100	100
10	z	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
11	4	56/70 (80%)	53 (95%)	2 (4%)	1 (2%)	6	3
16	0	49/55 (89%)	49 (100%)	0	0	100	100
17	1	44/46 (96%)	44 (100%)	0	0	100	100
18	2	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
19	B	222/241 (92%)	212 (96%)	9 (4%)	1 (0%)	24	23
20	C	204/233 (88%)	198 (97%)	5 (2%)	1 (0%)	24	23
21	D	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
22	E	154/167 (92%)	147 (96%)	7 (4%)	0	100	100
23	F	101/135 (75%)	97 (96%)	4 (4%)	0	100	100
24	G	151/179 (84%)	146 (97%)	5 (3%)	0	100	100
25	H	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
26	I	125/130 (96%)	118 (94%)	7 (6%)	0	100	100
27	J	96/103 (93%)	92 (96%)	3 (3%)	1 (1%)	12	9
28	M	113/118 (96%)	111 (98%)	2 (2%)	0	100	100
29	O	86/89 (97%)	86 (100%)	0	0	100	100
30	P	79/82 (96%)	74 (94%)	5 (6%)	0	100	100
31	Q	77/84 (92%)	74 (96%)	3 (4%)	0	100	100
32	R	64/75 (85%)	64 (100%)	0	0	100	100
33	S	82/92 (89%)	79 (96%)	3 (4%)	0	100	100
34	T	84/87 (97%)	84 (100%)	0	0	100	100
35	U	68/71 (96%)	67 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	e	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
38	f	175/179 (98%)	172 (98%)	3 (2%)	0	100	100
39	g	173/177 (98%)	166 (96%)	7 (4%)	0	100	100
40	h	147/149 (99%)	141 (96%)	6 (4%)	0	100	100
41	i	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
42	j	121/123 (98%)	117 (97%)	3 (2%)	1 (1%)	16	13
43	k	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
44	n	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
45	o	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
46	p	115/118 (98%)	115 (100%)	0	0	100	100
47	q	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
48	r	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
49	s	91/100 (91%)	88 (97%)	3 (3%)	0	100	100
50	t	100/104 (96%)	99 (99%)	1 (1%)	0	100	100
51	u	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
52	v	82/85 (96%)	78 (95%)	3 (4%)	1 (1%)	10	6
53	w	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
54	x	59/63 (94%)	58 (98%)	1 (2%)	0	100	100
55	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
All	All	5593/5913 (95%)	5428 (97%)	159 (3%)	6 (0%)	49	54

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	J	57	VAL
42	j	108	ARG
11	4	4	ASP
20	C	61	ALA
19	B	64	LYS

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	3	34/34 (100%)	34 (100%)	0	100	100
2	K	89/98 (91%)	89 (100%)	0	100	100
3	L	102/103 (99%)	102 (100%)	0	100	100
4	N	83/84 (99%)	83 (100%)	0	100	100
6	c	216/218 (99%)	216 (100%)	0	100	100
7	d	163/163 (100%)	163 (100%)	0	100	100
8	l	107/107 (100%)	107 (100%)	0	100	100
9	m	98/103 (95%)	98 (100%)	0	100	100
10	z	47/48 (98%)	47 (100%)	0	100	100
11	4	55/62 (89%)	54 (98%)	1 (2%)	51	61
16	0	46/49 (94%)	46 (100%)	0	100	100
17	1	38/38 (100%)	38 (100%)	0	100	100
18	2	51/52 (98%)	51 (100%)	0	100	100
19	B	186/199 (94%)	186 (100%)	0	100	100
20	C	170/190 (90%)	170 (100%)	0	100	100
21	D	172/173 (99%)	172 (100%)	0	100	100
22	E	119/126 (94%)	119 (100%)	0	100	100
23	F	90/116 (78%)	90 (100%)	0	100	100
24	G	126/147 (86%)	126 (100%)	0	100	100
25	H	104/105 (99%)	104 (100%)	0	100	100
26	I	105/107 (98%)	105 (100%)	0	100	100
27	J	86/90 (96%)	86 (100%)	0	100	100
28	M	93/96 (97%)	93 (100%)	0	100	100
29	O	76/77 (99%)	76 (100%)	0	100	100
30	P	65/65 (100%)	65 (100%)	0	100	100
31	Q	73/78 (94%)	73 (100%)	0	100	100
32	R	57/65 (88%)	57 (100%)	0	100	100
33	S	72/79 (91%)	72 (100%)	0	100	100
34	T	65/66 (98%)	65 (100%)	0	100	100
35	U	60/61 (98%)	59 (98%)	1 (2%)	53	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	e	165/165 (100%)	165 (100%)	0	100	100
38	f	148/150 (99%)	148 (100%)	0	100	100
39	g	136/138 (99%)	136 (100%)	0	100	100
40	h	114/114 (100%)	114 (100%)	0	100	100
41	i	116/116 (100%)	116 (100%)	0	100	100
42	j	104/104 (100%)	104 (100%)	0	100	100
43	k	103/103 (100%)	103 (100%)	0	100	100
44	n	86/87 (99%)	86 (100%)	0	100	100
45	o	99/100 (99%)	99 (100%)	0	100	100
46	p	89/90 (99%)	89 (100%)	0	100	100
47	q	84/84 (100%)	84 (100%)	0	100	100
48	r	93/93 (100%)	93 (100%)	0	100	100
49	s	80/84 (95%)	80 (100%)	0	100	100
50	t	83/85 (98%)	83 (100%)	0	100	100
51	u	78/78 (100%)	78 (100%)	0	100	100
52	v	62/63 (98%)	62 (100%)	0	100	100
53	w	67/68 (98%)	67 (100%)	0	100	100
54	x	54/55 (98%)	54 (100%)	0	100	100
55	y	48/49 (98%)	48 (100%)	0	100	100
All	All	4657/4825 (96%)	4655 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	4	1	MET
35	U	2	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
27	J	58	ASN
51	u	87	GLN
38	f	37	ASN
50	t	53	ASN

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Mol	Chain	Res	Type
45	o	10	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	A	1516/1542 (98%)	196 (12%)	28 (1%)
13	Y	68/76 (89%)	15 (22%)	0
14	Z	68/78 (87%)	10 (14%)	1 (1%)
15	a	2753/2904 (94%)	294 (10%)	0
36	X	9/10 (90%)	2 (22%)	0
5	b	118/120 (98%)	9 (7%)	0
All	All	4532/4730 (95%)	526 (11%)	29 (0%)

5 of 526 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	b	9	G
5	b	21	G
5	b	35	C
5	b	36	C
5	b	56	G

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	A	858	G
12	A	1505	G
12	A	993	G
12	A	1397	C
12	A	992	U

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

50 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
15	1MG	a	745	15	22,26,27	0.47	0	33,39,42	0.50	0
12	5MC	A	1407	12	18,22,23	0.31	0	26,32,35	0.67	0
15	PSU	a	2457	15	18,21,22	0.90	1 (5%)	22,30,33	0.61	0
12	MA6	A	1519	12	23,26,27	0.25	0	34,38,41	0.78	1 (2%)
15	6MZ	a	2030	15	22,25,26	0.37	0	30,36,39	0.62	0
12	G7M	A	527	12	23,26,27	0.72	1 (4%)	35,39,42	0.64	0
15	PSU	a	746	15,57	18,21,22	0.91	1 (5%)	22,30,33	0.60	0
14	5MU	Z	54	14	19,22,23	0.27	0	28,32,35	0.37	0
13	6MZ	Y	37	13	22,25,26	0.32	0	30,36,39	0.52	0
14	4SU	Z	8	14	18,21,22	0.38	0	26,30,33	1.17	3 (11%)
12	2MG	A	1207	12,58	23,26,27	0.38	0	32,38,41	0.47	0
15	6MZ	a	1618	15	22,25,26	0.34	0	30,36,39	0.59	0
15	5MU	a	1939	15,58	19,22,23	0.30	0	28,32,35	0.38	0
12	PSU	A	516	12	18,21,22	0.91	1 (5%)	22,30,33	0.62	0
15	5MU	a	747	15	19,22,23	0.26	0	28,32,35	0.32	0
15	2MA	a	2503	15,57,58	22,25,26	0.25	0	33,37,40	0.64	1 (3%)
15	PSU	a	955	15,58	18,21,22	0.88	1 (5%)	22,30,33	0.57	0
12	5MC	A	967	12	18,22,23	0.32	0	26,32,35	0.52	0
13	G7M	Y	46	13	23,26,27	0.72	1 (4%)	35,39,42	0.54	0
15	PSU	a	1911	15	18,21,22	0.88	1 (5%)	22,30,33	0.56	0
12	2MG	A	966	12	23,26,27	0.39	0	32,38,41	0.35	0
15	5MC	a	1962	15,58	18,22,23	0.34	0	26,32,35	0.49	0
15	OMG	a	2251	15,14,58	23,26,27	0.30	0	33,38,41	0.40	0
15	2MG	a	2445	15	23,26,27	0.39	0	32,38,41	0.40	0
13	PSU	Y	55	13	18,21,22	0.91	1 (5%)	22,30,33	0.59	0
15	OMC	a	2498	15,57	19,22,23	0.29	0	26,31,34	0.57	0
12	MA6	A	1518	12	23,26,27	0.24	0	34,38,41	0.69	1 (2%)
15	OMU	a	2552	15	19,22,23	0.21	0	26,31,34	0.38	0
13	4SU	Y	8	13	18,21,22	0.37	0	26,30,33	1.21	3 (11%)
15	3TD	a	1915	15	18,22,23	0.97	1 (5%)	22,32,35	0.68	0
15	PSU	a	1917	15	18,21,22	0.92	1 (5%)	22,30,33	0.62	0
2	IAS	K	119	2	6,7,8	0.91	0	6,8,10	0.97	0
14	G7M	Z	46	14	23,26,27	0.72	1 (4%)	35,39,42	0.55	0
15	2MG	a	1835	15	23,26,27	0.38	0	32,38,41	0.35	0
15	PSU	a	2504	15,58	18,21,22	0.84	1 (5%)	22,30,33	0.68	0
14	OMC	Z	32	14	19,22,23	0.27	0	26,31,34	0.35	0
15	PSU	a	2580	15	18,21,22	0.92	1 (5%)	22,30,33	0.74	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
12	4OC	A	1402	12	20,23,24	0.37	0	26,32,35	0.46	0
8	4D4	l	81	8	9,11,12	0.47	0	8,13,15	0.65	0
15	PSU	a	2604	15	18,21,22	0.89	1 (5%)	22,30,33	0.76	1 (4%)
12	2MG	A	1516	12	23,26,27	0.39	0	32,38,41	0.46	0
15	G7M	a	2069	15	23,26,27	0.71	1 (4%)	35,39,42	0.61	0
15	PSU	a	2605	15	18,21,22	0.91	1 (5%)	22,30,33	0.77	0
8	MS6	l	82	8	5,7,8	0.19	0	2,7,9	0.07	0
3	D2T	L	89	3	7,9,10	0.92	0	6,11,13	1.68	2 (33%)
13	5MU	Y	54	13	19,22,23	0.26	0	28,32,35	0.28	0
15	H2U	a	2449	15	18,21,22	0.63	0	21,30,33	0.78	2 (9%)
7	MEQ	d	150	7	8,9,10	0.42	0	5,10,12	0.63	0
12	UR3	A	1498	12	19,22,23	0.26	0	26,32,35	0.66	0
14	PSU	Z	55	14	18,21,22	0.92	1 (5%)	22,30,33	0.64	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
15	1MG	a	745	15	-	0/7/25/26	0/3/3/3
12	5MC	A	1407	12	-	0/7/25/26	0/2/2/2
15	PSU	a	2457	15	-	0/7/25/26	0/2/2/2
12	MA6	A	1519	12	-	2/11/29/30	0/3/3/3
15	6MZ	a	2030	15	-	1/9/27/28	0/3/3/3
12	G7M	A	527	12	-	1/7/25/26	0/3/3/3
15	PSU	a	746	15,57	-	2/7/25/26	0/2/2/2
14	5MU	Z	54	14	-	0/7/25/26	0/2/2/2
13	6MZ	Y	37	13	-	0/9/27/28	0/3/3/3
14	4SU	Z	8	14	-	0/7/25/26	0/2/2/2
12	2MG	A	1207	12,58	-	0/9/27/28	0/3/3/3
15	6MZ	a	1618	15	-	0/9/27/28	0/3/3/3
15	5MU	a	1939	15,58	-	0/7/25/26	0/2/2/2
12	PSU	A	516	12	-	0/7/25/26	0/2/2/2
15	5MU	a	747	15	-	1/7/25/26	0/2/2/2
15	2MA	a	2503	15,57,58	-	1/7/25/26	0/3/3/3
15	PSU	a	955	15,58	-	0/7/25/26	0/2/2/2
12	5MC	A	967	12	-	0/7/25/26	0/2/2/2
13	G7M	Y	46	13	-	3/7/25/26	0/3/3/3
15	PSU	a	1911	15	-	0/7/25/26	0/2/2/2
12	2MG	A	966	12	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	5MC	a	1962	15,58	-	0/7/25/26	0/2/2/2
15	OMG	a	2251	15,14,58	-	0/9/27/28	0/3/3/3
15	2MG	a	2445	15	-	1/9/27/28	0/3/3/3
13	PSU	Y	55	13	-	0/7/25/26	0/2/2/2
15	OMC	a	2498	15,57	-	0/9/27/28	0/2/2/2
12	MA6	A	1518	12	-	0/11/29/30	0/3/3/3
15	OMU	a	2552	15	-	0/9/27/28	0/2/2/2
13	4SU	Y	8	13	-	0/7/25/26	0/2/2/2
15	3TD	a	1915	15	-	2/7/25/26	0/2/2/2
15	PSU	a	1917	15	-	0/7/25/26	0/2/2/2
2	IAS	K	119	2	-	0/7/7/8	-
14	G7M	Z	46	14	-	1/7/25/26	0/3/3/3
15	2MG	a	1835	15	-	0/9/27/28	0/3/3/3
15	PSU	a	2504	15,58	-	0/7/25/26	0/2/2/2
14	OMC	Z	32	14	-	0/9/27/28	0/2/2/2
15	PSU	a	2580	15	-	0/7/25/26	0/2/2/2
12	4OC	A	1402	12	-	2/9/29/30	0/2/2/2
8	4D4	l	81	8	-	1/11/12/14	-
15	PSU	a	2604	15	-	0/7/25/26	0/2/2/2
12	2MG	A	1516	12	-	0/9/27/28	0/3/3/3
15	G7M	a	2069	15	-	2/7/25/26	0/3/3/3
15	PSU	a	2605	15	-	0/7/25/26	0/2/2/2
8	MS6	l	82	8	-	1/4/6/8	-
3	D2T	L	89	3	-	2/7/12/14	-
13	5MU	Y	54	13	-	0/7/25/26	0/2/2/2
15	H2U	a	2449	15	-	0/7/38/39	0/2/2/2
7	MEQ	d	150	7	-	2/8/9/11	-
12	UR3	A	1498	12	-	0/7/25/26	0/2/2/2
14	PSU	Z	55	14	-	0/7/25/26	0/2/2/2

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	Z	55	PSU	C6-C5	3.63	1.39	1.35
15	a	1915	3TD	C6-C5	3.63	1.39	1.35
15	a	1917	PSU	C6-C5	3.63	1.39	1.35
13	Y	55	PSU	C6-C5	3.60	1.39	1.35
15	a	746	PSU	C6-C5	3.59	1.39	1.35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	Y	8	4SU	C4-N3-C2	-4.36	123.10	127.34
14	Z	8	4SU	C4-N3-C2	-4.28	123.19	127.34
12	A	1518	MA6	C2-N1-C6	2.94	118.69	111.75
12	A	1519	MA6	C2-N1-C6	2.93	118.66	111.75
13	Y	8	4SU	C5-C4-N3	2.78	117.27	114.69

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L	89	D2T	CG-CB-SB-CB1
15	a	746	PSU	C2'-C1'-C5-C4
15	a	1915	3TD	C3'-C4'-C5'-O5'
15	a	1915	3TD	O4'-C4'-C5'-O5'
12	A	1519	MA6	O4'-C4'-C5'-O5'

There are no ring outliers.

6 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	A	1519	MA6	1	0
15	a	2030	6MZ	1	0
14	Z	8	4SU	1	0
15	a	1939	5MU	1	0
12	A	1518	MA6	1	0
15	a	2604	PSU	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 305 ligands modelled in this entry, 303 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
59	SCM	A	1601	-	23,25,25	0.26	0	26,39,39	0.65	0
60	VAL	Y	101	13	4,6,7	0.57	0	6,7,9	1.00	1 (16%)

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
59	SCM	A	1601	-	-	0/4/57/57	0/3/3/3
60	VAL	Y	101	13	-	0/5/6/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	Y	101	VAL	CB-CA-C	-2.07	110.15	112.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	A	1601	SCM	2	0
60	Y	101	VAL	1	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.

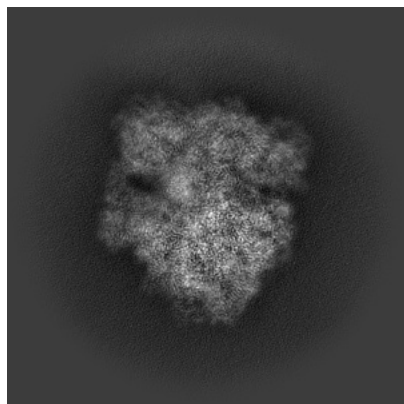
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-56830. These allow visual inspection of the internal detail of the map and identification of artifacts.

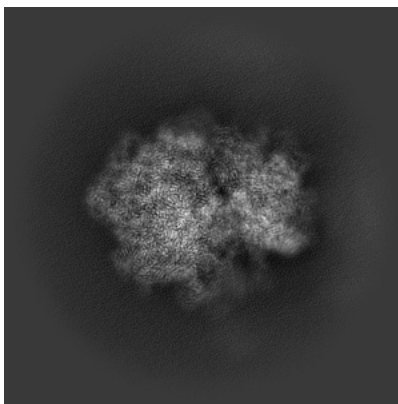
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

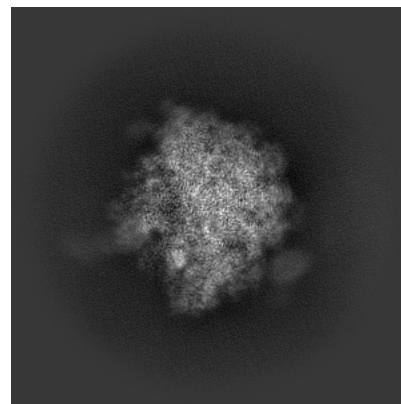
#### 6.1.1 Primary map



X

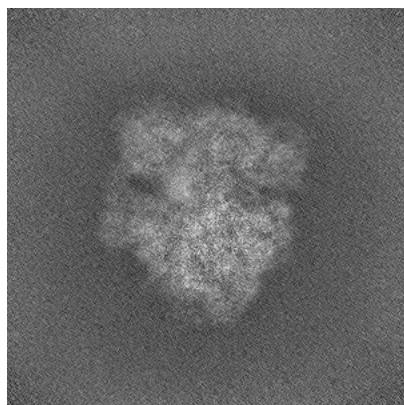


Y

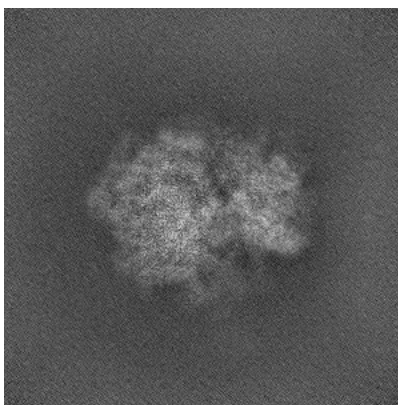


Z

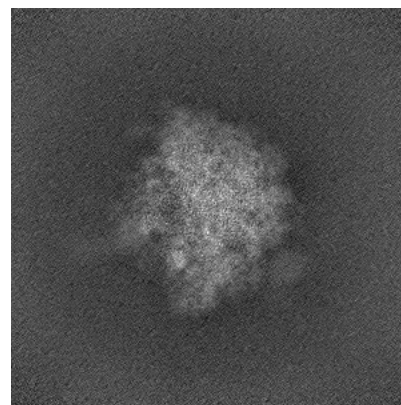
#### 6.1.2 Raw map



X



Y



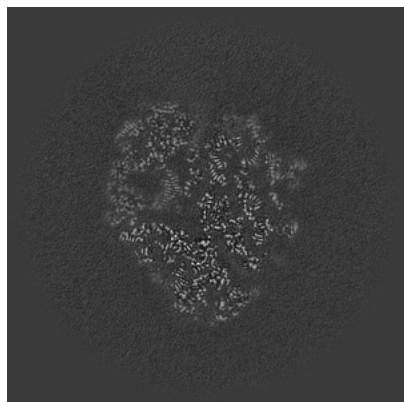
Z

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

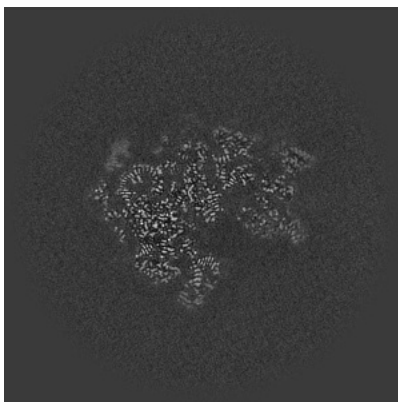


## 6.2 Central slices [i](#)

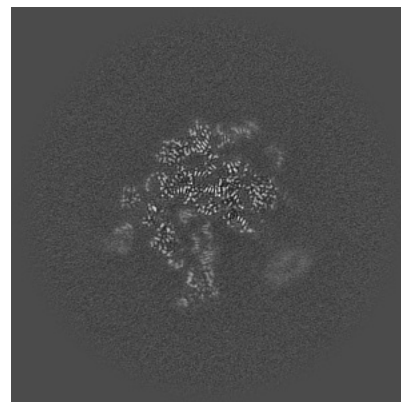
### 6.2.1 Primary map



X Index: 288

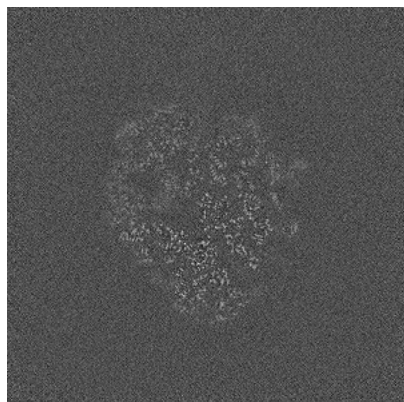


Y Index: 288

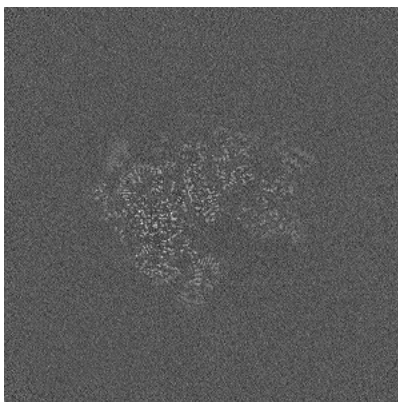


Z Index: 288

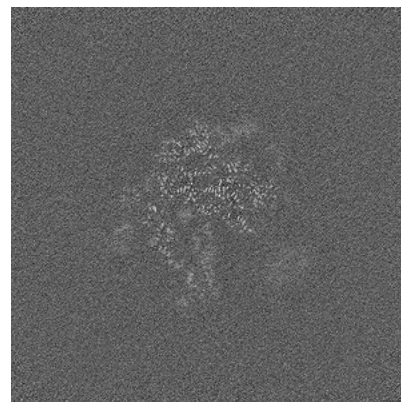
### 6.2.2 Raw map



X Index: 288



Y Index: 288



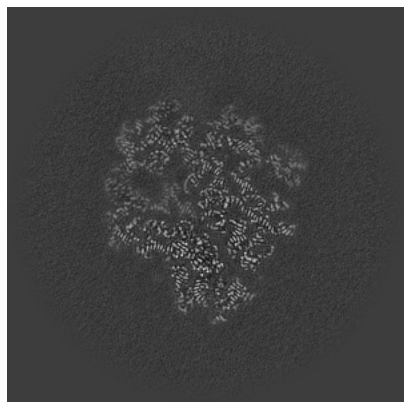
Z Index: 288

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

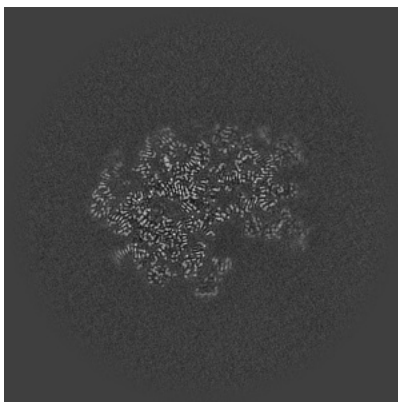


## 6.3 Largest variance slices [i](#)

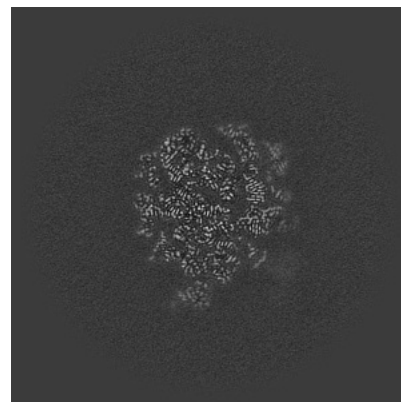
### 6.3.1 Primary map



X Index: 282

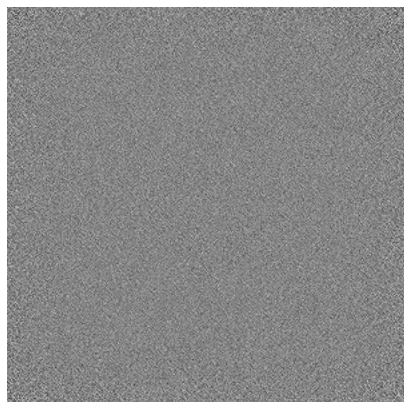


Y Index: 303

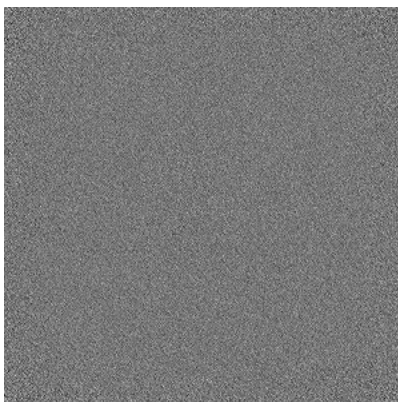


Z Index: 234

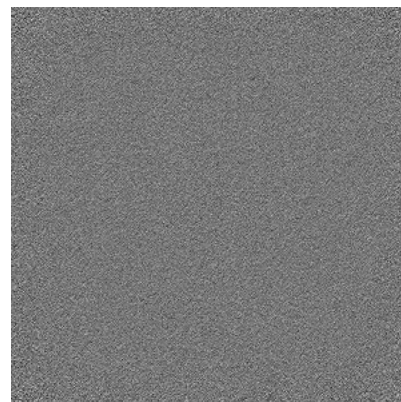
### 6.3.2 Raw map



X Index: 0



Y Index: 0

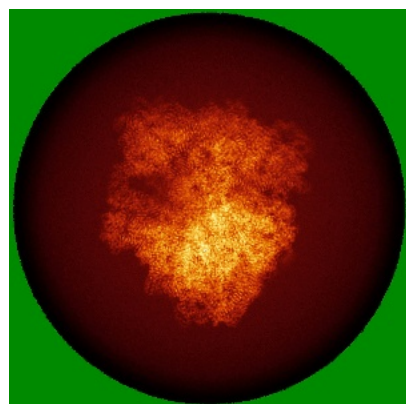


Z Index: 0

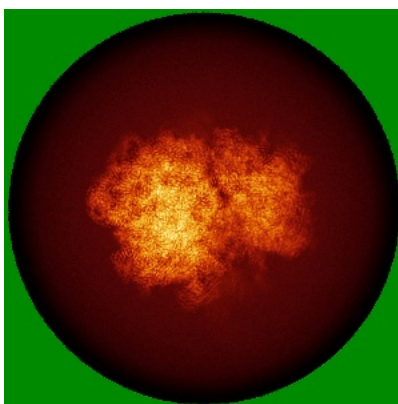
The images above show the largest variance slices of the map in three orthogonal directions.

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

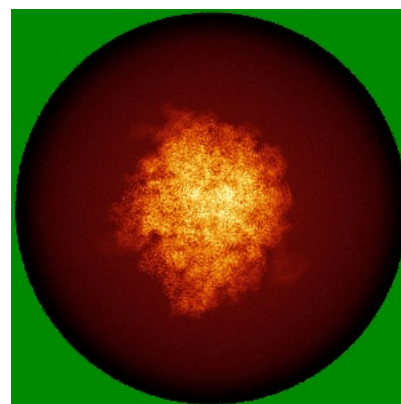
### 6.4.1 Primary map



X

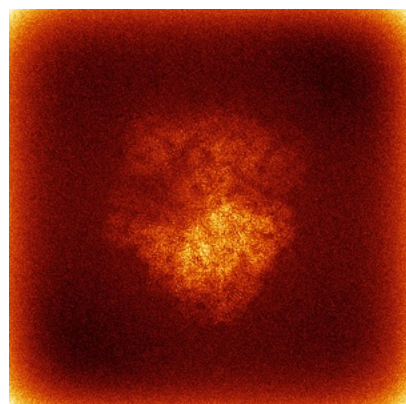


Y

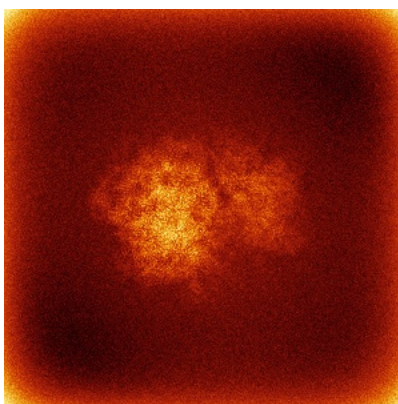


Z

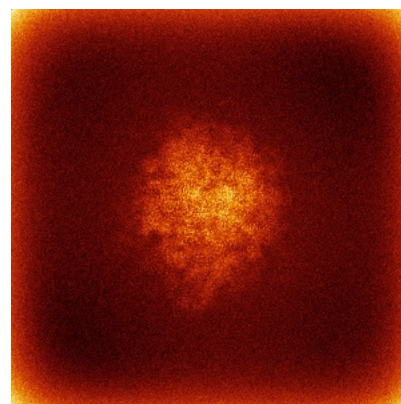
### 6.4.2 Raw map



X



Y

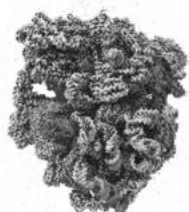


Z

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



X



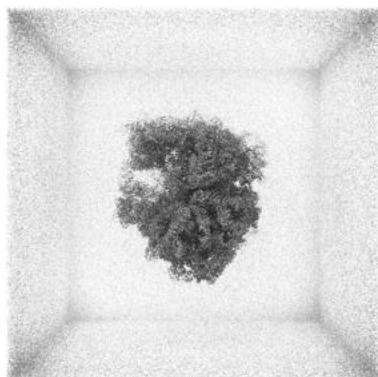
Y



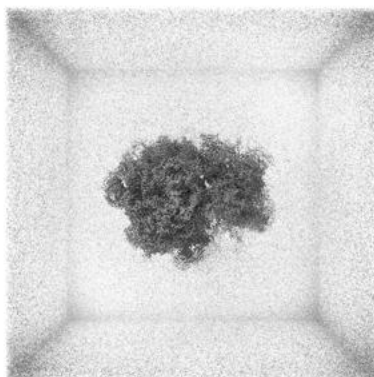
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0495. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

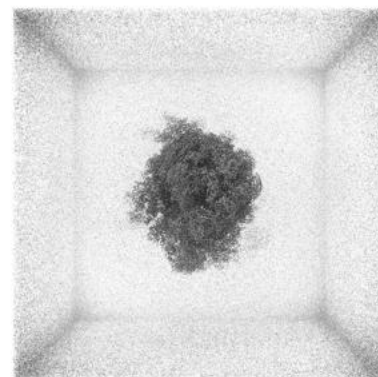
### 6.5.2 Raw map



X



Y



Z

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

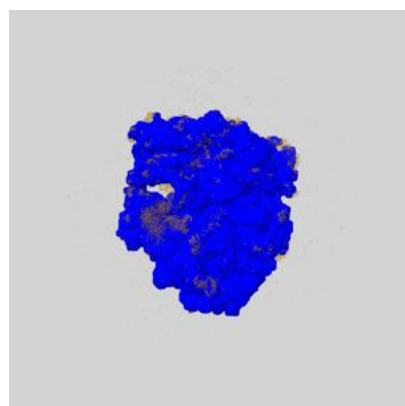
## 6.6 Mask visualisation [i](#)

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

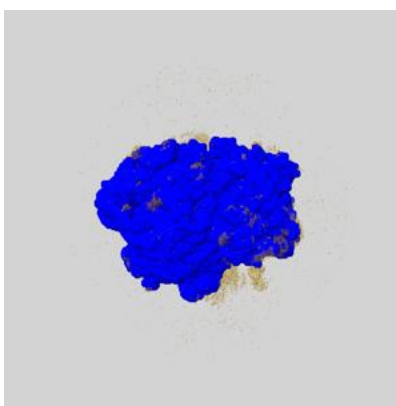
A mask typically either:

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

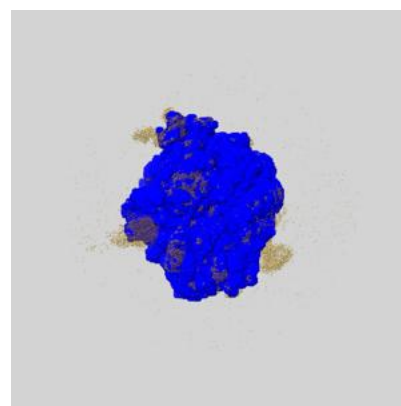
### 6.6.1 emd\_56830\_msk\_1.map [i](#)



X



Y

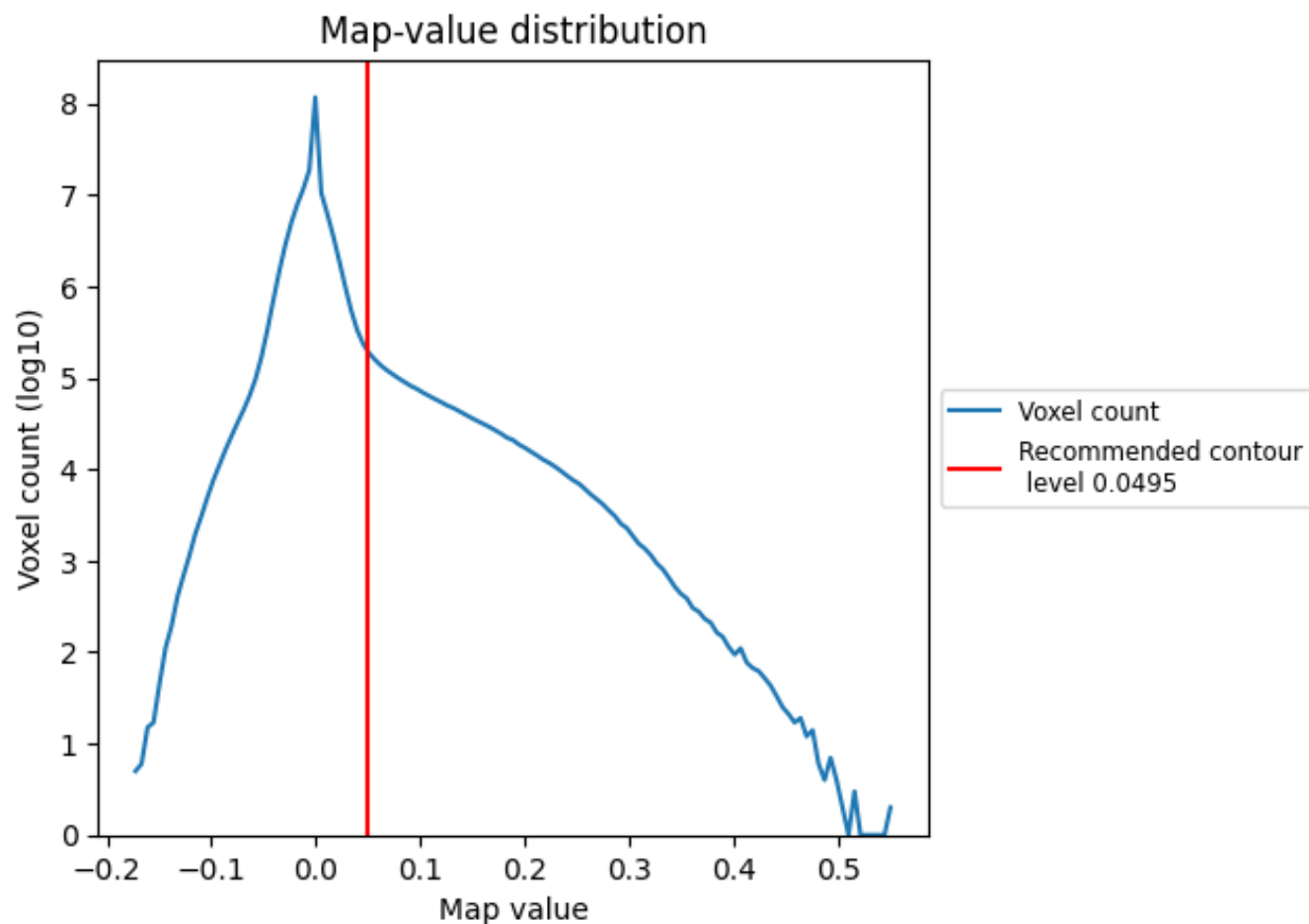


Z

## 7 Map analysis [i](#)

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

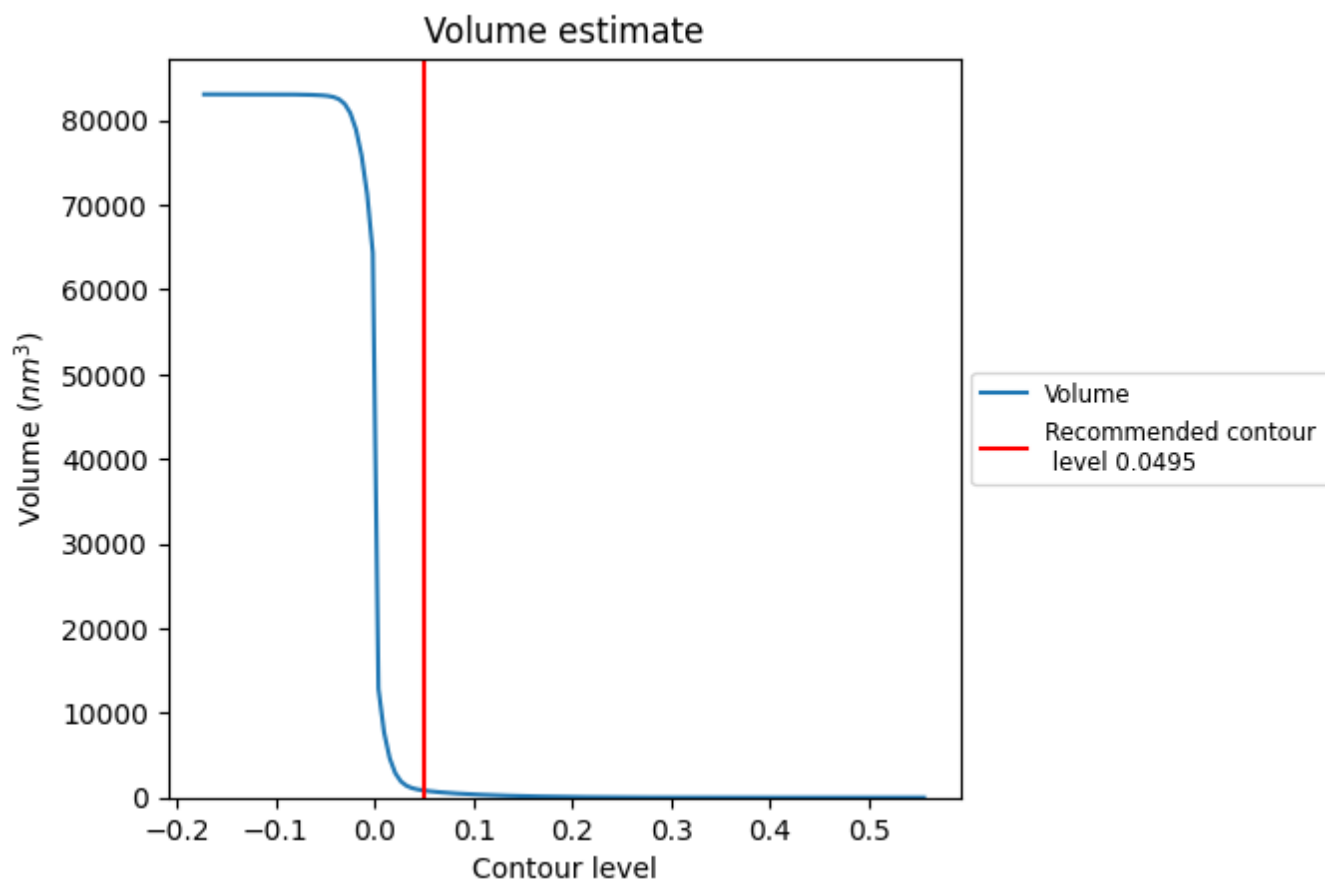
### 7.1 Map-value distribution [i](#)



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



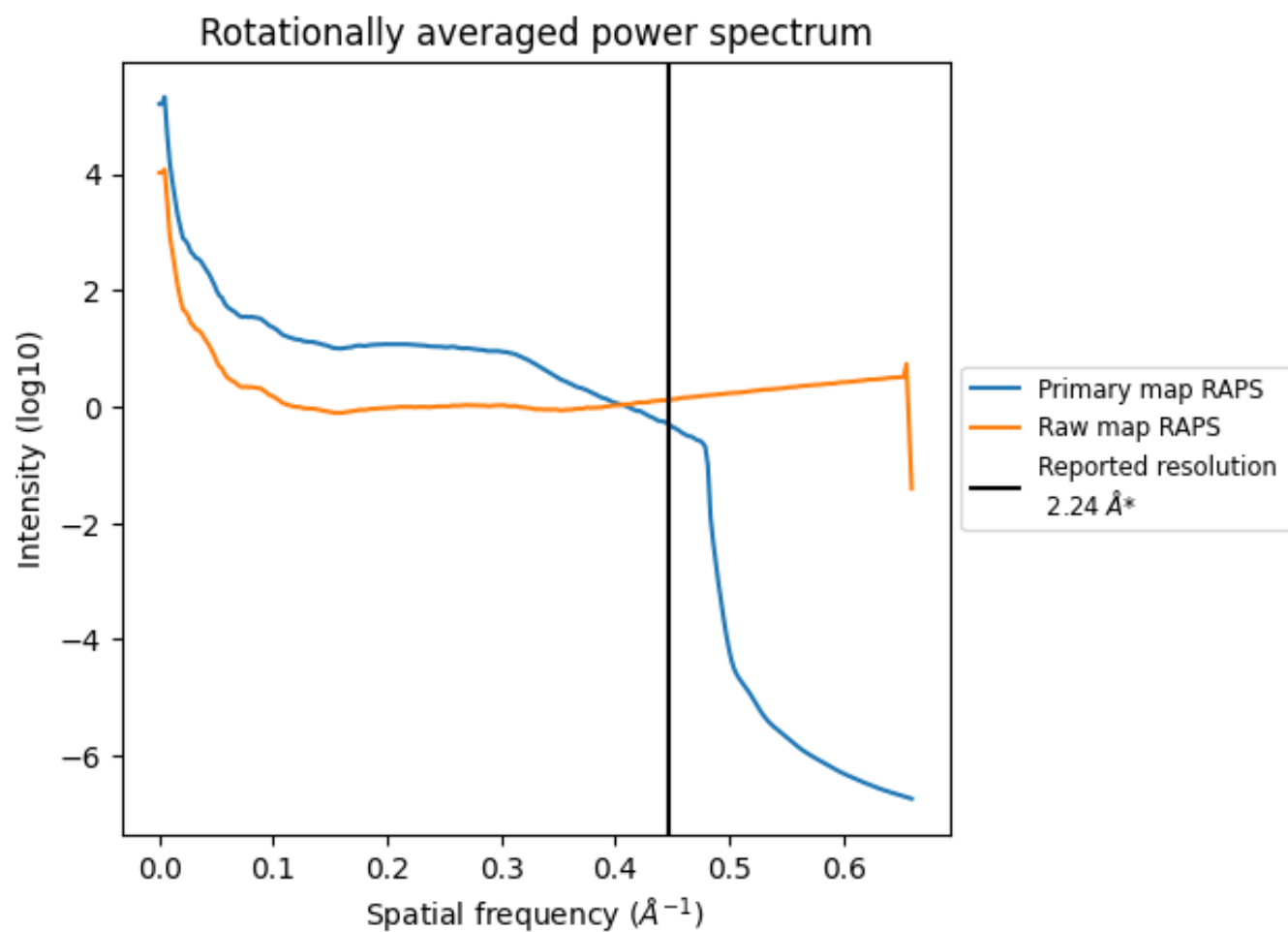
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 837 nm<sup>3</sup>; this corresponds to an approximate mass of 756 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 ⓘ

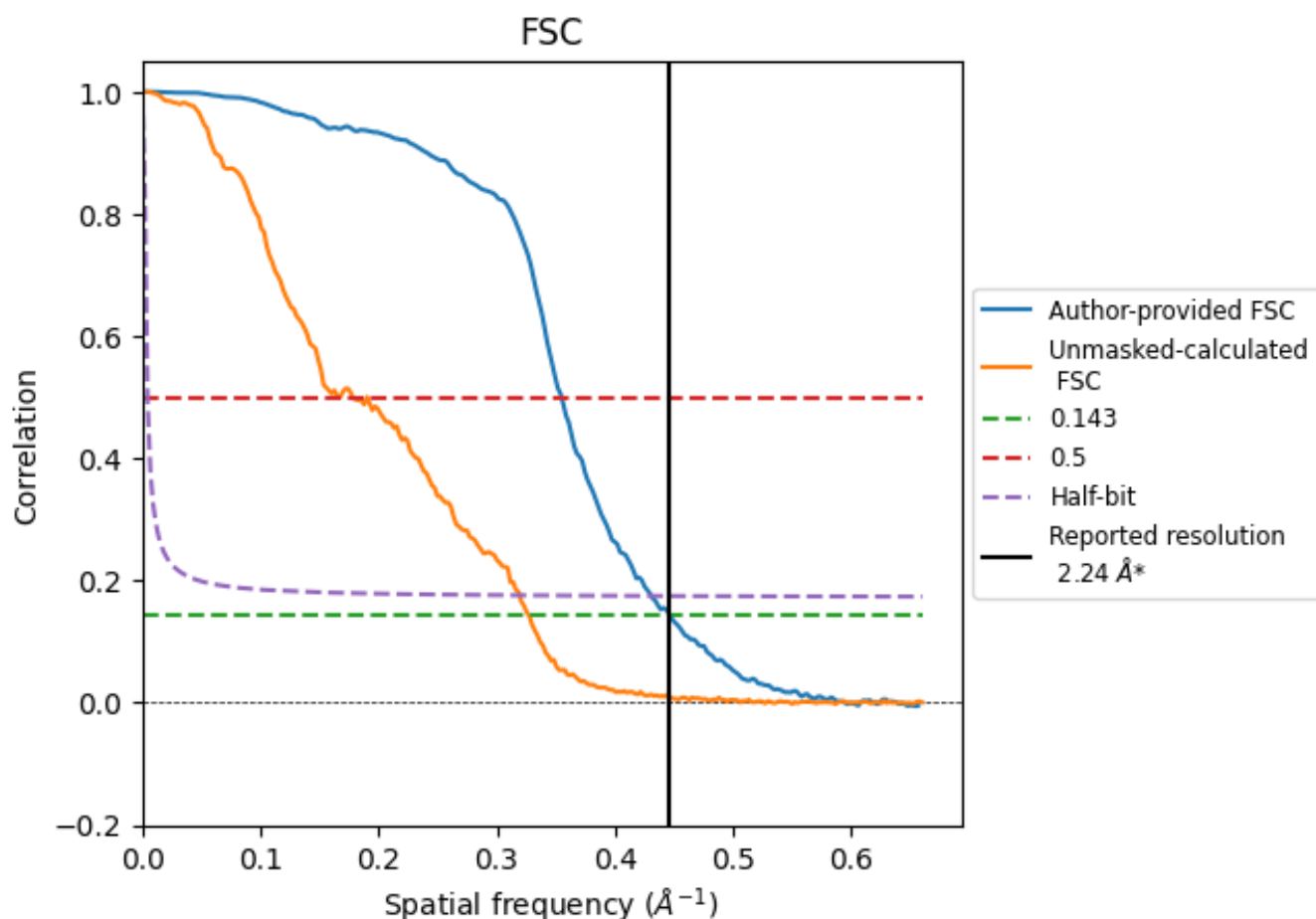


\*Reported resolution corresponds to spatial frequency of 0.446  $\text{\AA}^{-1}$

## 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  $0.446 \text{ \AA}^{-1}$



## 8.2 Resolution estimates [i](#)

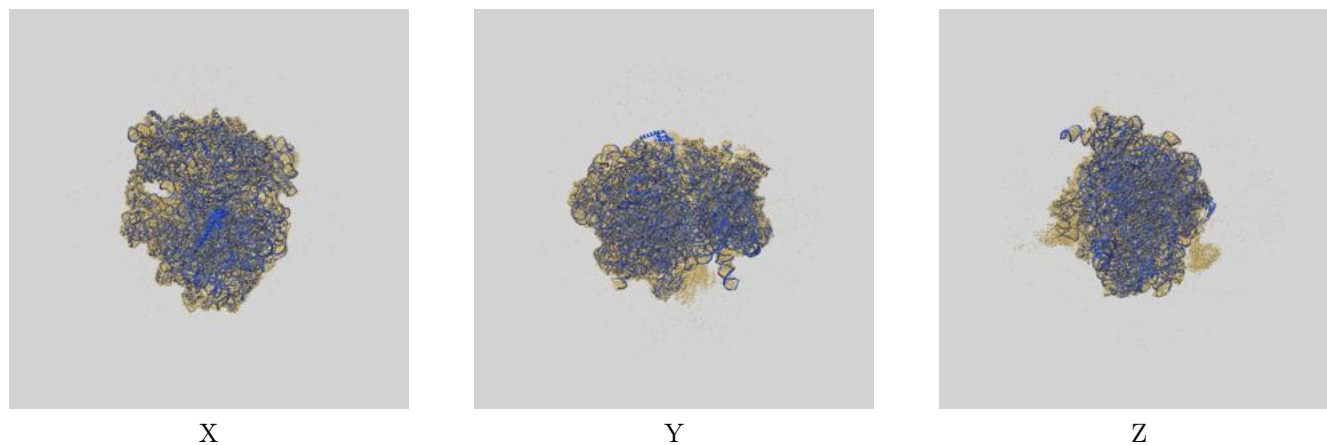
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.24	-	-
Author-provided FSC curve	2.24	2.82	2.32
Unmasked-calculated*	3.06	6.00	3.13

\*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 3.06 differs from the reported value 2.24 by more than 10 %

## 9 Map-model fit [i](#)

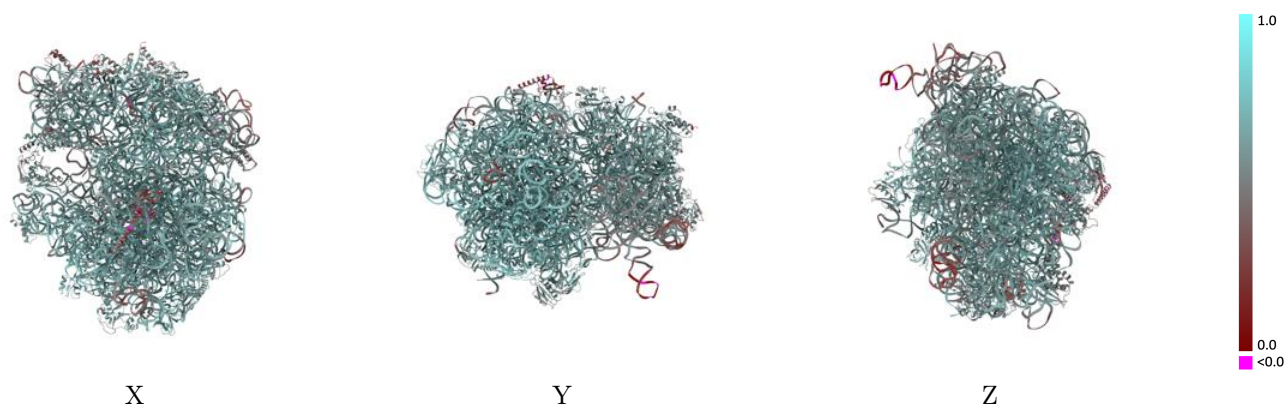
This section contains information regarding the fit between EMDB map EMD-56830 and PDB model 28UK. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

### 9.1 Map-model overlay [i](#)



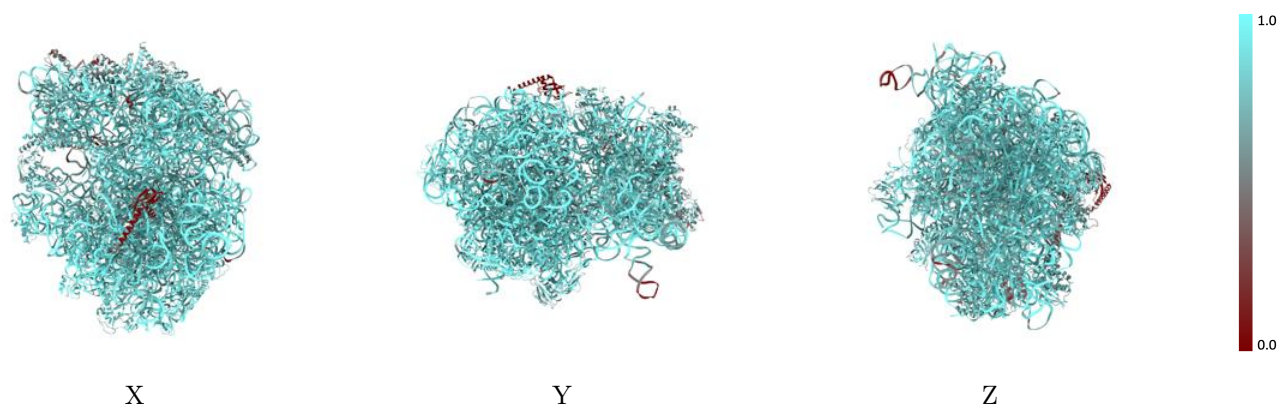
The images above show the 3D surface view of the map at the recommended contour level 0.0495 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



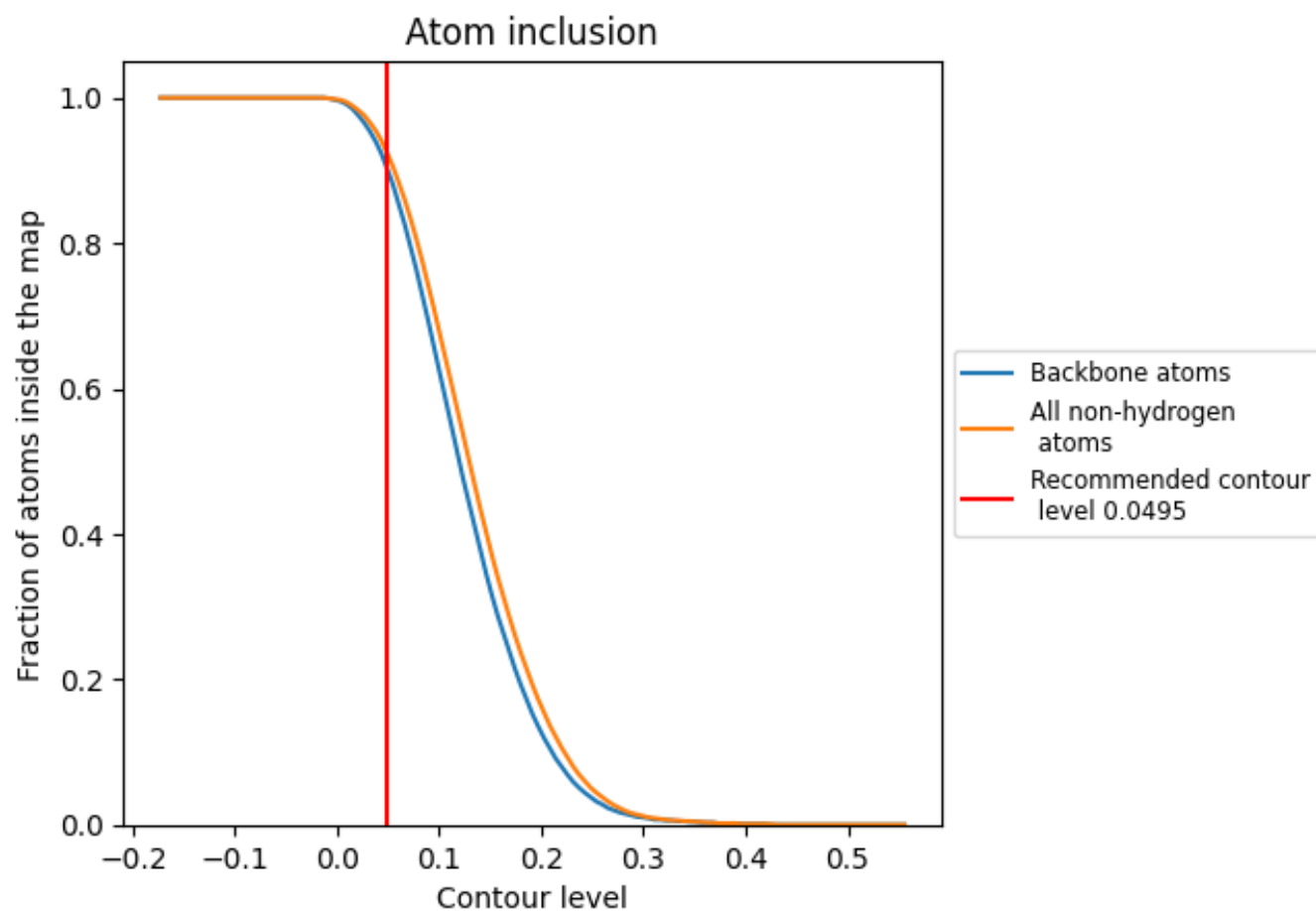
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0495).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 92% 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 (0.0495) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9230	 0.6330
0	 0.8950	 0.6590
1	 0.9660	 0.7070
2	 0.9630	 0.7070
3	 0.9350	 0.6710
4	 0.7270	 0.5100
A	 0.9340	 0.6030
B	 0.7510	 0.5490
C	 0.8190	 0.6000
D	 0.7130	 0.5360
E	 0.8950	 0.6400
F	 0.8170	 0.5830
G	 0.6730	 0.5120
H	 0.8920	 0.6430
I	 0.8150	 0.5700
J	 0.6990	 0.5160
K	 0.8590	 0.6200
L	 0.8580	 0.6310
M	 0.8180	 0.5860
N	 0.8590	 0.6130
O	 0.8700	 0.6210
P	 0.7620	 0.5420
Q	 0.8180	 0.6000
R	 0.8720	 0.6190
S	 0.8020	 0.5710
T	 0.8010	 0.5510
U	 0.6390	 0.5110
X	 0.9120	 0.6220
Y	 0.8930	 0.5820
Z	 0.8820	 0.5880
a	 0.9790	 0.6660
b	 0.9670	 0.6330
c	 0.9580	 0.6970
d	 0.9380	 0.6790
e	 0.9100	 0.6520



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Chain	Atom inclusion	Q-score
f	 0.7920	 0.5610
g	 0.8120	 0.5670
h	 0.2570	 0.3530
i	 0.9480	 0.6820
j	 0.9260	 0.6730
k	 0.9410	 0.6740
l	 0.9350	 0.6790
m	 0.9760	 0.7000
n	 0.9000	 0.6210
o	 0.9060	 0.6650
p	 0.9770	 0.7020
q	 0.9210	 0.6590
r	 0.9250	 0.6770
s	 0.8880	 0.6460
t	 0.8790	 0.6180
u	 0.8780	 0.6360
v	 0.9090	 0.6670
w	 0.9350	 0.6750
x	 0.8590	 0.6040
y	 0.9110	 0.6670
z	 0.9280	 0.6740